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Identification de caractéristiques communes et rares dans les ARN structurés dans la base de données Rfam

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Ce mémoire intitulé :

Identification de caractéristiques communes et rares dans les ARN structurés dans la base de données Rfam

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a été évalué par un jury composé des personnes suivantes :

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Résumé

Les ARN non codants (ARNnc) sont des transcrits d'ARN qui ne sont pas traduits en protéines et qui pourtant ont des fonctions clés et variées dans la cellule telles que la régulation des gènes, la transcription et la traduction. Parmi les nombreuses catégories d'ARNnc qui ont été découvertes, on trouve des ARN bien connus tels que les ARN ribosomiques (ARNr), les ARN de transfert (ARNt), les snoARN et les microARN (miARN). Les fonctions des ARNnc sont étroitement liées à leurs structures d'où l'importance de développer des outils de prédiction de structure et des méthodes de recherche de nouveaux ARNnc. Les progrès technologiques ont mis à la disposition des chercheurs des informations abondantes sur les séquences d'ARN. Ces informations sont accessibles dans des bases de données telles que Rfam, qui fournit des alignements et des informations structurelles sur de nombreuses familles d'ARNnc. Dans ce travail, nous avons récupéré toutes les séquences des structures secondaires annotées dans Rfam, telles que les boucles en épingle à cheveux, les boucles internes, les renflements « bulge », etc. dans toutes les familles d'ARNnc. Une base de données locale, RNAstem, a été créée pour faciliter la manipulation et la compilation des données sur les motifs de structure secondaire. Nous avons analysé toutes les boucles terminales et internes ainsi que les « bulges » et nous avons calculé un score d'abondance qui nous a permis d'étudier la fréquence de ces motifs. Tout en minimisant le biais de la surreprésentation de certaines classes d'ARN telles que l'ARN ribosomal, l'analyse des scores a permis de caractériser les motifs rares pour chacune des catégories d'ARN en plus de confirmer des motifs communs comme les boucles de type GNRA ou UNCG. Nous avons identifié des motifs abondants qui n'ont pas été étudiés auparavant tels que la « tetraloop » UUUU. En analysant le contenu de ces motifs en nucléotides, nous avons remarqué que ces régions simples brins contiennent beaucoup plus de nucléotides A et U. Enfin, nous avons exploré la possibilité d'utiliser ces scores pour la conception d'un filtre qui permettrait d'accélérer la recherche de nouveaux ARN non-codants. Nous avons développé un système de scores, RNAscore, qui permet d'évaluer un ARN en se basant sur son contenu en motifs et nous avons testé son applicabilité avec différents types de contrôles.

Mots clés : ARNnc, structure d'ARN, structure secondaire, Rfam, motifs

Abstract

Noncoding RNAs (ncRNAs) are RNA transcripts that are not translated into proteins yet they play important functional roles in the cell including gene regulation, transcription and translation. Among the many categories of ncRNAs that were discovered, we find the well-known ribosomal RNA (rRNA), transfer RNA (tRNA), snoRNA and microRNAs (miRNA). The functions of ncRNAs are tightly linked to their structural features. Thus, understanding and predicting RNA structure as well as developing methods to search for new ncRNAs help to gain insight into these molecules. Technological advances have made available abundant sequence information accessible in databases such as Rfam, which provides alignments and structural information of many ncRNA families. In this research project, we re trieved the information from the Rfam database about the sequences of all secondary structures such as hairpin loops, internal loops, bulges, etc. in all RNA families. A local database, RNAstem, was created to facilitate the use and manipulation of information about secondary structure motifs. We analyzed hairpin loops, bulges and internal loops using the compiled data about the frequencies of occurrence of each loop or bulge and calculated a frequency score. The frequency score is aimed to be an indicator for the abundance of a specific secondary structure motif. While minimizing the bias caused by the high redundancy of some RNA classes as ribosomal RNAs, the frequency score allowed us to identify the rare motifs in each category as well as the common ones. Our findings about the abundant motifs confirm what is already known from previous studies (ex. abundant GNRA or UNCG tetraloops). We found very large gaps between the most abundant and rare RNA structural features. Moreover, we discovered that "A" and "U" dominate single stranded RNA regions, whether they are bulges or loops. We further explored the possibility of using this data to improve current prediction tools for ncRNAs by applying a filter to new candidates. We developed a score system, RNAscore, that evaluates RNAs depending on their motif contents and we tested the program with many different controls.

Keywords: ncRNA, RNA structure, secondary structure, Rfam, motifs

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Liste des abréviations

A : adénine
ADN : acide désoxyribonucléiques
AdoCbl : adenosylcobalamine
ARN : acide ribonucléique
ARN MRP : *mitochondrial RNA processing*
ARN SRP : *signal recognition particle*
ARNm : ARN messager
ARNnc : ARN non codant
ARNr : ARN ribosomique
ARNsno : ARN nucléolaire
ARNt : ARN de transfert
BLAST : *Basic Local Alignment Search Tool*
C : cytosine
Cis-reg : *cis-regulatory*
CoTC ribozyme : *co-transcriptional cleavage ribozyme*
CRISPR : *clustered regularly interspaced short palindromic*
FMN : *flavin mononucleotide*
G : guanine
GEMM : *widespread Genes for the Environment, for Membranes and for Motility*
glmS ribozyme : *Glucosamine-6-phosphate activated ribozyme*
HCV : *Hepatitis C virus*
IRE : *Iron response element*
IRES : *Internal ribosome entry site*
lncRNA : *long non-coding RNA*
MAEB : *metabolism-associated element in Burkholderia*
Mg : magnésium
miARN : micro ARN

MOCO : *molybdenum cofactor*
NCM : *nucleotide cyclic motif*
pARNn (snRNA): petit ARN nucléaire (small nuclear RNA)
PDB : *Protein Data Bank*
pRNPn : petits ribonucléoprotéines nucléaires
protéines Sm : protéines *Sec1/Munc18-like*
Rfam : *Rna FAMilies*
RMN : résonance magnétique nucléaire
RNase P : ribonucléase P
RNP : ribonucléoprotéines
SAH : S-adenosylhomocystéine
SAM : S-adenosylméthionine
sARN (bact) : petits ARN bactérien (*small RNA*)
scaRNA : *Small Cajal body-specific RNA*
siARN : petits ARN interférents (*small interference RNA*)
SQL : *Structured Query Language*
TERC : *telomerase RNA component*
THF : *Tetrahydrofolate*
TPP : Thiamine pyrophosphate
U : uracil

« Emancipate yourselves from mental slavery.
None but ourselves can free our minds.»

« Light up the darkness.»
Bob Marley

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À ma Jana chérie, *you are my everything, you are my sunshine, my only sunshine*!

Chapitre 1 Introduction et Contexte

1.1 Introduction

La prédiction des structures de l'ARN et la recherche de nouveaux gènes à ARN sont des thématiques de la bioinformatique qui ont récemment connu beaucoup de développement (1). Grâce aux avancées technologiques, la nouvelle génération de séquençage à haut-débit génère de grandes quantités de données sur les génomes d'organismes appartenant à tous les règnes du vivant. Ceci a permis une grande expansion des bases de données incluant les bases de données spécialisées pour les familles d'ARN, telle que Rfam sur laquelle se base ce projet de recherche.

Cette abondance de données offre de nombreuses opportunités ainsi que des défis pour les bioinformaticiens qui se penchent sur la question de l'ARN pour mieux comprendre sa fonction et sa structure ainsi que développer des outils permettant de découvrir de nouveaux ARN non-codants (ARNnc). Les ARNnc sont des transcrits (ou régions de transcrits) qui ne sont pas traduits en protéines comme le sont les ARN messagers. L'expression d'un gène à ARN produit une molécule d'ARN fonctionnelle dont la fonction cellulaire est étroitement liée à la structure de la molécule. La difficulté que représente la recherche expérimentale des ARNnc par les techniques de biologie moléculaire et biochimie a propulsé le développement des méthodes bioinformatiques (2,3). La bioinformatique de l’ARN permet aux scientifiques d’améliorer la précision des prédictions de structures, de découvrir de nouveaux ARNnc et d’approfondir nos connaissances sur le fonctionnement de ces molécules dont les usages thérapeutiques sont prometteurs (4).

1.2 Les ARN non-codants

Le dogme central proposé par Francis Crick en 1957 (figure 1) (5) résume le transfert de l’information génétique dans la cellule à partir de l’ADN. L'ARN y figure comme l’intermédiaire dans la synthèse de protéines, un intermédiaire connu comme l’ARN messager. Les ARN ribosomiques (ARNr) et les ARN de transfert (ARNt), omniprésents dans les organismes vivants, sont les premiers exemples d'ARNnc qui étaient connus pour leurs rôles dans la traduction à l'époque où Crick a présenté le dogme central (6). La vue simpliste limitant l'ARN à la fonction de messager a été remise en question depuis la découverte des ribozymes, ARN ayant une fonction enzymatique. La ribonucléase P (RNase P) fut le premier ARN présentant des propriétés catalytiques qui a été découvert en 1983 (7). En parallèle, Thomas Cech et son équipe ont démontré que des introns de certains pré-ARNm chez *Tetrahymena* étaient autocatalytiques et pouvaient se cliver et se liguer sans l'intervention de protéines (8). Cette importante découverte des ribozymes a mené à un prix Nobel de chimie en 1989. Depuis, plusieurs autres types d'ARN issus de la transcription et qui ne subissent pas de traduction ont été découverts. L'appellation « ARN non-codants » (ARNnc) est utilisée pour les distinguer des ARN messagers.

La science de l'ARN a connu une révolution dans les deux dernières décennies durant lesquelles la découverte d'ARNnc a connu un rythme remarquable. Exemple de cette évolution, la première version de Rfam 1.0 a été lancée avec 25 familles d'ARNnc en 2003. Présentement on retrouve 2450 familles dans la dernière mise à jour de la base de données Rfam 12.0 (juillet 2014) (9).

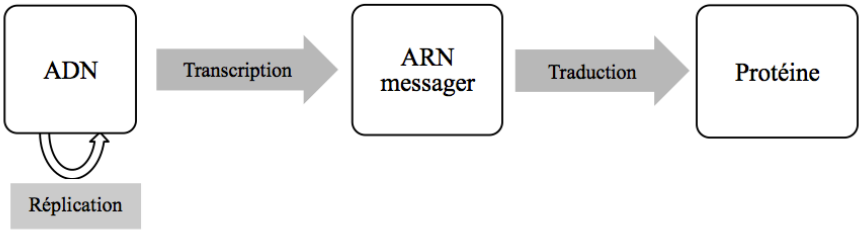

Figure 1. Le dogme central de Crick de la biologie moléculaire.

Ces ARN qui ne codent pas pour une protéine sont définis par « ce qu'ils ne sont pas » plutôt que par « ce qu'ils sont » en réalité ce qui engendre une grande hétérogénéité des ARNnc. Ils jouent de nombreuses fonctions cellulaires clés et variées incluant : la régulation, la localisation et la modification des transcrits, la modification de la chromatine et les altérations épigénétiques (figure 2) (10).

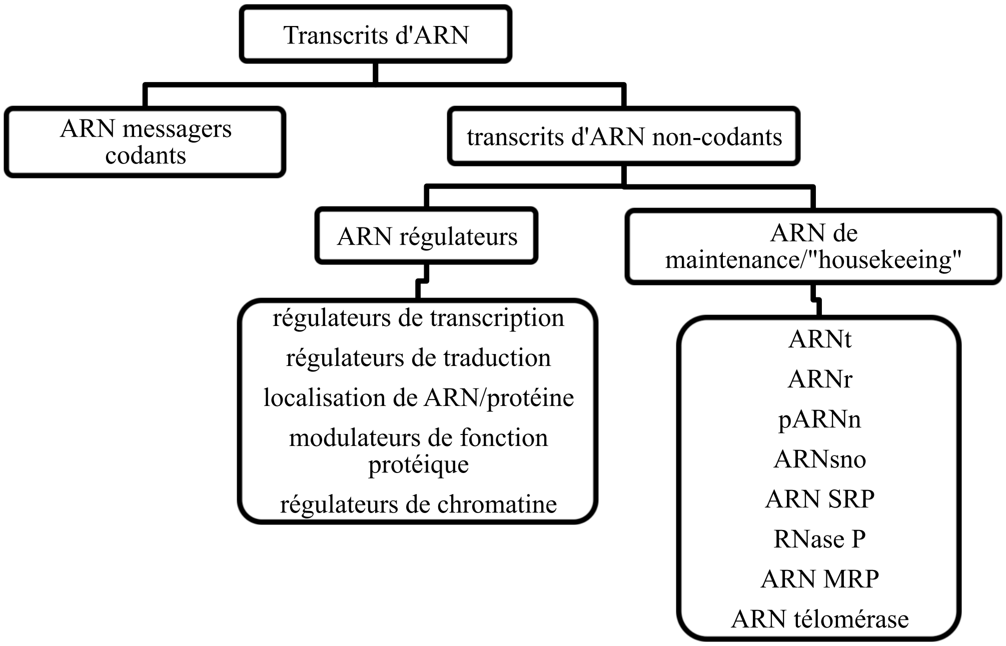

Figure 2. Transcrits d'ARN.
L'ARNnc a des fonctions cellulaires variées. Les ARNnc peuvent être classés en ARN régulateurs et en ARN de maintenance. Plusieurs de ces ARN forment avec des protéines des complexes appelés ribonucléoprotéines (RNP). pARNn : petits ARN nucléaires (« sRNA », ARN-U) jouent un rôle dans l'épissage de l'ARNm (snRNA). ARNsno : petits ARN nucléolaires (« small nucleolar RNA ») jouent un rôle dans la maturation d'autres ARN tels que l'ARNr, l'ARNt et les pARNn. ARN SRP : « signal recognition particle » reconnaît et lie le peptide signal jouant un rôle dans le trafic et la sécrétion des protéines. RNase P : ribonucléase P a pour fonction la maturation de l'ARNt. ARN MRP : sous-unité ARN de l'ARNase MRP (« mitochondrial RNA processing ») qui jouent plusieurs rôles importants dans les cellules eucaryotes. ARN de la télomérase : (TERC « telomerase RNA component ») sert de matrice pour l'extension du télomère. Adapté de (10).

Il existe plusieurs façons de classifier les ARNnc selon leurs caractéristiques et/ou fonctions. Nous avons considéré deux principales classes : une classe pour les ARNnc dont la fonction est reliée à la complémentarité avec une cible tandis que l'autre classe regroupe les ARNnc avec une « activité biochimique ». Les ARNnc de cette dernière classe ont la principale caractéristique commune d'avoir des structures suffisamment complexes pour effectuer des fonctions telles que la reconnaissance de molécules, la catalyse ou l'échafaudage de RNP. Ce groupe inclut les ARN structuraux adaptateurs tels que les ARNt. Il est à noter que cette classification n'est pas sans faille puisque certains ARN possèdent les deux critères de classification. Dans la réalisation de ce projet, ces ARN ont été classés dans le groupe qui représente la caractéristique dominante. Dans les deux sections qui suivent, nous explorons quelques exemples des principaux ARNnc les plus connus de chaque classe.

1.2.1 ARNnc dont la fonction est reliée à la complémentarité avec une cible

Plusieurs ARNnc accomplissent leurs fonctions grâce à une complémentarité avec leurs cibles. La reconnaissance de la cible se fait généralement grâce à la formation de paires de bases entre des régions simples brins de l'ARN et sa cible. Dans ce travail, nous référons à cette classe d'ARN par sa propriété « antisens ».

Plusieurs études ont révélé l'existence de nombreux petits ARN dans le noyau dont des petits ARN trouvés dans le nucléole, un pseudo compartiment du noyau (11). Ces petits ARN nucléolaires (ARNsno, « small nucleolar RNA ») jouent un rôle dans la maturation d'autres ARN, principalement l'ARNr ainsi que l'ARNt et les petits ARN nucléaires (pARNn). Un ARNsno s'associe à au moins quatre protéines pour guider la modification d'une base précise de l'ARNr. Il y a deux sous-familles principales : les ARNsno à boite C/D associés à la méthylation et les ARNsno à boite H/ACA associés à la pseudouridylation (des exceptions existent). Chacune des sous-familles est caractérisée par des motifs de séquences conservés et c'est l'élément antisens, complémentaire à la séquence cible contenant la base à modifier, qui permet à l'ARNsno de jouer son rôle de guide (12). Une sous-catégorie de snoARN appelée scaARN sont un hybride des ARNsno à boîte C/D et ceux à boîte H/ACA capable de guider les deux modifications de méthylation et pseudouridylation (13).

Les micro ARN (miARN), une famille d'ARN impliquée dans la régulation de la traduction, ont été découverts en l'année 2000 (14,15). Des centaines de gènes de miARN ont été identifiés depuis et beaucoup de ces derniers contrôlent l'expression génique en étant des répresseurs post-transcriptionnels (16). Les miARN sont de petits ARNnc d'environ 20 à 24 nucléotides exprimés dans les cellules eucaryotes animales et végétales (et dans certains virus). Ils ont une fonction de répression génique en se liant à l’ARNm cible grâce à leur séquence complémentaire. Ce sont des ARN très conservés, transcrits à partir de leurs propres gènes ou d’introns pour former une structure en épingle de cheveux pour être ensuite exportés et clivés dans le cytoplasme. À cause de leurs implications dans des maladies telles que le cancer, les miARN font l’objet de beaucoup d’études qui se penchent sur la dérégulation de ces molécules importantes afin de les utiliser comme marqueurs de diagnostic et développer de nouvelles approches thérapeutiques (17).

Il y d’autres ARNnc qui inhibent l’ARNm en étant complémentaire à une partie de la séquence tels que les ARN dénommés « antisens ». Les ARN antisens sont de longs transcrits qui fonctionnent en se liant généralement à l’extrémité 5′ de l’ARNm cible, contrairement aux miARN qui sont de courtes séquences dont la cible se trouve généralement à l’extrémité 3′ de l’ARNm. On a découvert un grand nombre d’ARN antisens transcrits naturellement dans les cellules mammifères. Les récentes études démontrent que ces ARN antisens ont des fonctions régulatrices dans la transcription et post-transcription jouant ainsi des rôles biologiques variés (18). Il existe aussi des petits ARN bactériens antisens « bacterial sRNA » qui sont capables de se lier par complémentarité à des régions d’ARNm cibles et en réguler l’expression. Les petits ARN sont des ARNnc très abondants dans les bactéries et ils sont impliqués dans plusieurs processus incluant le métabolisme du carbone, la réponse au stress et le « quorum sensing » pour nommer quelques exemples (19).

Les ARN CRISPR (« clustered regularly interspaced short palindromic repeats ») sont un autre exemple d’ARNnc antisens. On les retrouve dans environ 40% des bactéries séquencées et 90% des archéobactéries (20). Ils sont associés à des protéines pour former le système CRISPR/Cas qui est un système d’immunité procaryote permettant de résister aux éléments génétiques exogènes (plasmides et phages) en les clivant (21). L’ARN CRISPR a pour fonction de guider le complexe Cascade en se liant à l’ADN auquel il est complémentaire. La taille de ces ARN varie entre 24 et 48 paires de bases et ils forment généralement des structures en forme d’épingle à cheveux.

Ces quelques exemples illustrent la diversité des ARNnc que nous avons mis dans la classe « antisens » pour mettre en évidence leur point commun. Ces descriptions ne sont pas exhaustives, d’autres types d’ARNnc sont également inclus dans cette classe, et comme mentionné, certains ARN classés comme ayant une « activité biochimique » agissent parfois via une complémentarité de paires de bases avec leur cible.

1.2.2 ARNnc avec une « activité biochimique »

La découverte des ARN ayant une activité enzymatique a changé l’idée que seulement les protéines peuvent catalyser des réactions. On appelle ribozymes tous ces ARN ayant une activité catalytique et ils sont impliqués dans une variété de réactions et de fonctions telles que l’épissage de l’ARN, la maturation des ARNt et la réplication virale. Certains ribozymes sont autocatalytiques tels que les introns auto-épissables et les ribozymes hammerhead. Une grande variété de ribozymes ne portent pas nécessairement le nom « ribozyme » au sein de la base de données Rfam et contiennent de nombreuses familles d’ARN (le ribosome, les RNAses P, le riboswitch glmS, les introns auto-épissables, les petits ARN nucléaires) alors qu’on retrouve aussi plusieurs familles telles que les ribozymes Hammerhead, ribozymes VS (Varkud satellite), ribozymes Hairpin, ribozymes Vg1, etc.

Les ARN ribosomiques 5S avec ceux des petites et grandes sous-unités représentent 60% du ribosome, le reste étant des protéines. Le ribosome est un ribozyme puisque la grande sous-unité (50S chez les procaryotes, 60S chez les eucaryotes) catalyse la formation du lien peptidique dans la synthèse de protéines et qu’il n’y a aucun acide aminé, mais que des bases d’ARN dans son site catalytique (22).

Les petits ARN nucléaires, pARNn sont toujours associés avec un ensemble de protéines formant des ribonucléoprotéines (RNP) appelés pRNPn (snRNP) dont la fonction principale est l’épissage des ARN messagers. Chaque particule RNP est composée de plusieurs protéines Sm, les pARNn et les protéines pRNPn-spécifiques. Les composantes de pARNn ont une taille moyenne d’environ 150 nucléotides et les plus connues sont U1, U2, U4, U5 et U6. Bien que U1 et U2 font partie des ARNnc qui se lient par complémentarité à une cible, U4 en complexe avec U6 ont une activité catalytique permettant de cliver l’ARNm et tous ensemble ils forment le spliceosome (23,24).

Les riboswitch sont un autre type d'ARN non-codant ayant une fonction régulatrice des gènes. Le riboswitch glmS a une activité autolytique comme mécanisme de régulation de l'ARNm, il est à la fois ribozyme et riboswitch (25), mais nous le classons comme riboswitch. De façon générale, les riboswitchs se trouvent dans la portion 5' des ARNm et consistent en une région d'ARN appelée aptamère qui a un rôle de récepteur. En liant un métabolite spécifiquement, un riboswitch change de conformation ce qui induit une régulation transcriptionelle ou traductionnelle de l'expression (26). La figure 3 montre quelques exemples de riboswitch avec la séquence et structure secondaire consensus (27). On considère les riboswitch comme un exemple explicite de la relation structure-fonction des ARN.

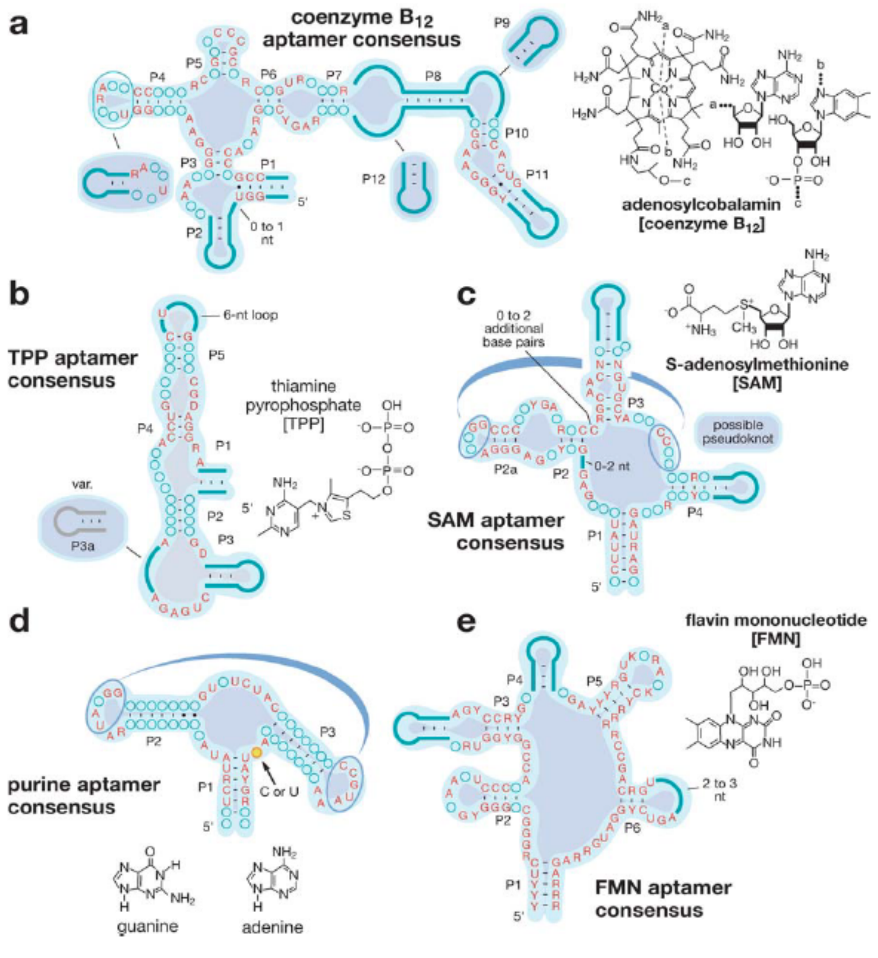

Figure 3. Séquences consensus et modèles de structures secondaires de riboswitch.
Les lettres en rouge représentent les nucléotides conservés dans plus de 90% des séquences alignées. *Tiré de* (27).

IRES « Internal ribosome entry site » se trouve aussi dans cette classe d'ARNnc. On retrouve ces ARN structurés dans la région non traduite d'ARN viral ainsi que dans certains ARNm et ils jouent un rôle dans l'initiation de la traduction. Des ARNnc qu'on nomme « thermoregulator » tels que cspA ou prfA *thermoregulator* sont aussi des éléments de la région 5' non-traduite et agissent sur l'expression des gènes en réponse à la chaleur. Ceux-ci ne sont que quelques exemples de plusieurs autres familles que nous classifions comme ayant une activité biochimique.

1.3 La structure de l'ARN

1.3.1 Relation Structure/fonction

Le principe selon lequel « la fonction de l'ARN est plus conservée que la structure et la structure est plus conservée que la séquence » (28) a été adopté depuis les années soixante et a été appuyé par l'analyse des nouveaux complexes d'ARN de grande taille tels que le ribosome (29). La richesse des nouvelles structures a propulsé le développement de nouvelles méthodes informatiques pour la classification des ARN, la description de leurs motifs structuraux, la détermination de leurs fonctions ainsi que la comparaison et la prédiction de leurs structures (30-33).

La conformation spatiale adoptée par l'ARNnc est déterminante pour sa fonction. La molécule simple brin peut se replier sur elle-même en formant des appariements (paires de bases) entre ses bases. Les paires de bases contigües forment des tiges alors que les régions non appariées forment des boucles. La nature de ces appariements et les motifs structuraux formés (tige, boucle etc.) contribuent à la stabilité de l'ARN. On utilise les principes de la thermodynamique et l'énergie libre pour évaluer la stabilité de la structure de l'ARN. La stabilité de la structure augmente quand son énergie libre est minimale.

1.3.2 Structure hiérarchique de l'ARN

La structure de l'ARN est hiérarchique (34). La figure 4 montre un exemple de la hiérarchie des structures d'un ARNt. La structure primaire est la séquence linéaire de nucléotides tandis que la structure secondaire est l'ensemble des paires de bases appariées formant des tiges (énergétiquement stabilisantes) et des régions simple-brin (déstabilisantes) telles que les boucles terminales, les renflements ou « bulges », les boucles internes et les jonctions (constituées par de multiples tiges-boucles). La structure tridimensionnelle est le repliement de l'ARN qui résulte de l'ensemble de tous les appariements de la structure secondaire en plus des interactions additionnelles entre les éléments de structure secondaire tels que les tiges-boucles. La structure tertiaire inclut les interactions à longue distance comme les pseudonœuds formés par l'interaction d'une boucle avec des bases situées à l'extérieur de la tige ainsi que les interactions triples qui résultent d'une interaction entre trois bases se trouvant dans le même plan et liées par des ponts hydrogènes. On y retrouve les sites d'interaction avec d'autres ARN, des protéines ou d'autres petites molécules On peut voir dans la figure 5 une représentation des structures tige-boucle ou en épingle à cheveux ainsi qu'un pseudonœud. Bien que la structure tertiaire définisse la conformation spatiale, il faut mentionner que la structure spatiale de l'ARN inclut les interactions avec des molécules séparées (par exemple les interactions entre les sous-unités du ribosome).

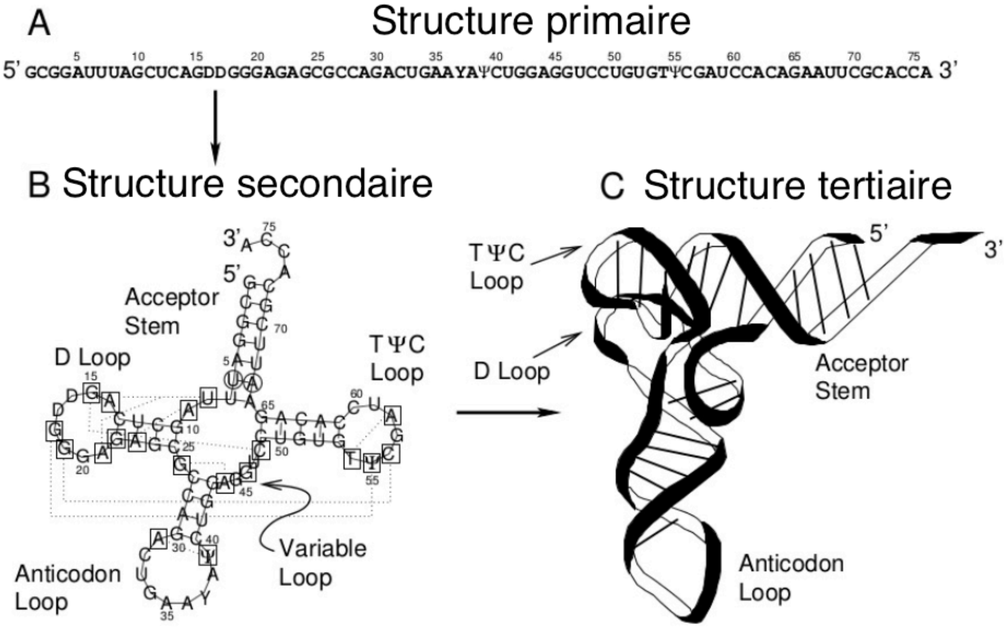

Figure 4. La structure primaire, secondaire et tertiaire d'un ARNt. Adapté de (35).

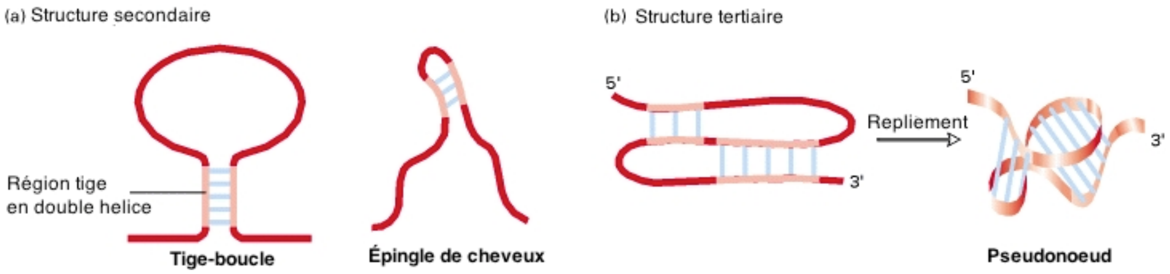

Figure 5. Structures secondaires et tertiaires de l'ARN. Adapté de (36).

1.3.3 Motifs structuraux

Certains éléments structuraux de l'ARN sont récurrents et représentent des motifs distincts qui ont été étudiés et caractérisés. En plus d'avoir des motifs d'ARN dans les structures secondaires, on a des motifs qui forment des interactions tertiaires, ou des motifs 3D. Les motifs peuvent contribuer à la stabilité globale de la structure de l'ARN et guider le repliement spécifique de la molécule en étant des sites de nucléation (37,38).

Parmi les motifs les plus connus, on retrouve des éléments structuraux de type tri-boucles « triloops » et des tetra-boucles « tetraloop » qui sont des boucles terminales dans une structure de type tige-boucle ou en épingle à cheveux de tailles 3 et 4 respectivement. Les tetraboucles les plus communes sont principalement du type GNRA, UNCG et CUUG. Nous élaborons plus sur les motifs structuraux secondaires étudiés dans le contexte de ce travail au début du chapitre 3.

Les motifs E, C et « kink-turn » sont des boucles internes qui forment en réalité des motifs avec plusieurs interactions tertiaires et des paires de bases non-canoniques. La boucle E du ribosome a été identifiée dans l'ARNr 5S et considérée comme une boucle interne au début. Ce motif s'avère un peu plus complexe, ayant une paire de base A-A parallèle, trois autres paires de bases non-canoniques et délimité par une ou deux paires G-A en tandem. Le motif Sarcin-Ricin, un renflement (« bulge ») d'une base G, est un sous-motif de la boucle E qu'on retrouve également dans d'autres familles d'ARN (jonctions de tiges-boucles). Le motif « kink-turn » est aussi une boucle interne qui a été identifiée à de multiples sites dans les ARNr 16S et 23S. On le trouve aussi dans le pARNn U4, certains riboswitchs et certains snoARN. Le motif tient son nom de la courbure causée par la boucle interne et qui est importante pour la fonction de l'ARNnc impliquée (39,40). Le motif C est également une boucle interne asymétrique de taille variable (longueur des segments simple brin) et qui se retrouve dans l'ARNr 23S.

La boucle T est une boucle qu'on retrouve dans une des tiges-boucles de l'ARNt et aussi dans certaines tiges-boucles des ARNr. La boucle T contient cinq nucléotides et forme des liaisons tertiaires avec d'autres éléments structuraux.

Le motif « UA-handle » est un exemple de motif qui se forme au repliement de la structure tertiaire et il fait partie d'autres motifs comme la «boucle T ». On y retrouve un « bulge » qui peut avoir une taille d'un nucléotide ou plus (41).

Ces éléments structuraux sont souvent des motifs de reconnaissance pour des protéines spécifiques (42). Ils sont généralement conservés au sein d'une famille d'ARN et sont souvent trouvés dans plusieurs familles d'ARN. Toutes ces caractéristiques les rendent utiles pour la prédiction de structure, l'identification des sites fonctionnels et la recherche d'ARNnc.

1.3.4 Modularité de la structure

La modularité est une caractéristique importante dans l'organisation biologique. Les ARN, tout comme les protéines, présentent des structures ayant des domaines. Les ARNt présents en copies multiples dans toutes les cellules vivantes présentent essentiellement les mêmes éléments structuraux (bras accepteur, bras anti-codon, bras T et D) et ne diffèrent que par quelques nucléotides dépendamment de l'acide aminé spécifique à l'ARNt (43). La modularité de la structure secondaire de l'ARN a été démontrée par la capacité de défaire des sous-structures individuelles sans affecter les autres éléments (44). Le repliement hiérarchique de l'ARN lui confère cette modularité. Les sous-structures secondaires et tertiaires se replient souvent de façon indépendante (34). Les motifs structuraux récurrents tels que les boucles GNRA et le motif sarcin-ricin sont considérés comme des unités modulaires (45). L'étude de la modularité de l'ARN est cruciale pour une bonne compréhension de la relation structure/fonction, de même que pour la conception de nouvelles molécules d'ARN synthétiques telles que la construction de nanoparticules (46).

1.4 Les outils bioinformatiques de prédiction de structure

Dans cette section, on essaiera de faire un survol sur les principaux outils bioinformatiques qui permettent de faire de la prédiction de structure en s'intéressant de plus proche à la structure secondaire.

La détermination de la structure de l'ARN avec les méthodes expérimentales demeure une tâche difficile et souvent couteuse malgré les progrès remarquables de la cristallographie par rayon X, la spectroscopie par résonance magnétique nucléaire (RMN) et les modifications chimiques de l'ARN. Les structures déterminées par ces techniques ne constituent qu'une faible portion des ARNnc connus. Ces techniques impliquent souvent la modification du milieu dans lequel se trouve l'ARN (différent du milieu cellulaire) et la fixation dans une seule conformation ce qui constitue une perte d'information pour une molécule ayant une structure dynamique. La prédiction de structure par la bioinformatique est un outil important pour contourner ces inconvénients et générer des hypothèses sur la relation structure/fonction de l'ARN. La prédiction de structure est utile pour l'interprétation et la conception des expériences de mutagénèse, l'identification de caractéristiques structurales conservées et la conception des stratégies de petits ARN interférents ("siRNA").

L'ARN se replie de façon hiérarchique donc la structure secondaire détermine la structure tertiaire. Ceci implique que la précision de la prédiction de la structure secondaire est déterminante pour obtenir une prédiction tertiaire optimale. Nous disposons actuellement de plusieurs programmes informatiques pour la prédiction de structure secondaire d'ARN (32). Les approches bioinformatiques développées trouvent une structure secondaire de l'ARN soit à partir d'une séquence, soit à partir d'un alignement de séquences multiples et dans ce dernier cas il s'agit d'une structure consensus. On distingue alors deux catégories de méthodes: d'un côté nous avons les approches thermodynamiques fondées sur l'importance de la stabilité de la structure et qui visent à trouver les structures les plus stables et d'un autre coté il y a les approches comparatives qui se basent sur l'importance de la conservation d'une structure commune pour un ensemble de séquences homologues. Il existe aussi des méthodes hybrides qui combinent les deux approches.

1.4.1 Les méthodes comparatives

Ces méthodes consistent à générer un alignement de séquences multiples et à chercher des motifs de covariation entre deux nucléotides. L'analyse comparative nécessite un bon alignement de séquences homologues provenant de plusieurs espèces et qui ont suffisamment de variation pour établir un alignement de qualité. On retrouve deux types d’approches dans ces méthodes : Il y a des méthodes qui cherchent des covariations sur des alignements préalables de séquences donc l’alignement précède le repliement et il y a des approches qui n’utilisent pas des alignements préalables où l’alignement et le repliement se font simultanément.

RNAalifold (47) est parmi les approches avec alignement préalable les plus utilisées. Cet algorithme trouve la structure commune par minimisation de l’énergie thermodynamique et il a été beaucoup utilisé pour la prédiction d’ARNnc notamment par le programme RNAz (48). RNAlishapes combine les idées de RNAalifold à celles de RNAshapes (une méthode thermodynamique) (49). Les approches du type « replier et aligner simultanément » sont basées sur l’algorithme de Sankoff (50) et les exemples les plus connus sont Foldalign (51) et Dynalign (52). Le degré de conservation des séquences homologues influence le type d’approches à choisir. Il reste que les deux types de méthodes se complémentent.

1.4.2 Les approches thermodynamiques

Les approches thermodynamiques génèrent les structures secondaires possibles à partir d'une séquence donnée et s’avèrent utiles lorsqu’on ne peut pas appliquer les approches comparatives (peu de séquences disponibles, pas ou trop de variations). Les méthodes thermodynamiques suivent généralement deux règles qui sont: maximiser les paires de bases et minimiser l'énergie libre de la structure, en d'autres termes augmenter la stabilité thermodynamique.

Nussinov a élaboré la première approche utilisant la programmation dynamique à la fin des années 70. L'algorithme de Nussinov et Jacobson a amélioré l'algorithme original de maximisation des paires de bases en y ajoutant des critères énergétiques. La majorité des algorithmes de minimisation de l'énergie libre se base sur l'algorithme de Nussinov et Jacobson dont l'algorithme de Zuker (53,54) qui utilise les règles énergétiques de Freier-Turner et incorpore les interactions d'empilements. L'algorithme de Zuker est implémenté dans deux programmes très utilisés: Mfold (55) et RNAfold (56). RNAsubopt (57) est une variation de RNAfold qui trouve toutes les structures sous-optimales situées à un intervalle d'énergie libre de la structure optimale. RNAshapes (58) perfectionne le calcul des structures sous-optimales en réduisant l'espace de solutions avec une approche utilisant l'abstraction des « formes » de structures. PKNOTS (59) est une extension de l'algorithme de Zuker qui permet la prédiction de structure secondaire avec pseudonœuds (motifs de structure tertiaire exclus des algorithmes cités ci-dessus).

1.4.3 Autres approches

Certaines approches utilisent des modèles d'énergies différents du modèle de Turner. CONTRAfold utilise un modèle d'énergie probabiliste obtenu par apprentissage des paramètres à partir d'un ensemble de séquences ayant des structures confirmées (60). Dans une nouvelle approche bayésienne, Parisien et Major ont proposé un modèle qui utilise une base de motifs appelés NCM pour « *Nucleotide Cyclic motifs* » extraits des structures 3D d'ARN disponibles dans les bases de données des structures cristallisées (31). Ces motifs contiennent des boucles ayant au plus 4 bases non-appariées ainsi que tous les types de paires de bases (canoniques et non-canoniques) ce qui améliore les prédictions. MC-Fold sert de base pour MC-Sym, un outil de prédiction de structure 3D. Le *pipeline* MC-Fold-MC-Sym a permis de prédire correctement plusieurs structures pour lesquelles le modèle de Turner ne donnait pas de bonnes prédictions.

Tous ces algorithmes ont permis de développer de puissants programmes contenant une compilation d'outils « *package*» d'alignement de séquences/structures, de repliement et de recherche d'homologie et de motifs d'ARN.

1.5 Découverte de nouveaux ARN non-codants

Comme mentionné dans les sections précédentes, les découvertes récentes d'ARNnc se multiplient. En 2007, 22 candidats d'ARN structurés dans les bactéries ont été identifiés par Weinberg *et. al.* à l'aide un pipeline automatisé utilisant la recherche d'homologie et CMfinder pour les alignements de séquences multiples (61). La figure 6 montre sept ARN parmi ces 22 ARN. Trois ans plus tard, la même équipe a utilisé un pipeline de génomique comparative intégrant les recherches d'homologie, l'algorithme RNAmotif ainsi que CMfinder pour trouver plus d'une centaine de candidats d'ARN structurés dans des métagénomes de bactéries et archéobactéries (62). On retrouve de nombreux ARN cis-régulateurs parmi ces nouveaux ARN structurés et d'intéressants candidats de riboswitch. Ces exemples d'études montrent l'importance des outils de recherche des nouveaux ARNnc et l'amplitude de ce qui reste à découvrir et à élucider pour ces ARN, leurs structures et fonctions cellulaires.

L'hétérogénéité des ARNnc et le manque de conservation au niveau de leurs séquences primaires rendent la tâche de recherche de nouveaux ARN beaucoup plus difficile que celles de séquences codantes. Il est important de combiner séquences et motifs structuraux dans les méthodes de recherche de nouveaux ARNnc (63). On distingue deux catégories de méthodes de recherche d'ARNnc: la recherche d'homologie qui trouve des ARN dont la famille est connue et il y a les outils de recherche *ab initio* (de novo) d'ARNnc.

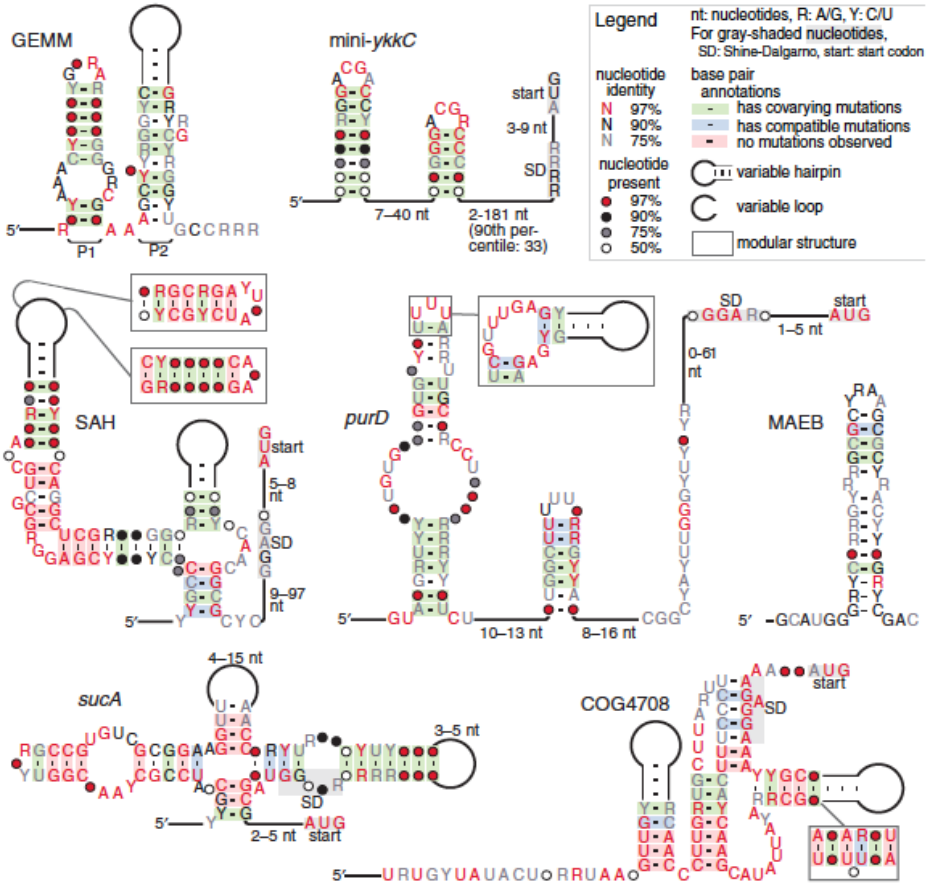

Figure 6. Séquences et structures consensus de nouveaux ARN identifiés par Weinberg *et al.* GEMM (« widespread Genes for the Environment, for Membranes and for Motility »), SAH, COG4708 et sucA sont des candidats de riboswith. Quant à eux, purD et mini-ykkc sont des candidats d'ARNnc cis-régulateurs. MAEB (« metabolism-associated element in Burkholderia ») est un candidat d'ARN régulateur probablement reconnu par une protéine. *Tiré de* (61).

1.5.1 Recherche d'ARNnc par approche d'homologie

Les approches d'homologie permettent la recherche de nouveaux ARNnc dont les familles sont déjà connues. Certains outils se basent uniquement sur la conservation de la séquence primaire tels que Blast (64) alors d'autres programmes intègrent l'information sur la structure secondaire de l'ARNnc et nous en donnons quelques exemples dans ce qui suit. On peut trouver la majorité des ARNr et ARNt en utilisant BLAST mais c'est inefficace pour les autres ARNnc parce que les séquences primaires d'ARNnc sont moins conservées. tRNAscan-

SE (65) utilise des modèles de covariance pour la séquence ainsi que la structure secondaire consensus mais c'est un outil qui est limité aux ARNt. Erpin (66) est un programme d'identification de motif d'ARN qui utilise un algorithme de programmation dynamique basé sur un profil de motifs. En partant d'un alignement de séquences d'ARN et l'annotation de structure secondaire, Erpin identifie les séquences homologues. Des outils appelés descripteurs d'ARN comme RNArobo (67) et RNAmotif (68) (qui sont des extensions de RNAmot (69)) ont été développés afin d'améliorer la recherche d'homologie en tenant compte de l'information sur les motifs.

Infernal (70) est un puissant outil de recherche d'homologie et il est utilisé pour maintenir la base de données Rfam. Infernal contient une compilation d'outils d'alignement de structure et de recherche de motifs basés sur un modèle de covariance. Pour chaque famille de Rfam, un modèle de covariance est obtenu à partir d'un alignement multiple annoté par une structure consensus. Il y a une vérification manuelle des alignements avant la construction du modèle ce qui assure la qualité de l'alignement. Infernal est un outil gourmand en ressources (temps de calcul et mémoire) et ceci est dû à l'usage du modèle de covariance. Ces méthodes de recherche par homologie sont plus performantes pour trouver des nouveaux membres d'ARNnc dont la famille est connue que pour découvrir de nouvelles familles d'ARNnc.

1.5.2 Recherche *ab initio* d'ARNnc

La recherche *ab initio* d'ARNnc permet d'identifier de nouveaux ARNnc appartenant ou pas à des familles connues. Ces outils sont basés sur des approches comparatives, thermodynamiques ou sur les biais de composition en nucléotides (cette dernière approche a été très peu développée). On dispose de plusieurs outils de recherche *de novo* d'ARNnc incluant RNAz (48) et QRNA (71) qui sont les plus populaires. EvoFold (72), ddbRNA (73) et MSARI (74) sont d'autres exemples. Les méthodes citées sont basées sur l'approche de génomique comparative et utilisent l'information de plusieurs séquences similaires pour trouver le plus d'information sur la conservation de la structure secondaire. Certains programmes comme RNAz utilisent à la fois des outils de prédiction de structure basés sur l'approche de stabilité thermodynamique (RNAfold) ainsi que la conservation de structure consensus dans l'alignement multiple (RNAalifold).

CMfinder (75) a été utilisé dans le cadre de ce travail pour détecter des ARN structurés dans des séquences homologues (voir chapitre 4). C'est un outil de prédiction de motifs d'ARN basé sur un modèle de covariance, mais avec l'avantage d'avoir des heuristiques soigneusement élaborées ce qui augmente son efficacité. La prédiction de structure combine l'énergie de repliement et la covariation de séquences. Ce programme crée en résultat un nouveau modèle de covariance qui peut être directement intégré à la recherche d'homologie à l'échelle du génome. Il peut être utilisé, par exemple avec Infernal, pour le raffinement automatique et l'expansion des familles d'ARN.

Certains outils ont été conçus pour la découverte de gènes à ARN dans une séquence génomique donnée (sans utilisation d'approches comparatives). smyRNA (76) est un outil qui se base sur les motifs dans la structure primaire et a démontré une capacité à trouver de nombreux nouveaux ARNnc. NCRNASCAN (59), utilise plutôt des paramètres de la structure secondaire, mais n'a pas prouvé son efficacité à trouver des ARNnc excepté pour les miARN. ncRNAscout (77) est une méthode plus récente de découverte *ab initio* qui combine les deux approches de smyRNA et NCRNASCAN pour une meilleure performance que ses deux prédécesseurs.

1.6 Rfam une base de données de familles d'ARNnc

L'application d'outils bioinformatiques puissants tels que CMfinder ou Infernal à la collection de données de séquences d'ADN en expansion continuelle facilite l'identification de nouveaux ARNnc et révèle aussi de nouveaux membres de familles déjà connues. Plusieurs bases de données ont été développées dans les récentes années pour les ARNnc. On retrouve certaines bases qui sont générales telles que Rfam qui contient toutes les familles d'ARNnc alors que NONCODE exclut les ARNt et ARNr. D'autres bases de données sont plus spécialisées comme miRBase pour les miARN, lncRNAdb pour les longs ARNnc ou snOPY pour les ARNsno.

Rfam est une base de données qui répertorie les ARNnc grâce à des alignements de séquences et des modèles de covariance. Infernal est l'outil utilisé pour maintenir Rfam (voir section 1.5.1). Rfam maintient les alignements, les consensus de structures secondaires, les modèles de covariances et les annotations correspondantes aux familles d'ARN. Chaque famille représente un ensemble de séquences qui ont une fonction comme ARNnc et ont un ancêtre commun. On y trouve les familles des ARNt, miARN, riboswitch etc. Rfam est souvent utilisée comme une source d'alignements de haute qualité pour tester des programmes d'analyse de séquence ou de repliement et pour l'entrainement machine. Rfam 10.0 a été mis en ligne au début de 2010 contenant une importante mise à jour suite à l'usage de la nouvelle version de l'algorithme d'Infernal v1.0. Les améliorations apportées par cette mise à jour ont permis une augmentation de 178% du nombre des régions de séquences couvertes par Rfam ainsi que l'augmentation de la taille de certains alignements (78). C'est cette version de Rfam que nous avons utilisée pour ce travail. La version 12.0 a récemment été publiée et contient actuellement 2450 familles d'ARNnc (9).

1.7 Mise en contexte et objectifs du projet de maîtrise

Alors que l'on dispose de plus en plus de séquences d'ADN et d'ARN provenant de la génomique et de la transcriptomique, la signification de la plupart de ces séquences reste encore à élucider. Plusieurs gènes à ARN restent à découvrir ainsi que leurs structures et fonctions. Jusqu'à présent aucune étude n'a essayé de répertorier tous les motifs structuraux (boucles « hairpin », boucles internes, combinaisons de paires de bases, etc.) par leurs abondances dans la base de données Rfam. Il y a eu beaucoup d'études sur des motifs spécifiques et généralement dans un contexte restreint (excluant toujours une partie des données). Pour ne nommer que quelques exemples, on trouve dans la littérature de nombreuses études sur les boucles à trois bases non-appariées appelé triloop (79-81), les boucles « tetraloop » de type GNRA, UNCG ou CUUG qui sont très abondantes et impliquées dans la fonction de nombreux ARNnc (82-86) et les structures d'épingle à cheveux (87,88). Cependant ce projet est innovateur dans le sens où il inclut toutes les caractéristiques structurées dans toutes les familles de Rfam, ce qui représente l'ensemble de toutes les séquences d'ARNnc à notre disposition. Notre analyse ne se limite pas aux motifs structuraux communs et expose les motifs rares restés jusqu'à présent dans l'ombre des structures abondantes. L'analyse de toutes les structures de toutes les séquences se trouvant dans Rfam pourrait potentiellement aider à ressortir des motifs qui sont sur- ou sous-représentés pour n'importe quels facteurs qui affecteraient leur sélection au cours de l'évolution. Ainsi, au-delà de la stabilité thermodynamique d'une structure donnée, des facteurs tels que la susceptibilité à être dégradé par des ribonucléases, à lier des protéines, à former des dimères, à être transcrit plus efficacement sont autant d'exemples de facteurs pouvant influer le cours de l'évolution, mais dont les programmes de prédictions ne tiennent généralement pas compte.

Notre hypothèse est qu'en tenant compte de l'abondance des motifs dans Rfam de façon exhaustive, nous serons capables de mieux évaluer un nouvel ARNnc et de discriminer entre les vrais et faux candidats prédits par les méthodes actuelles de recherche d'ARNnc.

Notre premier objectif dans ce travail est d'analyser tous les motifs de structure secondaire disponibles dans Rfam et de trouver les caractéristiques communes et rares. Les résultats de cette analyse sont présentés dans le chapitre 3. Notre deuxième objectif est d'exploiter la richesse des structures secondaires contenues dans les alignements de Rfam pour développer un système de score pour évaluer les ARN structurés et par la suite étudier la possibilité de faire des filtres pour les nouveaux candidats d'ARNnc basés sur ces informations. Le chapitre 4 présente le système de score développé et nous discutons de son applicabilité au chapitre 5.

Chapitre 2 Compilation des données de Rfam et la conception de la base de données RNAstem

Avant-propos

Ce chapitre présente un article en préparation pour une soumission à la revue *Database and ontologies.* Cette base de donnée fait partie des méthodes utilisées dans ce travail et a permis de compiler les données de Rfam afin d'en faciliter l'utilisation. J'ai participé à la conception de la base de données et de son site web. J'ai aussi testé le fonctionnement de la base de données. Je n'ai pas participé à la rédaction de cet article.

Database and ontologies

RNAstem: a relational database of stem-loop features in RNA

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2.1 Abstract

Motivation: Our understanding of RNA tertiary structures benefited a great deal from experimentally determined atomic resolution structures. Still, the 1102 structures currently available represent a very small fraction of known RNAs; the Rfam database lists nearly 2000 RNA families and over two million sequences. Many recurring small RNA motifs have been identified from mining RNA structural data, but a different organization of data is needed to fully take advantage of wealth of information provided by Rfam and growing amounts of data from sequencing projects.

Results: We introduce RNAstem, a web server to study RNA secondary structure. RNAstem is a MySQL database with an incomparable query flexibility that allows simple or global analysis of loops, bulges, internal loops, base paired regions, multistem junctions to look for conservation, covariation of motifs and discovery of novel motifs.

Availability: http://euler.bc.edu/meyerlab/RNAstem/

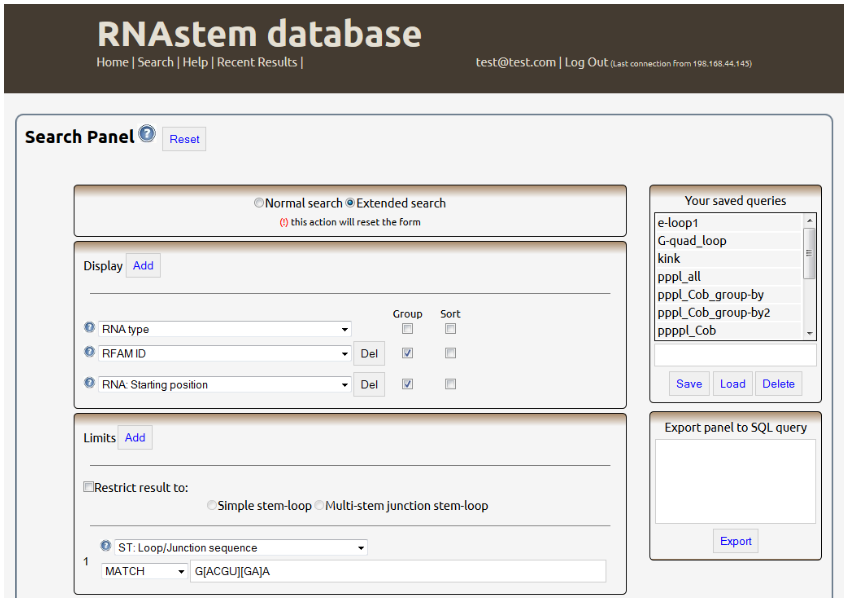
2.2 Introduction

Following many major discoveries of the past two decades RNA is now recognized as a complex multifunctional molecule. The wealth of available sequence data has been exploited by computational tools to find hundreds of non-coding RNAs. Many recurring small RNA motifs have been identified from mining RNA structural data; such as the notoriously stable GNRA and UNCG tetraloops, the most common RNA loops found in ribosomes (89,90). Such motifs have been useful for deepening our understanding of RNA structure and in the development of computational tools for RNA structure prediction. For instance, when folding a query sequence, the predictive tool Mfold takes into consideration the improvement in free-energy provided by a GNRA tetraloop in addition to that derived from base-pairing (91) and many computational tools that find novel RNA structures through comparative genomics rely in part on free-energy calculations (48,75,92-94). More sophisticated prediction tools, like MC-fold, attempt to consider most of the potential tertiary interactions (95). All of these approaches rely on data accumulated from the determination of three dimensional structures. However, the number of RNA sequences characterized in these studies represents a very small subset of available functional RNA sequences. There are currently 1102 RNA structures in the Protein Structure Databank (common repository for all biomolecule crystal structures (96)) derived from less than 100 families of RNA. In contrast, the Rfam database of RNA families (97) consisted of 1973 RNA families in 2009, with secondary structure alignments comprising over two million sequences.

To aid in the search of such constraints, we have built a database of all the stem-loops present in the Rfam database, which totals approximately 10,000,000 stem-loops. All the features of these hairpins have been extracted and listed in different tables with various information allowing complex queries.

2.3 Description

Stem-loop browsing and searches: A user-friendly interface allows casual visitors to look at any known RNA stem-loop, its sequence, structure, coordinates in corresponding sequence and species, as well as additional information like the overall conservation of that stem (see Figure 7).



test@test.com | Log Out (Last connection from 198.168.44.145)

○ Normal search ● Extended search

(!) this action will reset the form

	Group	Sort
RNA type	☐	☐
RFAM ID	☑	☐
RNA: Starting position	☑	☐

☐ Restrict result to:

○ Simple stem-loop ○ Multi-stem junction stem-loop

1 ST: Loop/Junction sequence

MATCH G[ACGU][GA]A

e-loop1
G-quad_loop
kink
pppl_all
pppl_Cob_group-by
pppl_Cob_group-by2
ppppl_Cob

Figure 7. Screenshot of interface.

Search by features and multiple conditions: Users interested in all the stems with a given feature set can easily access that information. For example, all the stems harbouring a GNRA tetraloop can be accessed by using the pattern G[ACGU][AG]A in conjunction with the “terminal loops” option. Other examples of information that can be fetched include the presence, size or sequence of any secondary structure element: terminal loops, internal loops, bulges or the stem itself. Queries can combine many different criteria simultaneously, for example, looking for all stems that have two bulges, one internal loop and a terminal loop of five bases that comprises GGA. Other examples include presence of a D-loop and a T-loop in the same RNA.

Complex queries: A schematic of the database tables is provided for users familiar with SQL to allow them to write their own queries. We therefore provide the full capabilities of SQL language, without the need for numerous options that would only add confusion to a user interface.

2.4 Implementation

The MySQL database has a web interface implemented in php. The server runs on UNIX. Simple queries are processed and displayed in real time. However, because of the size of the database and the complexity of some potential queries, compressed result files will be sent by email address of registered users.

2.5 Results

To highlight the potential of the database, we performed a query to identify all stems with at least one putative non-canonical bp (within Rfam aligned sequences). In this search, we find that the closing stem of most riboswitches is more likely to include a non-canonical bp than simple stem-loops, in contrast with other well known RNA families not known to be "structural-switches" (see table 1). This can be explained by a need for more flexible structures that allow switching where the aptamer and expression platform portions of riboswitches overlap, typically the closing stem of the aptamer (98).

Riboswitch	cl. NC	st. NC	cl.-st.	RNA (other)	cl. NC	st. NC	cl.-st.
Mg sensor	0.01	0.15	-0.14	RNaseP bact-b	0.08	0.18	-0.10
SAM-IV	0.02	0.22	-0.20	CPEB3	0.16	0.24	-0.08
Lysine	0.51	0.57	-0.06	RNaseP nuc	0.27	0.36	-0.09
Purine	0.58	0.55	0.03	CoTC ribozyme	0.49	0.56	-0.08
TPP	0.53	0.29	0.25	RNaseP bact a	0.37	0.27	0.09
Cobalamin	0.37	0.20	0.17	Hammerhead 1	0.47	0.34	0.13
AdoCbl(2)	0.61	0.29	0.32	RNase P	0.33	0.18	0.15
MOCO	0.98	0.46	0.52	RNaseP arch	0.48	0.25	0.24
SAM-I-IV	0.43	0.15	0.28	RNase MRP	0.54	0.27	0.28
AdoCbl(3)	0.37	0.12	0.25	Hammerhead 3	0.07	0.03	0.04
SAM	0.48	0.15	0.33	IRES HCV	0.58	0.71	-0.13
THF	0.77	0.20	0.58	U1	0.33	0.59	-0.26
Glycine	0.60	0.11	0.48	U11	0.28	0.47	-0.20
drz-agam-2	0.96	0.18	0.78	U1 yeast	0.11	0.08	0.03
FMN	0.59	0.01	0.58	tRNA	0.20	0.28	-0.08
Avg	0.52	0.24	0.28*	Avg	0.42	0.31	-0.01*

Table 1. Stems with non-canonical bp.

cl. NC, ratio of closing stem sequences with non-canonical bp over total number of sequences; st. NC, same ratio for the other stems; cl.-st, closing stem ratio from which the ratio of the other stems is subtracted; Avg, average. *P<0.005.

A simpler example of a query is a search for all instances of internal loops consisting of one “U” on each strand, opened by a CG bp and closed by a GC bp. This motif is found in type 1 myotonic dystrophy where a “CUG” repeat is overabundant, leading to the formation of a very long stem with numerous “U,U” internal loops. Recent work suggests that molecule interacting specifically with this motif is potentially a treatment of the disease (99). We found 2879 instances of this motif in Rfam, most of which are in 5S rRNA sequences, but not in the human 5S rRNA. Overall, this is not a common motif, suggesting that the molecule will have few off-target effects.

2.6 Conclusion

RNAstem represents a powerful tool for those interested in studying RNA secondary structure on a global scale. By providing the basic element of RNA structure, hairpins, it partially circumvents the problem of comparing different RNA families, thus allowing the user to look for general features applicable to any RNA.

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Chapitre 3 Identification des motifs communs et rares des ARN structurés dans la base de données Rfam

Avant-propos

Ce chapitre présente un article en préparation pour la revue Nucleic Acids Research et représente une première partie du projet avec les méthodes, résultats et discussion de cette partie. Ma contribution à cet article est d'avoir effectué l'analyse des données compilées à partir de Rfam, le développement du score d'abondance sous la supervision de Jonathan Perreault et François Major. Ma contribution dans la rédaction est d'environ 80%.

Identification of Common and Rare Features of Structured RNAs in the Rfam Database

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3.1 Abstract

Technological advances have made available abundant sequence information accessible in databases such as Rfam, which provides alignments and structural information of many noncoding RNA (ncRNA) families. We retrieved all the terminal loops, internal loops and bulges from Rfam. We compiled the corresponding data and calculated an abundance score. We found significant differences between the most abundant and rare RNA structural features. Pentaloops were unexpectedly more common than tetraloops in some RNA categories. Well-known loops such as GNRA and UNCG were found to be among the most common, but also others that have not been noticed before, such as the UUUU tetraloop. Moreover, we discovered that "A" and "U" dominate single stranded RNA regions, whether they are bulges or loops.

3.2 Introduction

The advances of high-throughput technologies such as next generation sequencing or tiled arrays allowed the discovery of many transcripts with functions unrelated to protein coding, so called noncoding RNAs (ncRNA). These RNAs are an important fraction of the transcriptome (100) and new families of ncRNAs are being revealed at a surprising pace (62), (78). NcRNA are well known for being structural elements as in ribosomal RNA but they also play a wide range of functions including regulation of gene expression, metabolic regulation, and microbial pathogenicity. The function of ncRNAs such as ribozymes and riboswitches, just to name a few, is tightly linked to their structure (27). Thus, understanding and predicting

RNA structure can bring considerable insight into these molecules (61,101-103). Secondary structures such as stem-loop hairpins are versatile building blocks that allow various complex structures to be formed. We only partially understand what the implications of such structures are and how they exert their biological function.

Nevertheless, there is a growing body of data on various small RNA structure motifs that help us apprehend the relation between structure and function. Terminal loops are among the simplest RNA structures and are important functional elements of RNA, making them very interesting to study. For example, the triloop motif is known to play a major role in a variety of organisms and pathways as in the promotion of some virus replication (88), (81), viral synthesis (104), and iron response (105), while tetraloop hairpins are very abundant and represent about 50% of all hairpins (83,106,107). Among the very well-studied tetraloops we find the stable GNRA tetraloops that make up to 50% of hairpins in rRNA (82), UNCG (85) and CUUG (84,108) that are also common in ribosomes. Many structured functional RNAs have bulges and internal loops that are important structurally and catalytically. GA/GA tandem mismatch, a symmetric 2X2 internal loop, modulates RNA metal binding in hammerhead ribozymes (109,110). The kink-turn (abbreviated to K-turn) is a common structural motif that has an asymmetrical-internal-loop structure and is known to bind proteins (111). Bulges are unpaired nucleotides on one side of a stem of base pairs and they confer a variety of RNA architectures and recognition sites for intra and intermolecular interactions (112). Iron-Response-Elements (IRE) are known to have a conserved C-bulge in the 5′ strand of the stem that is tightly linked to their function (31,113).

In order to improve our understanding on aspects of RNA structure that have not been as thoroughly studied as determination of thermodynamic stability, we used a different approach than most RNA structure studies. Rather than focusing on RNA structures for which 3D structures are available, we tried to get insights in structural and biological features of RNA by extracting all the simplest secondary structure elements from the millions of sequences in the RNA families database (Rfam) (114). As common secondary motifs that were extensively studied are generally very stable structures, we also aim to explore loops and bulges for which other parameters (aside from thermodynamic stability) could explain the observed abundance. We focused on small motifs such as terminal loops, internal loops and bulges having small sizes (5 bases or less) (see Figure 8A).

Undeniably, less research was inclined to explore rare motifs and, to our knowledge, no publication explored these aspects of the distribution of RNA structural motifs where a few motifs are very abundant, many others are less common and some are exceedingly rare. In an attempt to explore all of the above features and questions about ncRNA, this work is aimed to determine common and rare features of all RNA available in Rfam alignments. We retrieved the information from the Rfam database about the sequences of secondary structures such as terminal loops, internal loops and bulges in all existing RNAs. We compiled and analyzed the available data to find the most common and rare structural features.

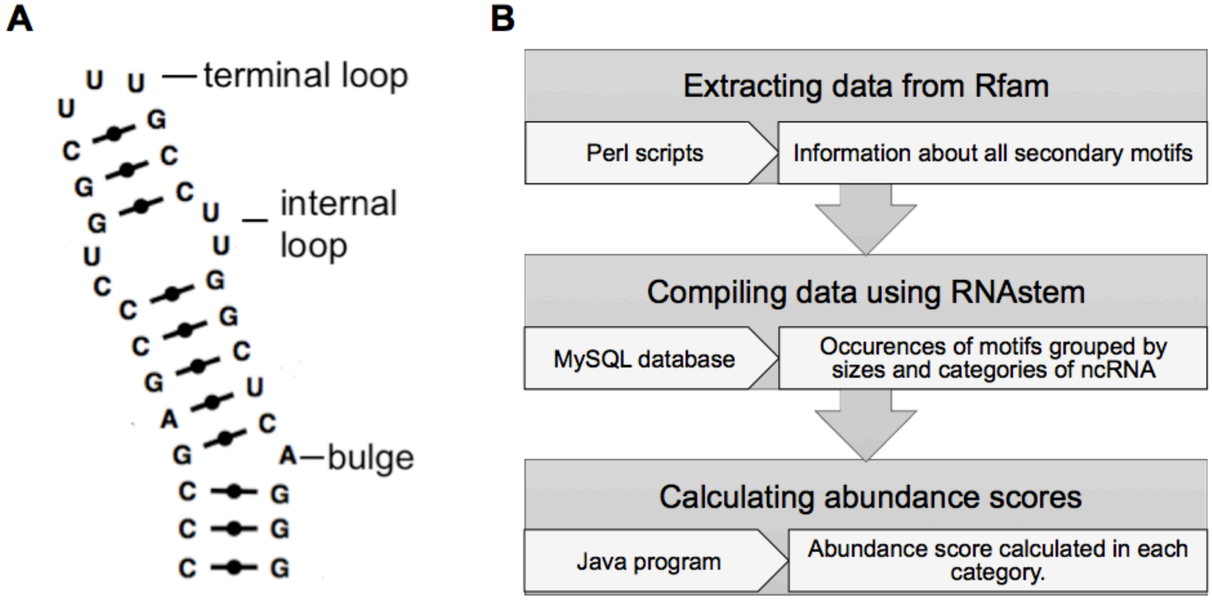

Figure 8. (A) Secondary structure of an RNA stem.

This structure was predicted by MC-fold and shows examples of the three basic secondary motifs that were studied: a terminal loop (triloop UUU), an internal loop (5′ CU-3′ UU) and a bulge (A).

(B) Flowchart of data extraction and analysis.

Different scripts and tools were used (on the left) to provide the output (on the right) required for the next step.

3.3 Materials And Methods

3.3.1 Data extraction and analysis

Full alignments of all noncoding RNA families available on Rfam (version 10) were retrieved from the database. A series of Perl scripts were used to extract information about all existing secondary motifs in these alignments such as stem-loops, bulges, internal loops and base pairs. We used a MySQL database, RNAstem, to facilitate data extraction (http://euler.bc.edu/meyerlab/RNAstem/). Data was compiled to identify all common and rare secondary structures in Rfam alignments. These loops and bulges consisting of so-called “single-stranded” regions are based solely on the Rfam annotation, even if many of them are well known to interact in various ways, such as the G and A of GNRA tetraloops. In fact, one of the goals of our analysis is to discover motifs that are likely to have such tertiary interactions. The steps for data extraction and analysis are summarized in Figure 8B.

3.3.2 Frequency score

A scoring system was elaborated to discriminate between rare and abundant structures. We calculated a score for each loop or bulge sequence of size N (for triloops, there are 64 possible triloop combinations: AAA, AAC, AAG..., UUU). We first compiled Rfam RNA families into 23 categories (see Table 2) based both on Rfam “Types” as well as statistical significance. Since there are often two levels of “Types” for a given RNA family, whenever too few sequences were available for one, the highest level was chosen. Conversely, for families such as small subunit rRNA, there are more than enough sequences for every sequence combination of the motifs to be found many times, they were therefore each chosen as a single category. Using these categories, the following formula was used to calculate a score:

$$\log((L_i+0.5)/\Sigma\, L_i)$$

where L_i is the number of instances of a specific loop of index i in a category and $\Sigma\, L_i$ is the sum of all loops of size N in the same category and 0.5 prevents log(0).

The log of the above ratio is calculated for the 23 RNA categories compiled from Rfam database (see Table 2) and then the average of logs for each sequence of loop or bulge is calculated between these categories. The average log represents the score we use as an indicator for the abundance of a specific motif. The more negative the score, the rarest the loop. If we were to calculate merely the average of the ratio of the relative occurrence to the total number of motifs, the discrimination for rare motifs is lost (zeroed). Calculating an average of logs allows us to give more weight to the rare motifs. We use a Java program to do these calculations. An example of how scores are calculated is depicted in Figure 12 in the supplementary data.

BIOCHEMICAL			***ANTISENSE***		
Translation	**Intron**	**Cis-Reg**	**Gene***	**Antisense**	**snoRNA**
5S	Ribozyme	IRES	Gene*	miRNA	H/ACA-box
5.8S	Splicing	Leader		CRISPR	scaRNA
SSU_rRNA_archea	snRNA	Riboswitch		Antisense	C/D-box
SSU_rRNA_bacteria	Intron	T-box			
SSU_rRNA_eukarya		Thermoregulator			
tRNA		Cis-Reg			

Table 2. RNA categories and supercategories.
*Gene is a classification of Rfam that encompasses numerous different families of RNA that are transcribed as single genes (typical example would be bacterial small RNAs such as RyhB) which makes it a supercategory in our classification. It is considered as ANTISENSE because most of the corresponding families are small RNAs that act through complementarity with their target. However, it also includes several genes for which this classification would be more controversial, such as the SRP RNA.

3.3.3 Superscores

Many RNA families in Rfam are not as large as the tRNA or the ribosomal categories, which form categories by themselves herein. Even when we merged families into 23 categories, many of these categories did not have enough motifs, which led to an under-representation of some loops or bulges. To deal with this issue and for a greater discrimination for rare loops, we grouped the 23 categories in 6 larger groups we conveniently named supergroups. Table 2 shows how the compiled categories were grouped.

While some categories needed to be merged in super categories for statistical significance, we later came to the conclusion that many intrinsic properties of different types of RNAs were too different to be compared. Therefore, the log scores were calculated independently for two different super-divisions. While *Gene*, *Inhibitory* and *Nuclear* were grouped in "*Antisense"* for having predominantly a function requiring base complementarity with a target, we grouped the three supercategories *Translation*, *Cleaving* and *Cis* in "*Biochemical"* for the biochemical function provided by their complex structures: catalysis and ligand binding. In principle, these divisions are not mutually exclusive, for example some RNA families can hybridize to a target to exert cleavage, but all RNA families were assigned to only one category, super category and division for our analysis.

3.4 Results

3.4.1 Abundance of motifs based on size

We first looked at the abundance of motifs based solely on their sizes. In Figure 9, we show the statistics for the terminal loops, bulges and internal loops. For each type of motif, we calculated the total occurrences (e.g. total number of all terminal loops of all sizes) then the occurrence for each motif size found in Rfam (Figure 9 A-C).

Tetraloops are the most abundant overall (Figure 9A), representing 37% of all terminal loops, which confirms what is already known about tetraloops (83). While they are the most common loops in *Biochemical* and are also very common for *Antisense* (2nd) (Figure 9D, Tables S1 and S21), pentaloops are the most abundant type of loop for the latter. Triloops are not as abundant at about 3% of all loops, although they are only slightly less abundant than tetraloops in *Antisense*. Interestingly, loops of size seven (heptaloops) are quite abundant (21%). This may be explained by the presence of two heptaloops in tRNAs, which are among the most abundant sequences in Rfam. This exemplifies the reasons underlying the scoring scheme based on logs averaged over many categories.

The most abundant bulges are the one-base bulges (see Figures 9B and 9E. Tables S2 and S22), representing over half of all existing bulges in ncRNA. Bulges of two and three bases are also relatively common. In general, bulges of small sizes (7 bases and less) are the most common making up over 99% of all bulges.

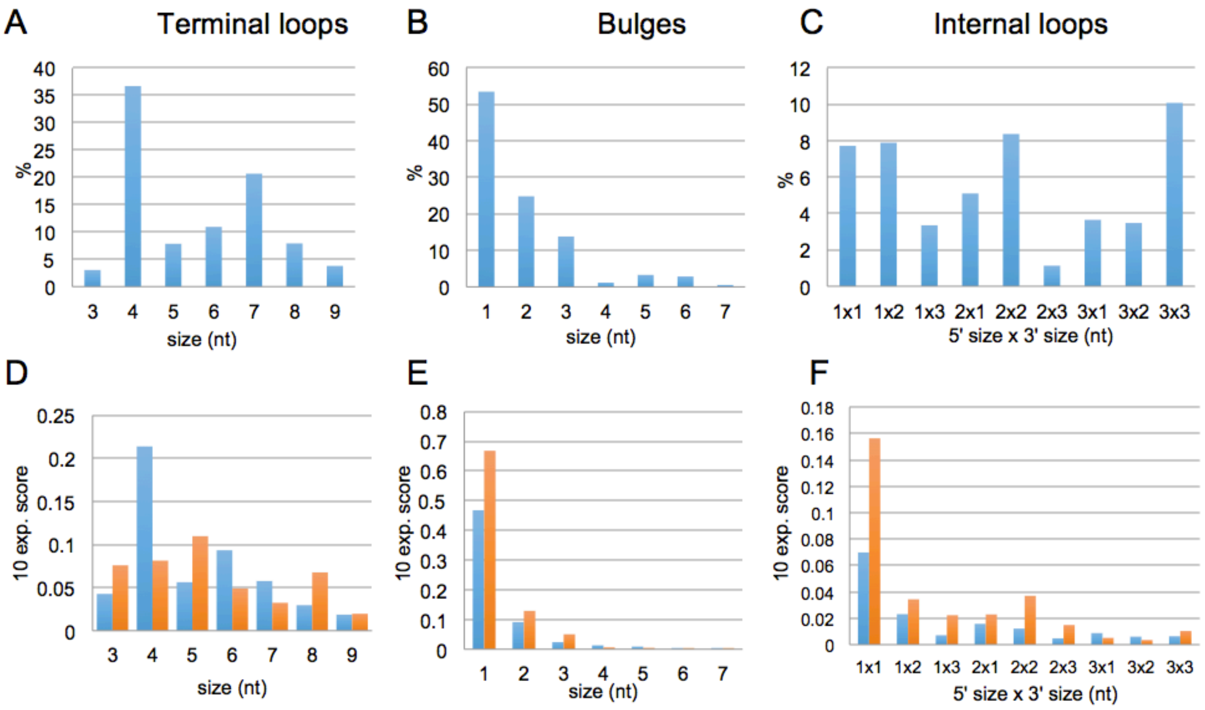

Figure 9. Motifs abundance by size in all of Rfam ncRNA.

Histograms on the top show percentages of terminal loop, bulges and internal loops by sizes that have the highest occurrences for each type of motifs (example tetraloops are the most abundant terminal loops representing 37% of all loops found in Rfam). These percentages do not reflect the relative abundance in the RNA categories. Graphs on the bottom show the abundance of motifs by size based on the abundance score in the 2 major classes of categories *Biochemical* (in blue) and *Antisense* (in red). The histograms are only grouped based on the size of the motifs and are not meant to be compared to each other as the abundance score is an indicator proper to each class of RNA. Tetraloops remain the highest in *Biochemical* while loops of size 5 are the most abundant terminal loops in *Antisense* class.

Internal loops also show the same tendency of small motifs being more common (Figures 9C and 9F, Tables S3 and S23). We note that the size range of internal loops is generally less than five nucleotides on each side: the 10 most common internal loops all have less than 5 nucleotides on each side and together they account for 60% of all internal loops. Size-symmetric internal loops are slightly more common, with 3 x 3 loops (three nucleotides on the 5′ side and three nucleotides on the 3′ side) being most common (10% of all internal loops). As with heptaloops, the score-based sorting contrasts sharply with overall data, likely because of numerous 3X3 internal loops in ribosomal RNAs. Indeed, scores indicate that in both categories 1X1 loops are the most common, followed by the 2X2, 1X2 and 2X1 loops. The symmetrical loop of size 4X4 although not shown in Figure 9F is more abundant than loops of sizes 3x3, 3x1 and 3x2 only in *Antisense* whereas in Biochemical it is further down the list of abundant tetraloops. The abundance of small-sized loops and bulges may be explained by the fact that thermodynamic stability of loops depends on size (115). Other factors could be the biological functions played by these motifs as well as pressure to have small genomes and RNAs, which is especially strong in bacteria and viruses.

3.4.2 Common and rare terminal loops, bulges and internal loops

We further used our score system to determine the abundance of all sequence combinations for the three types of secondary structure motifs (terminal loops, bulges and internal loops). Statistics on all possible sequence combinations for loops of sizes up to five bases, bulges up to four bases and internal loops of up to four bases were calculated separately. Larger structural elements (sizes greater than five) were not studied further because the numbers available of sequences did not provide significance for the growing number of sequence combinations as the size increases (six bases imply 4096 possible combinations, too many of which appear to be rare, often with no instances at all). While the analysis was done for all possible sequences of terminal loops of size 2 to 5 and bulges from size of 1 to 4 and a selection of internal loops, we only show the results for a few terminal loops in table 3 (complete score tables are available in the supplementary data Tables S4-S20 for *Biochemical* and Tables S24-S40 for *Antisense*). For each motif size, we sorted the loops from highest to lowest score. The most abundant and rarest loops are shown in table 3.

In biloops, triloops and tetraloops, most common loops in *Biochemical* are also abundant in *Antisense,* although the exact ranking of abundance differs. This pattern is also found in rare loops of size two to four while pentaloops have fewer similarities between the common loops of each group.

UU, AA and UA are the most common biloops in both *Biochemical* and *Antisense* while CC, GU, GC and CG are the less abundant loops. The triloops UAU and UUU are common in both groups. The most abundant triloop is CAU in *Biochemical* and UAA in *Antisense*. Examining the rare triloops shows overlap between *Biochemical* and *Antisense* with GCG and CGG triloops.

Our findings correlate with previous studies that identify three groups of terminal loops as the most common tetraloops: GNRA, UNCG and CUUG (where N represents any nucleotide and R is a purine) (83,116). Among the ten most abundant tetraloops in the *Biochemical*, we find six (out of the eight) GNRA tetraloops, two UNCG tetraloops and the CUUG tetraloop. We find more less-known tetraloops among the common tetraloops of the *Antisense* group, where three GNRAs and one UNCG also appear in the top ten most common loops. The GAAA tetraloop is the most common in *Biochemical* and the second most abundant in *Antisense*. GNRA is undeniably the most common tetraloop validated by the scores calculated for all of our compiled categories (before splitting into *Biochemical* and *Antisense*). A significant new finding is the abundance of the UUUU tetraloop, the most common loop in *Antisense* and the ninth in *Biochemical*. Little is known about this tetraloop found in the yeast SRP RNA (87,117).

Distribution of pentaloops in *Biochemical* and *Antisense* show less overlap than smaller terminal loops suggesting that these two groups differ in structural features. Pentaloops with consensus sequence GNNRA are quite common in *Biochemical* (GUCAA, GUUAA, GAUAA and GAAAA, rank 1st, 2nd, 3rd and 8th respectively). GNNRA may be a variation of the common GNRA tetraloop. UUUUU, UUUAU pentaloops are abundant in *Biochemical* (4th and 6th) as well as CUUGA and CUUGU (7th and 9th) and these pentaloops may be related to the abundant UUUU and CUUG tetraloops. It is interesting to note that UUUAU and CUUGU are also abundant in *Antisense* (7th and 9th).

	ABUNDANT				**RARE**			
	Biochemical		*Antisense*		*Biochemical*		*Antisense*	
	Loops	Score	Loops	Score	Loops	Score	Loops	Score
Biloops	UU	-0.5	UA	-0.9	CG	-2.0	CG	-2.1
	AA	-1.0	UU	-1.0	GC	-1.8	GC	-2.1
	AU	-1.1	AA	-1.1	GU	-1.7	CC	-1.6
	UA	-1.1	CA	-1.2	CC	-1.7	GU	-1.5
Triloops	CAU	-1.4	UAA	-1.7	CGG	-3.5	CGG	-3.5
	UUA	-1.4	UAU	-1.7	GGC	-3.4	CCG	-3.5
	UAU	-1.5	UUU	-1.8	GCG	-3.2	GCG	-3.5
	UUU	-1.5	ACC	-1.8	GGU	-3.0	GGG	-3.4
Tetraloops	GAAA*	-0.9	UUUU	-1.5	AGGG	-4.8	CGCG	-4.4
	GAGA*	-1.2	GAAA*	-1.6	ACGC	-4.7	CGCC	-4.3
	GCAA*	-1.2	AAAG	-1.7	CCGG	-4.6	CGUC	-4.1
	UUCG*	-1.5	UUCG *	-1.8	CGUC	-4.5	GCCG	-4.0
	GUGA*	-1.6	GGAA*	-1.9	GUGC	-4.3	CGCA	-4.0
	GUAA*	-1.7	GUAA*	-1.9	CGGA	-4.3	CGUA	-3.9
	CUUG	-1.7	GCAA*	-2.0	CGGC	-4.3	GCGG	-3.9
	GCGA*	-1.8	AAAA	-2.0	CGAU	-4.2	AGCG	-3.8
	UUUU	-1.8	GGAG	-2.1	GGGC	-4.2	AUCG	-3.8
	UACG*	-2.0	GAGU	-2.1	GACC	-4.2	CGGG	-3.8
Pentaloops	GUCAA	-2.2	UGCAU	-2.4	AUGCG	-5.0	GCGCU	-4.8
	GUUAA	-2.2	UCCAG	-2.5	CCGGG	-5.0	GCGGA	-4.8
	GAUAA	-2.2	UGGGC	-2.5	GGGGC	-5.0	GCGGC	-4.8
	UUUUU	-2.2	UGGGU	-2.5	GGGGU	-5.0	GCGUC	-4.8
	AAAUA	-2.3	UGUGU	-2.7	GGGCC	-5.0	GCUAC	-4.8
	UUUAU	-2.3	UUGCC	-2.7	CGACU	-5.0	GGGCC	-4.8
	CUUGA	-2.3	UUUAU	-2.7	GAGCU	-5.0	GGGCG	-4.8
	GAAAA	-2.4	UUUUG	-2.8	AGGUG	-5.0	GUCCG	-4.8
	CUUGU	-2.4	CUUGU	-2.8	CCGGU	-4.9	GUCGG	-4.8
	UAAUU	-2.4	AGAAA	-2.8	CGGGG	-4.9	UCGCG	-4.8

Table 3. Common and rare terminal loops.

Shown here are the most abundant and rare terminal loops in the two divisions *Biochemical* and *Antisense*. On the left, the top common loops are shown for loop sizes ranging from 2 to 5. A star next to a tetraloop indicates a frequent GNRA or UNCG tetraloops. The rarest loops are shown on the right. Note: for pentaloops, we are showing only part of the loops with the lowest scores (the complete list is available in supplementary data Table S4 and S24). Shaded motifs are found in the top most common or rare loops for both Biochemical and Antisense, note however that in most cases the loops not shaded are found in the counterpart group not too far from the top sequences.

We discovered certain consensus in the abundant pentaloops in *Biochemical*, such as GUNAA, GNYAA, UUUNN, CYUGU, YYYYG etc. Many of the common pentaloops in *Antisense* are either UNCAN, UGGGY or UUUNN types. Three of the abundant pentaloops in *Biochemical*: GAUAA, CUCAA and CUUGA (3rd, 7th and 13th respectively) are conserved pentaloops of the 16S RNA (118,119). GCU(A/C)A was reported as a conserved pentaloop that shows structural resemblance to UNCG tetraloop (120) but our analysis shows that this loop is not among the most abundant pentaloops in Rfam.

The log-based score that we used was largely intended to adequately represent the exceptional rarity of some motifs. This approach yielded many GC rich motifs, including some that are among the rarest for both *Antisense* and *Biochemical* categories, like “CGUC”. In our analysis of the rare loops in comparison to the abundant loops of different sizes, we noticed that common loops are more likely to be rich in A and U nucleotides while the rare ones have more C and G. We observed the same pattern in bulges and we verified this by statistical tests.

3.4.3 Base contents of motifs

The observation that abundant terminal loops and bulges were often rich in A and U while the rare ones had sequences with mostly C and G nucleotides led us to examine base content of motifs more closely. To verify these observations, we calculated the content of motifs in nucleotides using the RNAstem database. In table 4, the total percentages (taking all loops or bulges, regardless of the category) indicates that on average loops of size two to five contain 34% of A, 30% of U while C and G represent each 18% of the nucleotides found in terminal loops. We also calculated an average content to give equal weight to each category and thus eliminating the strong bias of the much more abundant ribosomal RNA (right side of the table). In this case, the average percentage in all loops is slightly different (A 31% and U 33%). However, if we examine tetraloops where G was relatively abundant in the total percentages with a 30%, there was a considerable difference when the ribosomal effect was corrected and G represents only 23% of nucleotides found in terminal tetraloops. Tetraloops may have a higher content in guanine due to the abundance of GNRA loops. This analysis indicates that about 2/3 of nucleotides in terminal loops are either A or U. We ran the same analysis on bulges of size one to five and it shows similar results where the average content of bulges is about 64% A or U and the nucleotides C and G represent 17 and 19% respectively of the nucleotides found in bulges. These results suggest that through evolution, selection generally favors the bases A and U in terminal loops and bulges.

A student T-test on terminal loop and bulge distribution to compare the scores of A/U-rich motifs to those of C/G-rich motifs confirms that terminal loops and bulges containing more A and U have a higher score that those that are C/G-rich. The score difference is statistically significant for all terminal loops of size two to five in both *Biochemical* and *Antisense*. Bulges of size one to five in *Biochemical* and *Antisense* showed the same results except for bulges of size one in *Antisense* where the scores of A and U bulges were not significantly higher than the scores of C and G bulges, but the small sample size makes it more difficult to prove a significant difference since there are only four bulges of size one.

Loop	**Total %**				**Categories Average %**			
size	**A**	**C**	**G**	**U**	**A**	**C**	**G**	**U**
2	27%	17%	12%	44%	28%	16%	16%	40%
3	31%	23%	11%	35%	32%	20%	14%	34%
4	37%	16%	**30%**	17%	33%	16%	**23%**	28%
5	38%	21%	15%	27%	28%	20%	19%	33%
6	36%	11%	23%	29%	33%	18%	20%	29%
Avr	***34%***	***18%***	***18%***	***30%***	***31%***	***18%***	***18%***	***33%***
Bulge size								
1	51%	9%	18%	21%	40%	16%	15%	29%
2	49%	11%	22%	19%	36%	18%	19%	27%
3	36%	15%	32%	17%	36%	21%	19%	24%
4	19%	12%	26%	43%	34%	15%	20%	31%
5	59%	1%	15%	25%	39%	15%	21%	25%
Avr	**43%**	**10%**	**23%**	**25%**	***37%***	***17%***	***19%***	***27%***

Table 4. Base content in terminal loops and bulges.

In this table, we calculated the base content of terminal loops and bulges. In the left side of the table, total percentages are calculated in all motifs found in Rfam alignments while on the right, the average percentages in the 23 compiled categories are shown. Calculating the average percentages reduces the effect of ribosomal RNA overrepresentation.

Discussion & Conclusion

While a lot of similitude can be found *Biochemical* and *Antisense* categories, differences between the typically highly structured *Biochemical* versus less structured *Antisense* abundant motifs support that these two groups show structural preferences for specific motifs, thus validating the elaboration of the two separate scores. In fact, they could potentially be used to help determine the function of newly discovered RNAs. When trying to use the scores that we computed to analyze newly discovered RNAs, it helped us to sort the new RNA in the *Antisense* or *Biochemical* groups (data not shown). However, in spite of statistical significance, the level of uncertainty associated with this “category assignment” makes it hard to use as a filter. For discoveries of novel RNA, we can think of using this scoring system to develop a filter that will improve current prediction tool, but future improvements including taxonomic data would likely be required for this to work. The two major groups *Biochemical* and *Antisense* could potentially be used to help determine the function of newly discovered RNAs. Indeed, following the partition of RNA categories into these groups, we found many differences between these two ensembles. When trying to use the scores that we determined for small RNA motifs to analyze newly discovered RNAs, it helped us to sort the new RNA in the *Antisense* or *Biochemical* groups (data not shown). In spite of statistical significance, the level of uncertainty associated with this “category assignment” makes it hard to use as a filter. Further study is required to have filters tailored to different types of RNAs and expand the two-score system.

However, the global analysis of Rfam data did led to interesting findings. We discovered that "A" and "U" nucleotides dominate single stranded RNA regions, whether they are bulges or loops. Since, to our knowledge, this fact was not reported in literature, we can only hypothesize about the reasons behind the abundance of A and U. Dominance of A and U may have evolved to avoid strong inter- or intra-molecular undesirable C-G base pairs in the folding process of RNA stems.

The data we report also suggests that some abundant internal loops especially in the 1X1 loops in *Biochemical* are probably stacking. Indeed, $5'$ C - $3'$ G and $5'$ U - $3'$ A internal loops are the most abundant in *Biochemical* supercategories. These are likely found at positions where non-canonical base pairs are observed in other sequences of the stockholm alignment. The occurrence of canonical base pairs at positions annotated as 1X1 internal loops is a good indication that bases are likely stacking to form a continuous stem. To some extent, this could be seen as an artifact of the Rfam alignment.

We found very large gaps between the most abundant and rare RNA structural features and it demonstrates that ncRNA has a preference to some structural motifs over other motifs that are rare. Different explanations are possible for this existing discrimination between motifs: thermodynamic stability as well as biological and evolutionary requirements. Past studies have rightfully highlighted the most frequent motifs (such as GNRA tetraloops) and many of these have been found to contribute to the stability of RNA structures. Highly stable motifs are also easier to crystallize or analyze through NMR, thus potentially causing an overrepresentation of these in available atomic resolution structures of RNAs. On the other hand, many motifs have not been noticed even though they are very abundant in RNA. Such is the case of the "UUUU" tetraloop which is found only 20 times in the PDB database, as per the September 2013 FRABASE update (121), as compared to the other top ten motifs which are found by hundreds and even thousands. The "AAAA" motif is also among the most abundant in both *Biochemical* and *Antisense* categories and is even less represented in PDBs (five times). Still, the overrepresentation of these two motifs in Rfam is indicative of some general usefulness for RNA function, whether it is for dynamics of the structure, interaction with A or U binding proteins like Hfq or functional base pairing with poly-A or poly-U RNAs, as the stabilizing effect of poly-Us for polyadenylated RNAs may suggest (122), even a higher instability permitting optimal turnover of the RNA may be selected for (113,123). Elucidation of the biological role(s) of these motifs will require further investigation, but will be important to unravel the functions of different types of basic RNA motifs.

In addition, when exploring correlation between abundance and stability, as predicted we found that abundant tetraloops tend to be more stable than rare ones. However, the correlation is not as clear as expected. Like we just mentioned, this is probably due to other factors influencing the observed frequency of RNA secondary structures. The correlation is more pronounced in *Biochemical* RNA categories, such as ribosomal RNA, where the abundant tetraloops are clearly more stable than the rarest. Whereas in other categories, especially in categories where primary sequence has a lot of importance, like miRNAs or snoRNAs, the relationship between the stability and abundance is weaker. A probable explanation could be that the function of these RNAs requires secondary structures with more flexibility and that the stability of the loop has less impact on the overall structure or rather than the other sequence requirements (complementarity to its target mRNA) are more important.

Contrary to abundant motifs, to our knowledge the rarest sequence combinations have not been the focus of any study. The higher GC% of rare motifs that we found is conceivably to prevent strong undesired base pairing. We also noticed that compared to the average loops, palindromic loops are rarer (i.e. loops that could potentially fold with themselves at the intermolecular level). This could potentially be explained by the fact that during transcription, nascent RNAs can be found in close proximity and can potentially interact with each other before they fold in their native hairpins. In the case of a palindromic loop, this could imply that two nascent RNAs could form a long duplex with perfect base complementarity from the 5′ to the 3′ end of the stems, including what was supposed to be the terminal loop if it had folded intramolecularly (see Figure 13). In other words, the stem formed by the intermolecular base pairs would be much stronger than the intramolecular stem. The fact that the abundance of palindromic sequences correlates in inverse fashion with the number of H-bonds of the potential intermolecular base pairs between the loops supports this trend. However, it is not easy to separate this correlation from the high GC% that we observed in rare loops.

Evidently, evolution increases representation of any generally favorable sequence combinations and would disfavor loops and bulges that are detrimental to RNA function. However, it can also lead to overrepresentation of some sequences for other reasons. There are a large number of pentaloops that closely resemble the GNRA consensus. In a specific case of a pentaloop of the GNR(N)A family, the common GAAAA loop was shown to adopt a GNRA-tetraloop fold, a feature that is central to the function of the RNA containing the stem-loop (124-126). While some of these loops, like GAUAA conserved in rRNA, may reflect a real function, it is likely that most of these are merely derivatives of the most common tetraloops, where the ancestral sequence had a one base insertion without any significant effect on fitness. This is somewhat verified by overrepresentation of pentaloops similar to other frequent tetraloops, namely UNCG and UUUU.

Protein binding sites are among the factors we can think of when considering selective pressure for (or against) some sequence combinations. This pressure could go both ways. For instance, an abundant protein specific for one RNA could select against the presence of its binding site in other RNAs because it would be titer the protein away from its functional binding site. Conversely, some proteins could also favor the presence of their binding sites when they provide more "generic" functions like stabilization, temporal control or localization. This could in part explain overrepresentation of AU bases in frequent loops and bulges since there are numerous AU-rich binding proteins, such as Hfq (127), AUF1(128), HuR (129), ELAV (130), etc. Then again, perhaps the fact single stranded regions tend to be more AU rich is the reason why many proteins bind these sites today. In some cases, evolution likely co-opted existing sequences for additional roles over time. Such might be the case of many "UUUU" tetraloops in bacteria for Hfq binding. It has recently been shown that the poly-U tail of Rho-independent terminators is important for Hfq binding (131). Since these stretches of Us are so common in bacteria, one can imagine that every now and then, mutations could convert the poly-U tail to a UUUU loop, a second terminator would provide this RNA with two poly-U binding sites for more efficient binding of Hfq.

Many of the proposed putative explanations of the observed frequencies rely on biological aspects that vary widely from species to the next. A more precise analysis is required to decipher links with function such as taking in account taxa. While there are clearly many criteria other than thermodynamic stability that govern the function and evolution of RNA structures, unraveling them will be a daunting task. This is complicated by the fact that there may very well be more than one explanation in many cases. New motifs and phenomenon were revealed that will require experimental approaches for a better understanding.

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Chapitre 4 Système de score pour l'évaluation de nouveaux candidats d'ARN non-codant

Mise en contexte

L'objectif principal de ce travail est l'élaboration d'un système de score basé sur l'abondance des motifs pour l'évaluation de nouveaux candidats d'ARN non-codant. À partir des tables de scores calculés pour les boucles terminales, les «bulges» et les boucles internes, nous avons conçu un programme, RNAscore, qui permet d'attribuer des scores globaux pour un alignement quelconque d'ARN.

Nous avons calculé les scores pour un échantillon d'alignements de Rfam de la version 10.1 (juin 2011) qui font partie de l'ensemble des données utilisées pour l'élaboration des scores. Ces ARN ont des fonctions confirmées et servent d'exemples de validation de RNAscore.

Par la suite, nous avons testé l'applicabilité de RNAscore sur différents contrôles. Comme contrôles positifs, nous avons choisis les nouvelles familles d'ARNnc ajoutées dans la version 11.0 de Rfam (Aout 2012) vu que ces ARN ne font pas partie des données de départ pour le calcul des scores d'abondance.

Nous avons testé plusieurs types de contrôles négatifs pour valider RNAscore comme filtre potentiel:

- des candidats d'ARN « fictifs » générés par CMfinder à partir de séquences codantes de protéines, intactes et/ou brouillées.
- des alignements de Rfam d'ARN connus dont la séquence est brouillée. Tout en provenant d'ARNnc, nous nous sommes assuré que la structure originale n'existe plus même si les séquences restent alignées.
- des motifs d'ARNnc qui ont été mutés provenant de nombreuses études expérimentales publiées.

- des ensembles aléatoires de séquences simulant des ARN hypothétiques.

4.1. RNAscore : Système de score

Les approches bioinformatiques utilisées pour la découverte de nouveaux ARN non-codants génèrent des milliers de candidats (61). Malgré l'avancement des logiciels et pipelines disponibles, il faut une étape de vérification manuelle de tous ces candidats afin d'identifier les plus intéressants. Cette sélection dépend de l'expertise de la personne qui analyse ces quantités importantes de données et nécessite beaucoup de temps. Un filtre capable de discriminer entre un ARN qui contient des motifs qu'on observe fréquemment dans Rfam et un ARN qui a plutôt des motifs rares pourrait accélérer cette étape de vérification. Les données sur l'abondance des motifs de structures secondaires peuvent être utiles pour développer un filtre afin d'accélérer l'étape de sélection des ARN qui méritent d'être étudiés davantage. Notre système de score est une tentative de développer un tel filtre afin d'évaluer des nouveaux candidats d'ARNnc en leur attribuant un score global basé sur leurs structures secondaires. Il est à préciser que l'objectif du travail n'est pas une évaluation de la qualité des alignements de Rfam ni des prédictions de structure secondaire.

Dans ce travail, un nouveau candidat est un alignement de séquences multiples d'ARN ayant une structure consensus et généré par un outil de recherche tel que CMfinder. Nous avons choisi CMfinder pour créer certains des contrôles utilisés pour tester notre système de score puisque c'est un outil de prédiction de motifs d'ARN qui a permis au cours des dernières années la découverte de nombreux ARNnc. Ce programme publié en 2005 prend au départ un ensemble de séquences qu'on suppose homologues et génère plusieurs possibilités d'alignements en détectant des motifs structuraux conservés. C'est un algorithme espérance-maximisation (« expectation maximization » EM) qui utilise un modèle de covariance (CM) pour décrire les motifs d'ARN, un modèle mixte fini pour décrire la distribution des motifs dans les séquences et un cadre EM pour faire la recherche dans l'espace motif. CMfinder présente une solution au problème de découverte de motifs lorsque les séquences sont peu ou très conservées, un problème qui affecte l'efficacité des méthodes de prédiction de structure basées sur l'analyse comparative de séquences. Les détails de l'algorithme sont disponibles dans (75).

4.1.1 Modification des scores :

Les tables de scores (voir annexe) pour les motifs individuels ont été utilisées afin d'attribuer un score global à un ARN donné constitué d'un alignement de séquences multiples. On évalue cet ARN en se basant sur l'ensemble de ses motifs structuraux (boucles terminales, boucles internes et « bulges »). Les scores ont été convertis pour en faciliter l'interprétation.

La valeur maximale (positive) est attribuée au motif le plus abondant et la valeur minimale (négative) est attribuée au motif le moins fréquent. Ces modifications donnent un intervalle de scores symétrique pour chaque motif. On peut voir un exemple dans la table 5.

bulge	Score original	Score converti
A	-0.412	0.28
U	-0.616	0.08
C	-0.668	0.02
G	-0.971	-0.28

Table 5. Superscores des « bulges » de taille 1 du groupe « Antisens ».
L'étendue (max - min)= 0.559**;** Le score converti = score - (max - étendue/2).

4.1.2. Q-score et Z-score

Pour une famille d'ARN ou un nouveau candidat d'ARN, tel qu'expliqué précédemment, l'alignement est compilé comme un ensemble de boucles terminales, de boucles internes et de « bulges ». Dans la perspective d'évaluer un ARN, nous lui attribuons un score global basé sur ses motifs de structures secondaires selon leurs scores d'abondance individuels. Pour chaque ARN ayant n motifs, on calcule deux scores :

- **Q-score** est le score global basé sur **les séquences des motifs**.

$$\textbf{Q-score} = \left[\sum_{i=1}^{n} \boldsymbol{score\ de\ séquence\ du\ motif_i} \Big/ \sum_{i=1}^{n} \boldsymbol{score_{max}\ motif_i} + \mathbf{1} \right] / \mathbf{2}$$

où i représente l'index du motif et le score_{max} est relatif au motif le plus abondant de même type et taille que le motif i. Par exemple, si le $i^{ème}$ motif est une boucle terminale «AAA » alors on additionne le score de séquence de cette boucle (0.74) à la somme $\sum_{i=1}^{n} \boldsymbol{score\ de\ séquence\ du\ motif_i}$. Le score$_{max}$ correspondant à cette boucle est celui de la boucle ayant le score le plus élevé de toutes les boucles de taille 3 (dans ce cas il sagit du score la boucle « CAU » = 0.96).

- Le Q-score est exprimé en ratio de la somme des scores des motifs individuels par rapport à la somme des scores maximaux. Ce score s'exprime sur une échelle de 0 à 1 (en additionnant 1 et divisant par 2). Par conséquent, un ARN contenant seulement des motifs parmi les plus abondants aura tendance à avoir un score proche de 1 alors que le score d'un ARN qui n'aurait que des motifs rares tendra vers 0.
- On calcule la somme des scores uniquement pour les motifs que l'on nomme motifs scorés (voir l'encadré qui suit pour la liste des motifs scorés). Le nombre de motifs scorés est inférieur ou égal au nombre total de motifs.

Les motifs scorés :
- Les boucles terminales de taille 2 à 5
- les boucles internes de taille 1x1, 1x2, 1x3, 2x1, 2x2, et 3x1
- et les « bulges » de taille 1 à 4 nt.

- **Z-score** est le score basé uniquement sur les tailles des motifs.

$$\textbf{Z-score} = \left[\sum_{i=1}^{n} \boldsymbol{score\ de\ taille\ du\ motif_i} \Big/ \sum_{i=1}^{n} \boldsymbol{score_{max}\ motif_i} + \mathbf{1} \right] / \mathbf{2}$$

où i représente l'index du motif et le score$_{max}$ est relatif au motif le plus abondant de même type que le motif i. La séquence du motif n'est pas importante pour le calcul du Z-score. En reprenant l'exemple précédent de la boucle « AAA », le score de taille correspondant aux boucles de taille 3 (1.79) est additionné à la somme $\sum_{i=1}^{n} \boldsymbol{score\ de\ taille\ du\ motif_i}$ tandis que le score$_{max}$ est celui des boucles de taille 4 (2.28) étant le type de boucles le plus abondant en terme de taille.

- Tous les motifs ont un score basé sur la taille dont on calcule la somme.

- Le Z-score est un ratio de la somme totale des scores par rapport à la somme des scores max. Tout comme le Q-score, le Z-score se situe aussi sur une échelle de 0 à 1.

Le calcul de RNAscore (Q-score et Z-score) passe par les étapes suivantes :

On commence par un fichier d'alignement (une famille de Rfam ou un résultat de CMfinder) qui est traité par trois scripts PERL:

- Rfam parser4.pl : script qui débloque l'alignement de Rfam pour que chaque séquence soit sur une ligne continue
- serial_sec_struc.pl : script qui décode la structure
- Stem-extractor-simple7.pl : script qui décortique l'alignement pour en extraire toutes les tiges-boucles et les motifs structuraux (boucles et « bulges »).

Le fichier « output » de Stem-extractor contient toutes les informations sur les motifs présents dans les tiges-boucles de l'alignement. J'ai développé un programme JAVA qui lit ce fichier, en extrait les informations sur toutes les structures secondaires et calcule les scores.

Fichier « output » de Stem-extractor sert de fichier « input » pour le programme JAVA RNAscore qui effectue les tâches suivantes:

- extraire les boucles terminales, les « bulges » et les boucles internes
- calculer le nombre de séquences, le nombre de motifs.
- calculer Q-score, Z-score

Cette première version de RNAscore basée sur les scores des six supercatégories a été raffinée par la suite pour calculer les scores Q-score et Z-score spécifiques aux deux groupes « activité biochimique » et « Antisens » (voir la section matériels et méthodes du chapitre 3).

4.1.3. RNAscore spécifique aux groupes « activité biochimique » et « Antisens »

Nous avons utilisé les scores de motifs spécifiques aux groupes « activité biochimique » et « Antisens » afin de développer une version RNAscore pour chaque groupe.

Nous avons donc trois types de scores: RNAscore global (23 catégories), RNAscore « activité biochimique » (*biochemical*) et RNAscore «antisens » (*antisense*). Nous avons calculé les Q-scores et Z-scores avec les trois versions de RNAscore pour tous les contrôles afin d'explorer s'il existe un avantage à utiliser les scores spécifiques aux groupes dans la détection d'ARN appartenant à un groupe donné.

On montre ci-dessous un exemple d'un alignement de Rfam du riboswitch SAM/SAH, un ARN utilisé dans la validation des scores (section 4.2). On peut voir la structure et la séquence consensus à la fin de l'alignement.

Alignement complet du riboswitch SAM/SAH

```
# STOCKHOLM 1.0
#=GF AC   RF01727
#=GF ID   SAM-SAH
#=GF DE   SAM/SAH riboswitch
#=GF AU   Yang J, Weinberg Z// (quelques lignes ont été coupées ici)
#=GF SQ   88

ABXF01000008.1/119484-119533             UACCUGCCACAACGGCUUCCUGGCGUGGCGGG.CUGAACCUC...AAUGGAGCA
AATR01000003.1/91067-91114               UAAGGCUUACAACGGCUACCUGAAGUAAG.UU.GACAUAAA....AACGGAGCA
ACCW01000016.1/156792-156744             CGCCUGUCACAACGGCUUCCUGACGUGAC.AG.GGAAAUCUU...AAUGGAGCA
ABXE01000008.1/209807-209759             AGACUGCCACAACGGCUUCCUGACGUGGU.GG.AAAAAUCUU...ACUGGAGCA
AAXZ01000012.1/36217-36265               UGUCCCCCUCAACGGCUUCCUGACGAGGC.GG.GCUUAACAA...AACGGAGCA
ACNW01000091.1/52818-52770               UUACCGUCACAACGGCUUCCUGGCGUGAU.GG.CUCGGUAUU...AAUGGAGCG
CP000830.1/1046963-1046915               CCGACGCUGCAACGGCUUCCUGGCGCAGCGGU.CGCUAUUC....AAUGGAGCA
CP000264.1/678143-678190                 ACUCCUCCACAACGGCUUCCUGACGUGGG.GG.AUUAUUUG....AAUGGAGCA
CP002224.1/728198-728247                 CAUCCCCCACAACGGCUUCCUGACGUGGC.GG.GUAAGAUUG..AAAUGGAGCA
CP002018.1/323815-323864                 CAUCCCCCACAACGGCUUCCUGACGUGGC.GG.GUAAGAUUG..AAAUGGAGCA
AAMS01000003.1/12007-12055               GUUCUGUCACAACGGCUUCCUGGCGUGAC.AG.GUUUUUCAU...AUCGGAGCA
AAMT01000035.1/1434-1386                 CAACCGCCACAACGGCUUCCUGACGUGGC.GG.GGAUAUCAU...AACGGAGCA
ABID01000011.1/17084-17036               AGAGCAUCACAACGGCUUCCUGACGUGGU.GC.GUAAUUUUU...AUUGGAGCA
AAOT01000020.1/3283-3235                 UCGCUGUCACAACGGCUUCCUGGCGUGGC.GG.UAAGAUCCC...AAUGGAGCG
AFPM01000085.1/701-750                   UCGCCGCCCCAACGGCUUCCUGACGGGGCAGG.UCUGAAAAU...ACCGGAGCA
ABSH01000031.1/84911-84863               ACUCGUCCGCAACGGCUUCCUGACGCGGAUCG.ACAUUUAA....ACUGGAGCA
ABSK01000009.1/52599-52551               UUUUAUCCACAACGGCUUCCUGAAGUGGA.UC.GACAUUUAA...ACUGGAGCA
AEPN01000002.1/106306-106354             UGACCGUCACAACGGCUUCCUGGCGUGAC.GG.CGUCAUUUU...AACGGAGCA
CP000489.1/1874599-1874647               UGACCGCCACAACGGCUUCCUGGCGUGGC.GG.CGUCAUUUC...AACGGAGCA
CP002897.1/756598-756645                 UGACCGUCACAACGGCUUCCUGGCGUGGC.GG.CGUCAUUC....AACGGAGCA
AATQ01000051.1/20133-20085               UCCCCGUCACAACGGCUUCCUGGCGUGAC.GG.CUGGUACCC...AAUGGAGCA
AFCF01000062.1/162358-162406             UACCUGUCACAACGGCUUCCUGGCGUGGCAAG.GCUAAACC....AAUGGAGCA
ABIF01000007.1/192066-192114             UUACUGCCACAACGGCUUCCUGGCGUGGC.AG.GCUAAACCC...AACGGAGCA
ABIE01000005.1/70619-70571               UUACUGCCACAACGGCUUCCUGGCGUGGC.AG.GCUAAACCC...AACGGAGCA
AFER01000002.1/940996-940947             CAACCGUCACAACGGCUUCCUGGCGUGAC.GG.GGUUAACCC..CAACGGAGCA
CP001312.1/1192313-1192361               UCACCACUCCAACGGCUUCCUGGCGGGGU.GG.GAACACAUC...AAUGGAGCA
FN552708.1/146-195                       CAACCGUCACAACGGCUUCCUGGCGUGAC.GG.GGUUAACCC..CAACGGAGCA
ACYY01000001.1/82076-82029               CGACCGUCACAACGGCUUCCUGGCGUGGC.GG.AAUUUCCC....AACGGAGCA
CP000578.1/343169-343120                 CAACCGUCACAACGGCUUCCUGGCGUGAC.GG.GGUUAACCC..CAACGGAGCA
CP001151.1/703619-703570                 CAACCGUCACAACGGCUUCCUGGCGUGAC.GG.GGUUAACCC..CAACGGAGCA
CP000662.1/776419-776468                 CAACCGUCACAACGGCUUCCUGGCGUGGC.GG.GGAUAACCC..CAACGGAGCA
CP000144.1/688624-688575                 CAACCGUCACAACGGCUUCCUGGCGUGAC.GG.GGUUAACCC..CAACGGAGCA
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AAYB01000002.1/503668-503715            AUUCUGUCACAACGGCUUCCUGACGUGGC.AG.AGAUUUUU....AAUGGAGCA
ABXS01000051.1/24818-24865              AAUCUGCCACAACGGCUUCCUGACGUGGC.UA.UUUAAUCU....AUUGGAGCA
AAYC01000001.1/142050-142098            UACCUGUCACAACGGCUUCCUGGCGUGACGAG.GUGACCUC....AGUGGAGCA
AANB01000001.1/292633-292681            GUCCUCUCACAACGGCUUCCUGACGUGACGAG.GUUAACCC....AAUGGAGCA
CP000362.1/3781791-3781742              AGCGAACCACAACGGCUUCCUGACGUGGU.UC.UUCAUUGGC..GAUUGGAGCG
ABCR01000003.1/393478-393430            AACCCGUCACAACGGCUUCCUGGCGUGAC.GG.CUGACAUAC...AAUGGAGCA
CP002623.1/543970-544019                AGCGAACCACAACGGCUUCCUGACGUGGU.UC.UUCAUUGGC..GAUUGGAGCG
AAMV01000006.1/34838-34885              AAUCCCCCACAACGGCUUCCUGGCGUGGC.GG.UGACAUUC....AAUGGAGCA
ABCL01000003.1/82568-82521              AAUCCCCCACAACGGCUUCCUGGCGUGGC.GG.UGACAUCA....AAUGGAGCA
AALY01000001.1/139779-139732            UCCCCGUCACAACGGCUUCCUGGCGUGGC.GG.AUGACCCU....AAUGGAGCG
ACNZ01000068.1/12000-12049              AUGCUGCCACAACGGCUUCCUGGCGUGGC.GG.AUAUUCAUU..CAAUGGAGCA
ABXM01000011.1/241752-241702            UUACUGCCACAACGGCUUCCUGGCGUGGCAGG.CUGAACCCC..CAACGGAGCA
CP000377.1/211359-211407                AUGCCGCCACAACGGCUUCCUGGCGUGGC.GG.AUCUCAUCC...AAUGGAGCA
CP000032.1/9372-9422                    GACCUGCCACAACGGCUUCCUGGCGUGGCGAG.GGAAACCUU..CAAUGGAGCA
ACNX01000023.1/85945-85896              UGCCCGUCACAACGGCUUCCUGGCGUGAC.GG.GGAAAAUCU..UAAUGGAGCG
AEYW01000003.1/121851-121899            UGCCCUUCACAACGGCUUCCUGACGUGAU.GG.GAAAAUCUU...AAUGGAGCA
AAYA01000008.1/121966-121918            ACCCCGUCACAACGGCUUCCUGGCGUGAC.GG.AGAAACCCG...AAUGGAGCA
AALV01000001.1/126167-126120            AAUCGGCCACAACGGCUUCCUGACGUGGC.UA.AGAAAUCU....AUUGGAGCA
AALZ01000001.1/70323-70276              AAUCGGCCACAACGGCUUCCUGACGUGGC.UA.AGAAAUCU....AUUGGAGCA
ACOA01000003.1/649118-649068            UAAUUGCCACAACGGCUUCCUGACGUGGCAGAGCAGUAGAA...UAUUGGAGCA
AAFY01026626.1/203-251                  GAAUUGCUACAACGGCUUCCUGACGUGGC.GA.UCUAUAUGA...ACUGGAGCA
AAFZ01022139.1/317-268                  AUGCCGCCCCAACGGCUUCCUGACGGGGC.GG.AUUCACUUU..AAAUGGAGCA
AACY020533904.1/2663-2615               GCGACCCCACAACGGCUUCCUGGCGUGGG.GA.CACACACAU...AAUGGAGCA
AACY022220959.1/246-198                 GUGCUGUCACAACGGCUUCCUGGCGUGGC.GG.CGAAAACCU...AAUGGAGCA
AACY022262901.1/198-151                 ACAUGUACGCAACGGCUUCCUGGCGCGUG.AA.CCGUAAUU....AUUGGAGCA
ABMI01085512.1/67-105                   ...CCGUCACAACGGCUUCCUGGCGUGGC.GG.CAGACAUUU...AA.......
ADIF01003913.1/410-361                  AAUGACCCACAACGGCUUCCUGACGUGGC.GC.ACAUAAGAA..AAUUGGAGCA
AACY020308077.1/1017-1066               GCGCUGCCACAACGGCUUCCUGGCGUGGC.GG.UCUGACAGU..CAAUGGAGCA
AACY021040428.1/508-461                 UAUUGCACGCAACGGCUUCCUGACGCGUG.AG.UUUUAAUU....AUCGGAGCA
AACY020064664.1/1378-1332               UCCUAGCUGCAACGGCUUCCUGGCGCAGCUUA.CAUUUU......AUUGGAGCA
AACY020255086.1/785-738                 UAUUGCACGCAACGGCUUCCUGACGCGUG.AG.UUUUAAUU....AUCGGAGCA
AACY020525991.1/1534-1483               CCGCUGUCACAACGGCUUCCUGGCGUGGC.GG.CUAAACCAUUUUAUCGGAGCA
ABMI01114022.1/24-74                    CCAUGCCCACAACGGCUUCCUGGCGUGGGUCA.CCUGUAUUC..CAAUGGAGCG
AACY023759949.1/393-346                 UAUUGCACGCAACGGCUUCCUGACGCGUG.AG.UUGUAAUU....AUCGGAGCA
AACY021789724.1/224-271                 UGAUGCACGCAACGGCUUCCUGACGCGUG.AG.AUUAAAUU....AUUGGAGCA
ABMI01039991.1/54-6                     AUCCCGUCACAACGGCUUCCUGGCGUGGC.GG.CAGACAUUU...AAUGGAGCA
AACY020589009.1/251-203                 ACGUCGUCACAACGGCUUCCUGGCGUGAC.GA.UACACAUCU...AAUGGAGCA
ACQI01011682.1/327-278                  AUCCUGCCACAACGGCUUCCUGGCGUGGU.GG.GAAUAACCC..CAAUGGAGCG
AACY022370156.1/216-170                 UCCUAGCUGCAACGGCUUCCUGGCGCAGCUUA.CAUUUU......AUUGGAGCA
AACY020081998.1/987-1034                AGAGACACGCAACGGCUUCCUGACGCGUG.AA.AUUAAAUU....AUUGGAGCA
AACY023873338.1/88-135                  UAUAGCACGCAACGGCUUCCUGACGCGUG.AG.CUUUAAUU....AUCGGAGCA
ABLU01142977.1/20-69                    CGACCGUCACAACGGCUUCCUGGCGUGGC.GG.AAUUUUUUU..CAAUGGAGCA
AACY020245805.1/1080-1127               UCCUACACGCAACGGCUUCCUGACGCGUG.AG.GUGUAAUC....AUUGGAGCA
ABPS01005437.1/199-153                  GGUCCGCCACAACGGCUUCCUGGCGUGGC.GG.CGUAACC.....AAUGGAGCA
ABPS01005991.1/96-143                   CGACCGCCACAACGGCUUCCUGGCGUGGC.GG.CGUAAAUC....AAUGGAGCG
AACY021083615.1/454-500                 CCGUAGCUGCAACGGCUUCCUGGCGCAGCUUA.CAUUUU......AUUGGAGCA
ABMI01051029.1/54-6                     AUCCCGUCACAACGGCUUCCUGGCGUGGC.GG.CAGACAUUU...AAUGGAGCA
AACY022514310.1/232-279                 AAUGUUCUACAACGGCUUCCUGACGUAGG.GC.AAUUCUUU....UUUGGAGCA
AACY020145469.1/1024-977                UGUGGCACGCAACGGCUUCCUGACGCGUG.AG.AUAAAAUU....AUUGGAGCA
AACY020253271.1/246-293                 AAUUGCACGCAACGGCUUCCUGACGCGUG.AG.UUUUAAUU....AUCGGAGCA
AACY020522644.1/2673-2625               AUCUCGCCACAACGGCUUCCUGACGUGGC.GG.CAGAACCCU...AAUGGAGCA
AACY023829178.1/189-238                 GCGCUGCCACAACGGCUUCCUGGCGUGGC.GG.UCUGACAGU..CAAUGGAGCA
AACY021643013.1/430-383                 UGUGGCACGCAACGGCUUCCUGACGCGUG.AG.AUUGAAUU....AUUGGAGCA
AACY020526688.1/2154-2202               CUCCUGUCACAACGGCUUCCUGGCGUGGC.GG.GCAACAUCC...AAUGGAGCA
AACY022603193.1/622-575                 UGAAACUUAUAACGGCUACCUGAAGUAAG.UU.UUUUUAUA....AACGGAGCA
AACY020223500.1/3303-3256               UAUUGCACGCAACGGCUUCCUGACGCGUG.AG.UUUUAAUU....AUCGGAGCA
#=GC SS_cons                            ...<<<<<<<..<<<....>>>..>>>>>.>>......................
#=GC RF                                 aaaccgcCACAACGGCUUCCUGaCGUGgc.gg.auuaaauau...AaUGGAGCA
```

Tous les motifs de cet alignement sont extraits afin de calculer les scores. Les données de sorties de RNAscore pour SAM/SAH sont présentés dans ce qui suit. Dans cet exemple tous les motifs sont scorés avec Q-score.

Résultats RNAscore pou riboswitch SAM/SAH :

```
Total number of sequences: 88
Loops: 88
Bulges: 14
Internal loops: 88
Number of scored motifs = 190
Total Number of motifs = 190

RNAscore
Sum Q-Score = 9.39              Sum Q-Score_max = 246.52        Q-Score = 0.5190452
Sum Z-Score =  344.1793         Sum Z-Score_max = 407.53998     Z-Score = 0.92226446

RNAscore biochemical
Sum Q-Score = -10.579998        Sum Q-Score_max = 312.05948     Q-Score = 0.4830481
Sum Z-Score = 345.94058         Sum Z-Score_max = 412.82        Z-Score = 0.9189969

RNAscore antisense
Sum Q-Score = -25.420027        Sum Q-Score_max = 239.7595      Q-Score = 0.4469885
Sum Z-Score = 334.4995          Sum Z-Score_max = 401.38        Z-Score = 0.9166868

Loops: 88 [CUUC, CUAC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC,
CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC,
CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC,
CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC,
CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC,
CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUUC, CUAC, CUUC]

Bulges: 14 [G, G, A, U, A, G, G, A, G, A, U, U, U, U]

Internal loops: 88 [AA-GC, AA-AA, AA-AC, AA-AC, AA-AC, AA-GC, AA-GC, AA-AC, AA-AC, AA-AC, AA-GC, AA-AC,
AA-AC, AA-GC, AA-AC, AA-AC, AA-AA, AA-GC, AA-GC, AA-GC, AA-GC, AA-GC, AA-GC, AA-GC, AA-GC, AA-GC, AA-
GC, AA-GC, AA-GC, AA-GC, AA-GC, AA-GC, AA-AC, AA-AC, AA-GC, AA-AC, AA-AC, AA-GC, AA-AC, AA-GC, AA-GC,
AA-GC, AA-GC, AA-GC, AA-GC, AA-GC, AA-GC, AA-AC, AA-GC, AA-AC, AA-AC, AA-AC, AA-AC, AA-AC, AA-GC, AA-
GC, AA-GC, AA-GC, AA-AC, AA-GC, AA-AC, AA-GC, AA-AC, AA-GC, AA-GC, AA-AC, AA-AC, AA-GC, AA-GC, AA-GC,
AA-GC, AA-AC, AA-AC, AA-GC, AA-AC, AA-GC, AA-GC, AA-GC, AA-GC, AA-AC, AA-AC, AA-AC, AA-AC, AA-GC, AA-
AC, AA-GC, AA-AA, AA-AC]
```

Exemple de calcul du Q-score pour la version RNAscore global :
SAM/SAH contient : 86 boucles « CUUC » 2 boucles « CUAC »,
5 *bulges* « G », 4 *bulges* « A », 5 *bulges* « U »,
50 boucles internes « AA-GC », 3 boucles internes AA-AA et 35 boucles internes AA-AC.

Sum Q-score = 86 x Q-score (boucle CUUC) + 2 x Q-score (boucle CUAC) +
5 x Q-score (*bulge* G) + 4 x Q-score (*bulge* A) + 5 x Q-score (*bulge* U) +
50 x Q-score (boucle interne AA-GC) + 3 x Q-score (boucle interne AA-AA) + 35 x Q-score (boucle interne AA-AC)
= 86 x (-0.31) + 2 x (-0.83) +5 x (-0.26) + 4 x (0.26) + 5 x (0.08) + 50 x (0.32) + 3 x (0.89) + 35 x (0.54)
= 9.39

Sum Q-score_max = 88 x Q-score_max (boucle de taille 4) + 14 x Q-score_max (*bulge* de taille 1) +
88 x Q-score_max (boucle interne de taille 2X2)
=88 x (1.5) +14 x (0.26) + 88 x (1.26)
=246.52

Q-score = (Sum Q-score/Sum Q-score_max +1)/2
=(9.39/246.52+1)/2
=**0.5190452**

4.2. Validation des scores

Nous avons commencé par tester RNAscore sur quelques alignements de Rfam 10.0, c'est-à-dire un échantillon de l'ensemble de données utilisé pour l'élaboration du système de scores. Les scores sont calculés selon les trois versions de RNAscore comme expliqué dans la section précédente. En d'autres mots nous avons un Q-score et un Z-score pour RNAscore global, RNAscore « Activité biochimique » et RNAscore « Antisens ». Nous calculons aussi la différence de score dQ et dZ. dQ est la différence [Q-score « Activité biochimique » moins Q-score « Antisens »] alors que dZ est la différence [Z-score « Activité biochimique » moins Z-score « Antisens »]. Nous avons calculé dQ et dZ pour examiner si ces différences sont significatives et si les versions RNAscore spécifiques à chaque groupe permettaient potentiellement de repérer une appartenance (ressemblance) à un groupe plus qu'à un autre. La table 6 montre les résultats d'un échantillon d'ARN qui sont connus.

Les moyennes des Q-scores de cet échantillon pour les trois versions de RNAscore ne montrent pas une très grande différence (0.54, 0.56 et 0.51) de même pour les moyennes des Z-scores (0.85, 0.85 et 0.86). La moyenne de dQ est de 0.05 et celle de dZ est -0.02. Considérant les écarts-types, on ne peut confirmer qu'il y a une réelle différence entre les versions de RNAscore. Rappelons que ces résultats ont été obtenus dans une perspective d'exploration plutôt qu'une validation puisque l'échantillon n'est pas très grand et provient des données de départ des scores.

Rfam ID	Clan Rfam	Nom de l'ARN	RnaScore		*Biochemical* RnaScore		*Antisense* RnaScore				Nb de séq.	Nb. motifs	
			Q	Z	Q	Z	Q	Z	dQ	dZ		Scorés	Total
RF00001	Gene; rRNA	5S	0.58	0.91	0.60	0.91	0.56	0.90	0.04	0.01	712	2895	3630
RF00037	Cis-reg	IRE_I	0.56	0.97	0.59	0.96	0.55	0.99	0.04	-0.03	3104	12460	12470
RF00057	Gene;sRNA	RyhB	0.51	0.83	0.47	0.82	0.57	0.83	-0.10	-0.01	958	1617	3825
RF00118	Gene; sRNA	rydB	0.47	0.88	0.53	0.85	0.29	0.92	0.24	-0.07	451	919	1370
RF00167	Cis-reg; riboswitch	Purine riboswitch	0.42	0.89	0.42	0.89	0.43	0.88	-0.01	0.01	1244	54	2517
RF00168	Cis-reg; riboswitch	Lysine riboswitch	0.57	0.74	0.62	0.73	0.49	0.75	0.13	-0.02	47	77	250
RF01517	Cis-reg	iscRS	0.57	0.90	0.55	0.89	0.56	0.92	-0.01	-0.03	435	876	2170
RF01688	Cis-reg	Actino-pnp	0.45	0.79	0.46	0.77	0.45	0.83	0.01	-0.06	392	614	850
RF01727	Cis-reg; riboswitch	SAM/SAH	0.52	0.92	0.48	0.92	0.45	0.92	0.04	0.00	88	190	190
RF01734	Cis-reg	crcB	0.53	0.55	0.56	0.55	0.51	0.53	0.05	0.02	1267	765	2543
RF01739	Cis-reg	glnA	0.69	0.91	0.71	0.90	0.68	0.91	0.02	-0.01	1434	1847	2869
RF01745	Cis-reg	manA RNA	0.47	0.79	0.54	0.78	0.39	0.79	0.15	-0.01	306	605	2282
RF01804	Cis-reg; thermoregulator	Lambda phage CIII thermoregulator element	0.48	0.96	0.55	0.96	0.52	0.94	0.03	0.02	183	731	731
RF01830	GENE	StyR-44	0.74	0.81	0.75	0.81	0.70	0.81	0.05	-0.01	931	3519	5388
RF01940	Gene; miRNA	hvt-mir-H	0.60	0.84	0.60	0.81	0.34	0.89	0.26	-0.08	12	12	24
RF02028	Gene; miRNA	mir-1827	0.53	0.97	0.51	0.97	0.62	0.97	-0.12	0.01	41	250	250
		Moyenne	0.54	0.85	0.56	0.85	0.51	0.86	0.05	-0.02			
		Écart-type	0.09	0.11	0.09	0.11	0.11	0.11	0.10	0.03			

Table 6. Application de RNAscore sur des ARNnc de Rfam 10.0.

RNAscore est le score global avant la répartition en deux groupes « Activité biochimique » et « Antisens ». La colonne Q désigne le score relatif à la séquence des motifs scorés alors que la colonne Z représente le score basé uniquement sur la taille de tous les motifs de l'ARN en question. dQ et dZ sont la différence du score « Activité biochimique » moins le score « Antisens » pour les scores Q et Z respectivement. Les Q-scores en bleu sont pour les ARN qui ont un Q-score plus élevé pour RNAscore activité biochimique alors que le rouge désigne le Q-score Antisens qui est plus élevé.

4.2.1 Application de RNAscore sur les nouvelles familles de Rfam 11.0

Lors de la création de la base de données RNAstem et du système de scores, nous avons compilé toutes les données de Rfam 10.0 qui était la version disponible au moment. Plus tard, Rfam a publié une mise à jour: la version 11.0 avec des nouvelles familles d'ARNnc ajoutées. Nous avons testé RNAscore sur ces nouveaux alignements qui servent de contrôles positifs puisque ce sont de vrais ARNnc et qu'ils ne faisaient pas partis de l'ensemble de données de départ. Nous avons sélectionné 103 ARN parmi les nouvelles familles de la version 11.0 de Rfam en plus de l'ARN Czc (communication personnelle par Zasha Weinberg et Ronald R. Breaker) qui est un nouvel ARN non-soumis à Rfam lors de l'analyse effectuée. Les résultats de RNAscore sont présentés dans la table 7 qui suit.

Deux de ces contrôles positifs, OrzO-P et FTX-1, n'avaient pas de motifs scorés ce qui ne permet pas de calculer le Q-score (ils ont un Z-score dû à la présence de motifs dont la taille dépasse celle des motifs scorés). Pour les 104 nouveaux ARNnc, les Q-scores moyens calculés selon les trois versions de RNAscore ne diffèrent pas beaucoup de celui des contrôles de validation (0.53, 0.51 et 0.55 pour RNAscore global, RNAscore « Activité biochimique » et RNAscore « Antisens » respectivement), mais on note un écart-type plus grand. L'écart entre les moyennes de Z-scores est encore plus petit (0.83, 0.82, 0.84). Ces résultats, ainsi que les résultats de l'échantillon de validation de la section précédente, situent la moyenne du Q-score pour des les ARN de Rfam environ au milieu de l'intervalle des valeurs de scores possibles (0 à 1) soit 0.5. Considérant l'écart-type, il est nécessaire de comparer les scores des contrôles positifs avec ceux des contrôles négatifs afin de déterminer si les scores discriminent entre un vrai et un faux ARN. Nous présentons les résultats de RNAscore sur deux types de contrôles négatifs dans les sections qui suivent.

Rfam ID	**Clan Rfam**	**Nom de l'ARN**	**RnaScore**		***Biochemical* RnaScore**		***Antisense* RnaScore**				**Nb de séq.**	**Nb. motifs**	
			Q	**Z**	**Q**	**Z**	**Q**	**Z**	**dQ**	**dZ**		**Scorés**	**Total**
-	*(ARNnc non-soumis à Rfam)*	Czc	0.55	0.85	0.56	0.83	0.56	0.88	**0.00**	-0.04	628	1685	2452
RF02032	Gene	GOLLD	0.58	0.78	**0.64**	0.76	0.46	0.80	**0.18**	-0.03	80	416	857
RF02033	Gene	HEARO	0.55	0.83	**0.57**	0.81	0.55	0.85	**0.02**	-0.03	458	1408	2657
RF02034	Gene	IMES-1	0.57	0.64	0.51	0.63	**0.60**	0.66	**-0.09**	-0.03	187	7	860
RF02035	Gene	IMES-2	0.76	0.86	**0.83**	0.85	0.65	0.88	**0.18**	-0.03	446	1645	2519
RF02036	Gene	IMES-3	0.77	0.85	**0.78**	0.85	0.74	0.83	**0.04**	0.03	37	194	265
RF02037	Gene	IMES-4	0.99	0.85	**0.99**	0.82	0.94	0.90	**0.06**	-0.07	32	32	96
RF02040	Gene; lncRNA	HOTTIP_1	0.45	0.92	**0.50**	0.91	0.46	0.91	**0.04**	0.00	50	100	100
RF02041	Gene; lncRNA	HOTTIP_2	0.61	0.82	**0.60**	0.80	0.51	0.84	**0.09**	-0.04	131	519	745
RF02042	Gene; lncRNA	HOTTIP_3	0.54	0.86	**0.54**	0.84	0.52	0.88	**0.02**	-0.04	74	528	995
RF02043	Gene; lncRNA	HOTTIP_4	0.39	0.90	0.36	0.89	**0.39**	0.93	**-0.03**	-0.04	73	375	486
RF02044	Gene; lncRNA	CDKN2B-AS_2	0.42	0.85	**0.45**	0.85	0.36	0.83	**0.10**	0.02	44	129	132
RF02045	Gene; lncRNA	CDKN2B-AS_3	0.62	0.71	0.44	0.67	**0.74**	0.79	**-0.30**	-0.11	63	64	191
RF02046	Gene; lncRNA	Sphinx_1	0.42	0.84	0.45	0.83	0.45	0.86	**0.00**	-0.03	149	296	743
RF02047	Gene; lncRNA	Sphinx_2	0.50	0.70	0.46	0.70	**0.58**	0.69	**-0.13**	0.01	244	483	1454
RF02048	Gene	STnc30	0.68	0.96	0.59	0.96	**0.79**	0.94	**-0.20**	0.02	99	495	594
RF02049	Gene; sRNA	STnc460	0.49	0.88	**0.52**	0.87	0.51	0.88	**0.02**	-0.01	16	130	161
RF02053	Gene; sRNA	STnc430	0.67	0.76	0.65	0.76	**0.72**	0.73	**-0.08**	0.04	424	1004	1877
RF02057	Gene; sRNA	STnc40	0.44	0.93	**0.48**	0.93	0.47	0.91	**0.01**	0.02	431	1298	1298
RF02058	Gene	STnc400	0.37	0.92	0.38	0.92	**0.46**	0.91	**-0.08**	0.01	38	82	117
RF02061	Gene; miRNA	mir-301	0.50	0.86	0.49	0.85	**0.50**	0.88	**-0.01**	-0.03	171	217	343
RF02073	Gene; sRNA	STnc260	0.74	0.85	**0.71**	0.84	0.63	0.85	**0.08**	-0.01	104	209	521
RF02077	Gene; sRNA	STnc220	0.33	0.92	0.24	0.88	**0.38**	1.00	**-0.14**	-0.12	96	192	192
RF02078	Gene; sRNA	STnc210	0.78	0.69	0.62	0.70	**0.91**	0.67	**-0.30**	0.03	107	103	525
RF02079	Gene; sRNA	STnc180	0.50	0.78	0.46	0.77	**0.51**	0.78	**-0.05**	-0.01	420	1598	2942
RF02081	Gene; sRNA	STnc550	0.47	0.82	0.43	0.81	**0.54**	0.82	**-0.11**	-0.01	471	2588	4437
RF02082	Gene; sRNA	STnc540	0.67	0.59	0.61	0.58	**0.72**	0.60	**-0.11**	-0.03	367	570	1296
RF02083	Gene; antitoxin	OrzO-P	-	0.89	-	0.88	-	0.87	-	0.01	372	0	744
RF02084	Gene	STnc130	0.17	0.96	**0.29**	0.96	0.20	0.94	**0.09**	0.02	443	446	893
RF02088	Gene; sRNA	STnc510	0.52	0.89	0.53	0.89	0.53	0.89	**0.00**	0.00	118	1667	2710
RF02089	Gene; lncRNA	CLRN1-AS1	0.91	0.93	**0.92**	0.92	0.87	0.93	**0.05**	0.00	55	55	110
RF02090	Gene; lncRNA	DAOA-AS1_1	0.46	0.69	0.44	0.69	**0.60**	0.68	**-0.17**	0.01	66	64	199
RF02091	Gene; lncRNA	DAOA-AS1_2	0.61	0.75	**0.63**	0.73	0.50	0.78	**0.13**	-0.04	95	123	477
RF02095	Gene; miRNA	mir-2985-2	0.46	0.70	**0.44**	0.71	0.43	0.67	**0.01**	0.03	302	290	613
RF02096	Gene; miRNA	mir-2973	0.50	0.78	0.42	0.79	**0.49**	0.75	**-0.07**	0.04	769	178	1698
RF02097	Gene; miRNA	mir-1662	0.40	0.82	0.28	0.79	**0.60**	0.88	**-0.32**	-0.08	7	7	14

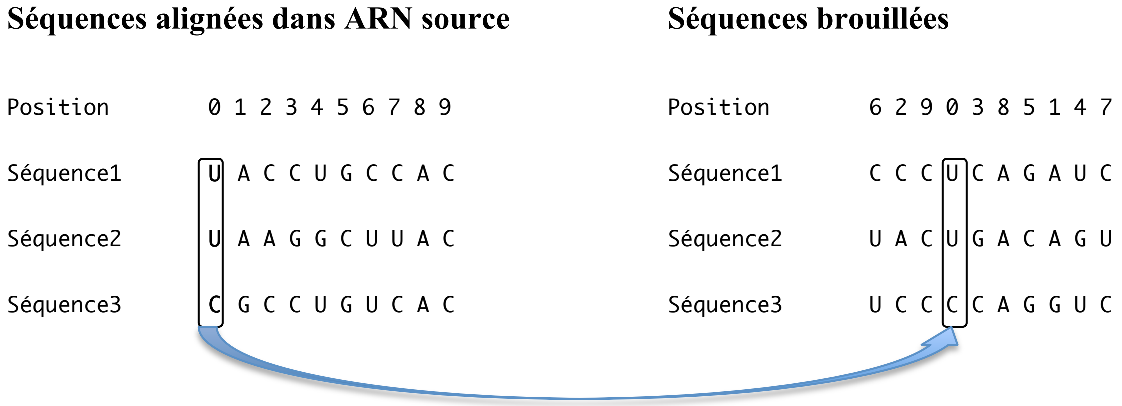
RF02099	Gene; sRNA	rivX	0.46	0.89	0.46	0.87	0.46	0.90	**0.00**	-0.03	16	96	144
RF02100	Gene; sRNA	tfoR	0.47	0.91	**0.49**	0.88	0.39	0.99	**0.10**	-0.11	115	453	462
RF02111	Gene	IS009	0.60	0.88	0.57	0.87	**0.60**	0.90	**-0.04**	-0.03	730	4278	5828
RF02119	Gene; lncRNA	FTX_1	0.97	0.86	0.97	0.84	0.97	0.89	**0.00**	-0.04	53	54	160
RF02120	Gene; lncRNA	FTX_2	-	0.57	-	0.55	-	0.58	**-**	-0.03	57	0	57
RF02121	Gene; lncRNA	FTX_3	0.45	0.72	0.43	0.70	**0.57**	0.74	**-0.14**	-0.03	55	56	168
RF02122	Gene; lncRNA	FTX_5	0.50	0.61	**0.53**	0.60	0.37	0.62	**0.16**	-0.02	57	62	277
RF02123	Gene; lncRNA	FTX_4	0.50	0.61	0.50	0.60	0.50	0.64	**0.00**	-0.05	46	46	94
RF02126	Gene; lncRNA	GHRLOS	0.61	0.93	0.57	0.92	**0.68**	0.96	**-0.11**	-0.05	45	139	186
RF02144	Gene	rsmX	0.45	0.95	0.45	0.93	**0.46**	0.97	**-0.01**	-0.04	173	752	927
RF02156	Gene; lncRNA	NPPA-AS1_1	0.49	0.90	0.50	0.88	**0.51**	0.91	**-0.01**	-0.03	47	272	382
RF02157	Gene; lncRNA	NPPA-AS1_2	0.54	0.84	**0.58**	0.84	0.45	0.85	**0.13**	-0.02	49	242	397
RF02158	Gene; lncRNA	NPPA-AS1_3	0.50	0.68	0.50	0.67	0.50	0.69	**0.00**	-0.02	69	65	139
RF02163	Gene; snRNA; snoRNA; CD-box	sR-tMet	0.90	0.58	**0.77**	0.58	0.68	0.59	**0.09**	-0.01	25	31	79
RF02179	Gene; lncRNA	ST7-AS1_1	0.70	0.56	0.65	0.54	**0.72**	0.60	**-0.06**	-0.06	103	6	209
RF02180	Gene; lncRNA	ST7-AS1_2	0.47	0.53	0.48	0.51	**0.53**	0.56	**-0.06**	-0.05	99	3	393
RF02194	Gene; antisense	HPnc0260	0.45	0.85	**0.38**	0.85	0.37	0.83	**0.01**	0.02	780	1968	4561
RF02197	Gene; lncRNA	TP73-AS1	0.41	0.94	0.38	0.93	**0.51**	0.96	**-0.13**	-0.03	26	127	204
RF02201	Gene; lncRNA	TTC28-AS1_4	0.31	0.88	0.29	0.87	**0.54**	0.87	**-0.25**	0.00	57	56	169
RF02211	Gene; lncRNA	ZFAT-AS1_1	0.48	0.86	0.47	0.86	**0.55**	0.84	**-0.08**	0.02	21	63	84
RF02212	Gene; lncRNA	ZFAT-AS1_2	0.49	0.74	0.47	0.74	**0.59**	0.74	**-0.11**	0.00	42	49	248
RF02213	Gene; lncRNA	ZFAT-AS1_3	0.49	0.99	0.42	0.99	**0.67**	0.98	**-0.24**	0.01	26	76	78
RF02214	Gene; miRNA	mir-56	0.50	0.87	0.30	0.87	**0.64**	0.86	**-0.34**	0.01	6	18	23
RF02221	Gene; sRNA	sRNA-Xcc1	0.86	0.69	**0.88**	0.69	0.82	0.69	**0.06**	0.00	774	685	2324
RF02222	Gene; sRNA	sX2	0.41	0.95	0.42	0.93	0.42	0.97	**0.00**	-0.03	22	132	132
RF02223	Gene; sRNA	sX4	0.44	0.77	0.39	0.76	**0.44**	0.76	**-0.05**	0.00	210	144	1039
RF02224	Gene; sRNA	sX5	0.46	0.94	0.44	0.94	**0.56**	0.93	**-0.12**	0.00	30	81	81
RF02225	Gene; sRNA	sX6	0.48	0.87	0.46	0.86	**0.54**	0.89	**-0.08**	-0.03	32	200	366
RF02226	Gene; sRNA	sX7	0.32	0.93	0.31	0.91	**0.32**	0.97	**-0.01**	-0.06	26	52	104
RF02227	Gene; sRNA	sX8	0.31	0.97	0.33	0.96	**0.35**	0.99	**-0.02**	-0.03	34	102	102
RF02228	Gene; sRNA	sX9	0.36	0.87	0.31	0.84	**0.45**	0.92	**-0.14**	-0.08	1935	5647	7745
RF02230	Gene; sRNA	sX11	0.62	0.92	0.58	0.90	**0.68**	0.95	**-0.11**	-0.04	30	90	159
RF02231	Gene; sRNA	sX12	0.63	0.70	**0.68**	0.69	0.55	0.71	**0.13**	-0.02	21	42	63
RF02232	Gene; sRNA	sX13	0.35	0.93	0.26	0.91	**0.58**	0.95	**-0.32**	-0.04	46	142	280
RF02233	Gene; sRNA	sX14	0.67	0.95	**0.64**	0.92	0.64	0.99	**0.01**	-0.07	22	110	110
RF02234	Gene; sRNA	sX15	0.52	0.77	**0.54**	0.78	0.52	0.77	**0.02**	0.01	29	115	171
RF02235	Gene; sRNA	asX1	0.37	0.94	0.36	0.93	**0.48**	0.94	**-0.12**	0.00	46	177	271
RF02236	Gene; sRNA	asX2	0.43	0.89	**0.45**	0.87	0.38	0.92	**0.08**	-0.05	6	18	24
RF02237	Gene; sRNA	asX3	0.44	0.89	0.46	0.88	**0.50**	0.89	**-0.04**	-0.01	13	77	137
RF02238	Gene; sRNA	asX4	0.48	0.92	0.42	0.91	**0.55**	0.94	**-0.13**	-0.03	21	239	324

RF02239	Gene; sRNA	asX6	0.27	0.89	0.25	0.89	**0.45**	0.86	**-0.20**	0.03	6	12	24
RF02240	Gene; sRNA	Xoo1	0.45	0.90	0.44	0.87	0.44	0.94	**0.00**	-0.07	31	105	160
RF02241	Gene; sRNA	Xoo2	0.26	0.86	**0.31**	0.84	0.16	0.90	**0.15**	-0.06	35	2	105
RF02242	Gene; sRNA	Xoo5	0.57	0.91	0.52	0.91	**0.60**	0.91	**-0.08**	0.01	37	149	259
RF02243	Gene; sRNA	Xoo8	0.54	0.73	0.52	0.71	**0.58**	0.75	**-0.06**	-0.03	156	729	1470
RF02244	Gene; miRNA	mir-785	0.80	0.80	**0.70**	0.78	0.68	0.83	**0.02**	-0.05	6	9	16
RF02245	Gene; miRNA	mir-788	0.59	0.89	0.44	0.87	**0.82**	0.91	**-0.38**	-0.04	6	12	18
RF02246	Gene; lncRNA	Six3os1_1	0.51	0.90	0.48	0.88	**0.51**	0.93	**-0.04**	-0.04	48	133	191
RF02253	Cis-reg	IRE_II	0.53	0.97	**0.56**	0.95	0.53	0.99	**0.02**	-0.04	714	2220	2220
RF02254	Gene; miRNA	mir-35	0.57	0.95	0.52	0.93	**0.63**	0.97	**-0.11**	-0.03	88	197	284
RF02259	Gene; lncRNA	Vax2os1_1	0.49	0.83	0.42	0.82	**0.53**	0.84	**-0.11**	-0.02	10	78	110
RF02260	Cis-reg	MAT2A_A	0.20	0.71	0.19	0.72	**0.20**	0.69	**-0.01**	0.03	171	176	515
RF02261	Cis-reg	MAT2A_B	0.77	0.79	**0.75**	0.78	0.68	0.79	**0.07**	-0.01	140	282	423
RF02262	Cis-reg	MAT2A_C	0.46	0.70	0.43	0.72	**0.61**	0.63	**-0.18**	0.10	155	157	467
RF02263	Cis-reg	MAT2A_D	0.20	0.80	0.08	0.77	**0.50**	0.86	**-0.42**	-0.09	169	170	339
RF02264	Cis-reg	MAT2A_E	0.64	0.75	0.62	0.75	**0.67**	0.73	**-0.05**	0.02	170	511	850
RF02265	Cis-reg	MAT2A_F	0.53	0.78	0.45	0.78	**0.59**	0.79	**-0.14**	-0.01	209	410	641
RF02266	Gene	XIST_intron	1.00	0.40	**1.00**	0.40	0.81	0.40	**0.19**	0.00	70	1	141
RF02268	Gene; sRNA	MtlS	0.85	0.84	**0.84**	0.82	0.81	0.86	**0.03**	-0.04	98	215	509
RF02269	Gene; sRNA	HPnc0580	0.52	0.96	**0.54**	0.94	0.50	0.97	**0.03**	-0.02	234	721	967
RF02270	Gene	nse_sRNA	0.51	0.94	0.50	0.93	**0.61**	0.95	**-0.11**	-0.02	50	145	200
RF02272	Gene; lncRNA	Vax2os1_3	0.47	0.75	0.45	0.74	**0.55**	0.75	**-0.09**	-0.02	46	146	286
RF02273	Gene	FsrA	0.78	0.93	**0.82**	0.92	0.78	0.92	**0.05**	0.01	37	18	92
RF02274	Gene	AniS	0.44	0.92	0.39	0.90	**0.61**	0.93	**-0.22**	-0.03	51	153	212
RF02275	Gene	Hammerhead_HH9	0.51	0.84	**0.58**	0.84	0.34	0.83	**0.24**	0.01	77	73	232
RF02276	Gene; ribozyme	Hammerhead_II	0.52	0.89	**0.55**	0.87	0.50	0.93	**0.05**	-0.06	156	342	478
RF02277	Gene; ribozyme	Hammerhead_HH10	0.27	0.82	0.28	0.82	**0.40**	0.80	**-0.13**	0.02	56	112	224
RF02278	Gene	Betaproteobacteria_toxic_sRNA	0.47	0.88	**0.47**	0.86	0.40	0.90	**0.07**	-0.03	356	86	718
Moyenne			0.53	0.83	0.51	0.82	0.55	0.84	-0.04	-0.02			
Écart type			0.17	0.11	0.17	0.11	0.15	0.12	0.13	0.03			

Table 7. Application de RNAscore sur les nouvelles familles d'ARNnc de Rfam 11.0.
RNAscore est le score global avant la répartition en deux groupes « Activité biochimique » et « Antisens ». La colonne Q désigne le score relatif à la séquence des motifs scorés alors que la colonne Z représente le score basé uniquement sur la taille de tous les motifs de l'ARN en question. dQ et dZ sont la différence du score « Activité biochimique » moins le score « Antisens » pour les scores Q et Z respectivement. Les Q-scores en bleu sont pour les ARN qui ont un Q-score plus élevé pour RNAscore activité biochimique alors que le rouge désigne le Q-score Antisens qui est plus élevé.

4.2.2. Application de RNAscore sur des contrôles négatifs

Une des étapes laborieuses de ce projet était l'élaboration des contrôles négatifs appropriés. Nous avions identifié certains motifs d'ARNnc qui ont été mutés expérimentalement et que nous avons utilisé dans la section suivante, mais il s'agissait de petits motifs qui ont été étudiés séparément et non d'un alignement d'ARN que nous pourrions comparer avec les nouvelles familles de Rfam. Nous avons donc créé des faux ARN structurés pour tester notre système de score. Des séquences d'ARN brouillées ont été soumises à CMfinder pour obtenir de faux ARN structurés ainsi que des séquences codantes des protéines aconitase et aminopeptidase dont certaines ont été aussi brouillées de la même façon que les séquences d'ARN. La figure 10 montre un exemple simplifié de la façon dont des séquences alignées ont été brouillées. Les trois séquences de dix bases chacune proviennent de l'alignement du riboswitch SAM/SAH (elles sont alignées). Avec un programme récursif, les bases ayant la même position dans toutes les séquences sont permutées avec les bases d'une position aléatoire. Le résultat est semblable à remanier les séquences en déplaçant des blocs verticalement. Ceci est dans l'objectif de garder l'alignement de séquences mais défaire la structure originale de l'ARN source.



Séquences alignées dans ARN source

Position	0	1	2	3	4	5	6	7	8	9
Séquence1	U	A	C	C	U	G	C	C	A	C
Séquence2	U	A	A	G	G	C	U	U	A	C
Séquence3	C	G	C	C	U	G	U	C	A	C

Séquences brouillées

Position	6	2	9	0	3	8	5	1	4	7
Séquence1	C	C	C	U	C	A	G	A	U	C
Séquence2	U	A	C	U	G	A	C	A	G	U
Séquence3	U	C	C	C	C	A	G	G	U	C

Figure 10. Conception des faux ARN.

Les positions dans les séquences brouillées sont celles des séquences originales.

Comme exemple d’un faux ARN, on montre ici un des faux ARN obtenus à partir des séquences brouillées du riboswitch SAM/SAH dont on a déjà présenté l’alignement complet de Rfam ainsi que les scores obtenus pour le vrai ARN. Nous avons soumis les 88 séquences brouillées à la version web du logiciel et en utilisant les paramètres par défaut. CMfinder a détecté une structure conservée en forme de tige-boucle dans 59 séquences des 88 de départ et les motifs sont différents de l’ARN original.

Résultats CMfinder SAMSAH-S3 (S3 pour « scrambled » et le numéro de candidat)

```
# STOCKHOLM 1.0

#=GF AC    sSAMSAH3
#=GF AU    CMfinder 0.1

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AACY0201454691/1024.977                 GAUAGAU.GUA.U..GGU.CGG.UG.A.A..ACGG.GC..UCGUGC.CA.UGUC
AACY0202235001/3303.3256                GACAGAU.GUU.U..GGU.CGG.UA.A.A..UCGG.GC..UCGU.UCCA.UGUC
AACY0202458051/1080.1127                GAUAGAU.AUG.U..GGU.CGG.C.CA.A..GCGG.GC.UC.GU.UCCA.UGUC
AACY0202532711/246.293                  GACAGAU.GUU.U..GGU.CGG.UA.A.A..UCGG.GC.A.CGU.UCCA.UGUC
AACY0202550861/785.738                  GACAGAU.GUU.U..GGU.CGG.UA.A.A..UCGG.GC..UCGU.UCCA.UGUC
AACY0203080771/1017.1066                GAUAGGU.U.AUU.A.GC.CGG.G.CA..CUCC.G.GC.GCGGC.CUCAA.GUC
AACY0205226441/2673.2625                GAUAGGU.C.CCU.A.G.ACGG.C.UA..CGCC.GG.C.ACGGU.CUCAA.GUC
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AACY0210836151/454.500                  GAUAGUU.A.CUU..GA.ACGA.CA....UUCCGGC.C..CGGU.U.CA.UGUC
AACY0216430131/430.383                  GAUAGAU.GUA.U..GGU.CGG.UG.A.A..UCGG.GC..UCGUGC.CA.UGUC
AACY0217897241/224.271                  GAUAGAU.GUA.U..GGU.CGG.UG.A.A..UCGG.GC..UCGU.UCCA.UGUC
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AACY0222629011/198.151                  GAUAGAU.GUC.U..GGC.CGA.U.CA.A..GCGG.GC.A.CGU.UCCA.UGUC
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ABMI010510291/54.6                      GAUAGGU.CUC.U.A.G.ACGG.U.UA.A.GCC.GG.C.ACGGC.CUCAA.GUC
ABMI011140221/24.74                     GGUAGCU.GUCUU.A.GC.CGA.U.CA.A..UCGG.GC..CCGGUCCCAA.GUC
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CP0011511/703619.703570                 GACAGGU.C.CGU.A.GG.CGG.CA.A.A.UCCGG.CC..CGAC.CCCAA.GUC
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#=GC SS.CONS                            ....<<<.<.......<<.<<<.........>>.>.>>...>>>.>........
#=GC RF                                 GAUAGGU.CUCUU.A.GU.CGG.UA.A.A.UCCGG.GC.ACGGC.CCCAAUGUC
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L'évaluation de ce résultat de CMfinder par RNAscore a donné les scores suivants :

Résultats RNAscore de SAMSAH-S3 :

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--------------------------------------------------------------------------------------------------------------------------------------------
Total number of sequences: 59
Loops: 59
Bulges: 38
Internal loops: 59
Number of scored motifs = 96
Total number of motifs = 156

RNAscore
Sum Q-Score = -8.150004          Sum Q-Score_max = 86.34007            Q-Score = 0.4528029
Sum Z-Score = 231.08974          Sum Z-Score_max = 338.19              Z-Score = 0.8416567

RNAscore biochemical
Sum Q-Score = 5.509997           Sum Q-Score_max = 106.78005           Q-Score = 0.5258007
Sum Z-Score = 233.00038          Sum Z-Score_max = 341.73              Z-Score = 0.84091294

RNAscore antisense
Sum Q-Score = -18.62             Sum Q-Score_max = 85.2199             Q-Score = 0.3907532
Sum Z-Score = 221.89012          Sum Z-Score_max = 334.06              Z-Score = 0.8321112

Loops: 59 [CAUU, UGAA, UGAA, UAAA, CCAA, UAAA, UAAA, GCACU, CUACG, ACACA, CUAAA, ACAA, CCAA,
UAAA, CAUU, UGAA, UGAA, CUAAA, UCAA, CAUU, UAUU, AGAA, UAAA, GCACU, UAAA, GAAAU, UUACU,
UAAUA, UCACG, UAAUA, CAAUA, CUACU, CCACA, UUAUA, CAACG, AAAUA, AAAAG, UGAUU, UUAAG, UUAAG,
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UCAA, GACU, CGAAU, CUACG, UAAUU, CGAAA, UUACA, AAGAGG, CUAAA, AAAAA, UGAUA, UAACA, CAAAU,
GGAU, CUAA, CAAAU, CAAAA, CAAAU, GGAU]

Bulges: 38 [G, G, G, G, G, G, G, G, G, U, G, G, C, G, G, G, G, G, G, G, G, G, G, A, G, G, G, G, U, G, G, U, C, G, G, G,
U]

Internal loops: 59 [CUUG-C, UAUG-AC, UAUG-U, UUUG-U, UGUG-UC, UUUG-A, UUUG-U, AUUA-GC, CCUA-AC,
CCUA-CUC, UGUA-C, CCUA-GC, UUUA-AC, UUUG-U, CUUG-C, UAUG-U, UAUG-U, CCUA-GC, UCUG-A, CUUG-C,
UAUA-AC, UUUA-UC, UUUG-U, AUUA-GC, UCUG-U, UUUA-GC, UAUC-AC, AUA-AC, CAUA-UC, AUA-AC, UUUA-
AC, CGUGA-GC, CAUA-AC, UAUA-AC, UGUGA-UC, CUUA-AC, UCUA-AC, UAUA-C, UCUA-AC, UCUA-AC, UCUUA-C,
CCUA-GC, UCUA-C, CCUAA-UC, CUUA-AC, UGUA-UC, AAUA-AC, ACUAA-UC, CGUA-AC, GAUA-AC, CGUA-UC,
CGUGA-GC, CGUA-C, GUUA-AC, UAUA-AC, CGUA-C, CGUA-C, CGUA-C, GUUA-AC]
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Malgré que nous avons créé et soumis de nombreuses séquences de faux ARN et que les séquences ont été brouillées par colonne de l'alignement, pour conserver un meilleur potentiel global de former des paires de bases (avec de la covariation), seulement un faible pourcentage a donné des résultats sur CMfinder. Ceci s'explique par le fait que les séquences choisies l'ont été parce que l'on présume qu'elles n'ont pas de structures d'ARN conservées donc il n'est pas surprenant que CMfinder n'ait pas prédit de structures secondaires dans la majorité de nos tentatives. Nous avons donc appliqué RNAscore pour les 34 candidats obtenus et les résultats sont présentés dans la table 8. Parmi les 34 faux ARN, trois n'ont pas de motifs scorés et par conséquent ils n'ont pas de Q-score. Les Q-scores moyens sont presque semblables dans les trois versions de RNAscore (0.51, 0.52 et 0.52 pour RNAscore global, RNAscore « Activité biochimique » et RNAscore « Antisens » respectivement); de même pour les Z-scores moyens (0.83, 0.82 et 0.83 pour RNAscore global, RNAscore « Activité biochimique » et RNAscore « Antisens » respectivement). Les écarts-types des Q-scores (0.18, 0.19 et 0.16) et ceux des Z-scores (0.12, 0.12 et 0.13) indiquent que les valeurs de scores des contrôles négatifs sont assez dispersées autour de la moyenne. Ces résultats n'appuient pas notre hypothèse selon laquelle les faux ARN auraient une moyenne de score inférieure à celle de vrais ARN. En comparant avec les résultats des nouvelles familles d'ARN et tenant compte de l'écart-type, on ne remarque pas une différence significative entre les moyennes de scores.

ARN/protéine source	Nom alignement CMfinder	RnaScore		*Biochemical* RnaScore		*Antisense* RnaScore		dQ	dZ	Nb de séq.	Nb. motifs	
		Q	Z	Q	Z	Q	Z				Scorés	Total
GOLLD	GOLLD-S1	0.45	0.88	0.42	0.86	0.47	0.91	-0.05	-0.05	17	139	174
	GOLLD-S2	0.67	0.80	0.67	0.80	0.63	0.79	0.04	0.00	13	68	120
	GOLLD-S3	0.67	0.90	0.63	0.89	0.59	0.91	0.04	-0.02	16	145	177
	GOLLD-S4	-	0.83	-	0.81	-	0.85	-	-0.04	6	0	12
SAM-SAH	SAMSAH-S1	0.45	0.95	0.51	0.93	0.34	1.00	0.17	-0.07	59	88	89
	SAMSAH-S2	0.51	0.76	0.56	0.76	0.37	0.75	0.18	0.00	59	59	119
	SAMSAH-S3	0.45	0.84	0.53	0.84	0.39	0.83	0.14	0.01	59	96	156
5S	5S-S1	0.45	0.92	0.50	0.92	0.48	0.90	0.02	0.02	15	46	47
	5S-S2	-	0.56	-	0.55	-	0.58	-	-0.03	60	0	60
	5S-S3	0.21	0.52	0.15	0.51	0.26	0.52	-0.10	-0.01	58	59	117
	5S-S4	0.53	0.77	0.53	0.76	0.52	0.77	0.02	-0.01	59	152	329
glnA	GlnA-S1	-	0.90	-	0.89	-	0.90	-	-0.01	39	0	39
Hammerhead HH9	HH9-S1	0.48	0.67	0.55	0.67	0.36	0.67	0.19	0.00	33	26	82
	HH9-S2	0.99	0.78	0.98	0.78	0.81	0.78	0.17	0.00	33	33	95
	HH9-S3	0.59	0.79	0.62	0.79	0.60	0.78	0.02	0.01	33	66	132
	HH9-S4	0.55	0.93	0.57	0.92	0.58	0.93	-0.01	-0.01	33	145	178
crcB	crcb-S1	0.51	0.89	0.42	0.88	0.64	0.91	-0.22	-0.03	15	24	40
	crcb-S2	0.31	0.95	0.33	0.93	0.32	0.97	0.01	-0.05	11	29	31
ryhB	ryhB-S1	0.72	0.86	0.65	0.83	0.78	0.90	-0.13	-0.07	25	11	36
IRE-I	IRE_I-S1	0.65	0.95	0.76	0.95	0.64	0.95	0.12	0.00	56	39	95
	IRE_I-S2	1.00	0.69	1.00	0.69	1.00	0.67	0.00	0.01	58	3	119
Lysin riboswitch	Lysine-S1	0.38	0.94	0.42	0.92	0.32	0.96	0.10	-0.04	7	20	28
	Lysine-S2	0.46	0.91	0.46	0.90	0.51	0.92	-0.04	-0.02	7	44	54
	Lysine-S3	0.18	0.81	0.19	0.79	0.36	0.84	-0.17	-0.05	8	10	18
	Lysine-S4	0.54	0.53	0.67	0.53	0.54	0.51	0.13	0.02	16	6	38
	Lysine-S5	0.37	0.99	0.36	0.99	0.51	0.97	-0.16	0.02	7	16	16
	Lysine-S6	0.61	0.87	0.62	0.86	0.59	0.89	0.03	-0.03	21	45	67
aconitase	aconitase-1*	0.59	0.96	0.49	0.95	0.73	0.97	-0.24	-0.02	4	13	17
	aconitase-2*	0.50	0.91	0.50	0.91	0.54	0.91	-0.03	0.00	5	17	19
	aconitase-3*	0.36	0.72	0.33	0.71	0.46	0.73	-0.13	-0.01	5	9	30
	aconitase-4*	0.27	0.78	0.22	0.78	0.36	0.75	-0.15	0.03	5	3	15
	aconitase-S1	0.48	0.95	0.55	0.94	0.50	0.96	0.05	-0.02	3	4	7
	aconitase-S2	0.59	0.85	0.59	0.84	0.63	0.84	-0.04	0.01	4	5	12
aminopeptidase	aminopeptidase-S1	0.44	0.88	0.42	0.88	0.44	0.87	-0.01	0.01	6	15	15
Moyenne		0.51	0.83	0.52	0.82	0.52	0.83	0.02	-0.02			
Écart-type		0.18	0.12	0.19	0.12	0.16	0.13	0.12	0.03			

Table 8. Application de RNAscore sur des contrôles négatifs.

Les ARN testés sont des séquences d'ARN brouillées ainsi que des séquences codantes de protéines (aconitase et aminopeptidase) dont certaines ont aussi été brouillées avant d'être soumises à CMfinder. Les scores des faux ARN structurés obtenus sont présentés.

* indique les séquences du gène codant pour l'aconitase provenant de différentes espèces de bactéries et qui n'ont pas été brouillées.

4.2.3. Application de RNAscore sur des motifs d'études mutationnelles

Nous avons testé RNAscore sur des motifs qui ont été modifiés par mutation ponctuelle et dont la fonction a été étudiée expérimentalement. Une recherche de littérature approfondie nous a permis de trouver plusieurs motifs (boucles terminales et internes ainsi que des « bulges ») qui ont été mutés et nous les avons divisés en deux groupes :

- les mutations qui ont engendré une perte de fonction

et

- les mutations qui n'ont pas eu d'effet inhibiteur, incluant certaines mutations qui ont causé une augmentation de l'activité de l'ARN.

Chaque motif provient d'une étude expérimentale distincte. Afin de tester RNAscore sur ces motifs, nous les avons regroupés et avons appliqué le score pour chaque ensemble de motifs de façon semblable à un ARN avec une collection de motifs.

Pour cette analyse, nous avons appliqué uniquement RNAscore global puisque ce test vise à comparer le score des motifs *wild-type* au score des motifs mutés.

	"Wild-Type"		Mutants		Nb. de motifs mutés			Nb. motifs	
	Q-Score	Z-score	Q-Score	Z-score	boucles terminales	*bulges*	boucles internes	Scorés	Total
Mutants avec perte de fonction	0.63	0.86	0.54	0.86	57	18	21	35	96
Mutants avec fonction active	0.35	0.89	0.41	0.89	13	0	11	14	24

Table 9. Application de RNAscore sur des motifs mutés.
Les Q-scores et Z-scores des motifs avant et après mutation calculés avec la version RNAscore global.

Nous notons que pour les mutations avec perte de fonction, le score global des motifs mutés est inférieur à celui du type sauvage (0.54 < 0.63). On observe l'effet contraire pour les mutations qui ont maintenu l'activité de l'ARN ou l'ont augmenté. Dans ce cas, le score global des motifs mutés augmente par rapport au type sauvage (0.41 > 0.35). Malgré que la tendance des résultats concorde avec notre hypothèse, l'écart entre les scores des motifs mutés et ceux des motifs de type sauvage demeure faible.

4.2.4 RNAscore d'un ensemble aléatoire de motifs scorés

Les contrôles négatifs générés par des séquences brouillées ont donné des scores assez divergents. Certains de ces faux ARN avaient peu ou pas de motifs scorés. Nous avons testé une approche différente qui consiste à former aléatoirement des ensembles de motifs scorés et considéré chaque ensemble comme un ARN hypothétique afin d'y attribuer un Q-score. Chaque contrôle consiste en une sélection aléatoire par un programme informatique de 1400 motifs scorés dont :

- 400 boucles terminales : 100 boucles au hasard de chacune des tailles 2, 3, 4 et 5,
- 400 « bulges »: 100 « bulges » au hasard de chacune des tailles 1 à 4 nucléotides et
- 600 boucles internes : 100 boucles au hasard pour chacune des tailles 1x1, 1x2, 1x3, 2x1, 2x2 et 3x1.

Les résultats des contrôles aléatoires pour les Q-scores calculés selon les 3 versions de RNAscore sont présentés dans la table X. Pour les trois versions de RNAscore (global, « activité biochimique » et « antisens »), nous avons calculé les Q-scores de 10 contrôles aléatoires. Les écarts-types sont très faibles ce qui démontre que les scores sont très serrés par rapport aux moyennes. Nous avons effectué des simulations d'ensembles aléatoires jusqu'à 1000 fois et nous avons trouvé que les moyennes (résultats non-présentés ici) ne diffèrent pas de celles des 10 échantillons de la table X. Les moyennes des Q-scores global et des Q-scores pour Antisens ont presque la même valeur de 0.48 alors que la moyenne pour les Q-scores « Activité biochimique » est un peu plus basse soit 0.44. Nous avons calculés les valeurs de scores situés à plus ou moins trois écarts-types ce qui représenterait 99% des valeurs de scores aléatoires selon une distribution normale. Ces intervalles seront utilisés ultérieurement dans la comparaison des contrôles positifs et négatifs.

	RNAscore Q-score	*Biochemical* Q-Score	*Antisense* Q-Score
contrôle aléatoire 1	0.478	0.442	0.485
contrôle aléatoire 2	0.485	0.438	0.478
contrôle aléatoire 3	0.481	0.435	0.485
contrôle aléatoire 4	0.476	0.435	0.489
contrôle aléatoire 5	0.480	0.434	0.483
contrôle aléatoire 6	0.480	0.436	0.488
contrôle aléatoire 7	0.486	0.441	0.477
contrôle aléatoire 8	0.481	0.438	0.488
contrôle aléatoire 9	0.486	0.436	0.487
contrôle aléatoire 10	0.475	0.433	0.476
Moyenne	**0.481**	**0.437**	**0.484**
Écart-Type (É-T)	0.004	0.003	0.005
Moyenne+3 É-T	0.492	0.446	0.498
Moyenne-3 É-T	0.469	0.428	0.469

Table 10. Q-scores des contrôles aléatoires. É-T : Écart-Type.

4.3. Détermination de fonction par les scores « activité biochimique » vs « antisens »

Tel qu'avancé au début de ce chapitre, nous avons développé les versions de RNAscore spécifiques aux deux groupes d'ARNnc « activité biochimique » et « antisens » afin de vérifier s'il y a un avantage à utiliser cette approche. Il existe une grande variété d'ARNnc ayant des fonctions et caractéristiques très différentes. Au niveau structural, on s'attend à ce que certaines différences existent entre les deux groupes et celles ci se manifesteraient par des différences de scores (dQ>0) selon la nature de l'ARN.

Notre hypothèse suppose que le Q-score calculé selon la version RNAscore spécifique au groupe auquel appartient un ARN donné serait plus élevé que le Q-score calculé selon la version du groupe auquel il n'appartient pas. Si cette hypothèse est vraie, RNAscore pourrait être utilisé pour la prédiction de la fonction d'un nouvel ARN en se basant sur ses scores « activité biochimique » et « antisens ». De plus, cela permettrait, en principe, d'avoir des scores avec un meilleur pouvoir discriminant puisqu'ils sont « adaptés » à l'ARNnc correspondant.

4.3.1 Capacité de discerner le type d'ARN : échantillon Rfam

Dans les résultats présentés à la section 4.2.1, la différence de scores « activité biochimique » versus « antisens » a été calculé pour les 104 nouvelles familles d'ARN (la colonne dQ et dZ). Dans cette analyse, nous accordons plus d'importance à la différence dQ que dZ étant donné que la différence des scores basés sur la taille des motifs est généralement faible en plus d'avoir un petit écart-type de -0.2.

La moyenne générale dans cette perspective n'est pas très informative. Nous avons donc sélectionné deux échantillons à partir des nouvelles familles de Rfam selon la classification de Rfam et dont la fonction est confirmée (sachant d'avance à quel groupe ils appartiennent). Dans l'échantillon 1, dQ aurait une valeur positive puisque nous supposons que le score « activité biochimique » est plus élevé que le score « antisens ». Les valeurs de dQ de l'échantillon 2 devraient plutôt être négatives. Les moyennes de dQ des deux échantillons ne contredisent pas notre hypothèse puisque le dQ moyen pour l'échantillon 1 est 0.06 et celui de l'échantillon 2 est -0.08. Cependant il y a un chevauchement à cause des écarts-types. Afin de vérifier que les dQ de l'échantillon 1 sont différents de ceux de l'échantillon 2, nous avons procédé à un test statistique. Le test de Student effectué compare les dQ de l'échantillon 1 (ARN ayant une activité biochimique) aux dQ de l'échantillon 2 (ARN ayant une activité antisens). Le résultat du test de Student rejette l'hypothèse nulle avec une probabilité de **0.008** ce qui confirme que la différence entre les valeurs dQ de ces deux échantillons est statistiquement significative.

	Rfam ID	Rfam clan	RNA	Activité biochimique Q-Score	Antisens Q-Score	dQ
Échantillon 1	RF02032	Gene	GOLLD	0.64	0.46	**0.18**
	RF02033	Gene	HEARO	0.57	0.55	**0.02**
	RF02034	Gene	IMES-1	0.51	0.60	**-0.09**
	RF02035	Gene	IMES-2	0.83	0.65	**0.18**
	RF02144	Gene	rsmX	0.45	0.46	**-0.01**
	RF02253	Cis-reg	IRE_II	0.56	0.53	**0.02**
	RF02266	Gene	XIST_intron	1.00	0.81	**0.19**
	RF02275	Gene	Hammerhead_HH9	0.58	0.34	**0.24**
	RF02276	Gene; ribozyme	Hammerhead_II	0.55	0.50	**0.05**
	RF02277	Gene; ribozyme	Hammerhead_HH10	0.28	0.40	**-0.13**
			czc	0.56	0.56	**0.00**
Échantillon 2	RF02044	Gene; lncRNA	CDKN2B-AS_2	0.45	0.36	**0.10**
	RF02045	Gene; lncRNA	CDKN2B-AS_3	0.44	0.74	**-0.30**
	RF02061	Gene; miRNA	mir-301	0.49	0.50	**-0.01**
	RF02089	Gene; lncRNA	CLRN1-AS1	0.92	0.87	**0.05**
	RF02090	Gene; lncRNA	DAOA-AS1_1	0.44	0.60	**-0.17**
	RF02091	Gene; lncRNA	DAOA-AS1_2	0.63	0.50	**0.13**
	RF02095	Gene; miRNA	mir-2985-2	0.44	0.43	**0.01**
	RF02096	Gene; miRNA	mir-2973	0.42	0.49	**-0.07**
	RF02097	Gene; miRNA	mir-1662	0.28	0.60	**-0.32**
	RF02156	Gene; lncRNA	NPPA-AS1_1	0.50	0.51	**-0.01**
	RF02157	Gene; lncRNA	NPPA-AS1_2	0.58	0.45	**0.13**
	RF02158	Gene; lncRNA	NPPA-AS1_3	0.50	0.50	**0.00**
	RF02163	Gene; snRNA; snoRNA; CD-box	sR-tMet	0.77	0.68	**0.09**
	RF02179	Gene; lncRNA	ST7-AS1_1	0.65	0.72	**-0.06**
	RF02180	Gene; lncRNA	ST7-AS1_2	0.48	0.53	**-0.06**
	RF02194	Gene; antisense	HPnc0260	0.38	0.37	**0.01**
	RF02197	Gene; lncRNA	TP73-AS1	0.38	0.51	**-0.13**
	RF02201	Gene; lncRNA	TTC28-AS1_4	0.29	0.54	**-0.25**
	RF02214	Gene; miRNA	mir-56	0.30	0.64	**-0.34**
	RF02244	Gene; miRNA	mir-785	0.70	0.68	**0.02**
	RF02245	Gene; miRNA	mir-788	0.44	0.82	**-0.38**
	RF02254	Gene; miRNA	mir-35	0.52	0.63	**-0.11**

	N	Moyenne dQ	É-T
Échantillon 1: Activité biochimique	11	0.06	0.12
Échantillon 2: Antisens	22	-0.08	0.16

Table 11. Échantillons pour Test de Student de dQ-score « Activité biochimique » vs « Antisens ».

4.3.2 Applicabilité de RNAscore comme filtre

À première vue les résultats de RNAscore pour les contrôles positifs et négatifs ne montrent pas de différence significative. Afin de mieux comparer les scores de contrôles positifs et négatifs, nous avons utilisé comme référence les intervalles de scores aléatoires présentés à la section 4.2.4.

On suppose que ces intervalles représentent les valeurs de scores qu'un ARN donné peut avoir si les motifs présents étaient sélectionnés aléatoirement. Nous avons analysé la répartition des contrôles testés selon leurs Q-scores en calculant le pourcentage des ARN ayant un score inclus dans l'intervalle de scores aléatoires, supérieur ou inférieur aux bornes de l'intervalle. Ceci nous permet d'avoir une vue globale des deux types de contrôles étudiés. La figure 11 montre la distribution des scores pour les trois versions utilisées de RNAscore.

Dans toutes les versions de RNAscore, les contrôles négatifs ont un pourcentage plus élevé que les contrôles positifs d'ARN ayant des scores inférieurs à l'intervalle aléatoire. En d'autres termes, les faux ARN auraient une plus grande proportion de faibles scores. D'un autre coté, plus que la moitié des contrôles positifs ont des scores élevés dépassant l'intervalle aléatoire soit 53%, 64% et 66%. Ces pourcentages sont plus élevés que leurs équivalents du côté des contrôles négatifs dans les trois versions de RNAscore.

Ceci indique que les vrais ARNnc analysés ont plus tendance à avoir un Q-score supérieur à tout score aléatoire. La répartition des résultats des contrôles négatifs ne permet pas d'avoir une conclusion parallèle puisque dans le cas de RNAscore global, la majorité des candidats avaient de faibles scores (51%) alors pour les 2 autres versions, 54% des candidats ont eu des scores supérieurs aux scores aléatoires.

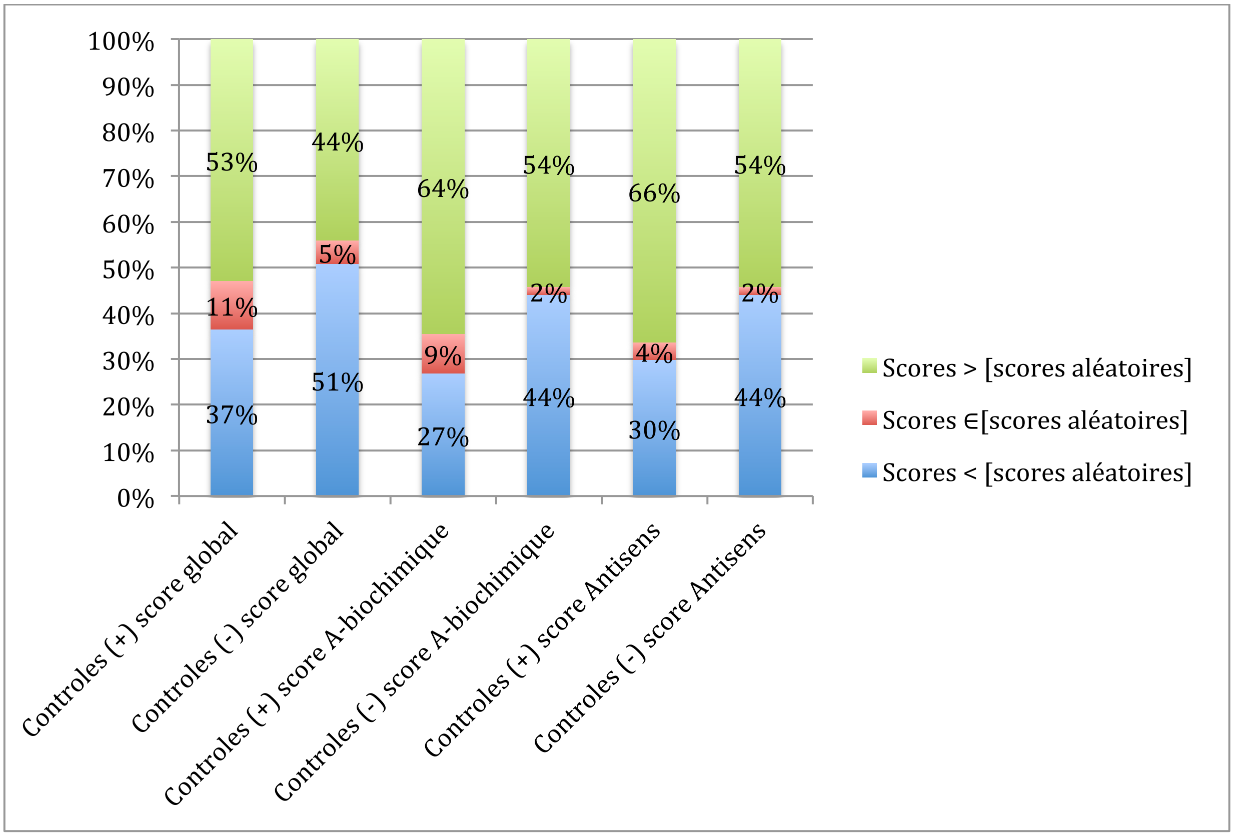

Figure 11. Répartition des scores des contrôles positifs et négatifs par rapport à l'intervalle des scores aléatoires.

Chapitre 5 Discussion et Conclusion

5.1 Indication de tendances

Les résultats de l'analyse de scores de motifs présentés au chapitre 3 nous ont permis d'identifier les structures les plus abondantes et rares dans tous les ARN de Rfam. Nous avons utilisé ces données pour élaborer un système de score en vue de développer un filtre visant à accélérer la découverte de nouveaux ARNnc. Nous avons testé ce nouveau système de scores RNAscore sur différents types de contrôles afin d'évaluer son applicabilité. RNAscore a été raffiné en deux versions spécifiques aux groupes «activité biochimique » et « antisens ». Cette partition a été motivée par les préférences spécifiques de ces groupes pour certains motifs, une différence qui a été démontrée statistiquement. Le groupe « activité biochimique » contient les familles d'ARNnc dont la structure a l'équivalent d'un site catalytique ou d'une pochette de liaison de ligand (analogue à ce que l'on trouverait chez une protéine) alors que le second groupe, comme son nom l'indique, regroupe les familles d'ARNnc ayant en commun une activité antisens. Au chapitre précédent, nous avons présentés les scores obtenus pour les contrôles avec nos trois versions de RNAscore.

Ces résultats nous ont permis de déceler une tendance où les moyennes des scores des vrais ARN (contrôles positifs) sont légèrement plus élevées que celles des contrôles négatifs. Les nouvelles familles de Rfam 11.0 ainsi que les faux ARN ont des scores moyens supérieurs à la moyenne de scores obtenus à partir de collections aléatoires de motifs. Ceci confirme que l'occurrence des motifs dans les ARNnc n'est pas aléatoire et que tous les motifs n'ont pas la même probabilité de se retrouver dans un ARN structuré.

Cette même tendance a été observée pour les motifs qui ont été mutés dans des études expérimentales. Le score global des motifs de type sauvage est plus élevé que le score de ces mêmes motifs lorsqu'ils subissent une mutation avec perte de fonction; ce qui indiquerait que les motifs de type sauvage (vrais ARN) ont un score plus élevé que les faux ARN. Par contre la tendance est inversée lorsque la mutation n'affecte pas la fonction ou si la mutation en augmente l'activité, le score est légèrement supérieur ou ne change pas. Une corrélation probable entre le score d'abondance et l'activité (affinité au substrat) de l'ARN serait un aspect intéressant à étudier pour les ARN tels que les ribozymes et riboswitchs.

D'un autre côté, nous avons trouvé que la différence des Q-scores calculés selon les deux versions de RNAscore, «activité biochimique » et « antisens », est statistiquement significative ce qui indique la pertinence des versions de RNAscore spécifiques aux groupes. La comparaison des Q-scores calculés d'un ARN pourrait aider à déterminer son appartenance au groupe de la version de RNAscore qui donne le Q-score le plus élevé. Cela serait particulièrement utile pour les ARNnc putatifs pour lesquels nous avons peu d'indice sur la fonction, par exemple lorsque le contexte génomique est peu connu (comme dans plusieurs études métagénomiques).

5.2 Faible pouvoir discriminant comme filtre

En testant RNAscore sur les différents contrôles, nous avons tenté d'établir les intervalles de valeurs que des ARNnc peuvent avoir comme scores. Notre hypothèse est que les scores des vrais ARN seraient supérieurs aux scores des faux ARN avec des intervalles bien distincts ou un minimum de chevauchement.

Les résultats de scores n'ont pas été discriminants entre les contrôles positifs et négatifs malgré les tendances observées. Pour être discriminant et utile dans le contexte d'un filtre permettant de classer des ARNnc prédits en fonction de leur vraisemblance, il eut fallu un accord beaucoup plus marqué entre les contrôles positifs et négatifs. Présentement, l'application de ces scores comme filtre risquerait soit de causer le rejet de nombreuses prédictions valides, soit de mener à l'étude d'un grand nombre de faux-positifs.

La table 12 résume toutes les moyennes de scores calculées et tenant compte des écarts-types, les intervalles de valeurs de scores des différents types de contrôles se chevauchent.

	RnaScore				*Biochemical* RnaScore				*Antisense* RnaScore			
Contrôles	Q	É-T	Z	É-T	Q	É-T	Z	É-T	Q	É-T	Z	É-T
validation	0.54	0.09	0.85	0.11	0.56	0.09	0.85	0.11	0.51	0.11	0.86	0.11
contrôles positifs	0.53	0.17	0.83	0.11	0.51	0.17	0.82	0.11	0.55	0.15	0.84	0.12
contrôles négatifs	0.51	0.18	0.83	0.12	0.52	0.19	0.82	0.12	0.52	0.16	0.83	0.13

Table 12. Comparaison des résultats de RNAscore sur les différents contrôles.
La colonne Q désigne le score relatif à la séquence des motifs scorés alors que la colonne Z représente le score basé uniquement sur la taille de tous les motifs de l'ARN en question. É-T : Écart-Type.

La taille des échantillons des contrôles négatifs est l'une des difficultés rencontrées dans ce projet. La conception des faux ARN à partir de séquences codantes et/ou brouillées n'était pas très efficace, ne générant souvent pas de résultats. Nous notons aussi que dans le cas où CMfinder trouve des candidats de faux ARN, le programme tente de donner les meilleures solutions ce qui favorise des structures très stables tout en réduisant les séquences de départ en nombre et en longueur. Ceci pourrait expliquer les scores élevés obtenus pour certains contrôles négatifs. Le Q-score est aussi limité par les motifs scorés ce qui pourrait affecter la qualité des scores basés sur la séquence. Cela pourrait ne refléter qu'une faible portion du contenu en motifs et ne serait pas assez représentatif (bien que la plupart des 104 nouvelles familles analysées de Rfam aient au moins un motif scoré, seulement huit d'entre elles ont tous leurs motifs qui sont scorés).

Pour contourner ces limitations, nous avons comparé les scores obtenus pour les nouvelles familles aux scores des faux ARN en prenant comme référence l'intervalle de valeurs des scores aléatoires. Les résultats à la fin du chapitre précédent montrent que l'échantillon de contrôles positifs contient plus d'ARN ayant un score dépassant la borne supérieure de l'intervalle aléatoire. Même si ces résultats indiqueraient que les vrais ARN ont un biais vers des scores plus élevés que des scores aléatoires, les contrôles négatifs n'ont pas donné de résultats concluants qui appuieraient cette hypothèse.

Certains des résultats décevant quant aux différences marginales entre les contrôles positifs et négatifs pourraient être expliqués par le fait que CMfinder utilise déjà certains motifs bien connus (tel que le GNRA) pour faire ses prédictions. Puisque les motifs avec le plus grand pouvoir discriminant sont ceux situés aux extrêmes des listes de scores, les motifs particulièrement abondant seront surreprésentés dans les vrais ARN, alors que les motifs très rares (dont ni CMfinder, ni la plupart des outils de prédiction ne tiennent compte) ne seront pas plus, ni moins, représentés que n'importe quel autre motif dans un faux-positifs, ce qui donnent en définitive assez peu de poids aux motifs à cet extrême de la liste de score. La majorité des motifs qui seraient trouvés dans de fausses prédictions d'ARNnc seraient soit bien scorés (car il y a un biais en ce sens dû aux outils de prédictions) soit neutres (car la plupart des motifs ont un faible écart de fréquence entre eux) et seuls quelques prédictions auraient « par chance » suffisamment des motifs rares permettant potentiellement de les désigner comme de faux-positifs.

5.3 Approches envisagées pour approfondir et améliorer

5.3.1. Subdiviser par clan

Notre approche consistait à compiler les familles de Rfam en 23 catégories afin de calculer un score d'abondance qui est une moyenne de log de ratios d'occurrence d'un motif précis. Pour améliorer la représentativité des motifs rares, nous avons réduit les 23 catégories en 6 supercatégories. Nous pensons qu'il serait pertinent de tester une approche différente dans la compilation des catégories pour améliorer le système de score telle que subdiviser les familles de Rfam par clan et recalculer les scores d'abondance. Ceci diminuerait les occurrences totales des motifs vu qu'un clan risque d'être beaucoup plus petit qu'une catégorie ou supercatégorie. Cependant cette approche augmenterait vraisemblablement la spécificité et permettrait d'obtenir une meilleure discrimination au niveau de RNAscore. Un désavantage de cette approche serait de réduire le pouvoir discriminant de la plupart des motifs très rares, mais comme noté plus haut, ces derniers s'avèrent peu utiles. Il s'agirait donc d'un sacrifice acceptable. Ce qui est plus problématique est que même certains motifs

« intermédiaires » sont peu ou pas représentés dans certains clans. Le deuxième désavantage serait de rendre beaucoup plus complexe la compilation et l'utilisation des scores si les clans sont ensuite compilés dans des systèmes de scores qui auraient plus de deux versions.

5.3.2. Tenir compte des espèces et de la composition en GC

La composition en nucléotides a été utilisée dans la recherche de nouveaux ARNnc (132,133). En effet, comme la structure des ARNnc est plus importante que pour les région codante ou les promoteurs, il y a un nombre minimal de paires de bases GC qui est requis pour avoir des structures stables(134). Ainsi, une région avec un %GC plus élevé peut être indicatrice de la présence d'un ARNnc. Chez des organismes à faible %GC cela peut représenter un pouvoir discriminant intéressant. Les ARNnc ont des biais de séquence qui existent chez certains organismes plus que d'autres. Il serait donc intéressant d'intégrer le %GC des régions de l'ARN qui forme des paires de base pour réaliser un filtre tenant compte de ces contraintes de façon plus précise que les études précédentes.

Un autre point majeur qui n'a pas été abordé dans notre étude concerne les variations entre espèces. En effet, la proportion des bases qui entre dans la composition des génomes varie grandement selon le groupe taxonomique concerné. Ainsi, *Streptomyces coelicolor* a un %GC de 72%, alors que pour *Saccharomyces cerevisiae* il est de 38% (135). Au-delà des paires de bases, cela a évidemment un impact sur les probabilités de trouver simplement par hasard des boucles GAAA ou GCGC par exemple. Cette information pourrait servir à mieux classifier la rareté ou l'abondance de motifs donnés en pondérant ceux-ci selon le %GC du motif et le %GC du génome de l'organisme d'où origine la séquence. Ainsi, nous avons simplifié l'analyse en considérant comme uniforme les probabilités d'occurrence aléatoire pour chaque motif (une chance sur 256). En réalité, pour la boucle GCGC les probabilités basées sur le %GC de *S. coelicolor* et de *S. cerevisiae* donneraient ~1/60 $((1/(72/2))^4)$ et ~1/767 $((1/(38/2))^4)$, respectivement, et seraient de ~1/1012 $((1/(72/2))*(1/(28/2))^3)$ et ~1/177 $((1/(38/2))*(1/(62/2))^3)$ pour la boucle GAAA pour les deux mêmes espèces. En d'autres mots, si GCGC est très rare chez *S. coelicolor* ou GAAA très abondant, cela renforcerait encore plus leurs caractères extrêmes. Cependant, une telle pondération implique de connaître le %GC du génome de l'organisme, ce qui n'est pas toujours le cas pour les séquences d'ARN trouvées dans Rfam. Cela sous-entend aussi que la distribution de ce %GC est uniforme dans le génome, ce que nous savons n'est pas le cas. Il n'est donc pas clair de quelle façon une pondération devrait être implémentée.

De plus, en tenant compte des différences entre espèces, nous pourrions potentiellement mieux expliquer certaines des fréquences observées. Par exemple, une séquence donnée étant liée par une protéine ribosomale pourrait se trouver à être particulièrement rare dans l'ensemble des ARN d'un organisme parce qu'autrement elle se trouverait liée par la très abondante protéine ribosomale. À l'opposé, la surreprésentation de certaines séquences dans certains groupes taxonomiques pourrait aussi correspondre un avantage notable de pouvoir lier une protéine donnée, telle que la protéine Hfq qui lie les petits ARN bactériens via leur séquence AU riche.

5.3.3. Évaluer d'autres éléments structuraux

Hormis les boucles et « bulges », d'autres parties de la structure des ARN seraient intéressantes à évaluer, notamment les paires de bases des tiges. Celles-ci sont primordiales à la formation de la structure secondaire et tertiaire. Néanmoins, bien que cet aspect soit plutôt bien étudié du point de vue des prédictions de structure et thermodynamique, il ne l'est pas autant pour ce qui est de biais potentiels, et de leurs implications, du point de vue biologique. Certains exemples sont connus et étudiés, comme la possibilité de glissement de l'ARN polymérase lors de la synthèse de régions homopolymères. Par contre, la diversité de composition, le nombre de paires de bases Wobble, la présence de répétitions ou la présence de motifs particuliers sont autant d'avenues qui pourraient être explorées d'une façon analogue à ce qui a été fait pour les régions dites « simple brin » dans ce mémoire.

5.4 Conclusion

Dans ce travail, nous avons identifié des caractéristiques communes et rares de tous les ARN non-codant disponibles dans la base de données Rfam. Nous avons exploré l'abondance des structures secondaires de l'ARN d'une façon différente de ce qui a été fait précédemment. Une base de données locale RNAstem a été créée pour faciliter l'extraction et la compilation des données sur la structure secondaire des alignements de Rfam.

Nous avons exploité ces données pour calculer un score d'abondance qui nous a permis d'étudier la fréquence des boucles terminales, des « bulges » et des boucles internes. Ce score corrige le biais de la surreprésentation de certaines classes d'ARN telle que l'ARN ribosomal et permet d'avoir une précision qu'on n'a pas en se basant uniquement sur les occurrences des motifs. Nos résultats confirment ce qui est déjà connu pour des boucles communes et qui ont été très étudiées comme les boucles de type GNRA ou UNCG. Notre travail a aussi permis d'identifier des motifs abondants qui n'ont pas été étudié auparavant tel que la boucle terminale UUUU. De plus, nous avons relevé une rareté surprenante pour certains motifs, ce qui n'avait pas été soulevé précédemment.

Nous avons exploré la possibilité d'utiliser ces scores pour la conception d'un filtre pour les candidats de nouveaux ARN non-codants. Dans cette perspective, nous avons développé un système de scores, RNAscore, qui permet d'évaluer un ARN en se basant sur son contenu en motifs et nous avons testé son applicabilité avec différents contrôles. Malgré que notre approche se soit avérée inefficace pour la discrimination entre des vrais ARN et de faux ARN, il y a un potentiel de perfectionnement de la méthode et nos résultats d'analyses ouvrent des pistes intéressantes pour de futures recherches.

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Annexe

A

	64 triloop sequences							
23 Categories	AAA	AAC	AAG	AAU	…	UUA	UUC	UUG	UUU
5S	20	5	25	11	…	7	4	49	13
5_8S	195	587	26	9048	…	129	127	446	253
antisense	136	16	0	24	…	9	61	0	7
CD-box	2	3	0	15	…	79	91	73	316
Cis-Reg	323	15	346	105	…	14352	135	2044	197
CRISPR	199	48	0	215	…	0	51	13	99
Gene	1096	36	192	57	…	435	42	85	189
HACA-box	26	227	13	41	…	14	197	69	1389
Intron	2157	200	94	184	…	203	27	89	296
IRES	45	3	487	19	…	53	61	18	163
leader	78	8	66	11	…	10	1	21	220
miRNA	17	36	32	11	…	17	6	5	9
riboswitch	102	12	45	40	…	330	62	66	145
ribozyme	48	415	10	27	…	348	20	52	316
scaRNA	8	0	1	0	…	0	1	0	0
snRNA	0	0	2	0	…	4	3	78	75
splicing	208	32	110	167	…	82	69	46	388
SSU_rRNA_archaea	63	36	132	324	…	131	91	92	455
SSU_rRNA_bacteria	549	534	207	1878	…	1778	1759	1075	4585
SSU_rRNA_eukarya	537	341	333	788	…	1015	2881	324	4633
T-box	92	12	4	54	…	67	99	47	174
Thermoregulator	356	1	9	43	…	1	0	2	30
tRNA	533	54	8	282	…	368	226	60	5939
Average logs of ratio	**-1.82**	**-2.38**	**-2.43**	**-2.02**	…	**-2.02**	**-2.16**	**-2.13**	**-1.55**

B

RRNA-small subunit		rRNA- 5S		riboswitch		miRNA		Ribozyme		snoRNA		tRNA	
CACG	14370	CCUC	455	**AAAA**	**68**	CUGU	527	**AAUA**	**418**	CCAG	120	**AGCA**	**197**
CUUG	14654	AUGA	565	**AUAA**	**70**	**CCAU**	**559**	**UUCG**	**444**	**AGCA**	**121**	AUAU	209
UAAG	15858	UUAA	599	AACU	73	GCUA	642	**UUUG**	**454**	UAGU	140	UGCA	210
UUUU	**15958**	**GCGA**	**647**	GAUU	90	AAGG	665	GUUG	532	UUAU	145	UUAU	225
AUCC	16827	GUUU	718	UCCC	100	**UAUA**	**945**	**UAUA**	**1170**	**AAAG**	**148**	AAUU	290
CAGG	19781	UUGA	799	UAUU	112	CUGC	1067	UAAA	1633	**UUCG**	**153**	**AAAA**	**424**
CUAG	21851	GAGG	1270	GCCC	144	CCAC	1134	**GCGA**	**1903**	UCAU	160	AGUA	425
CUCG	27107	**UACU**	**1353**	**GCGA**	**183**	CAUC	1151	CAAA	2002	CAAU	162	AUUU	477
UAUG	29737	**GAAA**	**1574**	**GUAA**	**248**	**GUCA**	**1330**	**AAAA**	**2613**	GAGU	178	**AAGA**	**515**
UAGG	36566	UCAC	1690	**UUUU**	**282**	**AAAA**	**1676**	GCAA	2802	**CCAU**	**179**	UGUU	613
UUAG	39965	GUCU	1762	ACCC	299	GAUG	1844	**GAGA**	**2891**	UUCU	193	**AACA**	**763**
CAAG	54891	**AAGA**	**1879**	GCAA	330	UCCA	2001	**GUUA**	**3537**	**UUUG**	**224**	**ACAA**	**1146**
UUCG	**405403**	GGGA	3277	**GUGA**	**353**	CUUU	2249	**GUGA**	**3539**	**GUCA**	**339**	**AAUA**	**1385**
GAAA	**638332**	**GUUA**	**4759**	**GAGA**	**445**	ACCA	3173	GUAA	4119	UUGU	399	AUUA	1466
GAGA	**645891**	**GUGA**	**32435**	CCCC	1528	GCCA	13484	**GUCA**	**20208**	**UUUU**	**408**	AGUG	5764
UACG	654193	**GAGA**	**39380**	**GAAA**	**1981**	**AAAG**	**16667**	**GAAA**	**36128**	UCUU	421	**AUAA**	**7519**
	2838711		101670		8912		63794		95901		8508		26332

Figure 12. Partial score calculation matrix for triloops (top) and common tetraloops (bottom).

The matrix is used to calculate the abundance score. For each triloop sequence, we have the occurrences in each of the 23 categories (example: triloop “AAA” there are 20 in 5S, 195 in 5.8S etc.). The log of the ratios occurrence/total number of loops are calculated for each cell of the matrix, then the average (seen at the bottom line) is used as an abundance score. Common motifs in one category are often among the most abundant in other categories as some tetraloops highlighted by different colors (bottom). Fro example, there are 645891 GAGA tetraloop in small subunit rRNA, 39380 GAGA in 5S, 445 in riboswitch category etc. Occurrences were compiled from an earlier version of Rfam (version 9). Bottom line shows the total number of tetraloops in each category (2838711 tetraloops in rRNA-small subunit).

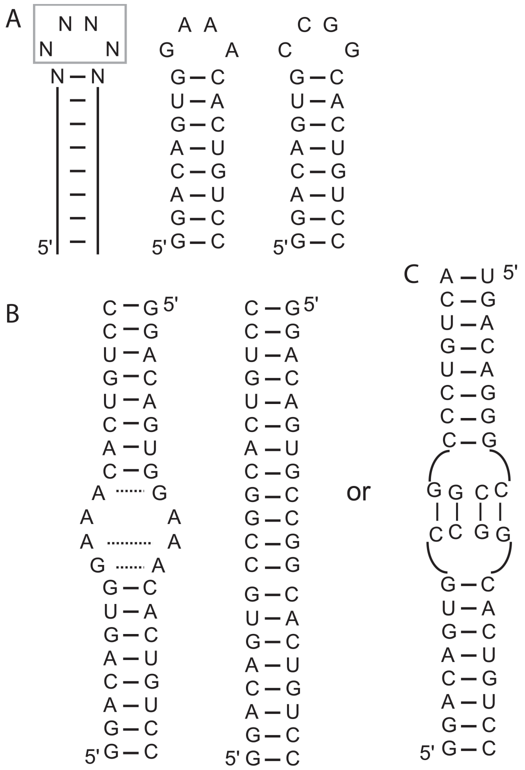

Figure 13. Possible intermolecular interactions.

(A) Small stem-loop model where the tetraloop changes. (B)-(C) Potential intermolecular base-pairs. Palindromic loops permit formation of uninterrupted helices.

Tables de scores S1 à S40 (supplementary data)

Table S1. Terminal loops-size

Range 4.818 * Median = max score - range/2
Median -3.079 * Centered score = score - range

Loop size	Score	SD	Centered Score
4	-0.670	0.458	2.41
6	-1.031	0.438	2.05
7	-1.243	0.569	1.84
5	-1.250	0.372	1.83
3	-1.366	0.502	1.71
8	-1.527	0.639	1.55
9	-1.731	0.640	1.35
10	-1.771	0.509	1.31
11	-2.054	0.813	1.03
2	-2.076	0.521	1.00
12	-2.300	0.843	0.78
1	-2.329	0.635	0.75
16	-2.680	0.989	0.40
13	-2.692	0.873	0.39
21	-2.777	1.091	0.30
20	-2.784	0.853	0.29
14	-2.803	1.087	0.28
18	-2.805	1.113	0.27
15	-2.815	1.057	0.26
17	-2.852	0.926	0.23
24	-2.955	0.710	0.12
19	-2.961	0.987	0.12
22	-2.994	0.970	0.08
23	-2.996	0.802	0.08
26	-3.166	0.880	-0.09
25	-3.215	0.932	-0.14
27	-3.291	1.295	-0.21
31	-3.377	1.075	-0.30
32	-3.473	1.152	-0.39
33	-3.497	1.095	-0.42
29	-3.498	1.359	-0.42
30	-3.592	1.266	-0.51
28	-3.656	1.434	-0.58
34	-3.739	1.084	-0.66
35	-3.837	1.208	-0.76
39	-3.843	1.154	-0.76
36	-3.884	1.111	-0.81
44	-3.890	1.203	-0.81
40	-3.930	1.210	-0.85
38	-4.008	1.177	-0.93
37	-4.097	1.166	-1.02
41	-4.180	1.147	-1.10
43	-4.249	1.152	-1.17
42	-4.282	1.258	-1.20
45	-4.299	1.214	-1.22
50	-4.343	1.185	-1.26
49	-4.372	1.165	-1.29
46	-4.412	1.116	-1.33
48	-4.412	1.118	-1.33
53	-4.428	1.135	-1.35
51	-4.450	1.123	-1.37
56	-4.457	1.063	-1.38
58	-4.475	1.181	-1.40
52	-4.475	1.084	-1.40
47	-4.480	1.119	-1.40
55	-4.536	1.120	-1.46
59	-4.541	1.216	-1.46
68	-4.549	1.380	-1.47
54	-4.574	1.142	-1.49
60	-4.576	1.048	-1.50
64	-4.586	1.152	-1.51
70	-4.601	1.230	-1.52
57	-4.614	1.019	-1.53
65	-4.614	1.049	-1.54
66	-4.624	1.042	-1.55

Loop size	Total loop count
4	6592509
7	3717336
6	1936636
8	1340414
5	1312907
9	673098
10	501550
3	470144
11	106760
32	100969
18	76722
12	76158
16	66462
2	58286
33	42384
26	40248
1	31612
27	27319
20	24058
14	21160
13	20907
22	18079
68	16263
24	15833
15	14392
19	14270
21	13290
30	12884
25	11158
23	10809
31	9162
17	9097
28	8327
29	7357
39	5300
44	3931
34	3459
40	2718
35	2503
70	2380
42	2114
38	1654
36	1513
45	1147
37	1105
75	1096
50	896
191	880
256	850
49	811
58	766
41	755
51	741
43	717
63	674
59	673
251	658
82	638
48	614
56	579
53	575
259	570
81	569
55	562
65	534

Category	Total loop count
5S	227478
5_8S	897420
Cis-reg	465113
Intron	255227
IRES	73612
leader	7320
riboswitch	71854
ribozyme	70005
snRNA	4764
splicing	151349
SSU_rRNA_archaea	262796
SSU_rRNA_bacteria	10327624
SSU_rRNA_eukarya	1307222
T-box	37661
thermoregulator	4648
tRNA	3307769

63	-4.633	1.174	-1.55
67	-4.655	1.118	-1.58
61	-4.670	1.081	-1.59
71	-4.684	1.099	-1.60
79	-4.721	1.074	-1.64
62	-4.728	1.086	-1.65
80	-4.741	1.114	-1.66
77	-4.755	1.018	-1.68
75	-4.755	1.210	-1.68
85	-4.759	1.049	-1.68
69	-4.773	0.959	-1.69
72	-4.776	1.039	-1.70
78	-4.786	1.054	-1.71
91	-4.790	0.993	-1.71
74	-4.793	1.059	-1.71
83	-4.821	1.065	-1.74
76	-4.822	1.118	-1.74
81	-4.834	1.055	-1.76
82	-4.857	1.100	-1.78
84	-4.860	1.068	-1.78
73	-4.870	1.055	-1.79
88	-4.900	1.075	-1.82
87	-4.941	1.133	-1.86
86	-4.946	1.075	-1.87
90	-4.972	0.971	-1.89
94	-4.972	1.017	-1.89
92	-4.989	1.011	-1.91
98	-5.003	0.963	-1.92
95	-5.003	1.131	-1.92
107	-5.026	1.061	-1.95
114	-5.058	0.959	-1.98
89	-5.061	0.960	-1.98
103	-5.064	1.019	-1.99
101	-5.073	0.991	-1.99
96	-5.074	1.038	-2.00
93	-5.076	1.066	-2.00
104	-5.083	0.976	-2.00
129	-5.086	0.994	-2.01
120	-5.095	1.049	-2.02
102	-5.102	0.983	-2.02
105	-5.102	0.977	-2.02
132	-5.103	1.013	-2.02
125	-5.111	0.906	-2.03
108	-5.112	1.006	-2.03
113	-5.113	0.937	-2.03
99	-5.114	0.964	-2.03
128	-5.114	0.971	-2.04
124	-5.125	0.987	-2.05
112	-5.129	0.983	-2.05
100	-5.130	1.001	-2.05
142	-5.137	1.116	-2.06
117	-5.142	0.951	-2.06
191	-5.143	1.198	-2.06
97	-5.144	1.031	-2.07
106	-5.147	0.954	-2.07
148	-5.148	0.945	-2.07
130	-5.158	1.121	-2.08
109	-5.159	1.075	-2.08
131	-5.171	1.106	-2.09
115	-5.175	1.057	-2.10
121	-5.178	0.934	-2.10
118	-5.180	1.023	-2.10
149	-5.188	1.079	-2.11
185	-5.189	1.066	-2.11
170	-5.189	1.100	-2.11
110	-5.191	1.038	-2.11
139	-5.191	1.046	-2.11
126	-5.194	0.984	-2.11
133	-5.194	1.045	-2.12

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241	182
185	177
103	175
239	173
72	168
142	167
265	166
273	166
232	160

123	-5.195	1.056	-2.12
147	-5.199	0.992	-2.12
141	-5.203	1.099	-2.12
138	-5.206	1.029	-2.13
143	-5.207	0.955	-2.13
192	-5.209	1.013	-2.13
168	-5.210	0.958	-2.13
146	-5.213	1.045	-2.13
152	-5.214	1.059	-2.14
184	-5.217	0.998	-2.14
186	-5.218	1.034	-2.14
167	-5.218	0.988	-2.14
181	-5.220	1.055	-2.14
153	-5.222	1.054	-2.14
187	-5.225	1.038	-2.15
251	-5.228	1.165	-2.15
140	-5.231	0.978	-2.15
248	-5.233	1.087	-2.15
116	-5.234	1.019	-2.16
155	-5.235	0.980	-2.16
111	-5.236	0.908	-2.16
218	-5.237	1.038	-2.16
134	-5.237	1.020	-2.16
119	-5.237	0.975	-2.16
238	-5.239	1.121	-2.16
268	-5.242	1.129	-2.16
256	-5.242	1.189	-2.16
151	-5.242	0.928	-2.16
201	-5.244	1.035	-2.16
188	-5.245	1.057	-2.17
196	-5.247	1.045	-2.17
122	-5.249	0.898	-2.17
269	-5.250	1.150	-2.17
259	-5.253	1.162	-2.17
176	-5.253	1.016	-2.17
171	-5.253	1.014	-2.17
270	-5.256	0.997	-2.18
255	-5.256	1.156	-2.18
250	-5.257	1.153	-2.18
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236	-5.258	1.127	-2.18
241	-5.259	1.085	-2.18
249	-5.260	1.147	-2.18
156	-5.260	0.995	-2.18
260	-5.260	1.146	-2.18
252	-5.261	1.120	-2.18
227	-5.261	1.044	-2.18
226	-5.263	1.086	-2.18
159	-5.263	0.912	-2.18
198	-5.264	1.061	-2.19
210	-5.266	1.011	-2.19
158	-5.266	1.001	-2.19
190	-5.266	1.056	-2.19
232	-5.267	1.079	-2.19
150	-5.268	0.996	-2.19
144	-5.269	0.988	-2.19
261	-5.269	1.102	-2.19
262	-5.270	1.100	-2.19
239	-5.270	1.084	-2.19
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266	-5.289	1.119	-2.21
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234	-5.290	1.116	-2.21
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233	-5.291	1.078	-2.21
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276	-5.295	1.049	-2.22
209	-5.296	1.011	-2.22
174	-5.296	1.001	-2.22
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193	-5.299	1.005	-2.22
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285	-5.300	1.027	-2.22
273	-5.300	1.095	-2.22
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294	-5.309	1.044	-2.23
277	-5.310	1.076	-2.23
222	-5.310	1.002	-2.23
211	-5.311	1.001	-2.23
221	-5.311	0.984	-2.23
291	-5.312	1.072	-2.23
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281	-5.318	1.011	-2.24
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215	-5.319	0.974	-2.24
225	-5.320	1.025	-2.24
189	-5.320	1.008	-2.24
195	-5.321	1.006	-2.24

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275	-5.336	1.108	-2.26
293	-5.339	1.025	-2.26
253	-5.340	1.101	-2.26
216	-5.340	0.980	-2.26
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219	-5.346	0.987	-2.27
301	-5.348	0.987	-2.27
205	-5.351	0.958	-2.27
214	-5.355	0.963	-2.28
283	-5.357	0.997	-2.28
315	-5.359	1.067	-2.28
331	-5.359	0.996	-2.28
278	-5.359	1.066	-2.28
296	-5.363	0.990	-2.28
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212	-5.367	0.962	-2.29
332	-5.371	0.959	-2.29
314	-5.375	0.975	-2.30
323	-5.375	0.975	-2.30
320	-5.378	0.972	-2.30
172	-5.381	0.932	-2.30
302	-5.384	0.966	-2.31
424	-5.388	0.944	-2.31
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341	-5.398	0.931	-2.32
346	-5.400	0.939	-2.32
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407	-5.405	0.932	-2.33
455	-5.405	0.932	-2.33
410	-5.408	0.935	-2.33
425	-5.411	0.934	-2.33
309	-5.411	0.995	-2.33
313	-5.411	0.995	-2.33
316	-5.411	0.995	-2.33
305	-5.414	0.991	-2.34
308	-5.414	0.945	-2.34
317	-5.414	0.987	-2.34
322	-5.414	0.991	-2.34
406	-5.414	0.934	-2.34
428	-5.414	0.934	-2.34
448	-5.414	0.934	-2.34
451	-5.414	0.934	-2.34
460	-5.414	0.934	-2.34
492	-5.414	0.945	-2.34
373	-5.423	0.933	-2.34
307	-5.428	0.940	-2.35
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408	-5.428	0.933	-2.35
414	-5.428	0.933	-2.35
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417	-5.428	0.933	-2.35
426	-5.428	0.933	-2.35
439	-5.428	0.933	-2.35
449	-5.428	0.933	-2.35

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384	-5.435	0.933	-2.36
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423	-5.435	0.933	-2.36
432	-5.435	0.933	-2.36
446	-5.435	0.933	-2.36
450	-5.435	0.933	-2.36
468	-5.435	0.933	-2.36
478	-5.435	0.933	-2.36
303	-5.444	0.970	-2.37
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372	-5.444	0.935	-2.37
387	-5.444	0.935	-2.37
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413	-5.444	0.935	-2.37
415	-5.444	0.935	-2.37
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385	-5.488	0.965	-2.41
386	-5.488	0.965	-2.41
389	-5.488	0.965	-2.41

394	1
398	1
400	1
403	1
404	1
409	1
411	1
412	1
420	1
421	1
422	1
434	1
435	1
437	1
440	1
441	1
442	1
444	1
445	1
454	1
456	1
464	1
465	1
466	1
469	1
472	1
473	1
474	1
475	1
489	1
490	1
494	1
506	1
510	1
516	1
531	1
675	1
756	1
918	1
312	0
319	0
321	0
326	0
330	0
335	0
336	0
338	0
342	0
343	0
344	0
347	0
352	0
353	0
354	0
359	0
360	0
362	0
363	0
364	0
368	0
369	0
374	0
375	0
378	0
379	0
383	0
385	0
386	0
389	0

Range 4.547 * Median = max score - range/2
Median -2.603 * Centered score = score - range

Bulge size	Score	SD	Centered score
1	-0.329	0.363	2.27
2	-1.039	0.659	1.56
3	-1.622	0.636	0.98
4	-1.882	0.579	0.72
5	-2.051	0.774	0.55
6	-2.448	1.056	0.15
7	-2.719	1.212	-0.12
8	-2.900	1.262	-0.30
9	-3.292	1.186	-0.69
10	-3.400	1.129	-0.80
11	-3.543	1.297	-0.94
12	-3.782	1.318	-1.18
13	-4.015	1.271	-1.41
14	-4.020	1.212	-1.42
20	-4.076	1.057	-1.47
15	-4.190	1.236	-1.59
19	-4.200	1.175	-1.60
22	-4.255	1.136	-1.65
18	-4.263	1.149	-1.66
21	-4.309	1.209	-1.71
16	-4.324	1.236	-1.72
17	-4.329	1.030	-1.73
27	-4.456	1.048	-1.85
23	-4.540	0.969	-1.94
24	-4.559	0.956	-1.96
26	-4.576	1.246	-1.97
29	-4.579	1.253	-1.98
32	-4.597	1.063	-1.99
30	-4.603	1.184	-2.00
28	-4.606	1.098	-2.00
43	-4.608	1.085	-2.01
25	-4.609	1.161	-2.01
35	-4.614	1.211	-2.01
31	-4.624	1.239	-2.02
38	-4.625	1.139	-2.02
39	-4.637	1.187	-2.03
41	-4.638	1.253	-2.03
42	-4.648	1.166	-2.05
36	-4.665	1.077	-2.06
33	-4.674	1.147	-2.07
34	-4.686	1.224	-2.08
40	-4.696	1.133	-2.09
45	-4.699	1.101	-2.10
51	-4.711	1.110	-2.11
44	-4.714	1.192	-2.11
37	-4.720	1.182	-2.12
75	-4.733	0.966	-2.13
50	-4.742	1.073	-2.14
47	-4.744	1.184	-2.14
48	-4.747	1.154	-2.14
58	-4.747	0.983	-2.14
46	-4.751	1.172	-2.15
49	-4.755	1.080	-2.15
57	-4.766	1.066	-2.16
56	-4.767	1.035	-2.16
73	-4.767	1.035	-2.16
68	-4.773	1.035	-2.17
70	-4.781	0.913	-2.18
55	-4.787	1.046	-2.18
63	-4.787	1.046	-2.18
54	-4.789	1.117	-2.19
52	-4.794	1.111	-2.19
59	-4.794	1.040	-2.19
72	-4.794	0.923	-2.19
238	-4.799	0.983	-2.20

Bulge size	Total bulge count
1	6475290
2	3080948
3	1687125
5	412601
6	356905
4	126436
7	63217
8	11832
9	2275
11	1755
19	1077
10	872
12	858
22	635
20	357
13	327
14	315
15	286
16	208
29	193
18	183
27	155
21	152
31	146
26	112
35	108
43	99
33	97
32	89
28	83
34	80
30	78
38	78
41	78
17	64
47	64
37	53
42	53
39	49
46	49
25	47
36	46
51	45
40	44
23	40
45	39
24	31
44	31
50	24
48	20
49	15
54	12
52	10
57	10
75	9
58	8
238	8
56	7
73	7
53	6
70	6
219	6
55	5
63	5
240	5

Category	Total bulge count
5S	118098
5_8S	2091
Cis-reg	184311
Intron	8791
IRES	22358
leader	2959
riboswitch	24399
ribozyme	38421
snRNA	823
splicing	35286
SSU_rRNA_archaea	242068
SSU_rRNA_bacteria	10073315
SSU_rRNA_eukarya	1356770
T-box	15175
thermoregulator	4559
tRNA	96539

61	-4.803	1.034	-2.20
67	-4.803	1.011	-2.20
94	-4.803	1.011	-2.20
53	-4.807	1.097	-2.20
219	-4.807	0.986	-2.20
240	-4.811	0.989	-2.21
64	-4.817	1.026	-2.21
82	-4.817	1.026	-2.21
239	-4.817	0.993	-2.21
71	-4.823	1.082	-2.22
84	-4.823	1.082	-2.22
62	-4.832	1.075	-2.23
79	-4.832	1.006	-2.23
146	-4.832	1.006	-2.23
165	-4.832	1.006	-2.23
174	-4.832	1.006	-2.23
177	-4.832	1.006	-2.23
201	-4.832	1.006	-2.23
216	-4.832	1.006	-2.23
217	-4.832	1.006	-2.23
218	-4.832	1.006	-2.23
233	-4.832	1.006	-2.23
309	-4.832	1.006	-2.23
60	-4.846	1.068	-2.24
65	-4.846	1.021	-2.24
69	-4.846	1.021	-2.24
76	-4.846	1.068	-2.24
77	-4.846	1.068	-2.24
78	-4.846	1.021	-2.24
85	-4.846	1.021	-2.24
86	-4.846	1.021	-2.24
91	-4.846	1.021	-2.24
93	-4.846	1.068	-2.24
97	-4.846	1.021	-2.24
99	-4.846	1.068	-2.24
100	-4.846	1.068	-2.24
107	-4.846	1.021	-2.24
110	-4.846	1.068	-2.24
111	-4.846	1.021	-2.24
132	-4.846	1.021	-2.24
166	-4.846	1.021	-2.24
180	-4.846	1.021	-2.24
188	-4.846	1.021	-2.24
191	-4.846	1.021	-2.24
192	-4.846	1.021	-2.24
195	-4.846	1.021	-2.24
197	-4.846	1.021	-2.24
203	-4.846	1.021	-2.24
211	-4.846	1.021	-2.24
214	-4.846	1.021	-2.24
215	-4.846	1.021	-2.24
222	-4.846	1.021	-2.24
228	-4.846	1.021	-2.24
230	-4.846	1.021	-2.24
236	-4.846	1.021	-2.24
237	-4.846	1.021	-2.24
241	-4.846	1.021	-2.24
246	-4.846	1.021	-2.24
247	-4.846	1.021	-2.24
66	-4.876	1.061	-2.27
74	-4.876	1.061	-2.27
80	-4.876	1.061	-2.27
81	-4.876	1.061	-2.27
83	-4.876	1.061	-2.27
87	-4.876	1.061	-2.27
88	-4.876	1.061	-2.27
89	-4.876	1.061	-2.27
90	-4.876	1.061	-2.27
92	-4.876	1.061	-2.27

59	4
68	4
72	4
239	4
61	3
67	3
71	3
84	3
94	3
62	2
64	2
79	2
82	2
146	2
165	2
174	2
177	2
201	2
216	2
217	2
218	2
233	2
309	2
60	1
65	1
69	1
76	1
77	1
78	1
85	1
86	1
91	1
93	1
97	1
99	1
100	1
107	1
110	1
111	1
132	1
166	1
180	1
188	1
191	1
192	1
195	1
197	1
203	1
211	1
214	1
215	1
222	1
228	1
230	1
236	1
237	1
241	1
246	1
247	1
66	0
74	0
80	0
81	0
83	0
87	0
88	0
89	0
90	0
92	0

Table S3. Internal loops-size

Range 3.847 * Median = max score - range/2
Median -3.079 * Centered score = score - range

5' size	3 'size	Score	SD	Centered Score
1	1	-1.156	1.048	1.92
1	2	-1.636	1.136	1.44
2	1	-1.803	0.756	1.28
2	2	-1.915	1.248	1.16
3	1	-2.059	1.021	1.02
1	3	-2.150	1.083	0.93
3	3	-2.198	1.345	0.88
3	2	-2.218	1.107	0.86
2	3	-2.322	0.965	0.76
4	3	-2.338	1.026	0.74
3	4	-2.491	1.247	0.59
4	1	-2.510	0.931	0.57
4	5	-2.553	0.966	0.53
5	5	-2.676	1.201	0.40
2	4	-2.694	1.076	0.39
5	1	-2.713	1.198	0.37
4	2	-2.717	0.860	0.36
6	5	-2.781	1.406	0.30
6	4	-2.799	1.157	0.28
4	4	-2.825	0.819	0.25
3	6	-2.868	1.236	0.21
3	5	-2.908	0.667	0.17
5	4	-2.911	1.087	0.17
6	3	-3.008	1.466	0.07
1	4	-3.089	1.096	-0.01
5	6	-3.117	1.126	-0.04
6	2	-3.133	1.105	-0.05
6	6	-3.150	1.147	-0.07
5	2	-3.157	1.039	-0.08
1	5	-3.177	1.227	-0.10
5	3	-3.330	0.940	-0.25
4	6	-3.341	0.710	-0.26
5	7	-3.379	1.394	-0.30
7	6	-3.396	1.264	-0.32
7	4	-3.403	0.872	-0.32
2	5	-3.420	0.978	-0.34
6	1	-3.442	0.953	-0.36
7	7	-3.548	1.449	-0.47
7	1	-3.587	1.086	-0.51
4	7	-3.587	0.914	-0.51
8	1	-3.634	1.151	-0.55
8	4	-3.669	1.184	-0.59
7	5	-3.672	1.169	-0.59
6	8	-3.672	1.518	-0.59
1	6	-3.673	1.000	-0.59
2	6	-3.692	0.967	-0.61
6	7	-3.710	1.204	-0.63
8	6	-3.732	1.329	-0.65
8	5	-3.790	1.072	-0.71
7	3	-3.795	1.083	-0.72
8	2	-3.796	1.172	-0.72
8	3	-3.846	1.187	-0.77
7	2	-3.863	1.112	-0.78
4	8	-3.876	1.248	-0.80
5	8	-3.887	0.925	-0.81
3	8	-3.931	1.151	-0.85
7	8	-3.965	1.378	-0.89
2	8	-3.966	1.185	-0.89
6	9	-3.975	1.361	-0.90
1	7	-3.993	0.921	-0.91
2	7	-4.004	1.049	-0.92
3	7	-4.024	0.878	-0.94
4	9	-4.075	1.221	-1.00
1	8	-4.081	0.814	-1.00
5	10	-4.091	1.025	-1.01
8	9	-4.095	1.226	-1.02

5' size	3 'size	Total i-loop count
3	3	1242499
2	2	1015455
3	4	931989
1	2	930514
1	1	731270
2	1	622137
3	2	433425
3	1	426903
4	2	420650
4	5	415644
6	4	410559
3	6	408370
5	7	395799
1	5	395067
6	5	389996
1	3	380526
2	4	358106
5	5	356249
4	3	336219
4	1	314319
4	10	200313
5	4	106450
2	3	89587
8	6	65994
5	6	56857
5	1	45267
7	6	24641
6	3	19320
7	4	18652
8	4	18028
4	4	17995
3	5	16398
3	8	13478
4	8	9416
4	9	9381
233	3	7567
1	4	7532
6	8	6736
7	5	5812
5	2	5287
4	11	5154
2	5	4942
5	3	4625
234	3	4611
6	6	4339
1	9	4174
4	7	3749
232	3	3734
7	7	3720
6	2	3523
4	6	3034
7	8	2994
1	18	2803
5	8	2759
3	7	2690
8	10	2470
7	13	2469
2	6	2377
8	3	2316
11	9	2306
235	3	2201
2	8	2181
8	13	2119
7	12	2064
7	15	1996
231	3	1990

Category	Total i-loop count
5S	776379
5_8S	225401
Cis-reg	318471
Intron	224397
IRES	71763
leader	3959
riboswitch	31854
ribozyme	13858
snRNA	116
splicing	78831
SSU_rRNA_archaea	200508
SSU_rRNA_bacteria	8548716
SSU_rRNA_eukarya	1333293
T-box	24117
thermoregulator	3854
tRNA	558

9	1	-4.102	1.158	-1.02
8	10	-4.106	1.249	-1.03
6	10	-4.125	1.225	-1.05
8	8	-4.126	1.182	-1.05
9	6	-4.132	1.213	-1.05
8	7	-4.134	1.231	-1.05
9	2	-4.142	1.086	-1.06
9	5	-4.148	1.189	-1.07
7	9	-4.166	1.333	-1.09
10	4	-4.169	1.066	-1.09
2	9	-4.169	0.880	-1.09
1	9	-4.178	1.117	-1.10
3	9	-4.189	0.846	-1.11
9	10	-4.193	1.173	-1.11
9	9	-4.196	1.261	-1.12
10	2	-4.199	1.157	-1.12
5	9	-4.202	0.960	-1.12
9	3	-4.208	1.054	-1.13
10	3	-4.208	1.258	-1.13
11	4	-4.219	1.091	-1.14
10	6	-4.219	1.090	-1.14
10	10	-4.220	1.202	-1.14
4	10	-4.230	1.505	-1.15
7	11	-4.235	1.195	-1.16
3	10	-4.237	0.952	-1.16
8	13	-4.245	1.254	-1.17
2	10	-4.253	0.874	-1.17
9	8	-4.293	1.180	-1.21
8	12	-4.295	1.042	-1.22
10	1	-4.295	1.265	-1.22
9	4	-4.299	1.028	-1.22
7	10	-4.305	1.310	-1.23
11	3	-4.313	1.236	-1.23
1	10	-4.318	0.830	-1.24
5	11	-4.326	0.903	-1.25
7	12	-4.345	1.048	-1.27
11	5	-4.345	1.078	-1.27
10	5	-4.351	1.095	-1.27
6	12	-4.357	1.067	-1.28
6	11	-4.357	1.131	-1.28
1	14	-4.358	1.088	-1.28
7	13	-4.398	1.102	-1.32
10	11	-4.412	1.297	-1.33
9	11	-4.414	1.152	-1.33
1	11	-4.414	1.029	-1.34
4	11	-4.414	1.274	-1.34
9	13	-4.428	1.102	-1.35
9	7	-4.433	1.175	-1.35
13	3	-4.433	1.089	-1.35
12	6	-4.442	1.213	-1.36
8	11	-4.447	1.133	-1.37
3	16	-4.449	0.918	-1.37
13	4	-4.455	1.150	-1.38
9	14	-4.466	1.071	-1.39
11	6	-4.467	1.057	-1.39
12	5	-4.477	1.107	-1.40
9	12	-4.480	1.128	-1.40
11	11	-4.488	1.112	-1.41
9	15	-4.494	1.111	-1.41
4	12	-4.498	1.042	-1.42
3	11	-4.498	0.960	-1.42
7	15	-4.508	1.085	-1.43
12	4	-4.511	1.177	-1.43
13	5	-4.513	1.107	-1.43
5	12	-4.515	0.986	-1.44
1	13	-4.518	1.074	-1.44
4	17	-4.518	1.003	-1.44
4	15	-4.520	0.978	-1.44
10	7	-4.522	1.192	-1.44

2	17	1894
1	6	1883
6	1	1843
236	3	1755
9	6	1717
7	3	1604
15	16	1545
6	10	1529
13	15	1472
10	10	1446
8	1	1393
7	1	1332
6	7	1173
5	15	1155
237	3	1132
6	14	1049
1	7	1014
1	8	1005
9	4	964
5	9	957
5	16	951
13	7	942
10	11	918
8	5	908
6	9	890
4	16	849
4	14	847
4	15	800
7	14	798
230	3	797
276	3	788
1	20	769
8	7	752
5	10	751
8	9	744
10	12	738
9	8	735
9	9	727
2	7	725
10	4	723
14	16	710
6	12	706
240	3	704
7	10	702
7	9	682
9	10	680
3	9	674
229	3	661
9	14	652
11	4	638
238	3	627
8	2	614
4	19	608
1	14	578
247	3	576
3	10	570
11	11	568
239	3	548
1	19	542
12	9	529
10	6	528
9	11	524
5	13	512
4	17	509
9	12	474
5	14	472
10	9	463
14	7	462
10	3	461

2	16	-4.524	1.010	-1.44
12	8	-4.530	1.259	-1.45
11	7	-4.532	1.242	-1.45
5	13	-4.532	1.003	-1.45
12	3	-4.535	1.152	-1.46
8	15	-4.535	1.025	-1.46
6	14	-4.541	1.058	-1.46
7	16	-4.546	1.044	-1.47
12	1	-4.560	1.099	-1.48
2	14	-4.560	1.016	-1.48
10	13	-4.564	1.122	-1.48
15	3	-4.567	1.124	-1.49
4	14	-4.567	0.991	-1.49
6	13	-4.567	1.043	-1.49
4	13	-4.570	0.999	-1.49
3	15	-4.575	0.913	-1.50
6	16	-4.575	1.026	-1.50
13	7	-4.576	1.199	-1.50
7	14	-4.577	1.062	-1.50
10	12	-4.579	1.058	-1.50
3	13	-4.583	0.966	-1.50
10	9	-4.583	1.142	-1.50
2	13	-4.584	1.051	-1.50
4	19	-4.587	1.129	-1.51
2	11	-4.587	1.031	-1.51
10	8	-4.589	1.210	-1.51
10	14	-4.589	1.107	-1.51
14	4	-4.592	1.130	-1.51
6	15	-4.594	1.085	-1.51
15	4	-4.594	0.996	-1.52
4	16	-4.597	0.978	-1.52
1	16	-4.598	0.982	-1.52
11	1	-4.599	1.099	-1.52
13	2	-4.606	1.440	-1.53
8	14	-4.609	1.079	-1.53
1	12	-4.611	0.941	-1.53
4	18	-4.613	0.988	-1.53
9	16	-4.617	1.119	-1.54
14	16	-4.619	1.147	-1.54
3	17	-4.620	0.945	-1.54
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15	16	-4.622	1.243	-1.54
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3	31	-4.623	1.248	-1.54
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3	30	-4.625	1.223	-1.55
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8	16	-4.637	1.048	-1.56
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8	18	-4.647	1.040	-1.57
6	17	-4.648	1.050	-1.57
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28	8	-4.973	1.276	-1.89
29	3	-4.973	1.266	-1.89
31	3	-4.973	1.235	-1.89
31	7	-4.973	1.214	-1.89
32	2	-4.973	1.276	-1.89
39	2	-4.973	1.285	-1.89
40	2	-4.973	1.285	-1.89
41	3	-4.973	1.285	-1.89
41	5	-4.973	1.235	-1.89
41	6	-4.973	1.235	-1.89
42	1	-4.973	1.285	-1.89
44	3	-4.973	1.285	-1.89
44	7	-4.973	1.235	-1.89
48	8	-4.973	1.235	-1.89
49	3	-4.973	1.235	-1.89
50	1	-4.973	1.285	-1.89
51	1	-4.973	1.285	-1.89
51	7	-4.973	1.256	-1.89
52	1	-4.973	1.235	-1.89
54	2	-4.973	1.214	-1.89
54	4	-4.973	1.235	-1.89
54	8	-4.973	1.235	-1.89
56	6	-4.973	1.235	-1.89
57	1	-4.973	1.285	-1.89
57	2	-4.973	1.285	-1.89
57	3	-4.973	1.214	-1.89
60	3	-4.973	1.214	-1.89
61	2	-4.973	1.235	-1.89
61	7	-4.973	1.235	-1.89
63	3	-4.973	1.235	-1.89
64	3	-4.973	1.235	-1.89
64	7	-4.973	1.285	-1.89
65	3	-4.973	1.235	-1.89
66	1	-4.973	1.285	-1.89
72	1	-4.973	1.235	-1.89
73	2	-4.973	1.235	-1.89
73	3	-4.973	1.235	-1.89
73	4	-4.973	1.235	-1.89
73	7	-4.973	1.235	-1.89
74	1	-4.973	1.285	-1.89

21	6	1
21	8	1
21	15	1
21	26	1
22	8	1
22	16	1
22	23	1
23	22	1
23	23	1
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25	6	1
25	8	1
26	6	1
26	7	1
27	2	1
28	2	1
28	7	1
28	8	1
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29	6	1
31	3	1
31	7	1
31	9	1
32	2	1
39	2	1
39	5	1
40	2	1
40	5	1
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41	5	1
41	6	1
42	1	1
42	5	1
44	3	1
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45	5	1
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56	6	1
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61	2	1
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63	3	1
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73	4	1
73	7	1
74	1	1
75	3	1

75	3	-4.973	1.235	-1.89
77	2	-4.973	1.285	-1.89
79	4	-4.973	1.235	-1.89
80	1	-4.973	1.285	-1.89
80	3	-4.973	1.235	-1.89
80	4	-4.973	1.235	-1.89
80	5	-4.973	1.235	-1.89
82	3	-4.973	1.235	-1.89
82	4	-4.973	1.235	-1.89
83	3	-4.973	1.235	-1.89
83	7	-4.973	1.235	-1.89
85	4	-4.973	1.235	-1.89
86	4	-4.973	1.235	-1.89
87	3	-4.973	1.235	-1.89
87	4	-4.973	1.235	-1.89
88	1	-4.973	1.235	-1.89
88	3	-4.973	1.235	-1.89
89	7	-4.973	1.235	-1.89
93	3	-4.973	1.235	-1.89
97	4	-4.973	1.235	-1.89
98	2	-4.973	1.235	-1.89
100	1	-4.973	1.235	-1.89
102	3	-4.973	1.235	-1.89
103	3	-4.973	1.235	-1.89
103	4	-4.973	1.235	-1.89
103	5	-4.973	1.235	-1.89
108	3	-4.973	1.235	-1.89
109	3	-4.973	1.235	-1.89
150	2	-4.973	1.235	-1.89
151	2	-4.973	1.235	-1.89
157	2	-4.973	1.235	-1.89
161	4	-4.973	1.235	-1.89
169	1	-4.973	1.285	-1.89
170	4	-4.973	1.235	-1.89
174	4	-4.973	1.235	-1.89
175	5	-4.973	1.285	-1.89
180	2	-4.973	1.235	-1.89
182	4	-4.973	1.235	-1.89
186	4	-4.973	1.235	-1.89
188	2	-4.973	1.235	-1.89
189	4	-4.973	1.235	-1.89
205	2	-4.973	1.235	-1.89
208	4	-4.973	1.235	-1.89
212	4	-4.973	1.235	-1.89
218	4	-4.973	1.235	-1.89
222	4	-4.973	1.235	-1.89
223	5	-4.973	1.235	-1.89
225	2	-4.973	1.235	-1.89
227	2	-4.973	1.235	-1.89
227	4	-4.973	1.235	-1.89
232	4	-4.973	1.235	-1.89
233	1	-4.973	1.235	-1.89
234	1	-4.973	1.235	-1.89
234	2	-4.973	1.235	-1.89
236	4	-4.973	1.235	-1.89
238	2	-4.973	1.235	-1.89
239	5	-4.973	1.235	-1.89
240	4	-4.973	1.235	-1.89
242	1	-4.973	1.235	-1.89
242	2	-4.973	1.235	-1.89
243	4	-4.973	1.235	-1.89
245	5	-4.973	1.235	-1.89
246	4	-4.973	1.235	-1.89
248	7	-4.973	1.235	-1.89
250	7	-4.973	1.235	-1.89
251	4	-4.973	1.235	-1.89
252	2	-4.973	1.235	-1.89
253	5	-4.973	1.235	-1.89
261	2	-4.973	1.235	-1.89

77	2	1
79	4	1
80	1	1
80	3	1
80	4	1
80	5	1
82	3	1
82	4	1
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98	2	1
100	1	1
102	3	1
103	3	1
103	4	1
103	5	1
108	3	1
109	3	1
150	2	1
151	2	1
157	2	1
161	4	1
169	1	1
170	4	1
174	4	1
175	5	1
180	2	1
182	4	1
186	4	1
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234	2	1
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240	4	1
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242	2	1
243	4	1
245	5	1
246	4	1
248	7	1
250	7	1
251	4	1
252	2	1
253	5	1
261	2	1

271	1	-4.973	1.235	-1.89
273	2	-4.973	1.235	-1.89
279	2	-4.973	1.235	-1.89
280	2	-4.973	1.235	-1.89
282	2	-4.973	1.235	-1.89
284	48	-4.973	1.235	-1.89
288	2	-4.973	1.235	-1.89
292	2	-4.973	1.235	-1.89
293	2	-4.973	1.235	-1.89
303	2	-4.973	1.235	-1.89
305	2	-4.973	1.235	-1.89
310	1	-4.973	1.235	-1.89
311	2	-4.973	1.235	-1.89
311	7	-4.973	1.235	-1.89
312	2	-4.973	1.235	-1.89
313	4	-4.973	1.235	-1.89
315	4	-4.973	1.235	-1.89
328	4	-4.973	1.235	-1.89
328	5	-4.973	1.235	-1.89
331	4	-4.973	1.235	-1.89
334	4	-4.973	1.235	-1.89
336	6	-4.973	1.235	-1.89
336	12	-4.973	1.235	-1.89
337	4	-4.973	1.235	-1.89
337	6	-4.973	1.235	-1.89
340	6	-4.973	1.235	-1.89
342	6	-4.973	1.235	-1.89
356	4	-4.973	1.235	-1.89
359	2	-4.973	1.235	-1.89
371	4	-4.973	1.235	-1.89
378	4	-4.973	1.235	-1.89
390	4	-4.973	1.235	-1.89
408	3	-4.973	1.235	-1.89
456	3	-4.973	1.235	-1.89
457	4	-4.973	1.235	-1.89
468	3	-4.973	1.235	-1.89
481	3	-4.973	1.235	-1.89
486	3	-4.973	1.235	-1.89
488	3	-4.973	1.235	-1.89
490	3	-4.973	1.235	-1.89
491	3	-4.973	1.235	-1.89
492	3	-4.973	1.235	-1.89
494	3	-4.973	1.235	-1.89
517	3	-4.973	1.235	-1.89
518	3	-4.973	1.235	-1.89
521	3	-4.973	1.235	-1.89
523	3	-4.973	1.235	-1.89
526	3	-4.973	1.235	-1.89
532	3	-4.973	1.235	-1.89
534	3	-4.973	1.235	-1.89
539	3	-4.973	1.235	-1.89
546	3	-4.973	1.235	-1.89
560	3	-4.973	1.235	-1.89
562	3	-4.973	1.235	-1.89
564	3	-4.973	1.235	-1.89
569	3	-4.973	1.235	-1.89
578	3	-4.973	1.235	-1.89
580	3	-4.973	1.235	-1.89
585	3	-4.973	1.235	-1.89
587	3	-4.973	1.235	-1.89
588	3	-4.973	1.235	-1.89
594	3	-4.973	1.235	-1.89
599	3	-4.973	1.235	-1.89
603	3	-4.973	1.235	-1.89
606	3	-4.973	1.235	-1.89
616	3	-4.973	1.235	-1.89
620	3	-4.973	1.235	-1.89
640	3	-4.973	1.235	-1.89
666	3	-4.973	1.235	-1.89

271	1	1
273	2	1
279	2	1
280	2	1
282	2	1
284	48	1
288	2	1
292	2	1
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303	2	1
305	2	1
310	1	1
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312	2	1
313	4	1
315	4	1
328	4	1
328	5	1
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336	12	1
337	4	1
337	6	1
340	6	1
342	6	1
356	4	1
359	2	1
371	4	1
378	4	1
390	4	1
408	3	1
456	3	1
457	4	1
468	3	1
481	3	1
486	3	1
488	3	1
490	3	1
491	3	1
492	3	1
494	3	1
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532	3	1
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546	3	1
560	3	1
562	3	1
564	3	1
569	3	1
578	3	1
580	3	1
585	3	1
587	3	1
588	3	1
594	3	1
599	3	1
603	3	1
606	3	1
616	3	1
620	3	1
640	3	1
666	3	1

Table S4. Terminal loops

Biloops		
Range	1.547	
Median	-1.281	
Loop	**Score**	**Centered score**
UU	-0.507	0.77
AA	-1.011	0.27
AU	-1.108	0.17
UA	-1.181	0.10
UC	-1.197	0.08
AC	-1.381	-0.10
CA	-1.469	-0.19
AG	-1.575	-0.29
UG	-1.576	-0.30
GA	-1.598	-0.32
GG	-1.615	-0.33
CU	-1.642	-0.36
CC	-1.712	-0.43
GU	-1.778	-0.50
GC	-1.802	-0.52
CG	-2.054	-0.77

Triloops		
Range	2.111	
Median	-2.467	
Loop	**Score**	**Centered score**
CAU	-1.412	1.06
UUA	-1.455	1.01
UAU	-1.556	0.91
UUU	-1.558	0.91
AUU	-1.690	0.78
UAA	-1.695	0.77
AAA	-1.738	0.73
GAA	-1.754	0.71
ACA	-1.837	0.63
UGU	-1.848	0.62
AAU	-1.923	0.54
AGU	-1.924	0.54
UUG	-1.932	0.53
CUA	-1.968	0.50
UCU	-1.997	0.47
AUA	-2.102	0.37
UGG	-2.112	0.36
CCU	-2.141	0.33
ACU	-2.157	0.31
GCA	-2.161	0.31
UUC	-2.179	0.29
CAA	-2.204	0.26
UAG	-2.222	0.25
AAG	-2.231	0.24
AUC	-2.244	0.22
AUG	-2.261	0.21
CUG	-2.323	0.14
UGA	-2.357	0.11
GUA	-2.361	0.11
GUU	-2.366	0.10
CAC	-2.373	0.09
AAC	-2.386	0.08
ACC	-2.445	0.02
UCG	-2.512	-0.05
UCC	-2.521	-0.05
CGA	-2.528	-0.06
GCC	-2.539	-0.07
CCC	-2.557	-0.09
ACG	-2.560	-0.09
UCA	-2.565	-0.10
CUU	-2.583	-0.12
AGA	-2.600	-0.13
GCU	-2.616	-0.15
UAC	-2.623	-0.16
GUC	-2.678	-0.21
GGG	-2.692	-0.22
CCG	-2.707	-0.24
AGC	-2.709	-0.24
CUC	-2.713	-0.25
CCA	-2.729	-0.26
GAU	-2.748	-0.28
CGC	-2.751	-0.28

Tetraloops		
Range	3.901	
Median	-2.915	
Loop	**Score**	**Centered score**
GAAA	-0.965	1.95
GAGA	-1.204	1.71
GCAA	-1.250	1.67
UUCG	-1.536	1.38
GUGA	-1.604	1.31
GUAA	-1.752	1.16
CUUG	-1.768	1.15
GCGA	-1.853	1.06
UUUU	-1.854	1.06
UACG	-2.062	0.85
UUUA	-2.075	0.84
UUUC	-2.077	0.84
UAAC	-2.317	0.60
GGAA	-2.322	0.59
GUCA	-2.346	0.57
UAAU	-2.368	0.55
UUUG	-2.398	0.52
AAAA	-2.427	0.49
AUAA	-2.438	0.48
UAUU	-2.452	0.46
ACAA	-2.467	0.45
UAAA	-2.479	0.44
GCAG	-2.479	0.44
AGCC	-2.490	0.43
GAAG	-2.503	0.41
GUUA	-2.528	0.39
UUAG	-2.576	0.34
UCCG	-2.590	0.32
GCAU	-2.613	0.30
UAUA	-2.641	0.27
AAAC	-2.651	0.26
GAUA	-2.671	0.24
AUUU	-2.686	0.23
UUCU	-2.698	0.22
UUAU	-2.702	0.21
CAAA	-2.726	0.19
CUCG	-2.736	0.18
UAAG	-2.749	0.17
UUGU	-2.761	0.15
UGAA	-2.762	0.15
UUCA	-2.774	0.14
CAAG	-2.783	0.13
UUGC	-2.807	0.11
UGAG	-2.830	0.09
CUUU	-2.843	0.07
AAUA	-2.849	0.07
AGUA	-2.861	0.05
UUAA	-2.875	0.04
GACA	-2.892	0.02
AACA	-2.899	0.02
AAAU	-2.902	0.01
UGCG	-2.933	-0.02

Pentaloops		
Range	2.876	
Median	-3.656	
Loop	**Score**	**Centered score**
GUCAA	-2.218	1.44
GUUAA	-2.230	1.43
GAUAA	-2.233	1.42
UUUUU	-2.294	1.36
AAAUA	-2.312	1.34
UUUAU	-2.354	1.30
CUUGA	-2.389	1.27
GAAAA	-2.421	1.24
CUUGU	-2.430	1.23
UAAUU	-2.468	1.19
CUCGA	-2.511	1.15
CAUUG	-2.540	1.12
CUCAA	-2.542	1.11
GAAAG	-2.585	1.07
CAAAA	-2.600	1.06
CUUAA	-2.601	1.05
AAACA	-2.606	1.05
GACAA	-2.613	1.04
CUCUG	-2.615	1.04
UUUUA	-2.624	1.03
UAACA	-2.638	1.02
UAACU	-2.699	0.96
UUAGU	-2.711	0.95
CUUUG	-2.730	0.93
CAAUG	-2.744	0.91
UUCGG	-2.747	0.91
UAAUA	-2.753	0.90
CAAGU	-2.765	0.89
GGAUA	-2.772	0.88
AUUAA	-2.787	0.87
CUCGU	-2.793	0.86
GAAAU	-2.794	0.86
UAACG	-2.813	0.84
AUUUU	-2.821	0.83
AAUAA	-2.822	0.83
AAAGA	-2.830	0.83
UUUGG	-2.850	0.81
GGAGA	-2.851	0.80
AGAAA	-2.853	0.80
UUUAA	-2.869	0.79
GAAUA	-2.871	0.78
AAAAA	-2.872	0.78
GUAUA	-2.879	0.78
CAAUA	-2.890	0.77
GGAAA	-2.898	0.76
GUAAA	-2.900	0.76
AUAAA	-2.905	0.75
UUAAU	-2.914	0.74
AAAAC	-2.919	0.74
UUAAG	-2.928	0.73
UUUCU	-2.931	0.73
AUUUA	-2.935	0.72

CAG	-2.761	-0.29
GAG	-2.796	-0.33
CGU	-2.826	-0.36
GGA	-2.829	-0.36
UGC	-2.850	-0.38
AGG	-2.880	-0.41
GUG	-2.938	-0.47
GAC	-3.051	-0.58
GGU	-3.068	-0.60
GCG	-3.223	-0.76
GGC	-3.408	-0.94
CGG	-3.523	-1.06

AUUA	-2.938	-0.02
GGGA	-2.962	-0.05
GGAG	-2.964	-0.05
CUAG	-2.965	-0.05
UACU	-3.003	-0.09
UUGG	-3.020	-0.10
CUCU	-3.020	-0.10
GUUU	-3.021	-0.11
UUAC	-3.022	-0.11
CUUC	-3.024	-0.11
UCAA	-3.030	-0.11
AAUU	-3.053	-0.14
AGCA	-3.054	-0.14
AGAA	-3.055	-0.14
AUCC	-3.072	-0.16
CGAA	-3.074	-0.16
CGUG	-3.081	-0.17
AAGA	-3.092	-0.18
GACG	-3.108	-0.19
UAUG	-3.120	-0.20
AAGU	-3.121	-0.21
GAAC	-3.126	-0.21
GCUA	-3.132	-0.22
GCCA	-3.137	-0.22
AGCU	-3.137	-0.22
UCUU	-3.145	-0.23
UCAC	-3.152	-0.24
UGUU	-3.161	-0.25
ACAU	-3.161	-0.25
UCUG	-3.168	-0.25
CAUG	-3.169	-0.25
AACU	-3.175	-0.26
CAUU	-3.200	-0.28
UAGA	-3.204	-0.29
CCCG	-3.205	-0.29
ACAG	-3.225	-0.31
CUAA	-3.226	-0.31
UCAG	-3.232	-0.32
GAGU	-3.242	-0.33
AUAU	-3.244	-0.33
GAGG	-3.245	-0.33
UCAU	-3.248	-0.33
GAAU	-3.252	-0.34
CAAC	-3.256	-0.34
CCUC	-3.265	-0.35
AUUG	-3.268	-0.35
GCUU	-3.271	-0.36
AUGA	-3.273	-0.36
UUCC	-3.280	-0.36
ACCC	-3.282	-0.37
CAGA	-3.292	-0.38
AUUC	-3.294	-0.38
GAUU	-3.295	-0.38
GGAU	-3.304	-0.39
UUGA	-3.308	-0.39
UCUC	-3.308	-0.39

UCAGC	-2.941	0.72
CUUGC	-2.942	0.71
CUAUG	-2.954	0.70
AUAAU	-2.972	0.68
CAAGA	-2.989	0.67
CACUG	-2.990	0.67
UUAGA	-2.991	0.67
UAUAU	-3.006	0.65
UUCUU	-3.017	0.64
UUGAC	-3.028	0.63
AAUUA	-3.032	0.62
AAUGA	-3.034	0.62
CUAAA	-3.041	0.62
GAGAG	-3.045	0.61
UUUCC	-3.045	0.61
CAAAG	-3.053	0.60
UAAAA	-3.054	0.60
UAACC	-3.061	0.60
UAAAU	-3.063	0.59
AACUA	-3.066	0.59
UAUAA	-3.066	0.59
GCAUA	-3.066	0.59
UUUGA	-3.073	0.58
CACGU	-3.082	0.57
UUUGU	-3.083	0.57
GCCAA	-3.085	0.57
GAAGA	-3.088	0.57
GAAAC	-3.093	0.56
GUAAU	-3.102	0.55
GGUUA	-3.103	0.55
GCAAG	-3.105	0.55
GAACA	-3.106	0.55
AUAUA	-3.108	0.55
AAAAU	-3.110	0.55
UUUAC	-3.119	0.54
UAAGA	-3.121	0.53
GUCUA	-3.124	0.53
UUAUU	-3.126	0.53
UUCAA	-3.127	0.53
GUUUA	-3.133	0.52
UUAUA	-3.138	0.52
CAUAG	-3.146	0.51
AUUAG	-3.146	0.51
GAUGA	-3.149	0.51
AUCAA	-3.151	0.51
CCCAA	-3.154	0.50
CGUUG	-3.156	0.50
UUAGG	-3.161	0.50
ACCCA	-3.161	0.50
GUUUC	-3.164	0.49
UUCGU	-3.165	0.49
UUAGC	-3.165	0.49
GGGGA	-3.167	0.49
GCUAA	-3.178	0.48
UUUUG	-3.178	0.48
GAGUA	-3.179	0.48

GUAU	-3.320	-0.40
AAAG	-3.322	-0.41
UAGG	-3.331	-0.42
GUUG	-3.344	-0.43
ACCU	-3.347	-0.43
CAAU	-3.347	-0.43
UGCU	-3.348	-0.43
CGCC	-3.352	-0.44
GUCU	-3.354	-0.44
ACUA	-3.362	-0.45
UGUG	-3.371	-0.46
AGUG	-3.374	-0.46
UAGU	-3.376	-0.46
UACA	-3.379	-0.46
GGUG	-3.380	-0.46
AUAC	-3.381	-0.47
UCCU	-3.383	-0.47
UCCA	-3.391	-0.48
UGAU	-3.409	-0.49
ACAC	-3.410	-0.49
AAUG	-3.428	-0.51
AUCA	-3.428	-0.51
CUGG	-3.432	-0.52
CCCC	-3.437	-0.52
GUAG	-3.438	-0.52
AACC	-3.440	-0.52
CACG	-3.450	-0.53
CCAA	-3.452	-0.54
GGUA	-3.462	-0.55
ACGA	-3.469	-0.55
ACUU	-3.470	-0.55
UAUC	-3.471	-0.56
AUCU	-3.477	-0.56
GUCC	-3.478	-0.56
CGAG	-3.479	-0.56
UACC	-3.486	-0.57
GGCA	-3.487	-0.57
CUUA	-3.490	-0.57
UGUA	-3.493	-0.58
CUGA	-3.501	-0.59
CUCC	-3.504	-0.59
AUAG	-3.505	-0.59
UGGU	-3.507	-0.59
GGGU	-3.512	-0.60
UCUA	-3.517	-0.60
GGUU	-3.522	-0.61
CUCA	-3.527	-0.61
AGAU	-3.538	-0.62
CCUU	-3.539	-0.62
CACU	-3.543	-0.63
UCCC	-3.546	-0.63
CCUG	-3.547	-0.63
GAUG	-3.559	-0.64
CCAG	-3.567	-0.65
CACA	-3.571	-0.66
UGAC	-3.573	-0.66

CGAAA	-3.182	0.47
CUGAC	-3.187	0.47
UUAAA	-3.190	0.47
CUACG	-3.193	0.46
UAUUU	-3.197	0.46
CUUAG	-3.201	0.46
UCUUU	-3.202	0.45
AAAUC	-3.204	0.45
UUUCA	-3.205	0.45
UUCUA	-3.208	0.45
CUUCG	-3.215	0.44
GAGAA	-3.217	0.44
CUUGG	-3.219	0.44
AUUAU	-3.219	0.44
CUAGC	-3.229	0.43
UGAAA	-3.233	0.42
UAAUG	-3.241	0.41
AAUAU	-3.247	0.41
CACCG	-3.260	0.40
GAGGA	-3.261	0.40
UUCCU	-3.261	0.39
UUGUG	-3.267	0.39
CACAA	-3.268	0.39
GGUAA	-3.274	0.38
AGAUA	-3.279	0.38
CAUUA	-3.287	0.37
CAACG	-3.288	0.37
CUAGU	-3.290	0.37
GUCAU	-3.291	0.37
CAAUU	-3.298	0.36
UUGAU	-3.299	0.36
CUCAG	-3.308	0.35
UACGA	-3.309	0.35
AAAUU	-3.309	0.35
AAGUA	-3.310	0.35
GUCUG	-3.311	0.35
UUCUG	-3.311	0.35
CAAGC	-3.312	0.34
UUCGA	-3.316	0.34
UUCAU	-3.318	0.34
CGCUG	-3.318	0.34
UAUUA	-3.322	0.33
GGACA	-3.326	0.33
CACAU	-3.327	0.33
AACAA	-3.332	0.32
AUGUA	-3.335	0.32
GUAAG	-3.337	0.32
UUUUC	-3.338	0.32
GGGAA	-3.339	0.32
CUUUU	-3.339	0.32
UCAGA	-3.340	0.32
GUCUU	-3.342	0.31
UCAGG	-3.344	0.31
UUAUG	-3.347	0.31
GUGAA	-3.352	0.30
AAACC	-3.355	0.30

AAGG	-3.575	-0.66
GUCG	-3.591	-0.68
CGUA	-3.602	-0.69
GCCU	-3.603	-0.69
AACG	-3.610	-0.69
CAUA	-3.611	-0.70
UGGA	-3.631	-0.72
CAGG	-3.635	-0.72
CUGU	-3.640	-0.72
GCAC	-3.645	-0.73
UGCC	-3.663	-0.75
AGAG	-3.683	-0.77
UAGC	-3.685	-0.77
UCGC	-3.688	-0.77
CAGU	-3.704	-0.79
CCAU	-3.707	-0.79
GUUC	-3.723	-0.81
UGCA	-3.726	-0.81
GAGC	-3.729	-0.81
AAUC	-3.734	-0.82
GUGU	-3.739	-0.82
AGUU	-3.757	-0.84
CUAU	-3.757	-0.84
GCGG	-3.769	-0.85
AUCG	-3.774	-0.86
ACCA	-3.777	-0.86
AUGG	-3.780	-0.86
CCCA	-3.786	-0.87
UCGG	-3.793	-0.88
CCGA	-3.802	-0.89
GACU	-3.810	-0.89
AUGC	-3.816	-0.90
ACUG	-3.836	-0.92
AAGC	-3.843	-0.93
CCCU	-3.851	-0.94
AGCG	-3.851	-0.94
AUGU	-3.853	-0.94
GCUG	-3.854	-0.94
GCCC	-3.855	-0.94
AGGA	-3.857	-0.94
GUGG	-3.861	-0.95
CCAC	-3.872	-0.96
UGGC	-3.875	-0.96
CUGC	-3.877	-0.96
ACGG	-3.897	-0.98
UCGU	-3.897	-0.98
AGUC	-3.898	-0.98
GCGU	-3.915	-1.00
ACUC	-3.926	-1.01
GGGG	-3.928	-1.01
CGUU	-3.959	-1.04
GGUC	-3.963	-1.05
GCUC	-3.966	-1.05
GUAC	-3.967	-1.05
GGCC	-3.974	-1.06
GGCU	-3.984	-1.07

AAUUU	-3.357	0.30
UACUU	-3.357	0.30
CUAGA	-3.360	0.30
AUGAU	-3.361	0.30
CUGGC	-3.373	0.28
GAAGU	-3.376	0.28
AGAAG	-3.382	0.27
UGAUA	-3.383	0.27
AUGAA	-3.384	0.27
CAAGG	-3.385	0.27
CAUUU	-3.386	0.27
UUUAG	-3.386	0.27
AGACA	-3.388	0.27
CAUGG	-3.389	0.27
GGCAA	-3.393	0.26
UAAUC	-3.393	0.26
CAUGA	-3.399	0.26
UUGGC	-3.399	0.26
CAGAG	-3.402	0.25
CAUAU	-3.406	0.25
CGCAA	-3.408	0.25
CACUA	-3.409	0.25
UGAAG	-3.411	0.24
AAACU	-3.415	0.24
ACAAA	-3.422	0.23
CCUAA	-3.424	0.23
AGAGA	-3.424	0.23
CGUGU	-3.426	0.23
GUUCA	-3.426	0.23
UAAAC	-3.428	0.23
UAGAU	-3.428	0.23
GAUAU	-3.433	0.22
UUUGC	-3.436	0.22
UCAAC	-3.440	0.22
GUUAU	-3.441	0.22
GACGA	-3.442	0.21
AAGAA	-3.442	0.21
GCAAA	-3.443	0.21
UUAAC	-3.443	0.21
GUUUU	-3.446	0.21
CCUGA	-3.446	0.21
CAACA	-3.447	0.21
CUCGC	-3.450	0.21
GUGUA	-3.451	0.21
GUUGG	-3.451	0.21
UUCAC	-3.456	0.20
CGCAU	-3.458	0.20
CUUCA	-3.461	0.20
AGCAA	-3.462	0.19
AUUGU	-3.468	0.19
UCACU	-3.468	0.19
CAUGU	-3.469	0.19
UCGCU	-3.480	0.18
GAUUA	-3.485	0.17
UUCCA	-3.488	0.17
CGAGU	-3.488	0.17

UGGG	-3.984	-1.07
UCGA	-3.993	-1.08
GAUC	-3.994	-1.08
CUAC	-4.001	-1.09
UGUC	-4.036	-1.12
CCUA	-4.063	-1.15
CGCG	-4.087	-1.17
CAGC	-4.088	-1.17
CCGC	-4.091	-1.18
GGCG	-4.095	-1.18
ACGU	-4.108	-1.19
CGCU	-4.113	-1.20
GGAC	-4.134	-1.22
CGCA	-4.149	-1.23
CACC	-4.157	-1.24
ACCG	-4.196	-1.28
GCGC	-4.207	-1.29
CAUC	-4.208	-1.29
AGGU	-4.209	-1.29
CGAC	-4.209	-1.29
GCCG	-4.211	-1.30
CGGU	-4.216	-1.30
CCGU	-4.230	-1.31
CGGG	-4.230	-1.31
AGGC	-4.233	-1.32
AGAC	-4.235	-1.32
GACC	-4.243	-1.33
GGGC	-4.271	-1.36
CGAU	-4.291	-1.38
CGGC	-4.296	-1.38
CGGA	-4.338	-1.42
GUGC	-4.363	-1.45
CGUC	-4.526	-1.61
CCGG	-4.599	-1.68
ACGC	-4.787	-1.87
AGGG	-4.866	-1.95

GGAUG	-3.489	0.17
UGAAU	-3.493	0.16
UUGAA	-3.502	0.15
UUGGU	-3.502	0.15
UAGAC	-3.503	0.15
GUCGA	-3.504	0.15
CACUU	-3.504	0.15
CAGUG	-3.505	0.15
CACAG	-3.510	0.15
AACCC	-3.512	0.14
UCUAA	-3.514	0.14
GUUAG	-3.517	0.14
UCCAA	-3.518	0.14
GUAUU	-3.518	0.14
UAAGU	-3.519	0.14
UUACG	-3.520	0.14
CUCAC	-3.532	0.12
AUAAG	-3.533	0.12
UGCCC	-3.535	0.12
AGCCC	-3.537	0.12
GCUUA	-3.538	0.12
UUCUC	-3.541	0.11
AAAGG	-3.542	0.11
AUUAC	-3.543	0.11
UCAUU	-3.544	0.11
AAAAG	-3.547	0.11
GUAAC	-3.549	0.11
AAUCA	-3.549	0.11
AAUGU	-3.549	0.11
GGGUA	-3.552	0.10
AUCAU	-3.553	0.10
CAACU	-3.554	0.10
AACCA	-3.555	0.10
UACAA	-3.556	0.10
ACCCU	-3.559	0.10
UCAGU	-3.560	0.10
UUGCU	-3.566	0.09
CGAAG	-3.570	0.09
GUUUG	-3.573	0.08
CAUAA	-3.574	0.08
CUUUA	-3.575	0.08
UUGCC	-3.579	0.08
ACGUA	-3.581	0.08
AUCUU	-3.581	0.07
AUAGA	-3.588	0.07
UAAAG	-3.588	0.07
CCCUG	-3.592	0.06
CGCAG	-3.594	0.06
UAUCA	-3.594	0.06
GUCUC	-3.597	0.06
CCUGU	-3.597	0.06
CAAUC	-3.598	0.06
GCACA	-3.602	0.05
UUUCG	-3.605	0.05
ACCAU	-3.606	0.05
AUCCU	-3.611	0.04
UCAAA	-3.613	0.04
UACGU	-3.614	0.04
ACCUA	-3.614	0.04
UACAU	-3.619	0.04
UUACA	-3.619	0.04

UGACC	-3.622	0.03
AACUU	-3.625	0.03
UGUAU	-3.628	0.03
CCAGU	-3.628	0.03
CUGGU	-3.629	0.03
CGUAA	-3.630	0.03
UCAAG	-3.633	0.02
UACCC	-3.637	0.02
GCUAU	-3.637	0.02
UGCUC	-3.640	0.02
UCCGG	-3.640	0.02
GUUCG	-3.641	0.02
AGUAG	-3.642	0.01
UGAUU	-3.644	0.01
AUAUU	-3.645	0.01
AGUUA	-3.645	0.01
UAUGA	-3.645	0.01
AUCUA	-3.647	0.01
CUAUU	-3.648	0.01
CCUUG	-3.648	0.01
UAUUC	-3.652	0.00
GCAAC	-3.653	0.00
CACGA	-3.654	0.00
AUUCA	-3.656	0.00
ACUAA	-3.663	-0.01
AAAUG	-3.663	-0.01
CAUCU	-3.663	-0.01
UCCAU	-3.665	-0.01
UUACC	-3.666	-0.01
UUCGC	-3.670	-0.01
UUCCG	-3.670	-0.01
ACACA	-3.672	-0.02
UCUCU	-3.673	-0.02
GCUGA	-3.673	-0.02
GUAGC	-3.676	-0.02
UCAAU	-3.677	-0.02
AUCAC	-3.679	-0.02
AUACA	-3.682	-0.03
GCUUU	-3.688	-0.03
GGCCC	-3.690	-0.03
CAAAU	-3.691	-0.03
CGGUG	-3.692	-0.04
AAUAG	-3.692	-0.04
CCAUG	-3.694	-0.04
UCCUA	-3.695	-0.04
AUUUG	-3.696	-0.04
AUAUC	-3.697	-0.04
GUCAG	-3.697	-0.04
AUCAG	-3.702	-0.05
CUCGG	-3.709	-0.05
UCUUA	-3.710	-0.05
CGUUU	-3.711	-0.05
CCCGC	-3.712	-0.06
CCAGC	-3.719	-0.06
GCGUA	-3.720	-0.06
GCUUC	-3.721	-0.06
GUACA	-3.722	-0.07
ACAGA	-3.722	-0.07
UUACU	-3.723	-0.07
UCCGC	-3.723	-0.07
CUUAU	-3.724	-0.07
CACCC	-3.724	-0.07
ACGAA	-3.730	-0.07
AUAGC	-3.732	-0.08
UGACU	-3.733	-0.08
UCACC	-3.733	-0.08
CUUAC	-3.733	-0.08
UUCCC	-3.735	-0.08
AUUGA	-3.736	-0.08

UAUUG	-3.736	-0.08
AUGAG	-3.737	-0.08
CUAUA	-3.738	-0.08
GAAUU	-3.739	-0.08
CCUAG	-3.741	-0.09
UCUCC	-3.742	-0.09
GGAUU	-3.743	-0.09
UAUGG	-3.745	-0.09
GCGAG	-3.746	-0.09
CCCGU	-3.747	-0.09
UGCAC	-3.747	-0.09
UGAGU	-3.751	-0.10
GUAGA	-3.757	-0.10
UCGGC	-3.758	-0.10
CCAGA	-3.759	-0.10
CAGCC	-3.762	-0.11
CCAGG	-3.763	-0.11
ACGAU	-3.767	-0.11
GCCCC	-3.769	-0.11
CUCAU	-3.772	-0.12
AUAGU	-3.772	-0.12
UCCCC	-3.774	-0.12
UGCGA	-3.774	-0.12
GGAAG	-3.775	-0.12
CUCUC	-3.778	-0.12
UGUGA	-3.778	-0.12
GUCCA	-3.779	-0.12
UCCUU	-3.779	-0.12
CUCCG	-3.780	-0.12
UGUAA	-3.780	-0.12
UGUGU	-3.784	-0.13
GGCUA	-3.784	-0.13
CAUGC	-3.784	-0.13
AUACU	-3.785	-0.13
UACAC	-3.786	-0.13
CUGGA	-3.788	-0.13
GGAAC	-3.790	-0.13
CGCGU	-3.794	-0.14
CAGCA	-3.796	-0.14
GGUUC	-3.797	-0.14
UGGUA	-3.798	-0.14
GCCUC	-3.799	-0.14
AAAGU	-3.799	-0.14
ACAAG	-3.800	-0.14
UUCAG	-3.804	-0.15
UACCA	-3.804	-0.15
AUAGG	-3.805	-0.15
ACUGG	-3.807	-0.15
ACCCC	-3.808	-0.15
AGUAA	-3.808	-0.15
ACAGG	-3.809	-0.15
UUGCA	-3.810	-0.15
GCCAU	-3.811	-0.16
UCAUA	-3.812	-0.16
GAUCU	-3.813	-0.16
CUAAG	-3.815	-0.16
CUCCA	-3.815	-0.16
GUUGA	-3.815	-0.16
GUGGA	-3.815	-0.16
AUUUC	-3.816	-0.16
AAGCA	-3.817	-0.16
AUGUG	-3.818	-0.16
UACUG	-3.820	-0.16
UAUAG	-3.820	-0.16
UGAUC	-3.820	-0.16
ACAUA	-3.824	-0.17
GUCCU	-3.824	-0.17
AGAAC	-3.826	-0.17
CCUGG	-3.826	-0.17

UCCAC	-3.826	-0.17
GAAUC	-3.827	-0.17
AUUGG	-3.830	-0.17
UUGUA	-3.831	-0.17
AUGGC	-3.832	-0.18
UAUGU	-3.835	-0.18
AUUCC	-3.836	-0.18
UCUAC	-3.839	-0.18
UACGG	-3.844	-0.19
AUAUG	-3.850	-0.19
ACUGA	-3.851	-0.20
UGCAA	-3.853	-0.20
UGGCU	-3.853	-0.20
AAGUG	-3.855	-0.20
CGAUA	-3.856	-0.20
GACCC	-3.856	-0.20
CAGUA	-3.858	-0.20
GAUUC	-3.859	-0.20
ACACG	-3.859	-0.20
CGCCC	-3.861	-0.20
AACUG	-3.861	-0.21
ACUUA	-3.862	-0.21
ACAGC	-3.863	-0.21
UGAAC	-3.863	-0.21
UAAGG	-3.864	-0.21
UUGUU	-3.867	-0.21
GCUCA	-3.868	-0.21
CCUGC	-3.869	-0.21
GUUGU	-3.869	-0.21
GGUGA	-3.869	-0.21
AAAGC	-3.871	-0.22
GGUUU	-3.873	-0.22
ACCAA	-3.874	-0.22
UGUUC	-3.875	-0.22
GAUAC	-3.879	-0.22
GCGAA	-3.879	-0.22
UCUCA	-3.879	-0.22
UUAUC	-3.886	-0.23
GUUCC	-3.889	-0.23
UACUC	-3.890	-0.23
GCCUA	-3.891	-0.24
UCAUC	-3.892	-0.24
CAUCG	-3.894	-0.24
UAGCU	-3.894	-0.24
UAUCU	-3.894	-0.24
ACGAG	-3.898	-0.24
GACCA	-3.900	-0.24
GGAGG	-3.901	-0.25
CCCUA	-3.903	-0.25
UGUUU	-3.903	-0.25
CUUCU	-3.904	-0.25
AUCCA	-3.907	-0.25
CGAUG	-3.907	-0.25
GACUA	-3.909	-0.25
ACGGA	-3.909	-0.25
AACGG	-3.911	-0.25
ACCUC	-3.912	-0.26
ACCUU	-3.914	-0.26
UCUGC	-3.914	-0.26
CGCGA	-3.917	-0.26
AUCGA	-3.918	-0.26
AUAAC	-3.918	-0.26
CUGUG	-3.919	-0.26
AGUUU	-3.920	-0.26
CUCUA	-3.921	-0.26
CGUAG	-3.921	-0.27
CCAUA	-3.923	-0.27
UGUCC	-3.923	-0.27
CCUCA	-3.924	-0.27

GCCUU	-3.925	-0.27
GCAGA	-3.925	-0.27
GAUCC	-3.927	-0.27
UGGAA	-3.928	-0.27
UAUAC	-3.934	-0.28
UGUAC	-3.936	-0.28
GAUCA	-3.939	-0.28
CUCCU	-3.941	-0.29
UCGCG	-3.941	-0.29
CAGGG	-3.943	-0.29
CCAAA	-3.944	-0.29
GCUUG	-3.946	-0.29
UCACA	-3.947	-0.29
AUGAC	-3.947	-0.29
CACCU	-3.949	-0.29
AGUCU	-3.951	-0.30
AGGAA	-3.952	-0.30
UCCCA	-3.953	-0.30
UCCGU	-3.955	-0.30
UAGCA	-3.956	-0.30
AUCGC	-3.956	-0.30
UUGAG	-3.956	-0.30
UCGAA	-3.958	-0.30
GCAAU	-3.959	-0.30
UGCUU	-3.960	-0.30
GACAU	-3.962	-0.31
UACCU	-3.964	-0.31
UCGAC	-3.967	-0.31
CGUAU	-3.969	-0.31
CUGUA	-3.971	-0.31
CCAUU	-3.971	-0.32
UGAGA	-3.973	-0.32
CCGAC	-3.974	-0.32
GUGAU	-3.974	-0.32
UCUGA	-3.975	-0.32
GCAGC	-3.976	-0.32
UGCCA	-3.978	-0.32
AGGAU	-3.978	-0.32
CCCCA	-3.979	-0.32
GUCAC	-3.983	-0.33
AGAGC	-3.986	-0.33
UCGGU	-3.988	-0.33
GACGC	-3.991	-0.33
CGAAU	-3.992	-0.34
CGACA	-3.994	-0.34
GCAUG	-3.995	-0.34
CACGG	-3.995	-0.34
CACGC	-3.995	-0.34
UCCUG	-3.998	-0.34
GAAUG	-3.999	-0.34
UCCCU	-3.999	-0.34
CUCUU	-4.003	-0.35
UUGCG	-4.003	-0.35
GGAAU	-4.006	-0.35
AUUCU	-4.007	-0.35
UUGGA	-4.007	-0.35
GUUAC	-4.008	-0.35
CCUAC	-4.008	-0.35
ACCGG	-4.009	-0.35
AACGU	-4.009	-0.35
UAGUA	-4.011	-0.36
UAGAA	-4.011	-0.36
CUUUC	-4.013	-0.36
GGUCA	-4.015	-0.36
CCCUU	-4.017	-0.36
GGAGU	-4.018	-0.36
ACUUG	-4.019	-0.36
GGCGA	-4.019	-0.36
GAGAU	-4.023	-0.37

AGGAG	-4.024	-0.37
GUGCA	-4.024	-0.37
CCUCG	-4.026	-0.37
AACAU	-4.027	-0.37
CCAUC	-4.032	-0.38
CAUCA	-4.033	-0.38
GUGAC	-4.034	-0.38
UCAUG	-4.038	-0.38
GUUCU	-4.041	-0.38
ACUUC	-4.042	-0.39
UGCAU	-4.043	-0.39
AGCAU	-4.048	-0.39
AUACG	-4.050	-0.39
CCUUA	-4.050	-0.39
CAUUC	-4.053	-0.40
AAGGU	-4.053	-0.40
GCUAG	-4.057	-0.40
UGGAU	-4.057	-0.40
CCACG	-4.062	-0.41
CCCAG	-4.063	-0.41
GCUAC	-4.066	-0.41
CAAAC	-4.067	-0.41
GAUGU	-4.068	-0.41
UACUA	-4.069	-0.41
UGUCU	-4.069	-0.41
CCCGA	-4.070	-0.41
AGAUG	-4.070	-0.41
AAUCC	-4.070	-0.41
CGUCU	-4.071	-0.41
AGUCA	-4.074	-0.42
ACUUU	-4.075	-0.42
UGUUA	-4.076	-0.42
GUAGU	-4.079	-0.42
GACGU	-4.080	-0.42
AGCCU	-4.080	-0.42
AGUAU	-4.081	-0.42
AGCCG	-4.083	-0.43
GGCCA	-4.083	-0.43
AGAAU	-4.086	-0.43
GGCUC	-4.088	-0.43
UCCUC	-4.091	-0.43
GAUUG	-4.091	-0.43
UCUAU	-4.091	-0.43
ACUCA	-4.092	-0.44
AGGUA	-4.093	-0.44
UGUUG	-4.093	-0.44
AGAUU	-4.093	-0.44
UAUCC	-4.093	-0.44
CCUUU	-4.096	-0.44
UACAG	-4.105	-0.45
UGACA	-4.106	-0.45
UACCG	-4.108	-0.45
UUGUC	-4.110	-0.45
AAUAC	-4.114	-0.46
GACUC	-4.114	-0.46
AAGUC	-4.117	-0.46
UGACG	-4.117	-0.46
CCAAG	-4.117	-0.46
AGUGA	-4.118	-0.46
UAGUU	-4.119	-0.46
AGCAG	-4.120	-0.46
AAUGG	-4.122	-0.47
GAGAC	-4.122	-0.47
CUACA	-4.123	-0.47
GGAUC	-4.123	-0.47
CUGAA	-4.124	-0.47
AUCUG	-4.124	-0.47
AAUUC	-4.125	-0.47
CGAGA	-4.128	-0.47

GGCAU	-4.130	-0.47
AUUCG	-4.132	-0.48
AUCCG	-4.133	-0.48
ACAAC	-4.134	-0.48
AGCUU	-4.134	-0.48
ACCAC	-4.135	-0.48
GCCAG	-4.136	-0.48
CGUGA	-4.141	-0.48
UGGUU	-4.141	-0.49
GAACC	-4.142	-0.49
AAGGC	-4.142	-0.49
AACUC	-4.143	-0.49
ACGAC	-4.143	-0.49
GCUGG	-4.145	-0.49
CCUCU	-4.147	-0.49
CUUCC	-4.148	-0.49
UAAGC	-4.149	-0.49
UACGC	-4.149	-0.49
UCUUC	-4.149	-0.49
ACUAG	-4.149	-0.49
ACCUG	-4.150	-0.49
UCACG	-4.150	-0.49
AAUCU	-4.151	-0.49
UUGGG	-4.151	-0.49
UCUCG	-4.153	-0.50
UAGGU	-4.155	-0.50
CAGUU	-4.156	-0.50
ACACC	-4.158	-0.50
CAGGC	-4.158	-0.50
GAACU	-4.158	-0.50
CCACC	-4.159	-0.50
CGCUU	-4.159	-0.50
CGUCA	-4.159	-0.50
CCUUC	-4.162	-0.51
GGUCC	-4.163	-0.51
AGCUA	-4.164	-0.51
GCACG	-4.165	-0.51
AGGAC	-4.166	-0.51
CUAAC	-4.168	-0.51
AGAGU	-4.172	-0.52
AGUUC	-4.172	-0.52
AAGCC	-4.172	-0.52
ACUGU	-4.176	-0.52
CUACC	-4.179	-0.52
GAGUU	-4.182	-0.53
AACCU	-4.185	-0.53
GGACG	-4.188	-0.53
AAGAG	-4.188	-0.53
UCUGG	-4.189	-0.53
GUAUG	-4.191	-0.54
AUGGU	-4.193	-0.54
GUCCC	-4.194	-0.54
GAUAG	-4.194	-0.54
CCAAU	-4.196	-0.54
UCGUA	-4.196	-0.54
UGCGU	-4.196	-0.54
CAGAU	-4.197	-0.54
CCUCC	-4.199	-0.54
CAGAA	-4.199	-0.54
GAACG	-4.200	-0.54
UGAUG	-4.200	-0.54
AUUGC	-4.206	-0.55
AUCGG	-4.206	-0.55
CGUGC	-4.207	-0.55
GCCUG	-4.212	-0.56
UGAGC	-4.214	-0.56
AAGGG	-4.214	-0.56
CUGAU	-4.215	-0.56
GGUAU	-4.216	-0.56

CUGAG	-4.219	-0.56
GAAGG	-4.219	-0.56
CUAGG	-4.221	-0.57
GAAGC	-4.222	-0.57
UGGGU	-4.223	-0.57
GUCCG	-4.224	-0.57
UCUUG	-4.225	-0.57
GCCCG	-4.226	-0.57
ACUAC	-4.226	-0.57
UGGCC	-4.227	-0.57
GUGAG	-4.229	-0.57
CGCGC	-4.232	-0.58
GUGGC	-4.235	-0.58
ACCGC	-4.236	-0.58
UGCUA	-4.237	-0.58
ACGCA	-4.238	-0.58
GGCAG	-4.243	-0.59
CAGCG	-4.244	-0.59
GACAG	-4.250	-0.59
UAGAG	-4.252	-0.60
CCGCC	-4.253	-0.60
AUCUC	-4.257	-0.60
CUACU	-4.257	-0.60
GGUCG	-4.260	-0.60
AAGAU	-4.261	-0.61
CUCCC	-4.261	-0.61
UAGGA	-4.263	-0.61
AGGCC	-4.263	-0.61
CGAGG	-4.263	-0.61
CUGUC	-4.265	-0.61
GUGGG	-4.266	-0.61
UGGAG	-4.266	-0.61
CAUCC	-4.267	-0.61
UGAGG	-4.267	-0.61
GAUUU	-4.267	-0.61
UGUGC	-4.270	-0.61
GACAC	-4.271	-0.62
AAACG	-4.274	-0.62
GCCCU	-4.274	-0.62
CCACA	-4.276	-0.62
UAGGC	-4.279	-0.62
CGGAU	-4.280	-0.62
UGGCA	-4.280	-0.62
CCACU	-4.282	-0.63
GCAGG	-4.282	-0.63
CGCUA	-4.286	-0.63
AUACC	-4.286	-0.63
CUGCC	-4.290	-0.63
CCCAC	-4.292	-0.64
GUUGC	-4.292	-0.64
CUAAU	-4.293	-0.64
GUGCG	-4.293	-0.64
AAGUU	-4.293	-0.64
AGCCA	-4.293	-0.64
GGCAC	-4.294	-0.64
GGCUU	-4.294	-0.64
AUCCC	-4.296	-0.64
AAUUG	-4.297	-0.64
GUCGC	-4.297	-0.64
UCCGA	-4.297	-0.64
CGAAC	-4.298	-0.64
CUGCG	-4.298	-0.64
CCUAU	-4.299	-0.64
UAGCC	-4.299	-0.64
CCGUG	-4.299	-0.64
UCGCC	-4.306	-0.65
GACCU	-4.308	-0.65
CAGGA	-4.309	-0.65
GCACC	-4.310	-0.65

UCUGU	-4.310	-0.65
CGCCU	-4.310	-0.65
UGGGC	-4.312	-0.66
AUGGG	-4.313	-0.66
ACAAU	-4.313	-0.66
AUCGU	-4.313	-0.66
CGACG	-4.315	-0.66
UGGGA	-4.315	-0.66
UGUGG	-4.322	-0.67
ACUCU	-4.323	-0.67
GGUAG	-4.324	-0.67
GCUCC	-4.327	-0.67
AUGUU	-4.331	-0.67
CGCUC	-4.331	-0.67
AACAC	-4.331	-0.68
GGGAG	-4.331	-0.68
CCCUC	-4.335	-0.68
UGCAG	-4.335	-0.68
AGUCC	-4.335	-0.68
AAGGA	-4.336	-0.68
AGCGC	-4.337	-0.68
CGCAC	-4.338	-0.68
GAUCG	-4.339	-0.68
ACAUU	-4.340	-0.68
ACACU	-4.341	-0.69
AUGGA	-4.341	-0.69
AAGCU	-4.347	-0.69
GGACU	-4.347	-0.69
ACGGC	-4.348	-0.69
CGGAA	-4.351	-0.70
GAGGG	-4.353	-0.70
CGCCA	-4.355	-0.70
ACUAU	-4.355	-0.70
CGACC	-4.359	-0.70
GUAUC	-4.363	-0.71
AACGA	-4.364	-0.71
UCGAU	-4.365	-0.71
GGAGC	-4.366	-0.71
GUACG	-4.368	-0.71
GCUGC	-4.368	-0.71
AGCUG	-4.371	-0.71
CCCGG	-4.372	-0.72
GCAUU	-4.373	-0.72
CGUGG	-4.375	-0.72
GGCGG	-4.376	-0.72
CGCCG	-4.379	-0.72
GUAGG	-4.379	-0.72
UGGUC	-4.379	-0.72
ACAUC	-4.381	-0.73
CACUC	-4.384	-0.73
ACAGU	-4.384	-0.73
UAUGC	-4.384	-0.73
UGGAC	-4.384	-0.73
GCUGU	-4.387	-0.73
GGGAC	-4.389	-0.73
UAGUG	-4.389	-0.73
AGUGG	-4.390	-0.73
GCAGU	-4.393	-0.74
AGCAC	-4.395	-0.74
CCCAU	-4.398	-0.74
CGUCC	-4.398	-0.74
GCCAC	-4.398	-0.74
GGUGC	-4.401	-0.75
CGUUC	-4.402	-0.75
GCGGG	-4.404	-0.75
GUGUG	-4.404	-0.75
CCCCC	-4.405	-0.75
GUCGG	-4.411	-0.75
GGUGG	-4.412	-0.76

AGUAC	-4.414	-0.76
CGGAC	-4.419	-0.76
AGAGG	-4.420	-0.76
GCGUU	-4.420	-0.76
GGCGC	-4.421	-0.77
AGUUG	-4.422	-0.77
CCCCG	-4.429	-0.77
AAGAC	-4.433	-0.78
AAGCG	-4.433	-0.78
AGGGA	-4.433	-0.78
UCGUU	-4.434	-0.78
CACCA	-4.435	-0.78
GAGCA	-4.435	-0.78
GGACC	-4.439	-0.78
CCGGC	-4.441	-0.78
GACUU	-4.446	-0.79
UCGUG	-4.447	-0.79
GCCGC	-4.448	-0.79
GCCGA	-4.451	-0.79
GGCUG	-4.458	-0.80
UCGCA	-4.458	-0.80
AACAG	-4.458	-0.80
ACGGG	-4.458	-0.80
GCCCA	-4.461	-0.80
GCUCU	-4.461	-0.80
GUGGU	-4.461	-0.80
UGCGC	-4.465	-0.81
GUGCU	-4.467	-0.81
GAGCC	-4.469	-0.81
GAUGC	-4.472	-0.82
ACCAG	-4.477	-0.82
GCGAC	-4.483	-0.83
UAUCG	-4.483	-0.83
UGCUG	-4.483	-0.83
GGGUG	-4.487	-0.83
GGGUU	-4.488	-0.83
CGUCG	-4.494	-0.84
GAGGU	-4.494	-0.84
UGGUG	-4.494	-0.84
CAGAC	-4.494	-0.84
GGGCA	-4.494	-0.84
GCGCA	-4.496	-0.84
UAGCG	-4.498	-0.84
UGUAG	-4.507	-0.85
ACAUG	-4.507	-0.85
GGCGU	-4.507	-0.85
CAACC	-4.509	-0.85
UGUCA	-4.517	-0.86
ACUCC	-4.518	-0.86
GCGAU	-4.522	-0.87
ACGUG	-4.527	-0.87
GAGUG	-4.527	-0.87
AGCGA	-4.530	-0.87
CUGCA	-4.530	-0.87
AGGGC	-4.530	-0.87
CGCGG	-4.531	-0.87
UCGUC	-4.531	-0.87
CCGUA	-4.537	-0.88
AUGUC	-4.543	-0.89
GGCCU	-4.543	-0.89
CUGUU	-4.543	-0.89
ACCGU	-4.551	-0.90
CGGAG	-4.552	-0.90
CCAAC	-4.557	-0.90
GGUUG	-4.557	-0.90
CGAGC	-4.557	-0.90
GUACU	-4.560	-0.90
UAGUC	-4.564	-0.91
AACGC	-4.564	-0.91

ACGCG	-4.564	-0.91
CAGUC	-4.564	-0.91
UCGGA	-4.567	-0.91
CUGGG	-4.570	-0.91
UGCGG	-4.573	-0.92
AUGCA	-4.580	-0.92
AGGCA	-4.588	-0.93
CGGGC	-4.588	-0.93
CGGUA	-4.588	-0.93
CACAC	-4.592	-0.94
ACCCG	-4.598	-0.94
GCGGA	-4.600	-0.94
AGCUC	-4.602	-0.95
CGUAC	-4.604	-0.95
GCGUG	-4.604	-0.95
GUCGU	-4.605	-0.95
GCAUC	-4.609	-0.95
UGGGG	-4.612	-0.96
AUGCC	-4.617	-0.96
GGUGU	-4.617	-0.96
UGCCU	-4.617	-0.96
GGGGG	-4.618	-0.96
AGACC	-4.626	-0.97
UCCAG	-4.628	-0.97
CUAUC	-4.631	-0.98
GCGGU	-4.631	-0.98
GUGUU	-4.631	-0.98
UCGGG	-4.631	-0.98
GCGCC	-4.631	-0.98
AGUGU	-4.637	-0.98
GCGCG	-4.637	-0.98
UAGGG	-4.640	-0.98
AGCGG	-4.647	-0.99
ACUGC	-4.647	-0.99
CCCCU	-4.653	-1.00
CCGAA	-4.653	-1.00
AGGUU	-4.666	-1.01
GAGUC	-4.666	-1.01
GGCCG	-4.666	-1.01
ACGUC	-4.668	-1.01
GAGGC	-4.668	-1.01
CCGCA	-4.672	-1.02
UCCCG	-4.672	-1.02
GCACU	-4.679	-1.02
CUGCU	-4.686	-1.03
UCGAG	-4.686	-1.03
CCGCG	-4.710	-1.05
GCUCG	-4.710	-1.05
GGGCG	-4.710	-1.05
CCGAU	-4.729	-1.07
CGAUU	-4.729	-1.07
GGUAC	-4.729	-1.07
GUACC	-4.733	-1.08
UGUCG	-4.733	-1.08
CCGUU	-4.740	-1.08
ACGUU	-4.747	-1.09
CGGCC	-4.747	-1.09
GGUCU	-4.747	-1.09
AGACG	-4.751	-1.09
CGUUA	-4.751	-1.09
AUGCU	-4.751	-1.09
CCGUC	-4.751	-1.09
CGAUC	-4.751	-1.09
CGGCA	-4.751	-1.09
GCCGU	-4.751	-1.09
UCUAG	-4.751	-1.09
AGUCG	-4.763	-1.11
GUGCC	-4.763	-1.11
AGACU	-4.771	-1.12

AGGCU	-4.776	-1.12
CAGGU	-4.776	-1.12
GCGGC	-4.776	-1.12
ACCGA	-4.776	-1.12
CAUAC	-4.776	-1.12
GAUGG	-4.790	-1.13
GACUG	-4.796	-1.14
GGGUC	-4.796	-1.14
AACCG	-4.806	-1.15
AAUCG	-4.806	-1.15
CCGAG	-4.806	-1.15
GACCG	-4.806	-1.15
GCCGG	-4.825	-1.17
UGCCG	-4.825	-1.17
AGCGU	-4.825	-1.17
GCGUC	-4.825	-1.17
AGAUC	-4.845	-1.19
AAUGC	-4.845	-1.19
AGGGG	-4.845	-1.19
AGGUC	-4.845	-1.19
CGGGA	-4.845	-1.19
GACGG	-4.853	-1.20
ACGCC	-4.861	-1.20
CAGCU	-4.861	-1.20
CGGCG	-4.861	-1.20
CGGGU	-4.869	-1.21
GAGCG	-4.869	-1.21
CCGGA	-4.869	-1.21
GGGAU	-4.869	-1.21
GUGUC	-4.869	-1.21
AGUGC	-4.899	-1.24
CGGCU	-4.899	-1.24
CGGUC	-4.899	-1.24
GGGCU	-4.899	-1.24
UGGCG	-4.899	-1.24
GCGCU	-4.899	-1.24
ACGGU	-4.910	-1.25
CGGUU	-4.922	-1.27
ACGCU	-4.935	-1.28
ACUCG	-4.935	-1.28
AGGGU	-4.949	-1.29
AGGCG	-4.984	-1.33
CCGCU	-4.984	-1.33
CCGGU	-4.984	-1.33
CGGGG	-4.984	-1.33
AGGUG	-5.029	-1.37
CGACU	-5.058	-1.40
GAGCU	-5.058	-1.40
GGGCC	-5.058	-1.40
AUGCG	-5.094	-1.44
CCGGG	-5.094	-1.44
GGGGC	-5.094	-1.44
GGGGU	-5.094	-1.44

Loop	Score	SD
UU	-0.507	0.229
AA	-1.011	0.075
AU	-1.108	0.468
UA	-1.181	0.021
UC	-1.197	0.431
AC	-1.381	0.238
CA	-1.469	0.051
AG	-1.575	0.227
UG	-1.576	0.174
GA	-1.598	0.116
GG	-1.615	0.325
CU	-1.642	0.156
CC	-1.712	0.318
GU	-1.778	0.187
GC	-1.802	0.481
CG	-2.054	0.198

Loop	Total loop count
AA	5251
AC	2334
AG	2101
AU	4482
CA	1950
CC	2117
CG	736
CU	1757
GA	1482
GC	1866
GG	2185
GU	1133
UA	3955
UC	8974
UG	1694
UU	16180

Supercategory	Total loop count
Intron	9625
Translation	42421
Cis -Reg	6151

Table S6. Triloops

Loop	Score	SD
CAU	-1.412	1.352
UUA	-1.455	0.720
UAU	-1.556	0.386
UUU	-1.558	0.257
AUU	-1.690	0.536
UAA	-1.695	0.787
AAA	-1.738	0.601
GAA	-1.754	0.175
ACA	-1.837	0.641
UGU	-1.848	1.037
AAU	-1.923	0.452
AGU	-1.924	1.146
UUG	-1.932	0.407
CUA	-1.968	0.409
UCU	-1.997	0.486
AUA	-2.102	0.175
UGG	-2.112	1.179
CCU	-2.141	1.025
ACU	-2.157	0.654
GCA	-2.161	0.653
UUC	-2.179	0.281
CAA	-2.204	0.258
UAG	-2.222	0.442
AAG	-2.231	0.440
AUC	-2.244	0.949
AUG	-2.261	0.547
CUG	-2.323	0.538
UGA	-2.357	0.993
GUA	-2.361	0.330
GUU	-2.366	0.322
CAC	-2.373	0.630
AAC	-2.386	0.718
ACC	-2.445	0.318
UCG	-2.512	0.441
UCC	-2.521	0.105
CGA	-2.528	0.399
GCC	-2.539	0.742
CCC	-2.557	0.769
ACG	-2.560	0.376
UCA	-2.565	0.192
CUU	-2.583	0.201
AGA	-2.600	0.260
GCU	-2.616	0.349
UAC	-2.623	0.456
GUC	-2.678	0.676
GGG	-2.692	0.918
CCG	-2.707	0.683
AGC	-2.709	0.269
CUC	-2.713	0.115
CCA	-2.729	0.428
GAU	-2.748	0.218
CGC	-2.751	0.862
CAG	-2.761	0.528
GAG	-2.796	0.121
CGU	-2.826	0.755
GGA	-2.829	0.243
UGC	-2.850	0.487
AGG	-2.880	0.678
GUG	-2.938	0.472
GAC	-3.051	0.119
GGU	-3.068	0.274
GCG	-3.223	0.152
GGC	-3.408	0.211
CGG	-3.523	0.387

Loop	Total loop count
AAA	5306
AAC	2255
AAG	1904
AAU	12981
ACA	22803
ACC	1279
ACG	1183
ACU	13596
AGA	919
AGC	635
AGG	647
AGU	80395
AUA	4104
AUC	3145
AUG	1714
AUU	15451
CAA	2043
CAC	2037
CAG	613
CAU	91743
CCA	586
CCC	1769
CCG	550
CCU	40586
CGA	1225
CGC	1411
CGG	100
CGU	1363
CUA	3138
CUC	749
CUG	2486
CUU	1546
GAA	7185
GAC	393
GAG	825
GAU	1296
GCA	11537
GCC	1000
GCG	367
GCU	1704
GGA	828
GGC	161
GGG	1767
GGU	287
GUA	3410
GUC	728
GUG	516
GUU	1380
UAA	8915
UAC	2217
UAG	1709
UAU	19080
UCA	1289
UCC	1728
UCG	2922
UCU	14104
UGA	2560
UGC	400
UGG	5676
UGU	8242
UUA	18878
UUC	5565
UUG	4509
UUU	17882

Supercategory	Total loop count
Intron	30409
Translation	372907
Cis -Reg	66006

Loop	Score	SD
GAAA	-0.965	0.476
GAGA	-1.204	0.347
GCAA	-1.250	0.324
UUCG	-1.536	0.527
GUGA	-1.604	0.576
GUAA	-1.752	0.318
CUUG	-1.768	0.556
GCGA	-1.853	0.538
UUUU	-1.854	0.489
UACG	-2.062	0.738
UUUA	-2.075	0.322
UUUC	-2.077	0.878
UAAC	-2.317	0.896
GGAA	-2.322	0.342
GUCA	-2.346	1.507
UAAU	-2.368	0.042
UUUG	-2.398	0.549
AAAA	-2.427	0.721
AUAA	-2.438	0.510
UAUU	-2.452	0.531
ACAA	-2.467	1.280
UAAA	-2.479	0.715
GCAG	-2.479	0.879
AGCC	-2.490	1.177
GAAG	-2.503	1.064
GUUA	-2.528	0.863
UUAG	-2.576	0.157
UCCG	-2.590	0.567
GCAU	-2.613	0.872
UAUA	-2.641	0.648
AAAC	-2.651	0.419
GAUA	-2.671	0.753
AUUU	-2.686	0.525
UUCU	-2.698	0.253
UUAU	-2.702	0.200
CAAA	-2.726	0.858
CUCG	-2.736	0.448
UAAG	-2.749	0.141
UUGU	-2.761	0.238
UGAA	-2.762	0.333
UUCA	-2.774	0.651
CAAG	-2.783	0.515
UUGC	-2.807	0.839
UGAG	-2.830	0.415
CUUU	-2.843	0.775
AAUA	-2.849	0.572
AGUA	-2.861	1.510
UUAA	-2.875	0.261
GACA	-2.892	0.213
AACA	-2.899	0.983
AAAU	-2.902	0.753
UGCG	-2.933	0.188
AUUA	-2.938	0.241
GGGA	-2.962	0.259
GGAG	-2.964	1.171
CUAG	-2.965	0.295
UACU	-3.003	0.537
UUGG	-3.020	0.732
CUCU	-3.020	0.886
GUUU	-3.021	0.270
UUAC	-3.022	0.355
CUUC	-3.024	0.407
UCAA	-3.030	0.243
AAUU	-3.053	0.425
AGCA	-3.054	0.716
AGAA	-3.055	0.172
AUCC	-3.072	0.327
CGAA	-3.074	0.683

Loop	Total loop count
AAAA	8135
AAAC	43343
AAAG	1255
AAAU	1865
AACA	3125
AACC	761
AACG	492
AACU	1015
AAGA	5161
AAGC	373
AAGG	5033
AAGU	4721
AAUA	2693
AAUC	611
AAUG	820
AAUU	3177
ACAA	14938
ACAC	638
ACAG	1438
ACAU	18797
ACCA	325
ACCC	1486
ACCG	219
ACCU	1603
ACGA	1149
ACGC	38
ACGG	411
ACGU	128
ACUA	754
ACUC	258
ACUG	472
ACUU	746
AGAA	4657
AGAC	404
AGAG	543
AGAU	784
AGCA	1854
AGCC	381878
AGCG	347
AGCU	1922
AGGA	356
AGGC	187
AGGG	96
AGGU	136
AGUA	8519
AGUC	594
AGUG	6055
AGUU	611
AUAA	12454
AUAC	807
AUAG	703
AUAU	1615
AUCA	858
AUCC	6117
AUCG	440
AUCU	737
AUGA	1745
AUGC	486
AUGG	326
AUGU	240
AUUA	4235
AUUC	2055
AUUG	2392
AUUU	5265
CAAA	4400
CAAC	11176
CAAG	35041
CAAU	2687

Supercategory	Total loop count
Intron	123970
Translation	6352055
Cis -Reg	106939

CGUG	-3.081	1.627
AAGA	-3.092	0.218
GACG	-3.108	1.309
UAUG	-3.120	0.605
AAGU	-3.121	0.037
GAAC	-3.126	0.162
GCUA	-3.132	0.523
GCCA	-3.137	0.671
AGCU	-3.137	0.575
UCUU	-3.145	0.521
UCAC	-3.152	0.301
UGUU	-3.161	0.300
ACAU	-3.161	0.556
UCUG	-3.168	0.164
CAUG	-3.169	0.182
AACU	-3.175	0.732
CAUU	-3.200	0.501
UAGA	-3.204	0.122
CCCG	-3.205	0.511
ACAG	-3.225	0.487
CUAA	-3.226	0.617
UCAG	-3.232	0.249
GAGU	-3.242	0.302
AUAU	-3.244	0.385
GAGG	-3.245	0.516
UCAU	-3.248	0.093
GAAU	-3.252	0.354
CAAC	-3.256	0.432
CCUC	-3.265	0.607
AUUG	-3.268	0.161
GCUU	-3.271	0.523
AUGA	-3.273	0.300
UUCC	-3.280	0.351
ACCC	-3.282	0.841
CAGA	-3.292	0.581
AUUC	-3.294	0.425
GAUU	-3.295	0.314
GGAU	-3.304	0.234
UUGA	-3.308	0.047
UCUC	-3.308	0.663
GUAU	-3.320	0.504
AAAG	-3.322	0.527
UAGG	-3.331	0.887
GUUG	-3.344	0.872
ACCU	-3.347	0.313
CAAU	-3.347	0.624
UGCU	-3.348	0.959
CGCC	-3.352	0.868
GUCU	-3.354	0.127
ACUA	-3.362	0.683
UGUG	-3.371	0.217
AGUG	-3.374	0.395
UAGU	-3.376	0.371
UACA	-3.379	0.788
GGUG	-3.380	1.484
AUAC	-3.381	0.642
UCCU	-3.383	0.366
UCCA	-3.391	0.587
UGAU	-3.409	0.501
ACAC	-3.410	0.707
AAUG	-3.428	0.638
AUCA	-3.428	0.458
CUGG	-3.432	0.775
CCCC	-3.437	1.480
GUAG	-3.438	0.372
AACC	-3.440	0.607
CACG	-3.450	0.182
CCAA	-3.452	0.568
GGUA	-3.462	0.428

CACA	853
CACC	147
CACG	3124
CACU	1251
CAGA	1040
CAGC	171
CAGG	13296
CAGU	339
CAUA	537
CAUC	238
CAUG	6389
CAUU	11334
CCAA	926
CCAC	224
CCAG	874
CCAU	1301
CCCA	248
CCCC	1836
CCCG	2002
CCCU	258
CCGA	410
CCGC	129
CCGG	125
CCGU	192
CCUA	164
CCUC	979
CCUG	737
CCUU	559
CGAA	1824
CGAC	154
CGAG	2053
CGAU	253
CGCA	326
CGCC	10074
CGCG	219
CGCU	181
CGGA	284
CGGC	69
CGGG	414
CGGU	484
CGUA	813
CGUC	60
CGUG	6806
CGUU	224
CUAA	1437
CUAC	351
CUAG	12762
CUAU	611
CUCA	720
CUCC	675
CUCG	27754
CUCU	1806
CUGA	930
CUGC	246
CUGG	726
CUGU	427
CUUA	815
CUUC	2407
CUUG	145951
CUUU	2177
GAAA	857531
GAAC	3575
GAAG	332915
GAAU	1794
GACA	6284
GACC	139
GACG	3039
GACU	1419
GAGA	636104

ACGA	-3.469	1.102
ACUU	-3.470	0.650
UAUC	-3.471	0.097
AUCU	-3.477	0.561
GUCC	-3.478	0.604
CGAG	-3.479	1.023
UACC	-3.486	0.238
GGCA	-3.487	0.182
CUUA	-3.490	0.413
UGUA	-3.493	0.662
CUGA	-3.501	0.449
CUCC	-3.504	1.061
AUAG	-3.505	0.481
UGGU	-3.507	0.279
GGGU	-3.512	0.618
UCUA	-3.517	0.590
GGUU	-3.522	0.558
CUCA	-3.527	0.805
AGAU	-3.538	0.378
CCUU	-3.539	0.554
CACU	-3.543	0.473
UCCC	-3.546	0.867
CCUG	-3.547	0.421
GAUG	-3.559	0.505
CCAG	-3.567	0.305
CACA	-3.571	0.352
UGAC	-3.573	0.289
AAGG	-3.575	0.409
GUCG	-3.591	0.601
CGUA	-3.602	0.594
GCCU	-3.603	0.109
AACG	-3.610	0.770
CAUA	-3.611	1.142
UGGA	-3.631	0.243
CAGG	-3.635	0.829
CUGU	-3.640	0.758
GCAC	-3.645	0.229
UGCC	-3.663	0.569
AGAG	-3.683	0.616
UAGC	-3.685	0.275
UCGC	-3.688	0.186
CAGU	-3.704	0.655
CCAU	-3.707	0.054
GUUC	-3.723	0.306
UGCA	-3.726	0.475
GAGC	-3.729	0.212
AAUC	-3.734	0.536
GUGU	-3.739	0.279
AGUU	-3.757	0.717
CUAU	-3.757	0.380
GCGG	-3.769	0.266
AUCG	-3.774	0.558
ACCA	-3.777	0.604
AUGG	-3.780	0.550
CCCA	-3.786	0.853
UCGG	-3.793	0.173
CCGA	-3.802	0.854
GACU	-3.810	0.131
AUGC	-3.816	0.503
ACUG	-3.836	0.348
AAGC	-3.843	0.506
CCCU	-3.851	0.811
AGCG	-3.851	0.651
AUGU	-3.853	0.642
GCUG	-3.854	0.238
GCCC	-3.855	0.984
AGGA	-3.857	0.470
GUGG	-3.861	0.456
CCAC	-3.872	0.709

GAGC	1468
GAGG	3876
GAGU	1851
GAUA	5027
GAUC	211
GAUG	1928
GAUU	1955
GCAA	689572
GCAC	1089
GCAG	218323
GCAU	155006
GCCA	1282
GCCC	279
GCCG	245
GCCU	1331
GCGA	255496
GCGC	139
GCGG	685
GCGU	487
GCUA	2587
GCUC	304
GCUG	566
GCUU	1126
GGAA	75525
GGAC	146
GGAG	4855
GGAU	1849
GGCA	1711
GGCC	681
GGCG	453
GGCU	248
GGGA	12647
GGGC	374
GGGG	412
GGGU	1375
GGUA	1133
GGUC	316
GGUG	2924
GGUU	1205
GUAA	73131
GUAC	327
GUAG	5960
GUAU	1014
GUCA	21626
GUCC	609
GUCG	519
GUCU	2152
GUGA	481692
GUGC	202
GUGG	1309
GUGU	612
GUUA	11701
GUUC	691
GUUG	1467
GUUU	3670
UAAA	5774
UAAC	259639
UAAG	14487
UAAU	27045
UACA	990
UACC	2992
UACG	390785
UACU	4317
UAGA	5602
UAGC	1724
UAGG	23016
UAGU	1569
UAUA	4662
UAUC	1751

UGGC	-3.875	0.699
CUGC	-3.877	0.579
ACGG	-3.897	1.121
UCGU	-3.897	0.113
AGUC	-3.898	0.254
GCGU	-3.915	0.484
ACUC	-3.926	0.486
GGGG	-3.928	0.322
CGUU	-3.959	0.672
GGUC	-3.963	1.139
GCUC	-3.966	0.625
GUAC	-3.967	0.526
GGCC	-3.974	0.590
GGCU	-3.984	0.868
UGGG	-3.984	0.160
UCGA	-3.993	0.436
GAUC	-3.994	0.546
CUAC	-4.001	0.467
UGUC	-4.036	0.528
CCUA	-4.063	0.562
CGCG	-4.087	0.791
CAGC	-4.088	0.513
CCGC	-4.091	0.819
GGCG	-4.095	0.302
ACGU	-4.108	0.878
CGCU	-4.113	0.674
GGAC	-4.134	0.585
CGCA	-4.149	0.174
CACC	-4.157	0.609
ACCG	-4.196	0.266
GCGC	-4.207	0.838
CAUC	-4.208	0.479
AGGU	-4.209	0.596
CGAC	-4.209	0.691
GCCG	-4.211	0.239
CGGU	-4.216	0.300
CCGU	-4.230	0.420
CGGG	-4.230	0.196
AGGC	-4.233	0.778
AGAC	-4.235	0.679
GACC	-4.243	0.529
GGGC	-4.271	0.025
CGAU	-4.291	0.245
CGGC	-4.296	0.904
CGGA	-4.338	0.162
GUGC	-4.363	0.136
CGUC	-4.526	0.523
CCGG	-4.599	0.145
ACGC	-4.787	0.446
AGGG	-4.866	0.046

UAUG	5535
UAUU	92443
UCAA	6570
UCAC	7350
UCAG	3863
UCAU	4365
UCCA	748
UCCC	733
UCCG	57147
UCCU	2106
UCGA	950
UCGC	1363
UCGG	1077
UCGU	825
UCUA	557
UCUC	860
UCUG	4133
UCUU	1465
UGAA	17014
UGAC	1301
UGAG	16613
UGAU	998
UGCA	494
UGCC	526
UGCG	10940
UGCU	687
UGGA	1079
UGGC	216
UGGG	902
UGGU	1045
UGUA	578
UGUC	192
UGUG	1666
UGUU	2330
UUAA	5344
UUAC	12046
UUAG	26111
UUAU	8020
UUCA	5032
UUCC	1887
UUCG	558528
UUCU	7159
UUGA	3622
UUGC	4439
UUGG	1516
UUGU	14759
UUUA	65146
UUUC	16522
UUUG	14338
UUUU	42884

Loop	Score	SD
GUCAA	-2.218	1.324
GUUAA	-2.230	0.865
GAUAA	-2.233	1.026
UUUUU	-2.294	0.340
AAAUA	-2.312	0.580
UUUAU	-2.354	0.203
CUUGA	-2.389	0.774
GAAAA	-2.421	0.493
CUUGU	-2.430	0.442
UAAUU	-2.468	1.279
CUCGA	-2.511	0.431
CAUUG	-2.540	0.492
CUCAA	-2.542	1.758
GAAAG	-2.585	0.837
CAAAA	-2.600	0.626
CUUAA	-2.601	1.289
AAACA	-2.606	0.455
GACAA	-2.613	1.415
CUCUG	-2.615	0.414
UUUUA	-2.624	0.389
UAACA	-2.638	1.148
UAACU	-2.699	0.817
UUAGU	-2.711	0.229
CUUUG	-2.730	0.489
CAAUG	-2.744	1.210
UUCGG	-2.747	1.323
UAAUA	-2.753	1.095
CAAGU	-2.765	1.032
GGAUA	-2.772	1.967
AUUAA	-2.787	0.490
CUCGU	-2.793	0.560
GAAAU	-2.794	0.608
UAACG	-2.813	1.639
AUUUU	-2.821	0.322
AAUAA	-2.822	0.586
AAAGA	-2.830	0.720
UUUGG	-2.850	0.414
GGAGA	-2.851	1.136
AGAAA	-2.853	0.491
UUUAA	-2.869	0.306
GAAUA	-2.871	0.727
AAAAA	-2.872	0.215
GUAUA	-2.879	0.010
CAAUA	-2.890	1.804
GGAAA	-2.898	0.409
GUAAA	-2.900	0.230
AUAAA	-2.905	0.175
UUAAU	-2.914	0.085
AAAAC	-2.919	0.566
UUAAG	-2.928	0.438
UUUCU	-2.931	0.714
AUUUA	-2.935	0.274
UCAGC	-2.941	1.299
CUUGC	-2.942	0.650
CUAUG	-2.954	1.177
AUAAU	-2.972	0.588
CAAGA	-2.989	0.385
CACUG	-2.990	1.233
UUAGA	-2.991	0.293
UAUAU	-3.006	0.353
UUCUU	-3.017	0.994
UUGAC	-3.028	1.130
AAUUA	-3.032	1.116
AAUGA	-3.034	0.279
CUAAA	-3.041	0.122
GAGAG	-3.045	0.904
UUUCC	-3.045	0.737
CAAAG	-3.053	0.946

Loop	Total loop count
AAAAA	1481
AAAAC	598
AAAAG	459
AAAAU	651
AAACA	9389
AAACC	288
AAACG	28
AAACU	889
AAAGA	567
AAAGC	85
AAAGG	146
AAAGU	209
AAAUA	22844
AAAUC	279
AAAUG	113
AAAUU	406
AACAA	2657
AACAC	77
AACAG	17
AACAU	106
AACCA	13165
AACCC	124
AACCG	9
AACCU	29
AACGA	80
AACGC	10
AACGG	142
AACGU	89
AACUA	2452
AACUC	40
AACUG	88
AACUU	102
AAGAA	1007
AAGAC	17
AAGAG	24
AAGAU	46
AAGCA	307
AAGCC	80
AAGCG	13
AAGCU	21
AAGGA	219
AAGGC	37
AAGGG	31
AAGGU	32
AAGUA	2335
AAGUC	30
AAGUG	50
AAGUU	44
AAUAA	7896
AAUAC	78
AAUAG	78
AAUAU	236
AAUCA	1091
AAUCC	97
AAUCG	9
AAUCU	48
AAUGA	660
AAUGC	7
AAUGG	80
AAUGU	188
AAUUA	15719
AAUUC	31
AAUUG	64
AAUUU	212
ACAAA	407
ACAAC	56
ACAAG	61
ACAAU	54

Supercategory	Total loop count
Intron	18938
Translation	1218388
Cis -Reg	72576

UAAAA	-3.054	0.201
UAACC	-3.061	0.904
UAAAU	-3.063	0.340
AACUA	-3.066	0.709
UAUAA	-3.066	0.133
GCAUA	-3.066	0.862
UUUGA	-3.073	0.515
CACGU	-3.082	0.634
UUUGU	-3.083	0.279
GCCAA	-3.085	0.185
GAAGA	-3.088	0.199
GAAAC	-3.093	0.863
GUAAU	-3.102	0.278
GGUUA	-3.103	0.553
GCAAG	-3.105	1.222
GAACA	-3.106	1.512
AUAUA	-3.108	0.064
AAAAU	-3.110	0.212
UUUAC	-3.119	0.315
UAAGA	-3.121	0.459
GUCUA	-3.124	1.057
UUAUU	-3.126	0.237
UUCAA	-3.127	0.621
GUUUA	-3.133	0.866
UUAUA	-3.138	0.201
CAUAG	-3.146	0.243
AUUAG	-3.146	0.643
GAUGA	-3.149	0.376
AUCAA	-3.151	0.461
CCCAA	-3.154	0.855
CGUUG	-3.156	1.142
UUAGG	-3.161	0.967
ACCCA	-3.161	0.939
GUUUC	-3.164	0.637
UUCGU	-3.165	0.113
UUAGC	-3.165	0.915
GGGGA	-3.167	1.292
GCUAA	-3.178	0.966
UUUUG	-3.178	0.137
GAGUA	-3.179	0.970
CGAAA	-3.182	0.614
CUGAC	-3.187	1.334
UUAAA	-3.190	0.238
CUACG	-3.193	0.803
UAUUU	-3.197	0.227
CUUAG	-3.201	0.475
UCUUU	-3.202	1.051
AAAUC	-3.204	0.563
UUUCA	-3.205	0.225
UUCUA	-3.208	0.612
CUUCG	-3.215	0.542
GAGAA	-3.217	0.397
CUUGG	-3.219	0.541
AUUAU	-3.219	0.502
CUAGC	-3.229	0.577
UGAAA	-3.233	0.275
UAAUG	-3.241	1.212
AAUAU	-3.247	0.976
CACCG	-3.260	1.146
GAGGA	-3.261	0.878
UUCCU	-3.261	0.101
UUGUG	-3.267	0.227
CACAA	-3.268	0.453
GGUAA	-3.274	0.065
AGAUA	-3.279	1.059
CAUUA	-3.287	0.612
CAACG	-3.288	0.561
CUAGU	-3.290	0.563
GUCAU	-3.291	0.802

ACACA	82
ACACC	36
ACACG	120
ACACU	36
ACAGA	117
ACAGC	105
ACAGG	261
ACAGU	18
ACAUA	62
ACAUC	57
ACAUG	12
ACAUU	45
ACCAA	460
ACCAC	40
ACCAG	27
ACCAU	128
ACCCA	325
ACCCC	636
ACCCG	23
ACCCU	1222
ACCGA	11
ACCGC	53
ACCGG	133
ACCGU	18
ACCUA	198
ACCUC	115
ACCUG	46
ACCUU	53
ACGAA	187
ACGAC	29
ACGAG	115
ACGAU	181
ACGCA	93
ACGCC	17
ACGCG	10
ACGCU	4
ACGGA	72
ACGGC	22
ACGGG	17
ACGGU	4
ACGUA	187
ACGUC	12
ACGUG	11
ACGUU	8
ACUAA	597
ACUAC	48
ACUAG	37
ACUAU	21
ACUCA	63
ACUCC	15
ACUCG	4
ACUCU	25
ACUGA	91
ACUGC	10
ACUGG	1218
ACUGU	39
ACUUA	84
ACUUC	90
ACUUG	50
ACUUU	44
AGAAA	736
AGAAC	58
AGAAG	234
AGAAU	81
AGACA	316
AGACC	30
AGACG	9
AGACU	8
AGAGA	235

CAAUU	-3.298	0.485
UUGAU	-3.299	0.276
CUCAG	-3.308	0.153
UACGA	-3.309	0.636
AAAUU	-3.309	0.461
AAGUA	-3.310	0.514
GUCUG	-3.311	0.610
UUCUG	-3.311	0.316
CAAGC	-3.312	0.568
UUCGA	-3.316	0.697
UUCAU	-3.318	0.391
CGCUG	-3.318	1.177
UAUUA	-3.322	0.355
GGACA	-3.326	1.353
CACAU	-3.327	0.536
AACAA	-3.332	0.637
AUGUA	-3.335	0.523
GUAAG	-3.337	0.520
UUUUC	-3.338	0.604
GGGAA	-3.339	0.448
CUUUU	-3.339	0.593
UCAGA	-3.340	0.232
GUCUU	-3.342	0.817
UCAGG	-3.344	0.674
UUAUG	-3.347	0.575
GUGAA	-3.352	0.334
AAACC	-3.355	0.421
AAUUU	-3.357	0.528
UACUU	-3.357	0.316
CUAGA	-3.360	0.238
AUGAU	-3.361	0.483
CUGGC	-3.373	0.880
GAAGU	-3.376	1.067
AGAAG	-3.382	0.573
UGAUA	-3.383	0.669
AUGAA	-3.384	0.312
CAAGG	-3.385	0.351
CAUUU	-3.386	0.887
UUUAG	-3.386	0.113
AGACA	-3.388	0.460
CAUGG	-3.389	0.778
GGCAA	-3.393	0.160
UAAUC	-3.393	0.457
CAUGA	-3.399	0.219
UUGGC	-3.399	1.713
CAGAG	-3.402	0.623
CAUAU	-3.406	1.404
CGCAA	-3.408	0.601
CACUA	-3.409	1.157
UGAAG	-3.411	0.682
AAACU	-3.415	0.407
ACAAA	-3.422	0.301
CCUAA	-3.424	0.346
AGAGA	-3.424	0.352
CGUGU	-3.426	0.948
GUUCA	-3.426	0.692
UAAAC	-3.428	0.192
UAGAU	-3.428	0.429
GAUAU	-3.433	0.378
UUUGC	-3.436	0.713
UCAAC	-3.440	0.804
GUUAU	-3.441	0.551
GACGA	-3.442	0.442
AAGAA	-3.442	0.399
GCAAA	-3.443	0.381
UUAAC	-3.443	0.357
GUUUU	-3.446	0.471
CCUGA	-3.446	0.414
CAACA	-3.447	1.169

AGAGC	91
AGAGG	27
AGAGU	39
AGAUA	309
AGAUC	7
AGAUG	61
AGAUU	45
AGCAA	405
AGCAC	89
AGCAG	44
AGCAU	34
AGCCA	43
AGCCC	524
AGCCG	59
AGCCU	35
AGCGA	36
AGCGC	22
AGCGG	26
AGCGU	6
AGCUA	146
AGCUC	14
AGCUG	17
AGCUU	179
AGGAA	63
AGGAC	70
AGGAG	62
AGGAU	86
AGGCA	19
AGGCC	55
AGGCG	3
AGGCU	7
AGGGA	39
AGGGC	14
AGGGG	7
AGGGU	9
AGGUA	325
AGGUC	7
AGGUG	5
AGGUU	15
AGUAA	149
AGUAC	16
AGUAG	137
AGUAU	48
AGUCA	62
AGUCC	29
AGUCG	12
AGUCU	82
AGUGA	66
AGUGC	5
AGUGG	92
AGUGU	8
AGUUA	673
AGUUC	51
AGUUG	18
AGUUU	238
AUAAA	1280
AUAAC	93
AUAAG	1176
AUAAU	6236
AUACA	322
AUACC	62
AUACG	82
AUACU	250
AUAGA	514
AUAGC	203
AUAGG	116
AUAGU	99
AUAUA	1075
AUAUC	714

CUCGC	-3.450	1.075
GUGUA	-3.451	0.465
GUUGG	-3.451	1.047
UUCAC	-3.456	0.413
CGCAU	-3.458	0.910
CUUCA	-3.461	0.692
AGCAA	-3.462	0.055
AUUGU	-3.468	0.599
UCACU	-3.468	0.235
CAUGU	-3.469	0.370
UCGCU	-3.480	0.569
GAUUA	-3.485	0.244
UUCCA	-3.488	0.617
CGAGU	-3.488	0.367
GGAUG	-3.489	1.046
UGAAU	-3.493	0.167
UUGAA	-3.502	0.117
UUGGU	-3.502	0.973
UAGAC	-3.503	0.427
GUCGA	-3.504	0.855
CACUU	-3.504	1.466
CAGUG	-3.505	1.890
CACAG	-3.510	0.950
AACCC	-3.512	0.653
UCUAA	-3.514	0.368
GUUAG	-3.517	0.188
UCCAA	-3.518	0.752
GUAUU	-3.518	0.109
UAAGU	-3.519	0.349
UUACG	-3.520	0.149
CUCAC	-3.532	0.810
AUAAG	-3.533	0.453
UGCCC	-3.535	1.369
AGCCC	-3.537	0.344
GCUUA	-3.538	0.720
UUCUC	-3.541	0.936
AAAGG	-3.542	1.090
AUUAC	-3.543	0.656
UCAUU	-3.544	0.329
AAAAG	-3.547	0.616
GUAAC	-3.549	0.603
AAUCA	-3.549	0.524
AAUGU	-3.549	0.550
GGGUA	-3.552	0.911
AUCAU	-3.553	0.537
CAACU	-3.554	0.277
AACCA	-3.555	1.395
UACAA	-3.556	0.274
ACCCU	-3.559	0.548
UCAGU	-3.560	1.142
UUGCU	-3.566	1.012
CGAAG	-3.570	0.535
GUUUG	-3.573	0.621
CAUAA	-3.574	0.191
CUUUA	-3.575	0.201
UUGCC	-3.579	0.265
ACGUA	-3.581	1.606
AUCUU	-3.581	0.411
AUAGA	-3.588	0.451
UAAAG	-3.588	0.258
CCCUG	-3.592	0.672
CGCAG	-3.594	0.983
UAUCA	-3.594	0.596
GUCUC	-3.597	0.599
CCUGU	-3.597	0.449
CAAUC	-3.598	1.129
GCACA	-3.602	0.811
UUUCG	-3.605	0.349
ACCAU	-3.606	0.625

AUAUG	703
AUAUU	626
AUCAA	2465
AUCAC	117
AUCAG	103
AUCAU	259
AUCCA	266
AUCCC	54
AUCCG	33
AUCCU	328
AUCGA	98
AUCGC	48
AUCGG	33
AUCGU	17
AUCUA	384
AUCUC	37
AUCUG	408
AUCUU	181
AUGAA	685
AUGAC	76
AUGAG	147
AUGAU	242
AUGCA	41
AUGCC	14
AUGCG	3
AUGCU	5
AUGGA	28
AUGGC	150
AUGGG	17
AUGGU	59
AUGUA	439
AUGUC	9
AUGUG	71
AUGUU	18
AUUAA	4582
AUUAC	174
AUUAG	515
AUUAU	297
AUUCA	357
AUUCC	108
AUUCG	104
AUUCU	44
AUUGA	141
AUUGC	30
AUUGG	63
AUUGU	194
AUUUA	1101
AUUUC	109
AUUUG	128
AUUUU	996
CAAAA	1281
CAAAC	125
CAAAG	13002
CAAAU	177
CAACA	184
CAACC	31
CAACG	295
CAACU	218
CAAGA	630
CAAGC	230
CAAGG	1292
CAAGU	629
CAAUA	7372
CAAUC	168
CAAUG	3732
CAAUU	2239
CACAA	807
CACAC	16
CACAG	2171

AUCCU	-3.611	0.365
UCAAA	-3.613	0.419
UACGU	-3.614	0.304
ACCUA	-3.614	1.138
UACAU	-3.619	0.560
UUACA	-3.619	0.273
UGACC	-3.622	0.902
AACUU	-3.625	0.586
UGUAU	-3.628	0.731
CCAGU	-3.628	0.563
CUGGU	-3.629	0.578
CGUAA	-3.630	0.417
UCAAG	-3.633	0.636
UACCC	-3.637	0.334
GCUAU	-3.637	0.997
UGCUC	-3.640	1.990
UCCGG	-3.640	1.126
GUUCG	-3.641	1.204
AGUAG	-3.642	0.551
UGAUU	-3.644	0.442
AUAUU	-3.645	0.411
AGUUA	-3.645	0.392
UAUGA	-3.645	0.311
AUCUA	-3.647	0.508
CUAUU	-3.648	0.766
CCUUG	-3.648	0.521
UAUUC	-3.652	0.319
GCAAC	-3.653	0.302
CACGA	-3.654	0.325
AUUCA	-3.656	0.412
ACUAA	-3.663	0.477
AAAUG	-3.663	0.462
CAUCU	-3.663	0.586
UCCAU	-3.665	0.745
UUACC	-3.666	0.290
UUCGC	-3.670	0.629
UUCCG	-3.670	0.562
ACACA	-3.672	0.742
UCUCU	-3.673	0.726
GCUGA	-3.673	0.054
GUAGC	-3.676	0.388
UCAAU	-3.677	0.243
AUCAC	-3.679	0.929
AUACA	-3.682	0.331
GCUUU	-3.688	0.841
GGCCC	-3.690	2.021
CAAAU	-3.691	0.937
CGGUG	-3.692	1.224
AAUAG	-3.692	0.746
CCAUG	-3.694	0.533
UCCUA	-3.695	1.296
AUUUG	-3.696	0.381
AUAUC	-3.697	0.443
GUCAG	-3.697	0.393
AUCAG	-3.702	0.544
CUCGG	-3.709	1.072
UCUUA	-3.710	0.156
CGUUU	-3.711	0.874
CCCGC	-3.712	0.713
CCAGC	-3.719	0.478
GCGUA	-3.720	0.363
GCUUC	-3.721	0.559
GUACA	-3.722	0.217
ACAGA	-3.722	1.087
UUACU	-3.723	0.444
UCCGC	-3.723	0.800
CUUAU	-3.724	0.391
CACCC	-3.724	0.739
ACGAA	-3.730	1.091

CACAU	221
CACCA	14
CACCC	651
CACCG	285
CACCU	83
CACGA	650
CACGC	156
CACGG	374
CACGU	1007
CACUA	658
CACUC	18
CACUG	1948
CACUU	653
CAGAA	40
CAGAC	26
CAGAG	2452
CAGAU	344
CAGCA	86
CAGCC	96
CAGCG	74
CAGCU	5
CAGGA	24
CAGGC	49
CAGGG	665
CAGGU	7
CAGUA	466
CAGUC	10
CAGUG	2976
CAGUU	39
CAUAA	322
CAUAC	11
CAUAG	1530
CAUAU	593
CAUCA	124
CAUCC	54
CAUCG	102
CAUCU	168
CAUGA	418
CAUGC	82
CAUGG	2681
CAUGU	210
CAUUA	336
CAUUC	43
CAUUG	3902
CAUUU	239
CCAAA	70
CCAAC	30
CCAAG	235
CCAAU	26
CCACA	33
CCACC	67
CCACG	56
CCACU	19
CCAGA	70
CCAGC	119
CCAGG	552
CCAGU	124
CCAUA	79
CCAUC	130
CCAUG	154
CCAUU	438
CCCAA	8299
CCCAC	30
CCCAG	67
CCCAU	87
CCCCA	50
CCCCC	13
CCCCG	16
CCCCU	13

AUAGC	-3.732	0.633
UGACU	-3.733	0.885
UCACC	-3.733	1.100
CUUAC	-3.733	0.538
UUCCC	-3.735	0.770
AUUGA	-3.736	0.241
UAUUG	-3.736	0.748
AUGAG	-3.737	0.267
CUAUA	-3.738	0.918
GAAUU	-3.739	0.272
CCUAG	-3.741	0.527
UCUCC	-3.742	0.860
GGAUU	-3.743	0.918
UAUGG	-3.745	0.521
GCGAG	-3.746	0.627
CCCGU	-3.747	0.233
UGCAC	-3.747	0.439
UGAGU	-3.751	0.326
GUAGA	-3.757	0.775
UCGGC	-3.758	1.424
CCAGA	-3.759	0.833
CAGCC	-3.762	0.413
CCAGG	-3.763	0.499
ACGAU	-3.767	0.443
GCCCC	-3.769	1.279
CUCAU	-3.772	0.662
AUAGU	-3.772	0.559
UCCCC	-3.774	1.151
UGCGA	-3.774	0.839
GGAAG	-3.775	0.307
CUCUC	-3.778	0.775
UGUGA	-3.778	0.552
GUCCA	-3.779	0.478
UCCUU	-3.779	0.918
CUCCG	-3.780	0.384
UGUAA	-3.780	0.258
UGUGU	-3.784	0.867
GGCUA	-3.784	0.546
CAUGC	-3.784	0.484
AUACU	-3.785	0.086
UACAC	-3.786	0.798
CUGGA	-3.788	0.992
GGAAC	-3.790	0.915
CGCGU	-3.794	0.945
CAGCA	-3.796	1.115
GGUUC	-3.797	0.956
UGGUA	-3.798	0.484
GCCUC	-3.799	0.289
AAAGU	-3.799	0.403
ACAAG	-3.800	0.688
UUCAG	-3.804	1.182
UACCA	-3.804	0.599
AUAGG	-3.805	0.396
ACUGG	-3.807	1.774
ACCCC	-3.808	1.507
AGUAA	-3.808	0.600
ACAGG	-3.809	1.452
UUGCA	-3.810	0.744
GCCAU	-3.811	0.943
UCAUA	-3.812	0.464
GAUCU	-3.813	0.642
CUAAG	-3.815	0.359
CUCCA	-3.815	0.829
GUUGA	-3.815	0.103
GUGGA	-3.815	0.297
AUUUC	-3.816	0.270
AAGCA	-3.817	0.253
AUGUG	-3.818	0.858
UACUG	-3.820	0.820

CCCGA	200
CCCGC	180
CCCGG	45
CCCGU	416
CCCUA	75
CCCUC	29
CCCUG	148
CCCUU	42
CCGAA	25
CCGAC	43
CCGAG	9
CCGAU	15
CCGCA	22
CCGCC	48
CCGCG	9
CCGCU	3
CCGGA	6
CCGGC	12
CCGGG	3
CCGGU	3
CCGUA	26
CCGUC	13
CCGUG	63
CCGUU	14
CCUAA	1142
CCUAC	197
CCUAG	641
CCUAU	18
CCUCA	59
CCUCC	34
CCUCG	65
CCUCU	29
CCUGA	515
CCUGC	120
CCUGG	115
CCUGU	228
CCUUA	43
CCUUC	31
CCUUG	271
CCUUU	34
CGAAA	684
CGAAC	125
CGAAG	1092
CGAAU	38
CGACA	45
CGACC	18
CGACG	64
CGACU	4
CGAGA	114
CGAGC	12
CGAGG	75
CGAGU	196
CGAUA	201
CGAUC	5
CGAUG	214
CGAUU	15
CGCAA	1182
CGCAC	23
CGCAG	325
CGCAU	130
CGCCA	31
CGCCC	54
CGCCG	15
CGCCU	16
CGCGA	241
CGCGC	25
CGCGG	27
CGCGU	56
CGCUA	25

UAUAG	-3.820	0.941
UGAUC	-3.820	0.780
ACAUA	-3.824	0.830
GUCCU	-3.824	0.713
AGAAC	-3.826	1.045
CCUGG	-3.826	0.243
UCCAC	-3.826	0.891
GAAUC	-3.827	0.892
AUUGG	-3.830	0.723
UUGUA	-3.831	0.342
AUGGC	-3.832	0.950
UAUGU	-3.835	0.251
AUUCC	-3.836	0.569
UCUAC	-3.839	0.697
UACGG	-3.844	0.781
AUAUG	-3.850	0.530
ACUGA	-3.851	0.489
UGCAA	-3.853	0.250
UGGCU	-3.853	1.024
AAGUG	-3.855	0.938
CGAUA	-3.856	1.264
GACCC	-3.856	1.256
CAGUA	-3.858	1.552
GAUUC	-3.859	0.379
ACACG	-3.859	0.836
CGCCC	-3.861	0.851
AACUG	-3.861	0.738
ACUUA	-3.862	0.349
ACAGC	-3.863	0.446
UGAAC	-3.863	0.227
UAAGG	-3.864	0.428
UUGUU	-3.867	0.304
GCUCA	-3.868	0.296
CCUGC	-3.869	0.220
GUUGU	-3.869	0.453
GGUGA	-3.869	0.288
AAAGC	-3.871	0.351
GGUUU	-3.873	0.342
ACCAA	-3.874	0.532
UGUUC	-3.875	0.710
GAUAC	-3.879	0.574
GCGAA	-3.879	0.381
UCUCA	-3.879	0.277
UUAUC	-3.886	0.188
GUUCC	-3.889	0.554
UACUC	-3.890	1.225
GCCUA	-3.891	1.127
UCAUC	-3.892	0.826
CAUCG	-3.894	0.500
UAGCU	-3.894	1.205
UAUCU	-3.894	0.309
ACGAG	-3.898	1.557
GACCA	-3.900	0.178
GGAGG	-3.901	0.493
CCCUA	-3.903	0.524
UGUUU	-3.903	0.463
CUUCU	-3.904	0.448
AUCCA	-3.907	0.357
CGAUG	-3.907	1.126
GACUA	-3.909	0.888
ACGGA	-3.909	1.013
AACGG	-3.911	1.066
ACCUC	-3.912	0.249
ACCUU	-3.914	0.585
UCUGC	-3.914	1.143
CGCGA	-3.917	0.191
AUCGA	-3.918	0.266
AUAAC	-3.918	0.336
CUGUG	-3.919	0.289

CGCUC	16
CGCUG	945
CGCUU	35
CGGAA	42
CGGAC	34
CGGAG	31
CGGAU	71
CGGCA	5
CGGCC	8
CGGCG	5
CGGCU	5
CGGGA	7
CGGGC	9
CGGGG	7
CGGGU	6
CGGUA	15
CGGUC	5
CGGUG	276
CGGUU	11
CGUAA	441
CGUAC	15
CGUAG	111
CGUAU	80
CGUCA	55
CGUCC	15
CGUCG	14
CGUCU	45
CGUGA	124
CGUGC	22
CGUGG	36
CGUGU	246
CGUUA	13
CGUUC	62
CGUUG	1142
CGUUU	143
CUAAA	1475
CUAAC	303
CUAAG	480
CUAAU	47
CUACA	126
CUACC	390
CUACG	5999
CUACU	25
CUAGA	1021
CUAGC	1986
CUAGG	292
CUAGU	1636
CUAUA	287
CUAUC	29
CUAUG	28533
CUAUU	1396
CUCAA	240618
CUCAC	892
CUCAG	935
CUCAU	152
CUCCA	246
CUCCC	30
CUCCG	271
CUCCU	100
CUCGA	2250
CUCGC	2333
CUCGG	3344
CUCGU	3792
CUCUA	123
CUCUC	62
CUCUG	3084
CUCUU	43
CUGAA	139
CUGAC	9173

AGUUU	-3.920	0.595
CUCUA	-3.921	0.847
CGUAG	-3.921	0.341
CCAUA	-3.923	0.852
UGUCC	-3.923	0.809
CCUCA	-3.924	0.664
GCCUU	-3.925	1.163
GCAGA	-3.925	0.430
GAUCC	-3.927	0.623
UGGAA	-3.928	0.469
UAUAC	-3.934	0.230
UGUAC	-3.936	0.691
GAUCA	-3.939	0.406
CUCCU	-3.941	0.180
UCGCG	-3.941	1.226
CAGGG	-3.943	0.712
CCAAA	-3.944	0.437
GCUUG	-3.946	0.440
UCACA	-3.947	0.913
AUGAC	-3.947	0.343
CACCU	-3.949	1.067
AGUCU	-3.951	1.065
AGGAA	-3.952	0.538
UCCCA	-3.953	0.612
UCCGU	-3.955	0.644
UAGCA	-3.956	1.465
AUCGC	-3.956	0.659
UUGAG	-3.956	0.647
UCGAA	-3.958	0.438
GCAAU	-3.959	0.549
UGCUU	-3.960	0.572
GACAU	-3.962	0.259
UACCU	-3.964	0.573
UCGAC	-3.967	1.072
CGUAU	-3.969	0.979
CUGUA	-3.971	0.579
CCAUU	-3.971	1.034
UGAGA	-3.973	0.237
CCGAC	-3.974	0.798
GUGAU	-3.974	0.622
UCUGA	-3.975	0.462
GCAGC	-3.976	0.551
UGCCA	-3.978	0.913
AGGAU	-3.978	0.362
CCCCA	-3.979	0.498
GUCAC	-3.983	0.592
AGAGC	-3.986	0.945
UCGGU	-3.988	0.699
GACGC	-3.991	1.133
CGAAU	-3.992	0.779
CGACA	-3.994	1.008
GCAUG	-3.995	0.735
CACGG	-3.995	0.537
CACGC	-3.995	0.571
UCCUG	-3.998	0.654
GAAUG	-3.999	0.181
UCCCU	-3.999	0.388
CUCUU	-4.003	0.695
UUGCG	-4.003	0.697
GGAAU	-4.006	0.324
AUUCU	-4.007	0.658
UUGGA	-4.007	1.057
GUUAC	-4.008	0.180
CCUAC	-4.008	1.075
ACCGG	-4.009	1.007
AACGU	-4.009	1.222
UAGUA	-4.011	0.608
UAGAA	-4.011	0.786
CUUUC	-4.013	0.582

CUGAG	74
CUGAU	64
CUGCA	14
CUGCC	38
CUGCG	82
CUGCU	10
CUGGA	247
CUGGC	150
CUGGG	18
CUGGU	102
CUGUA	51
CUGUC	38
CUGUG	88
CUGUU	13
CUUAA	93813
CUUAC	679
CUUAG	1909
CUUAU	123
CUUCA	405
CUUCC	35
CUUCG	820
CUUCU	79
CUUGA	32558
CUUGC	5851
CUUGG	1748
CUUGU	13731
CUUUA	249
CUUUC	41
CUUUG	3702
CUUUU	220
GAAAA	2196
GAAAC	336
GAAAG	11228
GAAAU	772
GAACA	2303
GAACC	48
GAACG	23
GAACU	31
GAAGA	1622
GAAGC	290
GAAGG	494
GAAGU	675
GAAUA	920
GAAUC	58
GAAUG	155
GAAUU	295
GACAA	127318
GACAC	71
GACAG	134
GACAU	270
GACCA	191
GACCC	62
GACCG	9
GACCU	92
GACGA	1422
GACGC	124
GACGG	18
GACGU	67
GACUA	1401
GACUC	37
GACUG	27
GACUU	23
GAGAA	1951
GAGAC	47
GAGAG	1166
GAGAU	77
GAGCA	31
GAGCC	12
GAGCG	6

GGUCA	-4.015	0.431
CCCUU	-4.017	0.672
GGAGU	-4.018	0.073
ACUUG	-4.019	0.702
GGCGA	-4.019	0.469
GAGAU	-4.023	0.833
AGGAG	-4.024	1.279
GUGCA	-4.024	0.361
CCUCG	-4.026	0.428
AACAU	-4.027	0.836
CCAUC	-4.032	0.563
CAUCA	-4.033	0.165
GUGAC	-4.034	0.321
UCAUG	-4.038	0.440
GUUCU	-4.041	0.384
ACUUC	-4.042	1.053
UGCAU	-4.043	0.377
AGCAU	-4.048	0.681
AUACG	-4.050	0.274
CCUUA	-4.050	0.491
CAUUC	-4.053	0.518
AAGGU	-4.053	0.748
GCUAG	-4.057	1.138
UGGAU	-4.057	0.707
CCACG	-4.062	0.733
CCCAG	-4.063	0.315
GCUAC	-4.066	1.228
CAAAC	-4.067	0.369
GAUGU	-4.068	0.974
UACUA	-4.069	0.422
UGUCU	-4.069	0.460
CCCGA	-4.070	0.264
AGAUG	-4.070	0.315
AAUCC	-4.070	0.171
CGUCU	-4.071	0.425
AGUCA	-4.074	0.251
ACUUU	-4.075	0.432
UGUUA	-4.076	0.264
GUAGU	-4.079	0.333
GACGU	-4.080	1.424
AGCCU	-4.080	0.580
AGUAU	-4.081	0.384
AGCCG	-4.083	0.265
GGCCA	-4.083	0.368
AGAAU	-4.086	0.310
GGCUC	-4.088	1.639
UCCUC	-4.091	0.889
GAUUG	-4.091	0.100
UCUAU	-4.091	0.427
ACUCA	-4.092	0.405
AGGUA	-4.093	0.500
UGUUG	-4.093	1.182
AGAUU	-4.093	0.405
UAUCC	-4.093	0.611
CCUUU	-4.096	0.573
UACAG	-4.105	0.332
UGACA	-4.106	0.609
UACCG	-4.108	0.308
UUGUC	-4.110	1.035
AAUAC	-4.114	0.678
GACUC	-4.114	1.059
AAGUC	-4.117	0.776
UGACG	-4.117	0.408
CCAAG	-4.117	0.431
AGUGA	-4.118	0.333
UAGUU	-4.119	0.535
AGCAG	-4.120	0.372
AAUGG	-4.122	0.604
GAGAC	-4.122	0.623

GAGCU	4
GAGGA	678
GAGGC	12
GAGGG	36
GAGGU	14
GAGUA	527
GAGUC	23
GAGUG	19
GAGUU	31
GAUAA	98040
GAUAC	69
GAUAG	140
GAUAU	223
GAUCA	67
GAUCC	48
GAUCG	215
GAUCU	81
GAUGA	2050
GAUGC	14
GAUGG	10
GAUGU	54
GAUUA	753
GAUUC	81
GAUUG	87
GAUUU	50
GCAAA	740
GCAAC	244
GCAAG	22129
GCAAU	368
GCACA	93
GCACC	19
GCACG	34
GCACU	21
GCAGA	132
GCAGC	63
GCAGG	66
GCAGU	32
GCAUA	307
GCAUC	99
GCAUG	66
GCAUU	60
GCCAA	1635
GCCAC	15
GCCAG	48
GCCAU	71
GCCCA	25
GCCCC	238
GCCCG	32
GCCCU	28
GCCGA	45
GCCGC	12
GCCGG	6
GCCGU	5
GCCUA	401
GCCUC	116
GCCUG	34
GCCUU	238
GCGAA	252
GCGAC	28
GCGAG	417
GCGAU	61
GCGCA	17
GCGCC	11
GCGCG	8
GCGCU	3
GCGGA	36
GCGGC	7
GCGGG	34
GCGGU	13

CUACA	-4.123	0.416
GGAUC	-4.123	0.640
CUGAA	-4.124	0.183
AUCUG	-4.124	0.908
AAUUC	-4.125	0.622
CGAGA	-4.128	0.301
GGCAU	-4.130	0.345
AUUCG	-4.132	0.066
AUCCG	-4.133	0.530
ACAAC	-4.134	0.269
AGCUU	-4.134	0.313
ACCAC	-4.135	1.132
GCCAG	-4.136	0.450
CGUGA	-4.141	0.160
UGGUU	-4.141	0.648
GAACC	-4.142	0.864
AAGGC	-4.142	1.161
AACUC	-4.143	0.540
ACGAC	-4.143	0.613
GCUGG	-4.145	0.494
CCUCU	-4.147	0.627
CUUCC	-4.148	0.473
UAAGC	-4.149	1.026
UACGC	-4.149	0.131
UCUUC	-4.149	0.054
ACUAG	-4.149	1.118
ACCUG	-4.150	0.376
UCACG	-4.150	0.334
AAUCU	-4.151	0.890
UUGGG	-4.151	0.459
UCUCG	-4.153	0.596
UAGGU	-4.155	1.279
CAGUU	-4.156	0.614
ACACC	-4.158	0.438
CAGGC	-4.158	1.297
GAACU	-4.158	0.956
CCACC	-4.159	0.785
CGCUU	-4.159	1.107
CGUCA	-4.159	0.465
CCUUC	-4.162	0.728
GGUCC	-4.163	1.357
AGCUA	-4.164	0.451
GCACG	-4.165	0.521
AGGAC	-4.166	1.148
CUAAC	-4.168	0.863
AGAGU	-4.172	0.421
AGUUC	-4.172	0.276
AAGCC	-4.172	0.061
ACUGU	-4.176	0.454
CUACC	-4.179	0.872
GAGUU	-4.182	0.546
AACCU	-4.185	0.665
GGACG	-4.188	0.592
AAGAG	-4.188	0.777
UCUGG	-4.189	0.293
GUAUG	-4.191	0.294
AUGGU	-4.193	0.143
GUCCC	-4.194	0.736
GAUAG	-4.194	0.336
CCAAU	-4.196	0.740
UCGUA	-4.196	0.839
UGCGU	-4.196	0.147
CAGAU	-4.197	0.851
CCUCC	-4.199	0.555
CAGAA	-4.199	0.420
GAACG	-4.200	0.707
UGAUG	-4.200	0.276
AUUGC	-4.206	0.711
AUCGG	-4.206	0.567

GCGUA	116
GCGUC	22
GCGUG	15
GCGUU	27
GCUAA	6237
GCUAC	95
GCUAG	116
GCUAU	90
GCUCA	271
GCUCC	21
GCUCG	9
GCUCU	21
GCUGA	280
GCUGC	24
GCUGG	35
GCUGU	22
GCUUA	1557
GCUUC	110
GCUUG	69
GCUUU	103
GGAAA	742
GGAAC	58
GGAAG	406
GGAAU	65
GGACA	994
GGACC	28
GGACG	35
GGACU	35
GGAGA	556
GGAGC	19
GGAGG	247
GGAGU	139
GGAUA	13728
GGAUC	77
GGAUG	382
GGAUU	120
GGCAA	763
GGCAC	41
GGCAG	63
GGCAU	45
GGCCA	50
GGCCC	768
GGCCG	7
GGCCU	13
GGCGA	48
GGCGC	26
GGCGG	59
GGCGU	12
GGCUA	86
GGCUC	116
GGCUG	17
GGCUU	21
GGGAA	383
GGGAC	33
GGGAG	79
GGGAU	6
GGGCA	14
GGGCC	4
GGGCG	7
GGGCU	5
GGGGA	471
GGGGC	3
GGGGG	13
GGGGU	3
GGGUA	150
GGGUC	7
GGGUG	18
GGGUU	13
GGUAA	778

CGUGC	-4.207	0.858
GCCUG	-4.212	0.862
UGAGC	-4.214	1.203
AAGGG	-4.214	0.442
CUGAU	-4.215	0.302
GGUAU	-4.216	0.707
CUGAG	-4.219	0.109
GAAGG	-4.219	0.717
CUAGG	-4.221	0.522
GAAGC	-4.222	0.823
UGGGU	-4.223	0.656
GUCCG	-4.224	0.663
UCUUG	-4.225	0.499
GCCCG	-4.226	0.607
ACUAC	-4.226	0.200
UGGCC	-4.227	1.068
GUGAG	-4.229	0.953
CGCGC	-4.232	0.563
GUGGC	-4.235	0.798
ACCGC	-4.236	1.135
UGCUA	-4.237	0.282
ACGCA	-4.238	1.643
GGCAG	-4.243	0.123
CAGCG	-4.244	0.348
GACAG	-4.250	0.383
UAGAG	-4.252	0.406
CCGCC	-4.253	0.610
AUCUC	-4.257	0.351
CUACU	-4.257	0.712
GGUCG	-4.260	1.037
AAGAU	-4.261	0.688
CUCCC	-4.261	0.564
UAGGA	-4.263	0.880
AGGCC	-4.263	0.437
CGAGG	-4.263	0.184
CUGUC	-4.265	0.268
GUGGG	-4.266	0.466
UGGAG	-4.266	0.466
CAUCC	-4.267	0.440
UGAGG	-4.267	0.147
GAUUU	-4.267	0.492
UGUGC	-4.270	0.938
GACAC	-4.271	0.182
AAACG	-4.274	0.431
GCCCU	-4.274	0.431
CCACA	-4.276	0.477
UAGGC	-4.279	1.317
CGGAU	-4.280	0.296
UGGCA	-4.280	1.013
CCACU	-4.282	1.009
GCAGG	-4.282	0.403
CGCUA	-4.286	0.667
AUACC	-4.286	0.328
CUGCC	-4.290	0.241
CCCAC	-4.292	0.401
GUUGC	-4.292	0.496
CUAAU	-4.293	1.359
GUGCG	-4.293	0.360
AAGUU	-4.293	0.514
AGCCA	-4.293	0.540
GGCAC	-4.294	1.152
GGCUU	-4.294	0.579
AUCCC	-4.296	0.366
AAUUG	-4.297	0.297
GUCGC	-4.297	0.633
UCCGA	-4.297	0.582
CGAAC	-4.298	0.291
CUGCG	-4.298	0.245
CCUAU	-4.299	0.725

GGUAC	15
GGUAG	32
GGUAU	25
GGUCA	51
GGUCC	46
GGUCG	19
GGUCU	8
GGUGA	126
GGUGC	20
GGUGG	22
GGUGU	8
GGUUA	369
GGUUC	74
GGUUG	12
GGUUU	83
GUAAA	1173
GUAAC	201
GUAAG	1345
GUAAU	1516
GUACA	153
GUACC	10
GUACG	78
GUACU	17
GUAGA	1442
GUAGC	391
GUAGG	35
GUAGU	159
GUAUA	1689
GUAUC	43
GUAUG	75
GUAUU	458
GUCAA	31934
GUCAC	68
GUCAG	143
GUCAU	2349
GUCCA	304
GUCCC	43
GUCCG	43
GUCCU	78
GUCGA	313
GUCGC	20
GUCGG	45
GUCGU	22
GUCUA	6094
GUCUC	348
GUCUG	1956
GUCUU	267
GUGAA	1307
GUGAC	255
GUGAG	75
GUGAU	67
GUGCA	66
GUGCC	12
GUGCG	39
GUGCU	26
GUGGA	200
GUGGC	25
GUGGG	35
GUGGU	25
GUGUA	755
GUGUC	6
GUGUG	30
GUGUU	29
GUUAA	18253
GUUAC	84
GUUAG	309
GUUAU	229
GUUCA	1585
GUUCC	77

UAGCC	-4.299	0.725
CCGUG	-4.299	1.078
UCGCC	-4.306	0.338
GACCU	-4.308	0.783
CAGGA	-4.309	1.085
GCACC	-4.310	0.682
UCUGU	-4.310	0.790
CGCCU	-4.310	0.883
UGGGC	-4.312	1.633
AUGGG	-4.313	0.962
ACAAU	-4.313	0.188
AUCGU	-4.313	0.748
CGACG	-4.315	0.265
UGGGA	-4.315	0.581
UGUGG	-4.322	0.723
ACUCU	-4.323	0.534
GGUAG	-4.324	0.394
GCUCC	-4.327	0.646
AUGUU	-4.331	0.641
CGCUC	-4.331	1.081
AACAC	-4.331	0.311
GGGAG	-4.331	0.214
CCCUC	-4.335	0.318
UGCAG	-4.335	0.244
AGUCC	-4.335	0.616
AAGGA	-4.336	0.514
AGCGC	-4.337	0.818
CGCAC	-4.338	0.470
GAUCG	-4.339	0.509
ACAUU	-4.340	0.207
ACACU	-4.341	0.533
AUGGA	-4.341	0.621
AAGCU	-4.347	0.530
GGACU	-4.347	0.540
ACGGC	-4.348	1.131
CGGAA	-4.351	0.217
GAGGG	-4.353	0.481
CGCCA	-4.355	0.539
ACUAU	-4.355	0.575
CGACC	-4.359	0.932
GUAUC	-4.363	0.327
AACGA	-4.364	0.195
UCGAU	-4.365	0.280
GGAGC	-4.366	0.697
GUACG	-4.368	0.728
GCUGC	-4.368	0.647
AGCUG	-4.371	0.590
CCCGG	-4.372	0.284
GCAUU	-4.373	0.189
CGUGG	-4.375	0.434
GGCGG	-4.376	0.188
CGCCG	-4.379	0.725
GUAGG	-4.379	0.436
UGGUC	-4.379	1.574
ACAUC	-4.381	0.187
CACUC	-4.384	0.592
ACAGU	-4.384	0.728
UAUGC	-4.384	0.908
UGGAC	-4.384	0.292
GCUGU	-4.387	0.474
GGGAC	-4.389	0.258
UAGUG	-4.389	0.443
AGUGG	-4.390	0.233
GCAGU	-4.393	0.446
AGCAC	-4.395	0.677
CCCAU	-4.398	0.675
CGUCC	-4.398	0.744
GCCAC	-4.398	0.744
GGUGC	-4.401	0.431

GUUCG	150
GUUCU	54
GUUGA	212
GUUGC	30
GUUGG	130
GUUGU	478
GUUUA	7487
GUUUC	786
GUUUG	223
GUUUU	216
UAAAA	1192
UAAAC	439
UAAAG	419
UAAAU	757
UAACA	1167
UAACC	337
UAACG	2353
UAACU	983
UAAGA	391
UAAGC	40
UAAGG	525
UAAGU	249
UAAUA	677
UAAUC	277
UAAUG	402
UAAUU	33451
UACAA	636
UACAC	68
UACAG	58
UACAU	107
UACCA	117
UACCC	156
UACCG	51
UACCU	60
UACGA	2314
UACGC	68
UACGG	1162
UACGU	669
UACUA	98
UACUC	62
UACUG	55
UACUU	299
UAGAA	90
UAGAC	238
UAGAG	81
UAGAU	241
UAGCA	71
UAGCC	18
UAGCG	12
UAGCU	114
UAGGA	22
UAGGC	35
UAGGG	14
UAGGU	67
UAGUA	40
UAGUC	22
UAGUG	33
UAGUU	45
UAUAA	1471
UAUAC	91
UAUAG	69
UAUAU	1697
UAUCA	169
UAUCC	43
UAUCG	28
UAUCU	85
UAUGA	634
UAUGC	16
UAUGG	189

CGUUC	-4.402	0.153
GCGGG	-4.404	0.907
GUGUG	-4.404	0.454
CCCCC	-4.405	0.788
GUCGG	-4.411	0.293
GGUGG	-4.412	0.368
AGUAC	-4.414	0.645
CGGAC	-4.419	0.323
AGAGG	-4.420	0.468
GCGUU	-4.420	0.468
GGCGC	-4.421	0.627
AGUUG	-4.422	0.524
CCCCG	-4.429	0.551
AAGAC	-4.433	0.485
AAGCG	-4.433	0.694
AGGGA	-4.433	0.300
UCGUU	-4.434	1.061
CACCA	-4.435	0.623
GAGCA	-4.435	0.339
GGACC	-4.439	0.850
CCGGC	-4.441	0.777
GACUU	-4.446	0.337
UCGUG	-4.447	0.554
GCCGC	-4.448	0.904
GCCGA	-4.451	0.131
GGCUG	-4.458	0.444
UCGCA	-4.458	0.217
AACAG	-4.458	0.642
ACGGG	-4.458	0.957
GCCCA	-4.461	0.933
GCUCU	-4.461	0.359
GUGGU	-4.461	0.933
UGCGC	-4.465	0.952
GUGCU	-4.467	0.889
GAGCC	-4.469	0.679
GAUGC	-4.472	0.553
ACCAG	-4.477	0.319
GCGAC	-4.483	0.331
UAUCG	-4.483	0.331
UGCUG	-4.483	1.255
GGGUG	-4.487	0.536
GGGUU	-4.488	1.240
CGUCG	-4.494	0.506
GAGGU	-4.494	0.506
UGGUG	-4.494	0.506
CAGAC	-4.494	0.340
GGGCA	-4.494	0.917
GCGCA	-4.496	0.413
UAGCG	-4.498	1.249
UGUAG	-4.507	0.489
ACAUG	-4.507	0.808
GGCGU	-4.507	0.808
CAACC	-4.509	0.722
UGUCA	-4.517	0.919
ACUCC	-4.518	1.207
GCGAU	-4.522	0.196
ACGUG	-4.527	0.785
GAGUG	-4.527	0.456
AGCGA	-4.530	0.641
CUGCA	-4.530	0.466
AGGGC	-4.530	1.243
CGCGG	-4.531	0.194
UCGUC	-4.531	0.194
CCGUA	-4.537	1.027
AUGUC	-4.543	0.801
GGCCU	-4.543	0.487
CUGUU	-4.543	0.605
ACCGU	-4.551	1.198
CGGAG	-4.552	0.080

UAUGU	315
UAUUA	893
UAUUC	151
UAUUG	79
UAUUU	564
UCAAA	134
UCAAC	139
UCAAG	103
UCAAU	185
UCACA	39
UCACC	72
UCACG	44
UCACU	542
UCAGA	359
UCAGC	937
UCAGG	1228
UCAGU	154
UCAUA	83
UCAUC	64
UCAUG	51
UCAUU	188
UCCAA	500
UCCAC	106
UCCAG	19
UCCAU	368
UCCCA	52
UCCCC	118
UCCCG	22
UCCCU	77
UCCGA	288
UCCGC	68
UCCGG	5365
UCCGU	241
UCCUA	770
UCCUC	29
UCCUG	42
UCCUU	79
UCGAA	260
UCGAC	285
UCGAG	20
UCGAU	47
UCGCA	35
UCGCC	30
UCGCG	49
UCGCU	334
UCGGA	45
UCGGC	158
UCGGG	29
UCGGU	39
UCGUA	28
UCGUC	27
UCGUG	24
UCGUU	25
UCUAA	396
UCUAC	148
UCUAG	13
UCUAU	85
UCUCA	95
UCUCC	77
UCUCG	71
UCUCU	115
UCUGA	55
UCUGC	90
UCUGG	76
UCUGU	25
UCUUA	229
UCUUC	93
UCUUG	32
UCUUU	403

CCAAC	-4.557	0.086
GGUUG	-4.557	0.510
CGAGC	-4.557	0.624
GUACU	-4.560	0.411
UAGUC	-4.564	0.742
AACGC	-4.564	0.847
ACGCG	-4.564	1.044
CAGUC	-4.564	0.847
UCGGA	-4.567	0.542
CUGGG	-4.570	0.828
UGCGG	-4.573	0.540
AUGCA	-4.580	0.103
AGGCA	-4.588	0.276
CGGGC	-4.588	1.006
CGGUA	-4.588	0.753
CACAC	-4.592	0.842
ACCCG	-4.598	0.146
GCGGA	-4.600	0.077
AGCUC	-4.602	0.923
CGUAC	-4.604	0.851
GCGUG	-4.604	1.209
GUCGU	-4.605	0.658
GCAUC	-4.609	0.538
UGGGG	-4.612	0.700
AUGCC	-4.617	0.430
GGUGU	-4.617	0.715
UGCCU	-4.617	0.485
GGGGG	-4.618	0.937
AGACC	-4.626	0.530
UCCAG	-4.628	0.668
CUAUC	-4.631	0.053
GCGGU	-4.631	0.453
GUGUU	-4.631	0.053
UCGGG	-4.631	0.530
GCGCC	-4.631	0.506
AGUGU	-4.637	0.640
GCGCG	-4.637	1.076
UAGGG	-4.640	0.788
AGCGG	-4.647	0.531
ACUGC	-4.647	0.529
CCCCU	-4.653	0.380
CCGAA	-4.653	0.532
AGGUU	-4.666	0.258
GAGUC	-4.666	0.534
GGCCG	-4.666	0.777
ACGUC	-4.668	0.403
GAGGC	-4.668	0.810
CCGCA	-4.672	0.088
UCCCG	-4.672	0.088
GCACU	-4.679	0.537
CUGCU	-4.686	0.922
UCGAG	-4.686	0.539
CCGCG	-4.710	0.666
GCUCG	-4.710	0.580
GGGCG	-4.710	0.622
CCGAU	-4.729	0.177
CGAUU	-4.729	0.177
GGUAC	-4.729	0.177
GUACC	-4.733	0.372
UGUCG	-4.733	0.372
CCGUU	-4.740	0.194
ACGUU	-4.747	0.725
CGGCC	-4.747	0.883
GGUCU	-4.747	0.883
AGACG	-4.751	0.403
CGUUA	-4.751	0.213
AUGCU	-4.751	0.832
CCGUC	-4.751	0.569
CGAUC	-4.751	0.832

UGAAA	915
UGAAC	284
UGAAG	158
UGAAU	343
UGACA	37
UGACC	178
UGACG	42
UGACU	189
UGAGA	135
UGAGC	31
UGAGG	54
UGAGU	204
UGAUA	189
UGAUC	79
UGAUG	45
UGAUU	122
UGCAA	195
UGCAC	115
UGCAG	35
UGCAU	147
UGCCA	59
UGCCC	211
UGCCG	8
UGCCU	12
UGCGA	1528
UGCGC	11
UGCGG	43
UGCGU	58
UGCUA	40
UGCUC	677
UGCUG	49
UGCUU	78
UGGAA	319
UGGAC	54
UGGAG	35
UGGAU	38
UGGCA	27
UGGCC	21
UGGCG	5
UGGCU	71
UGGGA	21
UGGGC	75
UGGGG	9
UGGGU	23
UGGUA	94
UGGUC	35
UGGUG	14
UGGUU	28
UGUAA	129
UGUAC	44
UGUAG	20
UGUAU	110
UGUCA	20
UGUCC	48
UGUCG	10
UGUCU	56
UGUGA	151
UGUGC	19
UGUGG	18
UGUGU	158
UGUUA	69
UGUUC	73
UGUUG	143
UGUUU	68
UUAAA	1129
UUAAC	576
UUAAG	3890
UUAAU	1964
UUACA	172

CGGCA	-4.751	0.832
GCCGU	-4.751	0.906
UCUAG	-4.751	0.569
AGUCG	-4.763	0.233
GUGCC	-4.763	0.233
AGACU	-4.771	0.438
AGGCU	-4.776	0.584
CAGGU	-4.776	1.015
GCGGC	-4.776	1.015
ACCGA	-4.776	0.256
CAUAC	-4.776	0.256
GAUGG	-4.790	0.597
GACUG	-4.796	0.319
GGGUC	-4.796	0.480
AACCG	-4.806	0.611
AAUCG	-4.806	0.308
CCGAG	-4.806	0.308
GACCG	-4.806	0.308
GCCGG	-4.825	0.530
UGCCG	-4.825	0.339
AGCGU	-4.825	1.072
GCGUC	-4.825	0.302
AGAUC	-4.845	0.959
AAUGC	-4.845	0.647
AGGGG	-4.845	0.647
AGGUC	-4.845	0.647
CGGGA	-4.845	0.374
GACGG	-4.853	0.293
ACGCC	-4.861	0.292
CAGCU	-4.861	0.592
CGGCG	-4.861	1.011
CGGGU	-4.869	0.672
GAGCG	-4.869	0.672
CCGGA	-4.869	0.416
GGGAU	-4.869	0.416
GUGUC	-4.869	0.416
AGUGC	-4.899	0.704
CGGCU	-4.899	0.466
CGGUC	-4.899	0.704
GGGCU	-4.899	0.466
UGGCG	-4.899	1.290
GCGCU	-4.899	0.923
ACGGU	-4.910	0.676
CGGUU	-4.922	0.305
ACGCU	-4.935	0.528
ACUCG	-4.935	0.528
AGGGU	-4.949	0.322
AGGCG	-4.984	0.808
CCGCU	-4.984	0.612
CCGGU	-4.984	0.808
CGGGG	-4.984	0.352
AGGUG	-5.029	0.401
CGACU	-5.058	0.437
GAGCU	-5.058	0.437
GGGCC	-5.058	0.437
AUGCG	-5.094	0.485
CCGGG	-5.094	0.485
GGGGC	-5.094	0.485
GGGGU	-5.094	0.485

UUACC	182
UUACG	351
UUACU	112
UUAGA	1058
UUAGC	273
UUAGG	10586
UUAGU	4437
UUAUA	1416
UUAUC	225
UUAUG	2529
UUAUU	1033
UUCAA	4461
UUCAC	820
UUCAG	720
UUCAU	882
UUCCA	456
UUCCC	67
UUCCG	253
UUCCU	826
UUCGA	1553
UUCGC	302
UUCGG	40258
UUCGU	845
UUCUA	3673
UUCUC	109
UUCUG	1363
UUCUU	486
UUGAA	425
UUGAC	7692
UUGAG	436
UUGAU	926
UUGCA	57
UUGCC	194
UUGCG	53
UUGCU	253
UUGGA	220
UUGGC	761
UUGGG	58
UUGGU	173
UUGUA	92
UUGUC	33
UUGUG	659
UUGUU	102
UUUAA	3774
UUUAC	940
UUUAG	691
UUUAU	7442
UUUCA	829
UUUCC	416
UUUCG	375
UUUCU	987
UUUGA	3356
UUUGC	265
UUUGG	4636
UUUGU	1146
UUUUA	8089
UUUUC	216
UUUUG	664
UUUUU	4306

Bulge size 1		
Range	0.588	
Median	-0.673	
Bulge	**Score**	**Centered score**
A	-0.378	0.29
U	-0.527	0.15
G	-0.846	-0.17
C	-0.967	-0.29

Bulge size 2		
Range	1.596	
Median	-1.524	
Bulge	**Score**	**Centered score**
AA	-0.726	0.80
AG	-1.205	0.32
AU	-1.241	0.28
GA	-1.258	0.27
CA	-1.325	0.20
UA	-1.448	0.08
AC	-1.485	0.04
UU	-1.551	-0.03
UG	-1.607	-0.08
GG	-1.644	-0.12
UC	-1.758	-0.23
CU	-1.789	-0.26
CG	-1.883	-0.36
GC	-2.031	-0.51
GU	-2.053	-0.53
CC	-2.322	-0.80

Bulge size 3		
Range	2.353	
Median	-2.315	
Bulge	**Score**	**Centered score**
GGA	-1.138	1.18
GAA	-1.425	0.89
AAA	-1.454	0.86
GAU	-1.540	0.77
AUA	-1.685	0.63
CUA	-1.737	0.58
UAA	-1.752	0.56
GUA	-1.816	0.50
GAG	-1.845	0.47
CAU	-1.922	0.39
UCA	-1.951	0.36
CAA	-1.953	0.36
ACA	-1.970	0.34
AAU	-1.977	0.34
AAG	-1.990	0.33
CAG	-2.072	0.24
UAU	-2.074	0.24
AUU	-2.133	0.18
CCA	-2.163	0.15
AGA	-2.168	0.15
GAC	-2.271	0.04
CCU	-2.278	0.04
AAC	-2.285	0.03
UUU	-2.415	-0.10
AGU	-2.441	-0.13
GCA	-2.454	-0.14
GUU	-2.468	-0.15
CUG	-2.469	-0.15
UUA	-2.496	-0.18
GGU	-2.518	-0.20
AGG	-2.581	-0.27
UAC	-2.619	-0.30
CUC	-2.625	-0.31
AUG	-2.626	-0.31
GUC	-2.650	-0.34
GGC	-2.661	-0.35
UUG	-2.676	-0.36
UAG	-2.692	-0.38
ACU	-2.698	-0.38
UGU	-2.724	-0.41
ACC	-2.741	-0.43
AUC	-2.757	-0.44
CCC	-2.759	-0.44
CUU	-2.782	-0.47
CCG	-2.790	-0.47
UGA	-2.796	-0.48
GGG	-2.800	-0.48
CAC	-2.802	-0.49
GUG	-2.927	-0.61
UCG	-2.964	-0.65
UUC	-2.967	-0.65
UGC	-2.990	-0.68
AGC	-3.010	-0.70
UCU	-3.046	-0.73
UCC	-3.076	-0.76
CGC	-3.105	-0.79
CGA	-3.109	-0.79
ACG	-3.112	-0.80
CGG	-3.130	-0.82
GCC	-3.176	-0.86
GCU	-3.192	-0.88
UGG	-3.232	-0.92
CGU	-3.449	-1.13
GCG	-3.491	-1.18

Bulge size 4		
Range	2.070	
Median	-3.013	
Bulge	**Score**	**Centered score**
AAGU	-1.978	1.03
AUAA	-2.072	0.94
AGAA	-2.145	0.87
AAAA	-2.156	0.86
UUUG	-2.246	0.77
ACAU	-2.270	0.74
UAUG	-2.270	0.74
AUUA	-2.290	0.72
GGAA	-2.291	0.72
UUAA	-2.329	0.68
AAGC	-2.336	0.68
AAAG	-2.343	0.67
UCAA	-2.347	0.67
AUAU	-2.352	0.66
UGAA	-2.360	0.65
CGAA	-2.401	0.61
GAAU	-2.420	0.59
AAAU	-2.430	0.58
CUAA	-2.441	0.57
UAGG	-2.455	0.56
CAAA	-2.471	0.54
AAUA	-2.474	0.54
UAAA	-2.482	0.53
UUCG	-2.484	0.53
UUUU	-2.488	0.52
CAGC	-2.507	0.51
AAGA	-2.509	0.50
GGGA	-2.527	0.49
AUUG	-2.534	0.48
UUUC	-2.550	0.46
AUAG	-2.555	0.46
CGAC	-2.582	0.43
AUCG	-2.591	0.42
GGGG	-2.596	0.42
UAAG	-2.656	0.36
UAAU	-2.657	0.36
GUAA	-2.665	0.35
UUUA	-2.675	0.34
GUAU	-2.677	0.34
AAAC	-2.691	0.32
AAUU	-2.699	0.31
UGUG	-2.705	0.31
UAUA	-2.710	0.30
AACA	-2.715	0.30
GUCG	-2.725	0.29
GAUU	-2.729	0.28
AGAU	-2.749	0.26
UUGG	-2.753	0.26
CUUG	-2.756	0.26
GAUA	-2.766	0.25
GACG	-2.773	0.24
ACAA	-2.776	0.24
UGAG	-2.786	0.23
AAUG	-2.797	0.22
AUCA	-2.808	0.20
AAGG	-2.822	0.19
CAAU	-2.826	0.19
GUUA	-2.828	0.19
GAGC	-2.829	0.18
UACG	-2.837	0.18
AUAC	-2.851	0.16
CCUA	-2.859	0.15
GAAA	-2.868	0.14
GAUG	-2.875	0.14

GAGU	-2.884	0.13
GAGA	-2.904	0.11
UAGC	-2.905	0.11
GCAA	-2.911	0.10
GGAU	-2.911	0.10
UCAG	-2.920	0.09
GAGG	-2.922	0.09
UUAG	-2.929	0.08
GAAG	-2.930	0.08
UAUU	-2.932	0.08
GCUA	-2.932	0.08
CUUC	-2.936	0.08
GUUG	-2.955	0.06
GCAU	-2.957	0.06
AGAG	-2.960	0.05
ACAG	-2.975	0.04
UCAU	-2.976	0.04
GUAG	-2.981	0.03
CAAC	-2.991	0.02
CUUA	-2.992	0.02
UUAU	-2.994	0.02
UUGA	-3.003	0.01
UAGA	-3.007	0.01
CAGA	-3.011	0.00
GGGC	-3.011	0.00
GAAC	-3.012	0.00
AGUA	-3.020	-0.01
CAAG	-3.048	-0.03
UGAU	-3.077	-0.06
GGUA	-3.082	-0.07
CUGA	-3.105	-0.09
GUCA	-3.105	-0.09
GGUG	-3.106	-0.09
CUAC	-3.108	-0.10
ACUU	-3.111	-0.10
UUCC	-3.114	-0.10
CCCC	-3.118	-0.11
GGGU	-3.118	-0.11
UCGG	-3.133	-0.12
UCCG	-3.141	-0.13
CAUA	-3.145	-0.13
ACCA	-3.147	-0.13
AUUU	-3.148	-0.13
AACC	-3.150	-0.14
AACG	-3.150	-0.14
ACAC	-3.150	-0.14
AUGU	-3.150	-0.14
GACA	-3.151	-0.14
CUCG	-3.155	-0.14
UUCU	-3.155	-0.14
AACU	-3.158	-0.15
ACUA	-3.163	-0.15
CAUU	-3.168	-0.15
CUAG	-3.170	-0.16
UAUC	-3.170	-0.16
GCAG	-3.171	-0.16
CAUC	-3.172	-0.16
UCUG	-3.175	-0.16
AAUC	-3.180	-0.17
GGAC	-3.185	-0.17
GGAG	-3.189	-0.18
AUUC	-3.192	-0.18
GUUC	-3.205	-0.19
UCAC	-3.229	-0.22
ACUG	-3.231	-0.22
CCUG	-3.233	-0.22
CAGG	-3.242	-0.23
UGGA	-3.242	-0.23
CUGU	-3.246	-0.23

UAAC	-3.246	-0.23
UAGU	-3.253	-0.24
CCAA	-3.257	-0.24
GCUG	-3.265	-0.25
GGUU	-3.269	-0.26
CGUG	-3.273	-0.26
UGGG	-3.277	-0.26
CCCA	-3.289	-0.28
AUGA	-3.309	-0.30
UCCA	-3.309	-0.30
CCAC	-3.310	-0.30
UGCG	-3.321	-0.31
UGUC	-3.323	-0.31
CACU	-3.340	-0.33
GUGG	-3.353	-0.34
AGCA	-3.358	-0.35
GUGU	-3.363	-0.35
GCGG	-3.370	-0.36
CUAU	-3.376	-0.36
AGGA	-3.377	-0.36
UCCU	-3.379	-0.37
CAUG	-3.381	-0.37
UGCU	-3.383	-0.37
AGUU	-3.388	-0.38
GUUU	-3.392	-0.38
CGAG	-3.399	-0.39
ACGA	-3.403	-0.39
CUUU	-3.403	-0.39
CCAG	-3.404	-0.39
CAGU	-3.405	-0.39
UUCA	-3.410	-0.40
GACU	-3.411	-0.40
UACA	-3.427	-0.41
GACC	-3.438	-0.43
CGAU	-3.440	-0.43
GUAC	-3.448	-0.44
ACGC	-3.456	-0.44
AUGG	-3.459	-0.45
AGGC	-3.462	-0.45
AGGG	-3.462	-0.45
UGAC	-3.462	-0.45
CUCA	-3.466	-0.45
UUGC	-3.466	-0.45
AUCC	-3.469	-0.46
CACC	-3.480	-0.47
GGCC	-3.486	-0.47
CCAU	-3.497	-0.48
GCCA	-3.497	-0.48
UCUC	-3.497	-0.48
UGGU	-3.497	-0.48
AGCU	-3.509	-0.50
CUGG	-3.509	-0.50
CGCA	-3.517	-0.50
ACCC	-3.522	-0.51
AUCU	-3.522	-0.51
UACC	-3.522	-0.51
UCGU	-3.522	-0.51
CACA	-3.523	-0.51
AGGU	-3.533	-0.52
CCGC	-3.533	-0.52
UACU	-3.536	-0.52
UCUU	-3.536	-0.52
GUGC	-3.552	-0.54
UCGA	-3.560	-0.55
GCCG	-3.564	-0.55
ACGG	-3.571	-0.56
CGUU	-3.571	-0.56
CUGC	-3.571	-0.56
GGCG	-3.571	-0.56

AUGC	-3.571	-0.56
UUAC	-3.582	-0.57
CUCU	-3.591	-0.58
GUGA	-3.591	-0.58
UUGU	-3.594	-0.58
UCCC	-3.607	-0.59
UCUA	-3.618	-0.61
GCAC	-3.625	-0.61
GAUC	-3.631	-0.62
CGUA	-3.648	-0.64
GGCA	-3.652	-0.64
UGUA	-3.652	-0.64
CCGG	-3.656	-0.64
CGCU	-3.656	-0.64
ACUC	-3.668	-0.66
AGAC	-3.668	-0.66
ACGU	-3.681	-0.67
CGGA	-3.681	-0.67
GCGA	-3.681	-0.67
GGUC	-3.686	-0.67
CGGG	-3.695	-0.68
UGUU	-3.695	-0.68
UCGC	-3.701	-0.69
UGCA	-3.706	-0.69
UGGC	-3.712	-0.70
CCGA	-3.717	-0.70
CCCU	-3.730	-0.72
GCCU	-3.730	-0.72
AGUG	-3.736	-0.72
CCUC	-3.736	-0.72
CCUU	-3.736	-0.72
CCCG	-3.743	-0.73
CGCG	-3.750	-0.74
AGCG	-3.766	-0.75
GCGC	-3.766	-0.75
UGCC	-3.766	-0.75
GUCC	-3.775	-0.76
AGUC	-3.793	-0.78
CACG	-3.804	-0.79
ACCU	-3.840	-0.83
CGCC	-3.840	-0.83
GUCU	-3.840	-0.83
ACCG	-3.854	-0.84
CGGU	-3.854	-0.84
GCUU	-3.854	-0.84
GCUC	-3.871	-0.86
AGCC	-3.889	-0.88
CCGU	-3.889	-0.88
CGGC	-3.909	-0.90
CUCC	-3.909	-0.90
GCCC	-3.909	-0.90
GGCU	-3.934	-0.92
CGUC	-4.048	-1.03
GCGU	-4.048	-1.03

Table S10. Bulges size 1

Bulge	Score	SD
A	-0.378	0.113
U	-0.527	0.145
G	-0.846	0.214
C	-0.967	0.130

Bulge	Total bulge count
A	3354550
C	558955
G	1193529
U	1362225

Supercategory	Total bulge count
Intron	51762
Translation	6231460
Cis -Reg	186037

Table S11. Bulges size 2

Bulge	Score	SD
AA	-0.726	0.572
AG	-1.205	0.812
AU	-1.241	0.387
GA	-1.258	0.325
CA	-1.325	0.397
UA	-1.448	0.097
AC	-1.485	0.313
UU	-1.551	0.205
UG	-1.607	0.614
GG	-1.644	1.001
UC	-1.758	0.117
CU	-1.789	0.318
CG	-1.883	0.540
GC	-2.031	0.563
GU	-2.053	0.462
CC	-2.322	0.535

Bulge	Total bulge count
AA	524977
AC	99402
AG	502403
AU	471446
CA	404469
CC	4038
CG	16937
CU	34712
GA	371322
GC	8018
GG	43349
GU	12764
UA	126620
UC	53342
UG	353068
UU	51581

Supercategory	Total bulge count
Intron	11836
Translation	3043312
Cis -Reg	23300

Table S12. Bulges size 3

Bulge	Score	SD
GGA	-1.138	0.569
GAA	-1.425	0.602
AAA	-1.454	0.879
GAU	-1.540	0.515
AUA	-1.685	1.566
CUA	-1.737	0.178
UAA	-1.752	0.152
GUA	-1.816	0.918
GAG	-1.845	0.601
CAU	-1.922	0.914
UCA	-1.951	0.578
CAA	-1.953	0.603
ACA	-1.970	1.142
AAU	-1.977	0.753
AAG	-1.990	0.545
CAG	-2.072	0.910
UAU	-2.074	0.568
AUU	-2.133	1.263
CCA	-2.163	1.158
AGA	-2.168	1.002
GAC	-2.271	0.833
CCU	-2.278	0.856
AAC	-2.285	0.668
UUU	-2.415	0.951
AGU	-2.441	0.650
GCA	-2.454	0.268
GUU	-2.468	0.610
CUG	-2.469	0.760
UUA	-2.496	0.676
GGU	-2.518	0.860
AGG	-2.581	1.161
UAC	-2.619	0.984
CUC	-2.625	0.280
AUG	-2.626	0.915
GUC	-2.650	0.368
GGC	-2.661	0.707
UUG	-2.676	0.633
UAG	-2.692	0.301
ACU	-2.698	1.035
UGU	-2.724	0.966
ACC	-2.741	0.975
AUC	-2.757	0.880
CCC	-2.759	0.919
CUU	-2.782	0.496
CCG	-2.790	0.576
UGA	-2.796	0.634
GGG	-2.800	0.489
CAC	-2.802	0.487
GUG	-2.927	0.706
UCG	-2.964	0.646
UUC	-2.967	0.053
UGC	-2.990	0.896
AGC	-3.010	0.518
UCU	-3.046	0.570
UCC	-3.076	0.494
CGC	-3.105	1.060
CGA	-3.109	0.524
ACG	-3.112	0.690
CGG	-3.130	0.448
GCC	-3.176	0.309
GCU	-3.192	0.337
UGG	-3.232	0.418
CGU	-3.449	0.206
GCG	-3.491	0.863

Bulge	Total bulge count
AAA	9909
AAC	2013
AAG	23204
AAU	2800
ACA	1713
ACC	601
ACG	230
ACU	486
AGA	1129
AGC	462
AGG	435
AGU	1262
AUA	2715
AUC	444
AUG	597
AUU	1139
CAA	5236
CAC	803
CAG	88455
CAU	227283
CCA	973
CCC	387
CCG	3397
CCU	60635
CGA	367
CGC	158
CGG	430
CGU	363
CUA	19463
CUC	4531
CUG	42787
CUU	976
GAA	247078
GAC	81907
GAG	48201
GAU	183009
GCA	2983
GCC	513
GCG	248
GCU	460
GGA	308534
GGC	23914
GGG	1215
GGU	44447
GUA	81163
GUC	5010
GUG	380
GUU	1224
UAA	44532
UAC	480
UAG	7426
UAU	3410
UCA	85568
UCC	517
UCG	462
UCU	357
UGA	543
UGC	235
UGG	901
UGU	430
UUA	1002
UUC	2089
UUG	773
UUU	694

Supercategory	Total bulge count
Intron	6371
Translation	1672174
Cis -Reg	6543

Bulge	Score	SD
AAGU	-1.978	0.235
AUAA	-2.072	0.949
AGAA	-2.145	0.809
AAAA	-2.156	0.838
UUUG	-2.246	1.710
ACAU	-2.270	1.322
UAUG	-2.270	0.051
AUUA	-2.290	0.679
GGAA	-2.291	0.228
UUAA	-2.329	0.462
AAGC	-2.336	1.705
AAAG	-2.343	0.739
UCAA	-2.347	1.003
AUAU	-2.352	1.074
UGAA	-2.360	0.645
CGAA	-2.401	1.220
GAAU	-2.420	0.642
AAAU	-2.430	0.729
CUAA	-2.441	0.228
UAGG	-2.455	1.397
CAAA	-2.471	0.508
AAUA	-2.474	0.859
UAAA	-2.482	1.060
UUCG	-2.484	1.648
UUUU	-2.488	0.953
CAGC	-2.507	1.425
AAGA	-2.509	0.942
GGGA	-2.527	0.545
AUUG	-2.534	0.274
UUUC	-2.550	0.856
AUAG	-2.555	0.587
CGAC	-2.582	0.273
AUCG	-2.591	0.229
GGGG	-2.596	0.749
UAAG	-2.656	0.825
UAAU	-2.657	1.038
GUAA	-2.665	0.755
UUUA	-2.675	0.671
GUAU	-2.677	0.976
AAAC	-2.691	0.867
AAUU	-2.699	1.056
UGUG	-2.705	0.490
UAUA	-2.710	0.737
AACA	-2.715	0.684
GUCG	-2.725	1.331
GAUU	-2.729	0.586
AGAU	-2.749	0.605
UUGG	-2.753	0.988
CUUG	-2.756	0.675
GAUA	-2.766	0.758
GACG	-2.773	0.682
ACAA	-2.776	0.716
UGAG	-2.786	0.178
AAUG	-2.797	0.614
AUCA	-2.808	0.385
AAGG	-2.822	0.632
CAAU	-2.826	0.660
GUUA	-2.828	0.309
GAGC	-2.829	1.447
UACG	-2.837	0.532
AUAC	-2.851	1.187
CCUA	-2.859	0.440
GAAA	-2.868	0.698
GAUG	-2.875	0.608
GAGU	-2.884	0.765
GAGA	-2.904	1.098
UAGC	-2.905	1.211
GCAA	-2.911	0.777

Bulge	Total bulge count
AAAA	299
AAAC	64
AAAG	229
AAAU	152
AACA	64
AACC	25
AACG	53
AACU	29
AAGA	137
AAGC	742
AAGG	52
AAGU	1503
AAUA	109
AAUC	26
AAUG	57
AAUU	166
ACAA	56
ACAC	21
ACAG	60
ACAU	278
ACCA	23
ACCC	12
ACCG	9
ACCU	10
ACGA	22
ACGC	10
ACGG	15
ACGU	5
ACUA	27
ACUC	12
ACUG	37
ACUU	33
AGAA	7312
AGAC	12
AGAG	46
AGAU	68
AGCA	28
AGCC	7
AGCG	17
AGCU	15
AGGA	30
AGGC	12
AGGG	48
AGGU	19
AGUA	36
AGUC	14
AGUG	21
AGUU	21
AUAA	281
AUAC	75
AUAG	1485
AUAU	215
AUCA	89
AUCC	10
AUCG	354
AUCU	12
AUGA	30
AUGC	15
AUGG	49
AUGU	33
AUUA	172
AUUC	57
AUUG	615
AUUU	65
CAAA	842
CAAC	43
CAAG	46
CAAU	50

Supercategory	Total bulge count
Intron	1713
Translation	119988
Cis -Reg	4228

GGAU	-2.911	0.091
UCAG	-2.920	0.506
GAGG	-2.922	0.571
UUAG	-2.929	0.696
GAAG	-2.930	0.321
UAUU	-2.932	0.725
GCUA	-2.932	0.122
CUUC	-2.936	1.208
GUUG	-2.955	0.335
GCAU	-2.957	1.038
AGAG	-2.960	0.504
ACAG	-2.975	0.503
UCAU	-2.976	0.625
GUAG	-2.981	0.129
CAAC	-2.991	0.557
CUUA	-2.992	0.494
UUAU	-2.994	0.695
UUGA	-3.003	0.309
UAGA	-3.007	0.583
CAGA	-3.011	0.373
GGGC	-3.011	0.610
GAAC	-3.012	0.452
AGUA	-3.020	0.686
CAAG	-3.048	0.387
UGAU	-3.077	0.306
GGUA	-3.082	0.453
CUGA	-3.105	0.615
GUCA	-3.105	0.561
GGUG	-3.106	0.538
CUAC	-3.108	1.003
ACUU	-3.111	0.781
UUCC	-3.114	0.786
CCCC	-3.118	0.564
GGGU	-3.118	0.979
UCGG	-3.133	0.351
UCCG	-3.141	1.040
CAUA	-3.145	0.833
ACCA	-3.147	0.671
AUUU	-3.148	0.513
AACC	-3.150	0.938
AACG	-3.150	0.642
ACAC	-3.150	1.030
AUGU	-3.150	0.430
GACA	-3.151	0.855
CUCG	-3.155	0.587
UUCU	-3.155	0.088
AACU	-3.158	0.610
ACUA	-3.163	0.639
CAUU	-3.168	0.462
CUAG	-3.170	0.537
UAUC	-3.170	0.650
GCAG	-3.171	0.954
CAUC	-3.172	0.489
UCUG	-3.175	0.983
AAUC	-3.180	0.684
GGAC	-3.185	0.399
GGAG	-3.189	0.302
AUUC	-3.192	1.121
GUUC	-3.205	0.880
UCAC	-3.229	0.800
ACUG	-3.231	0.280
CCUG	-3.233	0.344
CAGG	-3.242	0.860
UGGA	-3.242	0.614
CUGU	-3.246	1.098
UAAC	-3.246	0.656
UAGU	-3.253	0.813
CCAA	-3.257	0.281
GCUG	-3.265	0.338

CACA	13
CACC	16
CACG	13
CACU	26
CAGA	77
CAGC	122
CAGG	36
CAGU	25
CAUA	30
CAUC	31
CAUG	84
CAUU	66
CCAA	69
CCAC	17
CCAG	33
CCAU	16
CCCA	18
CCCC	29
CCCG	20
CCCU	22
CCGA	24
CCGC	15
CCGG	13
CCGU	7
CCUA	67
CCUC	21
CCUG	49
CCUU	21
CGAA	10406
CGAC	313
CGAG	74
CGAU	56
CGCA	9
CGCC	10
CGCG	19
CGCU	13
CGGA	31
CGGC	6
CGGG	10
CGGU	9
CGUA	39
CGUC	2
CGUG	24
CGUU	15
CUAA	810
CUAC	22
CUAG	26
CUAU	28
CUCA	47
CUCC	6
CUCG	399
CUCU	8
CUGA	27
CUGC	11
CUGG	35
CUGU	28
CUUA	409
CUUC	142
CUUG	1250
CUUU	24
GAAA	171
GAAC	47
GAAG	93
GAAU	135
GACA	49
GACC	168
GACG	351
GACU	23
GAGA	131

GGUU	-3.269	1.062
CGUG	-3.273	0.449
UGGG	-3.277	0.375
CCCA	-3.289	1.005
AUGA	-3.309	0.420
UCCA	-3.309	0.420
CCAC	-3.310	0.859
UGCG	-3.321	0.556
UGUC	-3.323	0.230
CACU	-3.340	0.617
GUGG	-3.353	0.498
AGCA	-3.358	0.482
GUGU	-3.363	0.603
GCGG	-3.370	0.427
CUAU	-3.376	0.433
AGGA	-3.377	0.290
UCCU	-3.379	0.506
CAUG	-3.381	0.198
UGCU	-3.383	0.934
AGUU	-3.388	0.679
GUUU	-3.392	0.439
CGAG	-3.399	0.464
ACGA	-3.403	0.536
CUUU	-3.403	0.466
CCAG	-3.404	0.280
CAGU	-3.405	0.328
UUCA	-3.410	0.589
GACU	-3.411	0.475
UACA	-3.427	0.551
GACC	-3.438	0.544
CGAU	-3.440	0.444
GUAC	-3.448	0.331
ACGC	-3.456	0.879
AUGG	-3.459	0.071
AGGC	-3.462	0.633
AGGG	-3.462	0.438
UGAC	-3.462	0.067
CUCA	-3.466	0.063
UUGC	-3.466	0.416
AUCC	-3.469	0.691
CACC	-3.480	0.568
GGCC	-3.486	0.447
CCAU	-3.497	0.506
GCCA	-3.497	0.252
UCUC	-3.497	0.435
UGGU	-3.497	0.506
AGCU	-3.509	0.523
CUGG	-3.509	0.051
CGCA	-3.517	0.654
ACCC	-3.522	0.504
AUCU	-3.522	0.504
UACC	-3.522	0.504
UCGU	-3.522	0.504
CACA	-3.523	0.632
AGGU	-3.533	0.304
CCGC	-3.533	1.003
UACU	-3.536	0.527
UCUU	-3.536	0.087
GUGC	-3.552	0.849
UCGA	-3.560	0.345
GCCG	-3.564	0.132
ACGG	-3.571	0.362
CGUU	-3.571	0.362
CUGC	-3.571	0.616
GGCG	-3.571	0.340
AUGC	-3.571	1.093
UUAC	-3.582	0.379
CUCU	-3.591	0.617
GUGA	-3.591	0.176

GAGC	131
GAGG	45
GAGU	40
GAUA	108
GAUC	44
GAUG	230
GAUU	138
GCAA	121
GCAC	16
GCAG	49
GCAU	56
GCCA	24
GCCC	6
GCCG	24
GCCU	8
GCGA	31
GCGC	17
GCGG	29
GCGU	2
GCUA	149
GCUC	8
GCUG	55
GCUU	9
GGAA	419
GGAC	71
GGAG	108
GGAU	123
GGCA	38
GGCC	15
GGCG	67
GGCU	5
GGGA	1451
GGGC	37
GGGG	86
GGGU	32
GGUA	285
GGUC	30
GGUG	33
GGUU	32
GUAA	805
GUAC	25
GUAG	118
GUAU	59
GUCA	37
GUCC	6
GUCG	7771
GUCU	10
GUGA	20
GUGC	12
GUGG	102
GUGU	15
GUUA	104
GUUC	25
GUUG	111
GUUU	18
UAAA	545
UAAC	36
UAAG	402
UAAU	153
UACA	38
UACC	12
UACG	331
UACU	11
UAGA	40
UAGC	55
UAGG	629
UAGU	21
UAUA	80
UAUC	26

UUGU	-3.594	0.658
UCCC	-3.607	0.671
UCUA	-3.618	0.277
GCAC	-3.625	0.491
GAUC	-3.631	0.262
CGUA	-3.648	0.243
GGCA	-3.652	0.239
UGUA	-3.652	0.239
CCGG	-3.656	0.519
CGCU	-3.656	0.286
ACUC	-3.668	0.530
AGAC	-3.668	0.530
ACGU	-3.681	1.125
CGGA	-3.681	0.214
GCGA	-3.681	0.214
GGUC	-3.686	0.211
CGGG	-3.695	0.559
UGUU	-3.695	0.559
UCGC	-3.701	0.574
UGCA	-3.706	0.201
UGGC	-3.712	0.382
CCGA	-3.717	0.198
CCCU	-3.730	0.196
GCCU	-3.730	0.598
AGUG	-3.736	0.196
CCUC	-3.736	0.196
CCUU	-3.736	0.196
CCCG	-3.743	0.197
CGCG	-3.750	0.199
AGCG	-3.766	0.205
GCGC	-3.766	0.205
UGCC	-3.766	0.683
GUCC	-3.775	0.490
AGUC	-3.793	0.224
CACG	-3.804	0.233
ACCU	-3.840	0.272
CGCC	-3.840	0.272
GUCU	-3.840	0.272
ACCG	-3.854	0.290
CGGU	-3.854	0.290
GCUU	-3.854	0.290
GCUC	-3.871	0.311
AGCC	-3.889	0.336
CCGU	-3.889	0.336
CGGC	-3.909	0.366
CUCC	-3.909	0.366
GCCC	-3.909	0.366
GGCU	-3.934	0.402
CGUC	-4.048	0.583
GCGU	-4.048	0.583

UAUG	765
UAUU	42
UCAA	291
UCAC	22
UCAG	73
UCAU	45
UCCA	30
UCCC	12
UCCG	1308
UCCU	25
UCGA	16
UCGC	7
UCGG	131
UCGU	12
UCUA	48
UCUC	38
UCUG	1039
UCUU	29
UGAA	1992
UGAC	48
UGAG	163
UGAU	51
UGCA	26
UGCC	5
UGCG	77
UGCU	22
UGGA	218
UGGC	9
UGGG	171
UGGU	16
UGUA	38
UGUC	43
UGUG	292
UGUU	10
UUAA	1435
UUAC	14
UUAG	816
UUAU	46
UUCA	204
UUCC	526
UUCG	24602
UUCU	82
UUGA	60
UUGC	17
UUGG	2738
UUGU	13
UUUA	651
UUUC	1266
UUUG	37281
UUUU	238

iLoop size 1x1			
Range		1.129	
Median		-1.425	
5'	**3'**	**Score**	**Centered score**
C	G	-0.860	0.56
U	A	-1.053	0.37
A	A	-1.100	0.32
A	U	-1.127	0.30
U	G	-1.215	0.21
U	U	-1.309	0.12
C	A	-1.425	0.00
A	G	-1.439	-0.01
G	A	-1.466	-0.04
G	U	-1.607	-0.18
G	C	-1.728	-0.30
G	G	-1.733	-0.31
U	C	-1.810	-0.39
C	C	-1.928	-0.50
C	U	-1.935	-0.51
A	C	-1.989	-0.56

iLoop size 1x2			
Range		1.828	
Median		-2.516	
5'	**3'**	**Score**	**Centered score**
G	AA	-1.602	0.91
C	UA	-1.710	0.81
A	UA	-1.770	0.75
C	AA	-1.823	0.69
A	UC	-1.859	0.66
G	UA	-1.901	0.62
C	GA	-1.969	0.55
A	AA	-2.029	0.49
A	GA	-2.066	0.45
U	AA	-2.077	0.44
A	CA	-2.078	0.44
A	CU	-2.124	0.39
G	AG	-2.156	0.36
C	CA	-2.157	0.36
U	UA	-2.165	0.35
U	UU	-2.182	0.33
A	UU	-2.199	0.32
C	CG	-2.243	0.27
G	CA	-2.275	0.24
A	AG	-2.284	0.23
C	CC	-2.291	0.23
G	UC	-2.307	0.21
C	CU	-2.311	0.21
U	CU	-2.338	0.18
U	AC	-2.356	0.16
C	UG	-2.364	0.15
C	AC	-2.368	0.15
U	AU	-2.376	0.14
G	AC	-2.386	0.13
G	CU	-2.396	0.12
G	UU	-2.431	0.09
C	UU	-2.467	0.05
G	GA	-2.515	0.00
U	UG	-2.519	0.00
G	AU	-2.547	-0.03
U	UC	-2.549	-0.03
C	GC	-2.555	-0.04
A	AU	-2.579	-0.06
C	UC	-2.653	-0.14
C	GG	-2.660	-0.14
A	UG	-2.666	-0.15
U	CA	-2.674	-0.16
C	AU	-2.675	-0.16
A	AC	-2.685	-0.17
C	GU	-2.702	-0.19
G	GC	-2.752	-0.24
G	CC	-2.755	-0.24
A	CG	-2.795	-0.28
G	UG	-2.836	-0.32
U	AG	-2.840	-0.32
C	AG	-2.919	-0.40
U	GA	-2.938	-0.42
U	CC	-2.953	-0.44
G	GG	-2.966	-0.45
A	CC	-3.003	-0.49
U	CG	-3.012	-0.50
A	GC	-3.084	-0.57
U	GU	-3.187	-0.67
G	CG	-3.210	-0.69
A	GU	-3.261	-0.74
U	GC	-3.325	-0.81
U	GG	-3.393	-0.88
A	GG	-3.428	-0.91
G	GU	-3.430	-0.91

iLoop size 2x1			
Range		2.125	
Median		-2.377	
5'	**3'**	**Score**	**Centered score**
AA	A	-1.315	1.06
GA	A	-1.323	1.05
AA	G	-1.605	0.77
AA	U	-1.652	0.73
AG	A	-1.768	0.61
GG	G	-1.929	0.45
GA	U	-1.962	0.41
GA	G	-2.012	0.36
AG	U	-2.017	0.36
AU	U	-2.078	0.30
GG	A	-2.098	0.28
UG	A	-2.141	0.24
UA	G	-2.157	0.22
CA	A	-2.209	0.17
UU	U	-2.246	0.13
CU	U	-2.267	0.11
UA	A	-2.312	0.07
AU	A	-2.328	0.05
GG	U	-2.345	0.03
AC	A	-2.372	0.01
UA	U	-2.381	0.00
AA	C	-2.384	-0.01
AG	G	-2.406	-0.03
UG	G	-2.429	-0.05
CA	G	-2.472	-0.09
GC	A	-2.480	-0.10
UC	U	-2.490	-0.11
GG	C	-2.577	-0.20
AG	C	-2.606	-0.23
AU	G	-2.611	-0.23
AU	C	-2.641	-0.26
UG	U	-2.649	-0.27
UC	A	-2.688	-0.31
UU	A	-2.702	-0.32
UC	G	-2.714	-0.34
GA	C	-2.759	-0.38
AC	C	-2.763	-0.39
CC	A	-2.778	-0.40
CU	A	-2.790	-0.41
CA	C	-2.794	-0.42
UU	C	-2.802	-0.42
CG	G	-2.802	-0.42
GU	C	-2.809	-0.43
CC	G	-2.809	-0.43
CU	C	-2.849	-0.47
UG	C	-2.867	-0.49
GU	U	-2.891	-0.51
CC	C	-2.991	-0.61
CA	U	-3.004	-0.63
CG	A	-3.005	-0.63
CG	U	-3.005	-0.63
GC	G	-3.022	-0.64
CG	C	-3.026	-0.65
CC	U	-3.030	-0.65
GU	A	-3.035	-0.66
UU	G	-3.042	-0.66
CU	G	-3.059	-0.68
UA	C	-3.081	-0.70
AC	U	-3.083	-0.71
GC	C	-3.180	-0.80
AC	G	-3.183	-0.81
GU	G	-3.219	-0.84
UC	C	-3.281	-0.90
GC	U	-3.440	-1.06

iLoop size 1x3			
Range		2.918	
Median		-3.265	
5'	3'	Score	Centered score
C	UCC	-1.806	1.46
A	GAA	-2.538	0.73
C	CUA	-2.611	0.65
G	AGG	-2.631	0.63
C	UGU	-2.654	0.61
U	AUG	-2.771	0.49
U	CCA	-3.024	0.24
U	AAG	-3.026	0.24
U	UUU	-3.035	0.23
A	UUU	-3.078	0.19
C	UUA	-3.106	0.16
U	UCC	-3.114	0.15
C	GCU	-3.119	0.15
C	GCC	-3.141	0.12
A	AAA	-3.185	0.08
C	CCA	-3.188	0.08
C	AAC	-3.192	0.07
C	UCU	-3.202	0.06
C	CCC	-3.205	0.06
U	AUA	-3.208	0.06
U	CUC	-3.212	0.05
U	AAA	-3.231	0.03
C	ACC	-3.247	0.02
A	AUA	-3.268	0.00
U	ACG	-3.280	-0.01
A	UGA	-3.284	-0.02
C	AAU	-3.289	-0.02
C	AUA	-3.305	-0.04
U	AUU	-3.314	-0.05
U	UUC	-3.329	-0.06
C	AGC	-3.335	-0.07
C	AAA	-3.359	-0.09
A	UAU	-3.378	-0.11
U	AUC	-3.381	-0.12
U	UAC	-3.382	-0.12
G	UAA	-3.388	-0.12
U	CUG	-3.402	-0.14
U	ACU	-3.409	-0.14
U	UAU	-3.413	-0.15
U	GAA	-3.432	-0.17
A	UCU	-3.432	-0.17
U	AAU	-3.439	-0.17
U	AGG	-3.455	-0.19
U	AAC	-3.461	-0.20
U	UCA	-3.464	-0.20
U	UUA	-3.465	-0.20
U	CAC	-3.470	-0.21
C	UGA	-3.481	-0.22
U	GAC	-3.498	-0.23
A	AAU	-3.502	-0.24
A	ACU	-3.502	-0.24
A	AAC	-3.505	-0.24
C	GAA	-3.506	-0.24
C	AUG	-3.506	-0.24
U	GUG	-3.510	-0.24
A	AUU	-3.522	-0.26
G	AAG	-3.529	-0.26
G	GAG	-3.542	-0.28
C	UAC	-3.555	-0.29
C	UAA	-3.567	-0.30
A	AAG	-3.567	-0.30
A	UUA	-3.585	-0.32
U	UAA	-3.585	-0.32
C	GGC	-3.587	-0.32
G	UAU	-3.588	-0.32

iLoop size 2x2			
Range		3.093	
Median		-3.083	
5'	3'	Score	Centered score
AA	GA	-1.536	1.55
GC	AA	-1.560	1.52
AA	AA	-1.580	1.50
UU	UU	-1.628	1.45
GA	GA	-2.005	1.08
GA	AA	-2.097	0.99
AA	CG	-2.219	0.86
UU	AU	-2.238	0.84
AU	UU	-2.294	0.79
AG	GA	-2.309	0.77
GC	GA	-2.336	0.75
AC	AA	-2.358	0.72
GA	CC	-2.370	0.71
AA	UU	-2.444	0.64
UA	AU	-2.581	0.50
UA	UU	-2.597	0.49
AA	AC	-2.602	0.48
CU	UU	-2.606	0.48
AU	AA	-2.616	0.47
UA	GA	-2.640	0.44
AU	UC	-2.643	0.44
CU	AA	-2.677	0.41
AU	CG	-2.683	0.40
UU	UC	-2.713	0.37
AA	AU	-2.718	0.36
AG	UC	-2.731	0.35
CU	UC	-2.734	0.35
UG	UU	-2.738	0.34
AA	CA	-2.754	0.33
UU	UA	-2.756	0.33
AG	AA	-2.760	0.32
UG	UG	-2.790	0.29
AC	UC	-2.817	0.27
AA	UC	-2.841	0.24
GA	UU	-2.848	0.23
AC	UU	-2.852	0.23
GA	UA	-2.873	0.21
AA	GC	-2.875	0.21
UU	GU	-2.894	0.19
CA	UU	-2.899	0.18
AG	CU	-2.902	0.18
AA	UA	-2.921	0.16
GC	AG	-2.935	0.15
CU	AU	-2.943	0.14
AU	AU	-2.946	0.14
UU	AA	-2.953	0.13
UA	CG	-2.958	0.12
CU	CG	-2.961	0.12
GA	AC	-2.975	0.11
GA	CA	-3.008	0.07
UG	CA	-3.016	0.07
UC	UU	-3.041	0.04
AG	UU	-3.042	0.04
AG	AU	-3.051	0.03
GU	AA	-3.055	0.03
UA	UA	-3.055	0.03
AU	UA	-3.075	0.01
GU	AU	-3.077	0.01
GG	CC	-3.079	0.00
AG	CA	-3.091	-0.01
GU	UC	-3.106	-0.02
GA	UC	-3.110	-0.03
AA	AG	-3.134	-0.05
GC	GC	-3.144	-0.06
UA	UC	-3.147	-0.06

iLoop size 3x1			
Range		2.922	
Median		-3.088	
5'	3'	Score	Centered score
CAA	A	-1.627	1.46
GGG	G	-2.081	1.01
UAA	A	-2.286	0.80
UAA	G	-2.311	0.78
CAC	A	-2.356	0.73
UAA	U	-2.416	0.67
UAA	C	-2.465	0.62
CAA	C	-2.493	0.59
AAA	A	-2.560	0.53
UUA	A	-2.593	0.50
UUA	G	-2.597	0.49
UUA	U	-2.624	0.46
ACC	G	-2.677	0.41
CCA	A	-2.810	0.28
AAU	U	-2.811	0.28
AGA	G	-2.845	0.24
ACA	A	-2.883	0.21
CCC	A	-2.918	0.17
AAA	G	-2.924	0.16
UUC	U	-2.930	0.16
CAA	G	-2.930	0.16
AUU	U	-2.932	0.16
AAU	A	-2.942	0.15
CUC	A	-2.964	0.12
GAA	A	-2.986	0.10
AAG	A	-2.990	0.10
UAG	G	-2.999	0.09
AAA	C	-3.003	0.09
AUU	A	-3.028	0.06
UUU	U	-3.029	0.06
UCA	A	-3.033	0.05
CAA	U	-3.033	0.05
GGA	G	-3.035	0.05
UGC	C	-3.042	0.05
CGG	A	-3.045	0.04
ACU	U	-3.060	0.03
AGG	G	-3.070	0.02
AUA	G	-3.083	0.01
CCU	A	-3.118	-0.03
UAC	C	-3.119	-0.03
UAC	G	-3.120	-0.03
CUA	G	-3.136	-0.05
UGC	U	-3.148	-0.06
GAA	G	-3.153	-0.06
CCU	C	-3.161	-0.07
UUC	C	-3.163	-0.08
ACA	G	-3.166	-0.08
AAG	C	-3.168	-0.08
AAC	G	-3.171	-0.08
UAG	C	-3.184	-0.10
GGA	U	-3.190	-0.10
UGC	G	-3.197	-0.11
AAA	U	-3.200	-0.11
UAG	A	-3.211	-0.12
GAG	G	-3.213	-0.12
UAU	U	-3.221	-0.13
ACA	U	-3.233	-0.15
UUA	C	-3.255	-0.17
CGA	A	-3.257	-0.17
AAG	G	-3.259	-0.17
CUA	A	-3.272	-0.18
UGU	A	-3.277	-0.19
AUU	G	-3.278	-0.19
CGA	G	-3.288	-0.20
CGC	A	-3.303	-0.21

U	UCU	-3.588	-0.32
G	ACA	-3.594	-0.33
C	GUA	-3.597	-0.33
A	UCA	-3.605	-0.34
G	UUC	-3.612	-0.35
C	AUU	-3.614	-0.35
G	UCC	-3.616	-0.35
C	AAG	-3.620	-0.35
C	CGC	-3.621	-0.36
C	ACG	-3.627	-0.36
C	ACU	-3.644	-0.38
C	AGA	-3.650	-0.39
A	UAC	-3.652	-0.39
A	ACC	-3.653	-0.39
A	GAU	-3.664	-0.40
C	UUU	-3.676	-0.41
U	CCG	-3.677	-0.41
G	GAA	-3.684	-0.42
A	AGA	-3.685	-0.42
C	UGC	-3.688	-0.42
G	UUA	-3.689	-0.42
C	UGG	-3.700	-0.43
U	CUA	-3.709	-0.44
U	UUG	-3.716	-0.45
A	UCC	-3.716	-0.45
C	UCA	-3.718	-0.45
G	ACU	-3.724	-0.46
C	AGU	-3.729	-0.46
A	GAG	-3.730	-0.47
A	CUA	-3.733	-0.47
A	CGA	-3.753	-0.49
A	GUG	-3.770	-0.50
A	CAC	-3.773	-0.51
A	UAA	-3.774	-0.51
U	GAG	-3.792	-0.53
G	AAA	-3.796	-0.53
A	GAC	-3.801	-0.54
U	CAG	-3.804	-0.54
C	CGU	-3.804	-0.54
G	AGA	-3.810	-0.54
C	GGA	-3.811	-0.55
G	AUU	-3.814	-0.55
A	CCU	-3.816	-0.55
G	AUA	-3.817	-0.55
A	UGU	-3.818	-0.55
U	UAG	-3.818	-0.55
G	AGU	-3.821	-0.56
C	GCA	-3.826	-0.56
U	CAU	-3.832	-0.57
C	GGU	-3.833	-0.57
C	CUC	-3.836	-0.57
A	GGA	-3.837	-0.57
A	AUG	-3.842	-0.58
U	ACC	-3.853	-0.59
U	ACA	-3.866	-0.60
A	GCU	-3.870	-0.60
A	CAA	-3.870	-0.60
C	CUU	-3.883	-0.62
A	ACA	-3.888	-0.62
A	GUA	-3.894	-0.63
U	GCG	-3.898	-0.63
G	AUG	-3.900	-0.63
G	UAG	-3.904	-0.64
U	CAA	-3.909	-0.64
G	AAC	-3.910	-0.64
G	GUA	-3.929	-0.66
C	GUG	-3.931	-0.67
G	UAC	-3.934	-0.67
C	ACA	-3.940	-0.68

UU	UG	-3.151	-0.07
CC	CA	-3.167	-0.08
GA	AU	-3.178	-0.10
UC	AA	-3.181	-0.10
UC	GU	-3.192	-0.11
AG	GG	-3.193	-0.11
GA	GG	-3.199	-0.12
AU	CU	-3.200	-0.12
UA	UG	-3.201	-0.12
GG	AA	-3.219	-0.14
GA	CU	-3.226	-0.14
AC	CG	-3.239	-0.16
AG	CG	-3.239	-0.16
AA	GU	-3.240	-0.16
CA	AU	-3.271	-0.19
CG	GA	-3.274	-0.19
CA	CG	-3.278	-0.20
UG	CG	-3.288	-0.21
CC	UU	-3.289	-0.21
UU	GA	-3.295	-0.21
CU	AG	-3.304	-0.22
AA	GG	-3.307	-0.22
AC	GU	-3.308	-0.23
UA	CU	-3.312	-0.23
UU	CU	-3.315	-0.23
CC	GU	-3.327	-0.24
AU	CA	-3.328	-0.25
AG	CC	-3.345	-0.26
UA	AC	-3.350	-0.27
AG	UA	-3.358	-0.28
AC	AG	-3.370	-0.29
GA	AG	-3.375	-0.29
GA	UG	-3.382	-0.30
AG	GU	-3.384	-0.30
GU	UU	-3.385	-0.30
CG	UC	-3.387	-0.30
GA	CG	-3.389	-0.31
CU	GU	-3.394	-0.31
CA	CA	-3.397	-0.31
UU	CG	-3.397	-0.31
GA	GC	-3.402	-0.32
GC	GG	-3.413	-0.33
GG	UU	-3.421	-0.34
CC	AA	-3.426	-0.34
UC	AU	-3.427	-0.34
UC	GA	-3.427	-0.34
GU	GU	-3.429	-0.35
UA	CC	-3.429	-0.35
AG	AG	-3.454	-0.37
GU	AC	-3.457	-0.37
CA	UG	-3.465	-0.38
AC	CA	-3.467	-0.38
GC	AU	-3.468	-0.39
AC	GA	-3.468	-0.39
AA	UG	-3.469	-0.39
GC	CA	-3.472	-0.39
UG	AU	-3.473	-0.39
AG	AC	-3.473	-0.39
GU	GA	-3.474	-0.39
CG	CA	-3.478	-0.40
UG	UA	-3.480	-0.40
UU	AG	-3.482	-0.40
GC	UA	-3.485	-0.40
AA	CU	-3.490	-0.41
AC	UA	-3.491	-0.41
UG	AA	-3.492	-0.41
CG	UG	-3.502	-0.42
UC	UG	-3.503	-0.42
AU	GU	-3.503	-0.42

AGU	U	-3.318	-0.23
UGG	A	-3.329	-0.24
GCU	U	-3.339	-0.25
GGA	A	-3.354	-0.27
CUU	G	-3.355	-0.27
GGG	A	-3.360	-0.27
UGA	A	-3.373	-0.29
AUA	A	-3.380	-0.29
AUA	U	-3.385	-0.30
UUU	G	-3.393	-0.30
AUU	C	-3.395	-0.31
UGG	G	-3.396	-0.31
AUC	G	-3.397	-0.31
UAG	U	-3.403	-0.31
CCU	U	-3.406	-0.32
UGC	A	-3.409	-0.32
GAG	A	-3.410	-0.32
GAU	U	-3.421	-0.33
ACA	C	-3.424	-0.34
UGA	U	-3.430	-0.34
GUU	U	-3.439	-0.35
UUC	G	-3.449	-0.36
CAG	A	-3.452	-0.36
UAC	U	-3.453	-0.37
AGA	U	-3.455	-0.37
GAG	U	-3.462	-0.37
AAG	U	-3.468	-0.38
GAC	A	-3.477	-0.39
GAA	U	-3.489	-0.40
GGA	C	-3.490	-0.40
CCC	G	-3.492	-0.40
CCA	G	-3.492	-0.40
CCC	U	-3.496	-0.41
AGC	G	-3.498	-0.41
GUU	C	-3.507	-0.42
CAG	C	-3.509	-0.42
UGU	G	-3.510	-0.42
AAC	U	-3.513	-0.42
AGC	A	-3.515	-0.43
AGA	A	-3.520	-0.43
UAC	A	-3.525	-0.44
GCA	G	-3.532	-0.44
UGG	C	-3.532	-0.44
CUU	A	-3.540	-0.45
CUG	G	-3.545	-0.46
UUG	U	-3.549	-0.46
CAU	A	-3.556	-0.47
AGU	G	-3.558	-0.47
AUC	C	-3.558	-0.47
CAG	G	-3.569	-0.48
CAC	U	-3.572	-0.48
CCU	G	-3.572	-0.48
UCG	U	-3.575	-0.49
CAU	G	-3.582	-0.49
CGC	C	-3.586	-0.50
AUG	U	-3.589	-0.50
AGU	A	-3.595	-0.51
AAU	G	-3.600	-0.51
AAU	C	-3.609	-0.52
UCC	G	-3.609	-0.52
GUG	G	-3.610	-0.52
GGG	U	-3.617	-0.53
GUA	C	-3.621	-0.53
CGA	C	-3.636	-0.55
ACG	U	-3.646	-0.56
CUA	C	-3.647	-0.56
UGA	C	-3.651	-0.56
UGU	U	-3.655	-0.57
CUA	U	-3.658	-0.57

G	CAA	-3.940	-0.68
U	AGA	-3.940	-0.68
G	CUC	-3.945	-0.68
G	CAG	-3.949	-0.68
U	UGC	-3.949	-0.68
U	UCG	-3.951	-0.69
C	AGG	-3.955	-0.69
U	GCU	-3.955	-0.69
U	CUU	-3.958	-0.69
A	GCA	-3.962	-0.70
G	UUU	-3.985	-0.72
A	UUG	-3.996	-0.73
U	CCC	-3.999	-0.73
A	AGG	-4.000	-0.73
G	UUG	-4.006	-0.74
G	CUA	-4.010	-0.74
A	CUC	-4.011	-0.75
A	CCA	-4.011	-0.75
C	UAU	-4.014	-0.75
C	GGG	-4.019	-0.75
G	GCA	-4.022	-0.76
C	AUC	-4.029	-0.76
C	UUC	-4.037	-0.77
C	GUC	-4.039	-0.77
G	UGA	-4.039	-0.77
C	CUG	-4.040	-0.77
A	UUC	-4.045	-0.78
U	GUU	-4.045	-0.78
C	GAG	-4.052	-0.79
C	CAC	-4.059	-0.79
U	UGU	-4.065	-0.80
U	CCU	-4.071	-0.81
U	UGA	-4.076	-0.81
U	GGG	-4.077	-0.81
C	GUU	-4.078	-0.81
C	UCG	-4.082	-0.82
A	CAU	-4.088	-0.82
C	CCG	-4.088	-0.82
U	GGU	-4.091	-0.83
G	CAC	-4.092	-0.83
U	AGU	-4.099	-0.83
A	CGC	-4.103	-0.84
G	GUG	-4.103	-0.84
U	GCA	-4.104	-0.84
G	GUC	-4.111	-0.85
G	ACC	-4.119	-0.85
G	GCC	-4.125	-0.86
U	CGC	-4.126	-0.86
U	UGG	-4.129	-0.86
C	CAA	-4.133	-0.87
U	GCC	-4.136	-0.87
G	CGG	-4.137	-0.87
G	AAU	-4.140	-0.88
A	AUC	-4.144	-0.88
A	CAG	-4.148	-0.88
G	CGU	-4.148	-0.88
U	AGC	-4.150	-0.88
C	CCU	-4.155	-0.89
C	GAU	-4.164	-0.90
G	GAU	-4.178	-0.91
G	ACG	-4.180	-0.91
G	AGC	-4.182	-0.92
G	UCA	-4.182	-0.92
G	CUU	-4.188	-0.92
G	UCU	-4.194	-0.93
G	CUG	-4.198	-0.93
U	GAU	-4.210	-0.94
G	GGG	-4.218	-0.95
U	GUA	-4.225	-0.96

UA	AA	-3.504	-0.42
CG	CG	-3.504	-0.42
UG	UC	-3.513	-0.43
AU	GA	-3.520	-0.44
CA	AA	-3.531	-0.45
GU	GC	-3.545	-0.46
GU	UA	-3.555	-0.47
AC	UG	-3.558	-0.48
CG	UU	-3.558	-0.48
CG	AA	-3.559	-0.48
AA	CC	-3.563	-0.48
GA	GU	-3.588	-0.51
GG	UC	-3.590	-0.51
AC	AC	-3.603	-0.52
UC	AG	-3.604	-0.52
GG	UA	-3.606	-0.52
AU	CC	-3.610	-0.53
GG	GA	-3.614	-0.53
CU	CU	-3.618	-0.54
UC	CG	-3.625	-0.54
CC	CG	-3.630	-0.55
UC	CU	-3.636	-0.55
CA	CU	-3.638	-0.56
UG	CU	-3.642	-0.56
CU	GG	-3.646	-0.56
CC	CC	-3.647	-0.56
UU	GG	-3.650	-0.57
AC	CC	-3.655	-0.57
CU	GC	-3.666	-0.58
CA	GU	-3.676	-0.59
AU	AC	-3.685	-0.60
GC	UU	-3.686	-0.60
UU	AC	-3.687	-0.60
UA	CA	-3.689	-0.61
CG	GU	-3.697	-0.61
GC	AC	-3.698	-0.62
CG	UA	-3.700	-0.62
CC	GA	-3.703	-0.62
AC	GG	-3.706	-0.62
AU	AG	-3.716	-0.63
CG	AU	-3.720	-0.64
GC	GU	-3.720	-0.64
CA	AG	-3.723	-0.64
AG	UG	-3.728	-0.65
GU	CU	-3.736	-0.65
CA	GA	-3.738	-0.66
CC	AG	-3.748	-0.67
UA	GU	-3.765	-0.68
UC	UA	-3.785	-0.70
CC	GG	-3.786	-0.70
AC	CU	-3.791	-0.71
CG	AG	-3.800	-0.72
CC	AU	-3.801	-0.72
GU	CC	-3.811	-0.73
CU	CC	-3.817	-0.73
GG	GG	-3.828	-0.75
UG	GC	-3.832	-0.75
AU	UG	-3.838	-0.76
UC	CA	-3.841	-0.76
CG	CC	-3.845	-0.76
GG	AU	-3.845	-0.76
CU	UG	-3.848	-0.77
CU	AC	-3.857	-0.77
GG	CA	-3.860	-0.78
CG	CU	-3.862	-0.78
CA	GC	-3.864	-0.78
CC	UA	-3.865	-0.78
CA	UC	-3.870	-0.79
GU	AG	-3.882	-0.80

UCA	G	-3.663	-0.58
UUC	A	-3.663	-0.58
CAG	U	-3.677	-0.59
AGU	C	-3.691	-0.60
UAU	A	-3.693	-0.60
GGU	C	-3.696	-0.61
CAC	C	-3.701	-0.61
GUG	A	-3.701	-0.61
UCU	U	-3.701	-0.61
UCU	A	-3.703	-0.62
UGA	G	-3.709	-0.62
UUG	C	-3.710	-0.62
CUC	G	-3.713	-0.62
GAC	C	-3.717	-0.63
GUG	C	-3.717	-0.63
ACG	C	-3.717	-0.63
GUC	U	-3.717	-0.63
ACU	G	-3.737	-0.65
UCU	G	-3.742	-0.65
GUC	G	-3.747	-0.66
CGC	U	-3.753	-0.66
GCU	C	-3.753	-0.66
CGA	U	-3.754	-0.67
GGC	C	-3.754	-0.67
AUC	U	-3.762	-0.67
UCA	C	-3.765	-0.68
UCA	U	-3.773	-0.69
GGU	G	-3.777	-0.69
UUU	A	-3.779	-0.69
CUC	C	-3.786	-0.70
AGC	C	-3.791	-0.70
CGU	G	-3.791	-0.70
CUC	U	-3.791	-0.70
GGC	A	-3.791	-0.70
GGU	U	-3.791	-0.70
GUA	A	-3.794	-0.71
CUG	C	-3.802	-0.71
GAG	C	-3.802	-0.71
GAA	C	-3.805	-0.72
AGA	C	-3.810	-0.72
CCA	U	-3.810	-0.72
GUA	G	-3.810	-0.72
CUG	A	-3.816	-0.73
GCA	A	-3.819	-0.73
AUC	A	-3.821	-0.73
CAU	C	-3.821	-0.73
CUG	U	-3.821	-0.73
CAU	U	-3.831	-0.74
UUG	A	-3.848	-0.76
UGU	C	-3.853	-0.76
AAC	A	-3.863	-0.77
ACU	C	-3.884	-0.80
UCC	U	-3.884	-0.80
ACU	A	-3.890	-0.80
UAU	G	-3.890	-0.80
GUG	U	-3.893	-0.81
CAC	G	-3.893	-0.81
UCG	G	-3.893	-0.81
UGG	U	-3.900	-0.81
UUG	G	-3.903	-0.81
ACC	C	-3.906	-0.82
AGG	A	-3.906	-0.82
CGC	G	-3.906	-0.82
AUG	A	-3.913	-0.83
CCG	C	-3.913	-0.83
GAU	A	-3.913	-0.83
GAU	C	-3.921	-0.83
UCG	A	-3.924	-0.84
AAC	C	-3.950	-0.86

C	GAC	-4.229	-0.96
A	CUG	-4.230	-0.96
G	UGU	-4.233	-0.97
A	GUU	-4.235	-0.97
G	GCG	-4.237	-0.97
A	GGG	-4.247	-0.98
G	CAU	-4.262	-1.00
A	AGU	-4.270	-1.01
A	UCG	-4.292	-1.03
A	CCC	-4.296	-1.03
C	CGG	-4.296	-1.03
A	GGU	-4.296	-1.03
U	GUC	-4.296	-1.03
G	UGC	-4.317	-1.05
C	CGA	-4.341	-1.08
G	CGA	-4.341	-1.08
G	CGC	-4.344	-1.08
C	CAG	-4.359	-1.09
C	UAG	-4.359	-1.09
G	CCU	-4.359	-1.09
G	GAC	-4.359	-1.09
A	ACG	-4.363	-1.10
A	AGC	-4.370	-1.10
U	CGU	-4.370	-1.10
G	UGG	-4.385	-1.12
A	GCG	-4.389	-1.12
A	CUU	-4.393	-1.13
A	GUC	-4.393	-1.13
A	UAG	-4.416	-1.15
C	UUG	-4.426	-1.16
G	AUC	-4.426	-1.16
C	GCG	-4.455	-1.19
G	GGA	-4.455	-1.19
A	UGC	-4.476	-1.21
C	CAU	-4.476	-1.21
A	GGC	-4.483	-1.22
A	GCC	-4.491	-1.23
G	CCG	-4.519	-1.25
G	GCU	-4.529	-1.26
A	UGG	-4.540	-1.27
G	GGC	-4.540	-1.27
U	GGC	-4.540	-1.27
G	CCC	-4.580	-1.31
G	CCA	-4.614	-1.35
G	UCG	-4.614	-1.35
U	GGA	-4.614	-1.35
G	GGU	-4.635	-1.37
A	CCG	-4.688	-1.42
A	CGG	-4.688	-1.42
A	CGU	-4.688	-1.42
G	GUU	-4.688	-1.42
U	CGA	-4.688	-1.42
U	CGG	-4.724	-1.46
UG	AG	-3.888	-0.81
GC	CC	-3.890	-0.81
GU	GG	-3.893	-0.81
CU	CA	-3.904	-0.82
GG	CU	-3.906	-0.82
GG	UG	-3.913	-0.83
GC	UC	-3.921	-0.84
UU	CA	-3.929	-0.85
CC	UG	-3.930	-0.85
UA	GC	-3.941	-0.86
UA	GG	-3.956	-0.87
AC	GC	-3.957	-0.87
CU	UA	-3.961	-0.88
UG	CC	-3.961	-0.88
UC	UC	-3.964	-0.88
UC	GC	-3.979	-0.90
UU	GC	-3.985	-0.90
UC	GG	-3.987	-0.90
UG	GU	-3.990	-0.91
CA	GG	-3.990	-0.91
UG	GA	-4.002	-0.92
CC	UC	-4.003	-0.92
AG	GC	-4.006	-0.92
GC	CU	-4.025	-0.94
AC	AU	-4.029	-0.95
UU	CC	-4.031	-0.95
CU	GA	-4.057	-0.97
GU	CA	-4.093	-1.01
UC	AC	-4.094	-1.01
AU	GG	-4.097	-1.01
AU	GC	-4.115	-1.03
GG	AC	-4.117	-1.03
GG	AG	-4.131	-1.05
GU	UG	-4.134	-1.05
CC	CU	-4.142	-1.06
CC	GC	-4.159	-1.08
GU	CG	-4.175	-1.09
CA	UA	-4.180	-1.10
GG	GC	-4.192	-1.11
UC	CC	-4.229	-1.15
CC	AC	-4.237	-1.15
GG	GU	-4.242	-1.16
UG	GG	-4.248	-1.17
CA	AC	-4.260	-1.18
UA	AG	-4.260	-1.18
GC	UG	-4.304	-1.22
CG	GC	-4.334	-1.25
GC	CG	-4.334	-1.25
UG	AC	-4.343	-1.26
CG	AC	-4.367	-1.28
GG	CG	-4.450	-1.37
CG	GG	-4.507	-1.42
CA	CC	-4.629	-1.55
AUG	G	-3.954	-0.87
CUU	C	-3.954	-0.87
GUA	U	-3.964	-0.88
AGC	U	-3.964	-0.88
CGG	U	-3.969	-0.88
GCC	A	-3.980	-0.89
ACG	G	-3.980	-0.89
CCA	C	-3.998	-0.91
UUU	C	-3.998	-0.91
ACC	A	-3.998	-0.91
GCG	A	-3.998	-0.91
GGC	U	-3.998	-0.91
GUC	A	-3.998	-0.91
GAC	G	-4.005	-0.92
GCA	U	-4.005	-0.92
GGC	G	-4.019	-0.93
GGG	C	-4.019	-0.93
CUU	U	-4.019	-0.93
GUU	A	-4.019	-0.93
GAU	G	-4.019	-0.93
UCG	C	-4.035	-0.95
GAC	U	-4.035	-0.95
UCC	C	-4.035	-0.95
AUA	C	-4.043	-0.96
GCU	G	-4.043	-0.96
AGG	U	-4.062	-0.97
CCC	C	-4.072	-0.98
UCC	A	-4.083	-1.00
GCA	C	-4.083	-1.00
CCG	A	-4.096	-1.01
GUU	G	-4.096	-1.01
GCG	C	-4.109	-1.02
GCU	A	-4.109	-1.02
CGG	G	-4.139	-1.05
GCG	G	-4.139	-1.05
GCG	U	-4.139	-1.05
AGG	C	-4.157	-1.07
CGU	A	-4.157	-1.07
CGU	C	-4.157	-1.07
UAU	C	-4.157	-1.07
UCU	C	-4.157	-1.07
CCG	G	-4.157	-1.07
ACG	A	-4.178	-1.09
GGU	A	-4.178	-1.09
CGU	U	-4.231	-1.14
AUG	C	-4.231	-1.14
GUC	C	-4.231	-1.14
ACC	U	-4.268	-1.18
GCC	C	-4.268	-1.18
GCC	G	-4.268	-1.18
CCG	U	-4.390	-1.30
CGG	C	-4.390	-1.30
GCC	U	-4.549	-1.46

Table S15. Internal loops 1x1

5'	3'	Score	SD
C	G	-0.860	0.168
U	A	-1.053	0.268
A	A	-1.100	0.698
A	U	-1.127	0.168
U	G	-1.215	0.752
U	U	-1.309	0.373
C	A	-1.425	0.357
A	G	-1.439	0.492
G	A	-1.466	0.579
G	U	-1.607	0.496
G	C	-1.728	0.219
G	G	-1.733	0.466
U	C	-1.810	0.428
C	C	-1.928	0.856
C	U	-1.935	0.363
A	C	-1.989	0.241

5'	3'	Total count
A	A	149092
A	C	8865
A	G	39559
A	U	71724
C	A	18322
C	C	11992
C	G	85398
C	U	7825
G	A	40987
G	C	18191
G	G	12274
G	U	51250
U	A	94030
U	C	10244
U	G	54192
U	U	56588

Supercategory	Total count
Intron	73985
Translation	569671
Cis -Reg	86877

Table S16. Internal loops 1x2

5'	3'	Score	SD
G	AA	-1.602	0.318
C	UA	-1.710	0.815
A	UA	-1.770	0.389
C	AA	-1.823	0.921
A	UC	-1.859	0.455
G	UA	-1.901	1.117
C	GA	-1.969	0.526
A	AA	-2.029	0.931
A	GA	-2.066	1.109
U	AA	-2.077	0.295
A	CA	-2.078	0.773
A	CU	-2.124	0.589
G	AG	-2.156	1.489
C	CA	-2.157	1.184
U	UA	-2.165	1.067
U	UU	-2.182	0.605
A	UU	-2.199	0.758
C	CG	-2.243	0.732
G	CA	-2.275	0.301
A	AG	-2.284	0.940
C	CC	-2.291	1.186
G	UC	-2.307	0.422
C	CU	-2.311	1.440
U	CU	-2.338	0.227
U	AC	-2.356	1.252
C	UG	-2.364	0.414
C	AC	-2.368	0.780
U	AU	-2.376	0.418
G	AC	-2.386	0.673
G	CU	-2.396	0.478
G	UU	-2.431	0.481
C	UU	-2.467	0.539
G	GA	-2.515	0.541
U	UG	-2.519	0.863
G	AU	-2.547	1.548
U	UC	-2.549	0.500
C	GC	-2.555	0.386
A	AU	-2.579	0.415
C	UC	-2.653	0.937
C	GG	-2.660	0.423
A	UG	-2.666	0.078
U	CA	-2.674	0.699
C	AU	-2.675	0.692
A	AC	-2.685	0.738
C	GU	-2.702	0.875
G	GC	-2.752	0.759
G	CC	-2.755	0.075
A	CG	-2.795	0.711
G	UG	-2.836	0.263
U	AG	-2.840	0.820
C	AG	-2.919	0.189
U	GA	-2.938	0.340
U	CC	-2.953	0.710
G	GG	-2.966	0.346
A	CC	-3.003	0.530
U	CG	-3.012	1.249
A	GC	-3.084	0.692
U	GU	-3.187	0.383
G	CG	-3.210	0.477
A	GU	-3.261	0.328
U	GC	-3.325	0.767
U	GG	-3.393	0.375
A	GG	-3.428	0.027
G	GU	-3.430	0.136

5'	3'	Total count
A	AA	7689
A	AC	724
A	AG	1614
A	AU	1007
A	CA	2047
A	CC	734
A	CG	486
A	CU	5150
A	GA	5203
A	GC	339
A	GG	337
A	GU	333
A	UA	8555
A	UC	35351
A	UG	1876
A	UU	35892
C	AA	143543
C	AC	1219
C	AG	1546
C	AU	861
C	CA	2646
C	CC	3032
C	CG	1478
C	CU	2968
C	GA	22244
C	GC	1143
C	GG	849
C	GU	17407
C	UA	146931
C	UC	1734
C	UG	2129
C	UU	3030
G	AA	45624
G	AC	1504
G	AG	292336
G	AU	53285
G	CA	5422
G	CC	1386
G	CG	1590
G	CU	3112
G	GA	1102
G	GC	615
G	GG	714
G	GU	320
G	UA	14573
G	UC	2530
G	UG	1629
G	UU	2207
U	AA	4736
U	AC	6116
U	AG	919
U	AU	1724
U	CA	542
U	CC	285
U	CG	337
U	CU	3835
U	GA	571
U	GC	316
U	GG	236
U	GU	259
U	UA	5417
U	UC	989
U	UG	684
U	UU	2030

Supercategory	Total count
Intron	46675
Translation	861600
Cis -Reg	8767

5'	3'	Score	SD
AA	A	-1.315	0.976
GA	A	-1.323	0.530
AA	G	-1.605	0.247
AA	U	-1.652	0.910
AG	A	-1.768	1.276
GG	G	-1.929	0.841
GA	U	-1.962	0.815
GA	G	-2.012	1.436
AG	U	-2.017	0.507
AU	U	-2.078	0.776
GG	A	-2.098	0.956
UG	A	-2.141	0.153
UA	G	-2.157	0.526
CA	A	-2.209	0.375
UU	U	-2.246	1.037
CU	U	-2.267	1.294
UA	A	-2.312	0.628
AU	A	-2.328	0.550
GG	U	-2.345	0.417
AC	A	-2.372	0.905
UA	U	-2.381	1.074
AA	C	-2.384	0.355
AG	G	-2.406	0.145
UG	G	-2.429	0.534
CA	G	-2.472	0.447
GC	A	-2.480	0.246
UC	U	-2.490	1.364
GG	C	-2.577	0.800
AG	C	-2.606	0.572
AU	G	-2.611	0.465
AU	C	-2.641	1.024
UG	U	-2.649	0.937
UC	A	-2.688	1.292
UU	A	-2.702	0.750
UC	G	-2.714	0.950
GA	C	-2.759	0.790
AC	C	-2.763	1.054
CC	A	-2.778	0.816
CU	A	-2.790	0.521
CA	C	-2.794	1.172
UU	C	-2.802	1.061
CG	G	-2.802	0.678
GU	C	-2.809	0.769
CC	G	-2.809	0.767
CU	C	-2.849	1.304
UG	C	-2.867	0.593
GU	U	-2.891	0.862
CC	C	-2.991	0.350
CA	U	-3.004	1.029
CG	A	-3.005	0.502
CG	U	-3.005	0.714
GC	G	-3.022	0.386
CG	C	-3.026	1.146
CC	U	-3.030	0.392
GU	A	-3.035	0.165
UU	G	-3.042	1.068
CU	G	-3.059	0.669
UA	C	-3.081	0.448
AC	U	-3.083	1.263
GC	C	-3.180	1.140
AC	G	-3.183	0.173
GU	G	-3.219	0.576
UC	C	-3.281	1.162
GC	U	-3.440	0.965

5'	3'	Total count
AA	A	139899
AA	C	1393
AA	G	28141
AA	U	2505
AC	A	525
AC	C	157
AC	G	543
AC	U	124
AG	A	6815
AG	C	549
AG	G	2506
AG	U	6983
AU	A	908
AU	C	255
AU	G	753
AU	U	949
CA	A	1587
CA	C	175
CA	G	748
CA	U	130
CC	A	190
CC	C	267
CC	G	186
CC	U	243
CG	A	188
CG	C	153
CG	G	255
CG	U	142
CU	A	423
CU	C	108
CU	G	162
CU	U	1172
GA	A	33155
GA	C	783
GA	G	250207
GA	U	1251
GC	A	3801
GC	C	51
GC	G	239
GC	U	45
GG	A	55505
GG	C	295
GG	G	60556
GG	U	1037
GU	A	876
GU	C	326
GU	G	188
GU	U	149
UA	A	781
UA	C	174
UA	G	2358
UA	U	333
UC	A	213
UC	C	100
UC	G	175
UC	U	708
UG	A	5579
UG	C	211
UG	G	701
UG	U	215
UU	A	240
UU	C	203
UU	G	186
UU	U	1234

Supercategory	Total count
Intron	1972
Translation	605865
Cis -Reg	13172

5'	3'	Score	SD
C	UCC	-1.806	1.983
A	GAA	-2.538	1.699
C	CUA	-2.611	1.573
G	AGG	-2.631	1.733
C	UGU	-2.654	1.684
U	AUG	-2.771	2.085
U	CCA	-3.024	1.373
U	AAG	-3.026	1.990
U	UUU	-3.035	0.795
A	UUU	-3.078	0.765
C	UUA	-3.106	1.270
U	UCC	-3.114	0.315
C	GCU	-3.119	0.209
C	GCC	-3.141	1.165
A	AAA	-3.185	0.409
C	CCA	-3.188	0.752
C	AAC	-3.192	0.633
C	UCU	-3.202	1.545
C	CCC	-3.205	1.381
U	AUA	-3.208	0.944
U	CUC	-3.212	1.653
U	AAA	-3.231	0.834
C	ACC	-3.247	0.713
A	AUA	-3.268	0.983
U	ACG	-3.280	2.278
A	UGA	-3.284	0.592
C	AAU	-3.289	0.568
C	AUA	-3.305	1.005
U	AUU	-3.314	0.653
U	UUC	-3.329	0.306
C	AGC	-3.335	0.616
C	AAA	-3.359	0.490
A	UAU	-3.378	1.785
U	AUC	-3.381	0.580
U	UAC	-3.382	1.121
G	UAA	-3.388	1.416
U	CUG	-3.402	0.698
U	ACU	-3.409	0.830
U	UAU	-3.413	0.893
U	GAA	-3.432	0.328
A	UCU	-3.432	0.577
U	AAU	-3.439	0.815
U	AGG	-3.455	1.239
U	AAC	-3.461	1.332
U	UCA	-3.464	0.491
U	UUA	-3.465	1.236
U	CAC	-3.470	1.121
C	UGA	-3.481	0.934
U	GAC	-3.498	0.678
A	AAU	-3.502	0.709
A	ACU	-3.502	2.118
A	AAC	-3.505	0.674
C	GAA	-3.506	0.148
C	AUG	-3.506	1.487
U	GUG	-3.510	1.191
A	AUU	-3.522	0.800
G	AAG	-3.529	0.273
G	GAG	-3.542	0.697
C	UAC	-3.555	0.564
C	UAA	-3.567	0.637
A	AAG	-3.567	0.350
A	UUA	-3.585	1.051
U	UAA	-3.585	0.536
C	GGC	-3.587	0.509
G	UAU	-3.588	1.344
U	UCU	-3.588	0.769
G	ACA	-3.594	0.975
C	GUA	-3.597	0.825

5'	3'	Total count
A	AAA	143
A	AAC	74
A	AAG	68
A	AAU	64
A	ACA	27
A	ACC	37
A	ACG	10
A	ACU	1092
A	AGA	174
A	AGC	6
A	AGG	16
A	AGU	14
A	AUA	157
A	AUC	10
A	AUG	49
A	AUU	78
A	CAA	52
A	CAC	39
A	CAG	63
A	CAU	35
A	CCA	55
A	CCC	15
A	CCG	4
A	CCU	45
A	CGA	80
A	CGC	14
A	CGG	4
A	CGU	2
A	CUA	135
A	CUC	18
A	CUG	36
A	CUU	34
A	GAA	3404
A	GAC	36
A	GAG	94
A	GAU	55
A	GCA	40
A	GCC	5
A	GCG	35
A	GCU	60
A	GGA	182
A	GGC	18
A	GGG	8
A	GGU	7
A	GUA	46
A	GUC	12
A	GUG	80
A	GUU	22
A	UAA	50
A	UAC	57
A	UAG	29
A	UAU	559
A	UCA	886
A	UCC	341
A	UCG	69
A	UCU	262
A	UGA	113
A	UGC	7
A	UGG	12
A	UGU	37
A	UUA	330
A	UUC	128
A	UUG	109
A	UUU	633
C	AAA	360
C	AAC	464
C	AAG	299
C	AAU	89

Supercategory	Total count
Intron	31324
Translation	335824
Cis -Reg	12385

A	UCA	-3.605	0.911
G	UUC	-3.612	1.420
C	AUU	-3.614	0.803
G	UCC	-3.616	1.136
C	AAG	-3.620	0.690
C	CGC	-3.621	0.515
C	ACG	-3.627	0.753
C	ACU	-3.644	0.398
C	AGA	-3.650	0.646
A	UAC	-3.652	1.188
A	ACC	-3.653	0.818
A	GAU	-3.664	0.215
C	UUU	-3.676	0.151
U	CCG	-3.677	1.440
G	GAA	-3.684	0.984
A	AGA	-3.685	0.554
C	UGC	-3.688	1.008
G	UUA	-3.689	1.339
C	UGG	-3.700	0.227
U	CUA	-3.709	1.860
U	UUG	-3.716	1.403
A	UCC	-3.716	0.952
C	UCA	-3.718	0.722
G	ACU	-3.724	0.773
C	AGU	-3.729	0.603
A	GAG	-3.730	1.039
A	CUA	-3.733	0.347
A	CGA	-3.753	1.337
A	GUG	-3.770	0.615
A	CAC	-3.773	1.026
A	UAA	-3.774	0.638
U	GAG	-3.792	0.948
G	AAA	-3.796	0.543
A	GAC	-3.801	0.505
U	CAG	-3.804	1.273
C	CGU	-3.804	0.459
G	AGA	-3.810	0.251
C	GGA	-3.811	0.212
G	AUU	-3.814	0.659
A	CCU	-3.816	0.592
G	AUA	-3.817	0.598
A	UGU	-3.818	0.966
U	UAG	-3.818	1.228
G	AGU	-3.821	0.920
C	GCA	-3.826	0.341
U	CAU	-3.832	0.480
C	GGU	-3.833	0.423
C	CUC	-3.836	0.999
A	GGA	-3.837	0.835
A	AUG	-3.842	0.132
U	ACC	-3.853	0.966
U	ACA	-3.866	1.095
A	GCU	-3.870	1.275
A	CAA	-3.870	0.041
C	CUU	-3.883	0.164
A	ACA	-3.888	0.468
A	GUA	-3.894	1.099
U	GCG	-3.898	0.678
G	AUG	-3.900	0.137
G	UAG	-3.904	0.428
U	CAA	-3.909	0.431
G	AAC	-3.910	0.766
G	GUA	-3.929	1.013
C	GUG	-3.931	0.256
G	UAC	-3.934	0.450
C	ACA	-3.940	0.147
G	CAA	-3.940	0.333
U	AGA	-3.940	0.478
G	CUC	-3.945	1.172

C	ACA	55
C	ACC	1274
C	ACG	124
C	ACU	117
C	AGA	175
C	AGC	699
C	AGG	144
C	AGU	69
C	AUA	246
C	AUC	31
C	AUG	523
C	AUU	78
C	CAA	208
C	CAC	40
C	CAG	15
C	CAU	19
C	CCA	105
C	CCC	1640
C	CCG	33
C	CCU	60
C	CGA	17
C	CGC	70
C	CGG	9
C	CGU	79
C	CUA	2227
C	CUC	60
C	CUG	36
C	CUU	38
C	GAA	89
C	GAC	23
C	GAG	44
C	GAU	35
C	GCA	34
C	GCC	641
C	GCG	8
C	GCU	410
C	GGA	37
C	GGC	340
C	GGG	33
C	GGU	82
C	GUA	89
C	GUC	33
C	GUG	28
C	GUU	18
C	UAA	499
C	UAC	423
C	UAG	43
C	UAU	56
C	UCA	407
C	UCC	305229
C	UCG	99
C	UCU	11749
C	UGA	117
C	UGC	504
C	UGG	51
C	UGU	2239
C	UUA	772
C	UUC	404
C	UUG	27
C	UUU	84
G	AAA	87
G	AAC	45
G	AAG	145
G	AAU	41
G	ACA	76
G	ACC	27
G	ACG	24
G	ACU	51
G	AGA	81

G	CAG	-3.949	0.754
U	UGC	-3.949	0.844
U	UCG	-3.951	1.310
C	AGG	-3.955	0.526
U	GCU	-3.955	0.812
U	CUU	-3.958	0.464
A	GCA	-3.962	0.886
G	UUU	-3.985	0.392
A	UUG	-3.996	0.458
U	CCC	-3.999	0.651
A	AGG	-4.000	0.840
G	UUG	-4.006	0.492
G	CUA	-4.010	0.091
A	CUC	-4.011	0.742
A	CCA	-4.011	0.274
C	UAU	-4.014	0.702
C	GGG	-4.019	0.313
G	GCA	-4.022	1.069
C	AUC	-4.029	0.315
C	UUC	-4.037	0.989
C	GUC	-4.039	0.390
G	UGA	-4.039	1.188
C	CUG	-4.040	0.355
A	UUC	-4.045	0.697
U	GUU	-4.045	0.111
C	GAG	-4.052	0.299
C	CAC	-4.059	0.226
U	UGU	-4.065	0.694
U	CCU	-4.071	0.288
U	UGA	-4.076	0.487
U	GGG	-4.077	0.840
C	GUU	-4.078	0.249
C	UCG	-4.082	0.477
A	CAU	-4.088	1.294
C	CCG	-4.088	0.208
U	GGU	-4.091	0.171
G	CAC	-4.092	0.640
U	AGU	-4.099	0.541
A	CGC	-4.103	0.696
G	GUG	-4.103	0.696
U	GCA	-4.104	0.794
G	GUC	-4.111	0.245
G	ACC	-4.119	0.201
G	GCC	-4.125	0.236
U	CGC	-4.126	0.915
U	UGG	-4.129	0.333
C	CAA	-4.133	0.827
U	GCC	-4.136	0.810
G	CGG	-4.137	0.821
G	AAU	-4.140	0.235
A	AUC	-4.144	0.858
A	CAG	-4.148	0.364
G	CGU	-4.148	0.225
U	AGC	-4.150	0.978
C	CCU	-4.155	0.562
C	GAU	-4.164	0.205
G	GAU	-4.178	0.189
G	ACG	-4.180	0.221
G	AGC	-4.182	0.230
G	UCA	-4.182	0.306
G	CUU	-4.188	0.442
G	UCU	-4.194	0.285
G	CUG	-4.198	0.169
U	GAU	-4.210	0.161
G	GGG	-4.218	0.625
U	GUA	-4.225	0.592
C	GAC	-4.229	0.151
A	CUG	-4.230	0.223
G	UGU	-4.233	0.772

G	AGC	18
G	AGG	2647
G	AGU	361
G	AUA	26
G	AUC	27
G	AUG	37
G	AUU	271
G	CAA	55
G	CAC	42
G	CAG	72
G	CAU	85
G	CCA	7
G	CCC	9
G	CCG	14
G	CCU	43
G	CGA	17
G	CGC	48
G	CGG	20
G	CGU	39
G	CUA	35
G	CUC	42
G	CUG	28
G	CUU	12
G	GAA	173
G	GAC	43
G	GAG	80
G	GAU	32
G	GCA	30
G	GCC	34
G	GCG	17
G	GCU	5
G	GGA	4
G	GGC	12
G	GGG	9
G	GGU	6
G	GUA	20
G	GUC	37
G	GUG	14
G	GUU	4
G	UAA	234
G	UAC	35
G	UAG	22
G	UAU	107
G	UCA	50
G	UCC	137
G	UCG	7
G	UCU	46
G	UGA	33
G	UGC	20
G	UGG	36
G	UGU	14
G	UUA	96
G	UUC	146
G	UUG	23
G	UUU	21
U	AAA	211
U	AAC	353
U	AAG	5703
U	AAU	107
U	ACA	85
U	ACC	49
U	ACG	6865
U	ACU	68
U	AGA	23
U	AGC	29
U	AGG	292
U	AGU	22
U	AUA	191
U	AUC	65

A	GUU	-4.235	0.149
G	GCG	-4.237	0.634
A	GGG	-4.247	0.542
G	CAU	-4.262	0.612
A	AGU	-4.270	0.646
A	UCG	-4.292	0.563
A	CCC	-4.296	0.171
C	CGG	-4.296	0.368
A	GGU	-4.296	0.508
U	GUC	-4.296	0.413
G	UGC	-4.317	0.446
C	CGA	-4.341	0.046
G	CGA	-4.341	0.046
G	CGC	-4.344	0.480
C	CAG	-4.359	0.037
C	UAG	-4.359	0.456
G	CCU	-4.359	0.456
G	GAC	-4.359	0.456
A	ACG	-4.363	0.251
A	AGC	-4.370	0.480
U	CGU	-4.370	0.441
G	UGG	-4.385	0.417
A	GCG	-4.389	0.411
A	CUU	-4.393	0.404
A	GUC	-4.393	0.073
A	UAG	-4.416	0.371
C	UUG	-4.426	0.356
G	AUC	-4.426	0.356
C	GCG	-4.455	0.174
G	GGA	-4.455	0.617
A	UGC	-4.476	0.209
C	CAU	-4.476	0.289
A	GGC	-4.483	0.280
A	GCC	-4.491	0.450
G	CCG	-4.519	0.242
G	GCU	-4.529	0.300
A	UGG	-4.540	0.223
G	GGC	-4.540	0.223
U	GGC	-4.540	0.530
G	CCC	-4.580	0.203
G	CCA	-4.614	0.204
G	UCG	-4.614	0.204
U	GGA	-4.614	0.204
G	GGU	-4.635	0.213
A	CCG	-4.688	0.257
A	CGG	-4.688	0.257
A	CGU	-4.688	0.723
G	GUU	-4.688	0.257
U	CGA	-4.688	0.257
U	CGG	-4.724	0.301

U	AUG	9954
U	AUU	74
U	CAA	26
U	CAC	105
U	CAG	84
U	CAU	27
U	CCA	327
U	CCC	14
U	CCG	235
U	CCU	39
U	CGA	4
U	CGC	17
U	CGG	3
U	CGU	14
U	CUA	782
U	CUC	612
U	CUG	106
U	CUU	21
U	GAA	75
U	GAC	87
U	GAG	79
U	GAU	26
U	GCA	25
U	GCC	23
U	GCG	45
U	GCU	27
U	GGA	7
U	GGC	4
U	GGG	29
U	GGU	21
U	GUA	14
U	GUC	11
U	GUG	191
U	GUU	28
U	UAA	44
U	UAC	144
U	UAG	129
U	UAU	61
U	UCA	57
U	UCC	206
U	UCG	107
U	UCU	62
U	UGA	103
U	UGC	16
U	UGG	24
U	UGU	15
U	UUA	189
U	UUC	256
U	UUG	254
U	UUU	162

5'	3'	Score	SD
AA	GA	-1.536	1.141
GC	AA	-1.560	1.179
AA	AA	-1.580	0.980
UU	UU	-1.628	0.294
GA	GA	-2.005	1.052
GA	AA	-2.097	1.015
AA	CG	-2.219	0.600
UU	AU	-2.238	0.793
AU	UU	-2.294	0.783
AG	GA	-2.309	0.963
GC	GA	-2.336	0.681
AC	AA	-2.358	0.909
GA	CC	-2.370	0.655
AA	UU	-2.444	0.935
UA	AU	-2.581	0.445
UA	UU	-2.597	0.633
AA	AC	-2.602	0.435
CU	UU	-2.606	1.238
AU	AA	-2.616	0.302
UA	GA	-2.640	1.433
AU	UC	-2.643	1.037
CU	AA	-2.677	0.078
AU	CG	-2.683	1.851
UU	UC	-2.713	0.313
AA	AU	-2.718	0.842
AG	UC	-2.731	1.310
CU	UC	-2.734	0.743
UG	UU	-2.738	0.768
AA	CA	-2.754	0.536
UU	UA	-2.756	0.695
AG	AA	-2.760	0.753
UG	UG	-2.790	1.062
AC	UC	-2.817	0.597
AA	UC	-2.841	0.435
GA	UU	-2.848	0.496
AC	UU	-2.852	0.891
GA	UA	-2.873	0.694
AA	GC	-2.875	0.362
UU	GU	-2.894	0.763
CA	UU	-2.899	0.369
AG	CU	-2.902	0.358
AA	UA	-2.921	0.623
GC	AG	-2.935	1.147
CU	AU	-2.943	0.930
AU	AU	-2.946	0.599
UU	AA	-2.953	0.175
UA	CG	-2.958	0.467
CU	CG	-2.961	0.648
GA	AC	-2.975	0.513
GA	CA	-3.008	1.795
UG	CA	-3.016	0.713
UC	UU	-3.041	0.332
AG	UU	-3.042	0.933
AG	AU	-3.051	0.931
GU	AA	-3.055	0.473
UA	UA	-3.055	0.605
AU	UA	-3.075	0.278
GU	AU	-3.077	1.168
GG	CC	-3.079	0.899
AG	CA	-3.091	1.333
GU	UC	-3.106	0.455
GA	UC	-3.110	0.763
AA	AG	-3.134	0.991
GC	GC	-3.144	0.687
UA	UC	-3.147	1.118
UU	UG	-3.151	1.145
CC	CA	-3.167	0.377
GA	AU	-3.178	0.746

5'	3'	Total count
AA	AA	19196
AA	AC	1456
AA	AG	3949
AA	AU	378
AA	CA	2888
AA	CC	65
AA	CG	1713
AA	CU	218
AA	GA	377012
AA	GC	663
AA	GG	908
AA	GU	641
AA	UA	2206
AA	UC	630
AA	UG	180
AA	UU	2233
AC	AA	32802
AC	AC	266
AC	AG	373
AC	AU	283
AC	CA	13847
AC	CC	1253
AC	CG	383
AC	CU	165
AC	GA	430
AC	GC	47
AC	GG	30
AC	GU	497
AC	UA	2344
AC	UC	536
AC	UG	397
AC	UU	265
AG	AA	753
AG	AC	90
AG	AG	127
AG	AU	2058
AG	CA	173
AG	CC	332
AG	CG	84
AG	CU	578
AG	GA	2081
AG	GC	25
AG	GG	91
AG	GU	134
AG	UA	241
AG	UC	268
AG	UG	88
AG	UU	174
AU	AA	2927
AU	AC	68
AU	AG	78
AU	AU	591
AU	CA	808
AU	CC	112
AU	CG	3665
AU	CU	189
AU	GA	360
AU	GC	157
AU	GG	37
AU	GU	384
AU	UA	442
AU	UC	27831
AU	UG	52
AU	UU	2940
CA	AA	234
CA	AC	57
CA	AG	100
CA	AU	141

Supercategory	Total count
Intron	1989
Translation	964242
Cis -Reg	45305

UC	AA	-3.181	0.389
UC	GU	-3.192	0.363
AG	GG	-3.193	1.221
GA	GG	-3.199	1.112
AU	CU	-3.200	0.758
UA	UG	-3.201	0.682
GG	AA	-3.219	0.685
GA	CU	-3.226	0.642
AC	CG	-3.239	0.611
AG	CG	-3.239	1.383
AA	GU	-3.240	0.992
CA	AU	-3.271	0.988
CG	GA	-3.274	1.384
CA	CG	-3.278	0.194
UG	CG	-3.288	0.755
CC	UU	-3.289	0.829
UU	GA	-3.295	1.217
CU	AG	-3.304	0.544
AA	GG	-3.307	0.282
AC	GU	-3.308	0.413
UA	CU	-3.312	0.834
UU	CU	-3.315	0.989
CC	GU	-3.327	0.343
AU	CA	-3.328	0.393
AG	CC	-3.345	0.645
UA	AC	-3.350	0.574
AG	UA	-3.358	1.930
AC	AG	-3.370	0.224
GA	AG	-3.375	0.852
GA	UG	-3.382	0.815
AG	GU	-3.384	1.534
GU	UU	-3.385	0.760
CG	UC	-3.387	0.915
GA	CG	-3.389	0.633
CU	GU	-3.394	0.426
CA	CA	-3.397	0.850
UU	CG	-3.397	1.442
GA	GC	-3.402	0.934
GC	GG	-3.413	1.004
GG	UU	-3.421	0.885
CC	AA	-3.426	0.729
UC	AU	-3.427	0.311
UC	GA	-3.427	0.154
GU	GU	-3.429	0.471
UA	CC	-3.429	1.129
AG	AG	-3.454	1.362
GU	AC	-3.457	0.614
CA	UG	-3.465	0.711
AC	CA	-3.467	1.561
GC	AU	-3.468	0.333
AC	GA	-3.468	0.119
AA	UG	-3.469	0.489
GC	CA	-3.472	0.304
UG	AU	-3.473	0.609
AG	AC	-3.473	1.101
GU	GA	-3.474	0.797
CG	CA	-3.478	1.333
UG	UA	-3.480	0.963
UU	AG	-3.482	0.818
GC	UA	-3.485	0.360
AA	CU	-3.490	0.293
AC	UA	-3.491	1.278
UG	AA	-3.492	0.523
CG	UG	-3.502	0.829
UC	UG	-3.503	0.281
AU	GU	-3.503	0.092
UA	AA	-3.504	0.606
CG	CG	-3.504	0.085
UG	UC	-3.513	0.812

CA	CA	413
CA	CC	2
CA	CG	336
CA	CU	123
CA	GA	238
CA	GC	179
CA	GG	76
CA	GU	87
CA	UA	34
CA	UC	82
CA	UG	129
CA	UU	917
CC	AA	1220
CC	AC	15
CC	AG	223
CC	AU	38
CC	CA	1025
CC	CC	110
CC	CG	304
CC	CU	18
CC	GA	102
CC	GC	19
CC	GG	143
CC	GU	1119
CC	UA	129
CC	UC	51
CC	UG	40
CC	UU	318
CG	AA	89
CG	AC	7
CG	AG	155
CG	AU	69
CG	CA	65
CG	CC	28
CG	CG	339
CG	CU	20
CG	GA	115
CG	GC	12
CG	GG	10
CG	GU	79
CG	UA	74
CG	UC	76
CG	UG	148
CG	UU	65
CU	AA	2522
CU	AC	51
CU	AG	477
CU	AU	1027
CU	CA	99
CU	CC	50
CU	CG	4843
CU	CU	171
CU	GA	36
CU	GC	62
CU	GG	119
CU	GU	1208
CU	UA	52
CU	UC	12835
CU	UG	991
CU	UU	3702
GA	AA	64049
GA	AC	857
GA	AG	480
GA	AU	627
GA	CA	36516
GA	CC	1196
GA	CG	1130
GA	CU	746
GA	GA	146053

AU	GA	-3.520	0.920
CA	AA	-3.531	0.370
GU	GC	-3.545	0.876
GU	UA	-3.555	1.277
AC	UG	-3.558	0.146
CG	UU	-3.558	0.990
CG	AA	-3.559	0.706
AA	CC	-3.563	0.757
GA	GU	-3.588	1.186
GG	UC	-3.590	0.766
AC	AC	-3.603	1.340
UC	AG	-3.604	0.564
GG	UA	-3.606	0.630
AU	CC	-3.610	0.458
GG	GA	-3.614	0.638
CU	CU	-3.618	1.166
UC	CG	-3.625	0.114
CC	CG	-3.630	0.138
UC	CU	-3.636	0.244
CA	CU	-3.638	1.016
UG	CU	-3.642	0.703
CU	GG	-3.646	0.652
CC	CC	-3.647	0.369
UU	GG	-3.650	1.456
AC	CC	-3.655	0.798
CU	GC	-3.666	0.582
CA	GU	-3.676	0.486
AU	AC	-3.685	0.807
GC	UU	-3.686	0.090
UU	AC	-3.687	0.372
UA	CA	-3.689	0.705
CG	GU	-3.697	1.064
GC	AC	-3.698	0.128
CG	UA	-3.700	1.774
CC	GA	-3.703	0.302
AC	GG	-3.706	1.312
AU	AG	-3.716	0.462
CG	AU	-3.720	1.762
GC	GU	-3.720	0.104
CA	AG	-3.723	0.279
AG	UG	-3.728	1.464
GU	CU	-3.736	0.877
CA	GA	-3.738	0.688
CC	AG	-3.748	0.221
UA	GU	-3.765	0.143
UC	UA	-3.785	0.284
CC	GG	-3.786	0.166
AC	CU	-3.791	0.679
CG	AG	-3.800	0.679
CC	AU	-3.801	0.689
GU	CC	-3.811	0.615
CU	CC	-3.817	0.623
GG	GG	-3.828	0.680
UG	GC	-3.832	1.786
AU	UG	-3.838	0.478
UC	CA	-3.841	1.017
CG	CC	-3.845	1.302
GG	AU	-3.845	1.478
CU	UG	-3.848	1.008
CU	AC	-3.857	0.450
GG	CA	-3.860	0.686
CG	CU	-3.862	1.386
CA	GC	-3.864	0.348
CC	UA	-3.865	0.257
CA	UC	-3.870	0.251
GU	AG	-3.882	0.657
UG	AG	-3.888	0.513
GC	CC	-3.890	0.472
GU	GG	-3.893	0.864

GA	GC	1442
GA	GG	2268
GA	GU	1197
GA	UA	1916
GA	UC	671
GA	UG	558
GA	UU	694
GC	AA	46777
GC	AC	221
GC	AG	1354
GC	AU	172
GC	CA	244
GC	CC	45
GC	CG	12
GC	CU	36
GC	GA	1603
GC	GC	189
GC	GG	146
GC	GU	167
GC	UA	199
GC	UC	32
GC	UG	42
GC	UU	169
GG	AA	465
GG	AC	52
GG	AG	140
GG	AU	50
GG	CA	103
GG	CC	207
GG	CG	15
GG	CU	135
GG	GA	1005
GG	GC	20
GG	GG	128
GG	GU	65
GG	UA	155
GG	UC	173
GG	UG	72
GG	UU	190
GU	AA	1558
GU	AC	135
GU	AG	55
GU	AU	950
GU	CA	182
GU	CC	52
GU	CG	35
GU	CU	38
GU	GA	141
GU	GC	67
GU	GG	51
GU	GU	213
GU	UA	63
GU	UC	285
GU	UG	29
GU	UU	223
UA	AA	311
UA	AC	1148
UA	AG	57
UA	AU	1344
UA	CA	123
UA	CC	52
UA	CG	1799
UA	CU	174
UA	GA	54311
UA	GC	106
UA	GG	158
UA	GU	141
UA	UA	327
UA	UC	113

CU	CA	-3.904	0.269
GG	CU	-3.906	1.029
GG	UG	-3.913	0.706
GC	UC	-3.921	0.723
UU	CA	-3.929	0.329
CC	UG	-3.930	0.704
UA	GC	-3.941	1.028
UA	GG	-3.956	0.929
AC	GC	-3.957	0.380
CU	UA	-3.961	0.733
UG	CC	-3.961	0.343
UC	UC	-3.964	0.696
UC	GC	-3.979	0.452
UU	GC	-3.985	0.922
UC	GG	-3.987	0.922
UG	GU	-3.990	0.921
CA	GG	-3.990	0.346
UG	GA	-4.002	1.036
CC	UC	-4.003	0.362
AG	GC	-4.006	1.618
GC	CU	-4.025	0.437
AC	AU	-4.029	0.804
UU	CC	-4.031	0.499
CU	GA	-4.057	0.432
GU	CA	-4.093	0.751
UC	AC	-4.094	1.333
AU	GG	-4.097	0.440
AU	GC	-4.115	0.736
GG	AC	-4.117	0.927
GG	AG	-4.131	0.725
GU	UG	-4.134	0.485
CC	CU	-4.142	0.623
CC	GC	-4.159	0.585
GU	CG	-4.175	0.499
CA	UA	-4.180	0.949
GG	GC	-4.192	0.562
UC	CC	-4.229	0.887
CC	AC	-4.237	0.627
GG	GU	-4.242	0.682
UG	GG	-4.248	0.681
CA	AC	-4.260	0.679
UA	AG	-4.260	0.679
GC	UG	-4.304	0.680
CG	GC	-4.334	0.674
GC	CG	-4.334	1.050
UG	AC	-4.343	0.688
CG	AC	-4.367	1.278
GG	CG	-4.450	0.741
CG	GG	-4.507	0.785
CA	CC	-4.629	1.112

UA	UG	526
UA	UU	1533
UC	AA	1455
UC	AC	21
UC	AG	73
UC	AU	191
UC	CA	1042
UC	CC	11
UC	CG	184
UC	CU	139
UC	GA	425
UC	GC	134
UC	GG	127
UC	GU	1237
UC	UA	222
UC	UC	29
UC	UG	211
UC	UU	551
UG	AA	133
UG	AC	32
UG	AG	252
UG	AU	384
UG	CA	485
UG	CC	54
UG	CG	2270
UG	CU	58
UG	GA	70
UG	GC	49
UG	GG	62
UG	GU	125
UG	UA	389
UG	UC	83
UG	UG	4480
UG	UU	406
UU	AA	836
UU	AC	96
UU	AG	169
UU	AU	4389
UU	CA	115
UU	CC	30
UU	CG	7447
UU	CU	347
UU	GA	217
UU	GC	129
UU	GG	134
UU	GU	8002
UU	UA	575
UU	UC	1457
UU	UG	13631
UU	UU	23685

5'	3'	Score	SD
CAA	A	-1.627	1.660
GGG	G	-2.081	1.584
UAA	A	-2.286	0.488
UAA	G	-2.311	0.778
CAC	A	-2.356	0.788
UAA	U	-2.416	0.980
UAA	C	-2.465	1.775
CAA	C	-2.493	1.339
AAA	A	-2.560	0.925
UUA	A	-2.593	0.853
UUA	G	-2.597	0.231
UUA	U	-2.624	0.950
ACC	G	-2.677	1.071
CCA	A	-2.810	0.221
AAU	U	-2.811	1.331
AGA	G	-2.845	0.524
ACA	A	-2.883	1.005
CCC	A	-2.918	0.572
AAA	G	-2.924	0.816
UUC	U	-2.930	1.248
CAA	G	-2.930	1.460
AUU	U	-2.932	0.772
AAU	A	-2.942	0.978
CUC	A	-2.964	1.710
GAA	A	-2.986	0.757
AAG	A	-2.990	1.105
UAG	G	-2.999	1.216
AAA	C	-3.003	1.622
AUU	A	-3.028	1.239
UUU	U	-3.029	1.199
UCA	A	-3.033	1.009
CAA	U	-3.033	1.291
GGA	G	-3.035	0.179
UGC	C	-3.042	2.091
CGG	A	-3.045	0.827
ACU	U	-3.060	0.496
AGG	G	-3.070	0.928
AUA	G	-3.083	0.854
CCU	A	-3.118	0.801
UAC	C	-3.119	1.470
UAC	G	-3.120	0.607
CUA	G	-3.136	1.161
UGC	U	-3.148	1.475
GAA	G	-3.153	0.322
CCU	C	-3.161	1.433
UUC	C	-3.163	1.649
ACA	G	-3.166	0.769
AAG	C	-3.168	1.017
AAC	G	-3.171	1.621
UAG	C	-3.184	0.869
GGA	U	-3.190	1.367
UGC	G	-3.197	1.184
AAA	U	-3.200	0.900
UAG	A	-3.211	0.415
GAG	G	-3.213	0.134
UAU	U	-3.221	1.258
ACA	U	-3.233	0.780
UUA	C	-3.255	1.108
CGA	A	-3.257	0.152
AAG	G	-3.259	0.898
CUA	A	-3.272	1.195
UGU	A	-3.277	1.188
AUU	G	-3.278	0.683
CGA	G	-3.288	1.001
CGC	A	-3.303	1.456
AGU	U	-3.318	0.916
UGG	A	-3.329	0.538
GCU	U	-3.339	0.909

5'	3'	Total count
AAA	A	184
AAA	C	118
AAA	G	123
AAA	U	83
AAC	A	13
AAC	C	5
AAC	G	117
AAC	U	35
AAG	A	73
AAG	C	60
AAG	G	38
AAG	U	59
AAU	A	81
AAU	C	15
AAU	G	26
AAU	U	81
ACA	A	161
ACA	C	51
ACA	G	118
ACA	U	169
ACC	A	6
ACC	C	10
ACC	G	462
ACC	U	3
ACG	A	6
ACG	C	9
ACG	G	9
ACG	U	53
ACU	A	11
ACU	C	9
ACU	G	136
ACU	U	170
AGA	A	28
AGA	C	8
AGA	G	181
AGA	U	24
AGC	A	18
AGC	C	32
AGC	G	50
AGC	U	10
AGG	A	10
AGG	C	3
AGG	G	173
AGG	U	14
AGU	A	12
AGU	C	20
AGU	G	22
AGU	U	41
AUA	A	102
AUA	C	6
AUA	G	157
AUA	U	125
AUC	A	10
AUC	C	14
AUC	G	49
AUC	U	9
AUG	A	40
AUG	C	2
AUG	G	30
AUG	U	127
AUU	A	68
AUU	C	21
AUU	G	81
AUU	U	140
CAA	A	374564
CAA	C	602
CAA	G	529
CAA	U	127

Supercategory	Total count
Intron	1087
Translation	413069
Cis -Reg	12387

GGA	A	-3.354	0.559
CUU	G	-3.355	1.083
GGG	A	-3.360	0.093
UGA	A	-3.373	0.638
AUA	A	-3.380	1.166
AUA	U	-3.385	1.093
UUU	G	-3.393	1.203
AUU	C	-3.395	1.145
UGG	G	-3.396	0.515
AUC	G	-3.397	0.954
UAG	U	-3.403	0.960
CCU	U	-3.406	1.498
UGC	A	-3.409	1.113
GAG	A	-3.410	0.112
GAU	U	-3.421	1.007
ACA	C	-3.424	0.692
UGA	U	-3.430	1.130
GUU	U	-3.439	1.323
UUC	G	-3.449	1.226
CAG	A	-3.452	0.890
UAC	U	-3.453	0.588
AGA	U	-3.455	0.872
GAG	U	-3.462	0.736
AAG	U	-3.468	1.204
GAC	A	-3.477	1.569
GAA	U	-3.489	0.968
GGA	C	-3.490	0.803
CCC	G	-3.492	1.660
CCA	G	-3.492	1.109
CCC	U	-3.496	1.494
AGC	G	-3.498	0.566
GUU	C	-3.507	1.227
CAG	C	-3.509	0.568
UGU	G	-3.510	0.158
AAC	U	-3.513	0.812
AGC	A	-3.515	1.627
AGA	A	-3.520	0.809
UAC	A	-3.525	0.770
GCA	G	-3.532	0.941
UGG	C	-3.532	1.049
CUU	A	-3.540	0.919
CUG	G	-3.545	0.925
UUG	U	-3.549	0.761
CAU	A	-3.556	0.753
AGU	G	-3.558	1.042
AUC	C	-3.558	1.459
CAG	G	-3.569	1.053
CAC	U	-3.572	0.659
CCU	G	-3.572	1.133
UCG	U	-3.575	1.472
CAU	G	-3.582	1.060
CGC	C	-3.586	1.614
AUG	U	-3.589	0.297
AGU	A	-3.595	1.297
AAU	G	-3.600	0.849
AAU	C	-3.609	1.374
UCC	G	-3.609	1.260
GUG	G	-3.610	0.653
GGG	U	-3.617	1.350
GUA	C	-3.621	0.326
CGA	C	-3.636	0.681
ACG	U	-3.646	0.287
CUA	C	-3.647	0.368
UGA	C	-3.651	1.075
UGU	U	-3.655	0.828
CUA	U	-3.658	1.181
UCA	G	-3.663	0.914
UUC	A	-3.663	1.425
CAG	U	-3.677	0.921

CAC	A	14745
CAC	C	19
CAC	G	16
CAC	U	31
CAG	A	980
CAG	C	75
CAG	G	52
CAG	U	43
CAU	A	477
CAU	C	10
CAU	G	48
CAU	U	11
CCA	A	445
CCA	C	4
CCA	G	20
CCA	U	12
CCC	A	145
CCC	C	3
CCC	G	20
CCC	U	18
CCG	A	11
CCG	C	6
CCG	G	3
CCG	U	1
CCU	A	65
CCU	C	50
CCU	G	15
CCU	U	21
CGA	A	346
CGA	C	32
CGA	G	89
CGA	U	17
CGC	A	190
CGC	C	22
CGC	G	10
CGC	U	26
CGG	A	105
CGG	C	1
CGG	G	8
CGG	U	7
CGU	A	3
CGU	C	3
CGU	G	14
CGU	U	2
CUA	A	171
CUA	C	39
CUA	G	518
CUA	U	26
CUC	A	85
CUC	C	13
CUC	G	17
CUC	U	14
CUG	A	27
CUG	C	19
CUG	G	28
CUG	U	12
CUU	A	29
CUU	C	30
CUU	G	46
CUU	U	7
GAA	A	93
GAA	C	11
GAA	G	208
GAA	U	21
GAC	A	40
GAC	C	13
GAC	G	21
GAC	U	5
GAG	A	124

AGU	C	-3.691	0.662
UAU	A	-3.693	1.045
GGU	C	-3.696	1.051
CAC	C	-3.701	0.973
GUG	A	-3.701	0.544
UCU	U	-3.701	0.756
UCU	A	-3.703	1.338
UGA	G	-3.709	0.780
UUG	C	-3.710	1.058
CUC	G	-3.713	1.396
GAC	C	-3.717	1.611
GUG	C	-3.717	0.776
ACG	C	-3.717	1.240
GUC	U	-3.717	1.138
ACU	G	-3.737	0.573
UCU	G	-3.742	0.961
GUC	G	-3.747	1.035
CGC	U	-3.753	1.308
GCU	C	-3.753	1.291
CGA	U	-3.754	1.188
GGC	C	-3.754	1.086
AUC	U	-3.762	1.199
UCA	C	-3.765	0.978
UCA	U	-3.773	0.385
GGU	G	-3.777	0.856
UUU	A	-3.779	0.989
CUC	C	-3.786	1.422
AGC	C	-3.791	1.846
CGU	G	-3.791	1.223
CUC	U	-3.791	1.564
GGC	A	-3.791	0.874
GGU	U	-3.791	1.223
GUA	A	-3.794	1.001
CUG	C	-3.802	1.008
GAG	C	-3.802	1.220
GAA	C	-3.805	0.894
AGA	C	-3.810	1.013
CCA	U	-3.810	0.806
GUA	G	-3.810	0.830
CUG	A	-3.816	0.834
GCA	A	-3.819	1.023
AUC	A	-3.821	0.917
CAU	C	-3.821	0.917
CUG	U	-3.821	1.254
CAU	U	-3.831	0.842
UUG	A	-3.848	0.529
UGU	C	-3.853	1.402
AAC	A	-3.863	0.626
ACU	C	-3.884	0.934
UCC	U	-3.884	0.934
ACU	A	-3.890	0.672
UAU	G	-3.890	0.530
GUG	U	-3.893	0.545
CAC	G	-3.893	0.895
UCG	G	-3.893	0.895
UGG	U	-3.900	0.532
UUG	G	-3.903	0.532
ACC	C	-3.906	0.699
AGG	A	-3.906	0.699
CGC	G	-3.906	0.699
AUG	A	-3.913	0.535
CCG	C	-3.913	1.051
GAU	A	-3.913	0.913
GAU	C	-3.921	1.260
UCG	A	-3.924	0.924
AAC	C	-3.950	1.106
AUG	G	-3.954	0.550
CUU	C	-3.954	0.550
GUA	U	-3.964	0.555

GAG	C	7
GAG	G	253
GAG	U	40
GAU	A	14
GAU	C	8
GAU	G	19
GAU	U	138
GCA	A	17
GCA	C	12
GCA	G	35
GCA	U	21
GCC	A	9
GCC	C	3
GCC	G	3
GCC	U	0
GCG	A	8
GCG	C	4
GCG	G	8
GCG	U	8
GCU	A	4
GCU	C	8
GCU	G	6
GCU	U	34
GGA	A	68
GGA	C	251
GGA	G	396
GGA	U	160
GGC	A	12
GGC	C	9
GGC	G	7
GGC	U	8
GGG	A	148
GGG	C	7
GGG	G	5932
GGG	U	25
GGU	A	6
GGU	C	11
GGU	G	13
GGU	U	14
GUA	A	20
GUA	C	46
GUA	G	28
GUA	U	28
GUC	A	6
GUC	C	4
GUC	G	11
GUC	U	11
GUG	A	23
GUG	C	19
GUG	G	38
GUG	U	16
GUU	A	7
GUU	C	47
GUU	G	11
GUU	U	18
UAA	A	826
UAA	C	1887
UAA	G	550
UAA	U	541
UAC	A	42
UAC	C	43
UAC	G	89
UAC	U	47
UAG	A	740
UAG	C	167
UAG	G	1495
UAG	U	1374
UAU	A	29
UAU	C	3

AGC	U	-3.964	0.652
CGG	U	-3.969	0.805
GCC	A	-3.980	0.677
ACG	G	-3.980	0.981
CCA	C	-3.998	1.181
UUU	C	-3.998	1.403
ACC	A	-3.998	0.854
GCG	A	-3.998	0.705
GGC	U	-3.998	1.001
GUC	A	-3.998	0.854
GAC	G	-4.005	0.581
GCA	U	-4.005	0.581
GGC	G	-4.019	0.738
GGG	C	-4.019	0.738
CUU	U	-4.019	1.024
GUU	A	-4.019	1.024
GAU	G	-4.019	0.591
UCG	C	-4.035	1.398
GAC	U	-4.035	0.916
UCC	C	-4.035	0.916
AUA	C	-4.043	1.053
GCU	G	-4.043	1.053
AGG	U	-4.062	0.628
CCC	C	-4.072	1.297
UCC	A	-4.083	0.999
GCA	C	-4.083	0.649
CCG	A	-4.096	0.662
GUU	G	-4.096	0.662
GCG	C	-4.109	0.883
GCU	A	-4.109	1.133
CGG	G	-4.139	0.710
GCG	G	-4.139	0.710
GCG	U	-4.139	0.710
AGG	C	-4.157	0.963
CGU	A	-4.157	0.963
CGU	C	-4.157	0.963
UAU	C	-4.157	1.125
UCU	C	-4.157	0.963
CCG	G	-4.157	1.580
ACG	A	-4.178	0.756
GGU	A	-4.178	0.756
CGU	U	-4.231	1.086
AUG	C	-4.231	1.298
GUC	C	-4.231	0.825
ACC	U	-4.268	0.874
GCC	C	-4.268	0.874
GCC	G	-4.268	0.874
CCG	U	-4.390	1.051
CGG	C	-4.390	1.051
GCC	U	-4.549	1.297

UAU	G	47
UAU	U	62
UCA	A	125
UCA	C	24
UCA	G	47
UCA	U	36
UCC	A	4
UCC	C	5
UCC	G	15
UCC	U	9
UCG	A	13
UCG	C	5
UCG	G	16
UCG	U	28
UCU	A	18
UCU	C	3
UCU	G	28
UCU	U	21
UGA	A	71
UGA	C	13
UGA	G	56
UGA	U	20
UGC	A	68
UGC	C	1113
UGC	G	42
UGC	U	332
UGG	A	256
UGG	C	20
UGG	G	58
UGG	U	44
UGU	A	54
UGU	C	21
UGU	G	96
UGU	U	21
UUA	A	246
UUA	C	30
UUA	G	1336
UUA	U	5425
UUC	A	11
UUC	C	43
UUC	G	27
UUC	U	64
UUG	A	63
UUG	C	26
UUG	G	43
UUG	U	500
UUU	A	22
UUU	C	4
UUU	G	86
UUU	U	153

Table S21. Terminal loops-size

Range 4.102 * Median = max score - range/2
Median -3.015 * Centered score = score - range

Loop size	Score	SD	Centered Score
5	-0.964	0.384	2.05
4	-1.094	0.409	1.92
3	-1.116	0.506	1.90
8	-1.171	0.532	1.84
6	-1.310	0.467	1.70
7	-1.490	0.442	1.52
10	-1.510	0.565	1.50
9	-1.707	0.447	1.31
12	-1.876	0.400	1.14
11	-1.909	0.959	1.11
14	-2.163	0.625	0.85
13	-2.176	0.636	0.84
2	-2.318	0.671	0.70
20	-2.455	0.594	0.56
15	-2.486	0.888	0.53
16	-2.495	0.998	0.52
1	-2.533	0.752	0.48
18	-2.592	0.756	0.42
19	-2.704	0.490	0.31
17	-2.715	0.929	0.30
21	-2.810	0.930	0.20
22	-2.880	0.563	0.13
23	-2.960	0.664	0.05
25	-3.014	0.866	0.00
24	-3.081	0.940	-0.07
29	-3.162	0.944	-0.15
26	-3.192	0.909	-0.18
28	-3.209	0.868	-0.19
35	-3.235	0.663	-0.22
31	-3.266	0.927	-0.25
27	-3.306	1.026	-0.29
37	-3.325	0.724	-0.31
32	-3.349	0.950	-0.33
33	-3.350	0.857	-0.34
30	-3.357	1.017	-0.34
36	-3.389	0.863	-0.37
42	-3.392	0.986	-0.38
34	-3.403	0.777	-0.39
46	-3.450	1.136	-0.44
41	-3.464	0.944	-0.45
39	-3.482	0.924	-0.47
38	-3.507	1.113	-0.49
43	-3.529	0.924	-0.51
59	-3.537	1.108	-0.52
48	-3.540	1.074	-0.53
47	-3.558	0.881	-0.54
51	-3.560	1.068	-0.55
45	-3.561	1.064	-0.55
50	-3.567	1.070	-0.55
49	-3.580	1.052	-0.57
44	-3.582	1.047	-0.57
55	-3.608	0.902	-0.59
40	-3.609	1.046	-0.59
58	-3.609	1.105	-0.59
54	-3.634	1.064	-0.62
52	-3.642	1.024	-0.63
61	-3.644	1.239	-0.63
53	-3.665	0.999	-0.65
57	-3.678	1.170	-0.66
60	-3.723	1.149	-0.71
62	-3.723	1.253	-0.71
56	-3.767	1.102	-0.75
69	-3.795	1.152	-0.78
68	-3.801	1.148	-0.79
63	-3.819	1.116	-0.80

Loop size	Total loop count
5	112397
8	97138
4	80510
3	80337
6	49580
7	29460
11	24911
10	24090
9	15397
13	14422
2	14079
97	13300
12	12315
95	11457
14	7653
96	7650
16	6290
21	6040
15	5413
25	5303
17	5107
94	4604
18	4496
1	4391
98	3099
20	2927
24	2340
19	2222
23	1883
22	1787
27	1776
29	1749
26	1722
62	1710
59	1667
93	1627
28	1538
61	1481
58	1381
30	1230
32	1079
31	1049
37	1044
57	1024
99	969
42	942
92	920
33	916
60	904
41	881
43	852
34	848
40	847
66	829
68	827
70	825
35	823
63	821
64	793
36	757
69	748
46	744
90	742
86	736
45	729

Category	Total loop count
antisense	138087
CD-box	48163
CRISPR	22066
Gene	249573
HACA-box	110779
miRNA	136398
scaRNA	4071

65	-3.830	1.133	-0.82
70	-3.846	1.162	-0.83
66	-3.855	1.179	-0.84
64	-3.859	1.142	-0.84
67	-3.867	1.079	-0.85
97	-3.872	1.692	-0.86
72	-3.932	1.116	-0.92
73	-3.958	1.147	-0.94
77	-3.966	1.128	-0.95
84	-3.978	1.111	-0.96
71	-3.997	1.069	-0.98
96	-4.015	1.505	-1.00
83	-4.016	1.110	-1.00
86	-4.017	1.180	-1.00
88	-4.023	1.095	-1.01
85	-4.024	1.152	-1.01
74	-4.027	1.152	-1.01
95	-4.034	1.607	-1.02
80	-4.044	1.105	-1.03
94	-4.046	1.413	-1.03
79	-4.059	1.177	-1.04
75	-4.067	1.207	-1.05
89	-4.071	1.207	-1.06
92	-4.071	1.258	-1.06
78	-4.093	1.200	-1.08
90	-4.098	1.308	-1.08
98	-4.098	1.380	-1.08
82	-4.111	1.126	-1.10
76	-4.121	1.195	-1.11
93	-4.134	1.268	-1.12
87	-4.137	1.203	-1.12
81	-4.146	1.137	-1.13
101	-4.181	1.059	-1.17
91	-4.189	1.165	-1.17
100	-4.220	1.096	-1.21
99	-4.246	1.275	-1.23
107	-4.278	0.992	-1.26
102	-4.395	0.916	-1.38
110	-4.425	0.817	-1.41
104	-4.463	0.929	-1.45
108	-4.477	0.838	-1.46
111	-4.520	0.852	-1.51
112	-4.524	0.819	-1.51
114	-4.527	0.729	-1.51
119	-4.537	0.736	-1.52
109	-4.538	0.759	-1.52
103	-4.539	1.003	-1.52
105	-4.543	0.995	-1.53
113	-4.547	0.777	-1.53
118	-4.552	0.880	-1.54
106	-4.568	0.741	-1.55
115	-4.592	0.930	-1.58
116	-4.592	0.999	-1.58
127	-4.596	0.826	-1.58
117	-4.614	1.001	-1.60
122	-4.645	0.862	-1.63
123	-4.668	0.894	-1.65
137	-4.707	0.906	-1.69
140	-4.715	0.793	-1.70
141	-4.725	0.772	-1.71
124	-4.730	0.665	-1.72
129	-4.730	0.650	-1.72
169	-4.735	0.927	-1.72
125	-4.745	0.799	-1.73
120	-4.749	0.826	-1.73
139	-4.749	0.891	-1.73
135	-4.793	0.807	-1.78
131	-4.798	0.620	-1.78
149	-4.798	0.573	-1.78

56	718
73	701
47	692
38	687
39	685
72	679
50	663
44	655
48	649
74	628
51	607
67	604
65	591
77	586
85	572
75	536
89	534
91	527
71	523
49	521
52	508
87	505
76	503
84	503
78	481
54	476
55	442
83	440
88	432
80	431
53	422
79	368
100	362
81	337
82	328
101	273
107	160
102	126
103	103
169	103
104	90
117	71
105	68
116	68
110	61
108	59
118	51
111	49
115	45
112	41
109	35
127	35
137	34
113	32
123	32
114	29
119	29
122	29
139	28
136	27
106	26
403	22
511	22
160	19
120	18
172	18
301	18
140	16
125	15

121	-4.809	0.780	-1.79
147	-4.809	0.703	-1.79
184	-4.809	0.780	-1.79
128	-4.817	0.715	-1.80
136	-4.817	0.927	-1.80
143	-4.824	0.628	-1.81
132	-4.830	0.670	-1.81
162	-4.830	0.745	-1.81
403	-4.830	0.752	-1.81
511	-4.830	0.752	-1.81
138	-4.838	0.731	-1.82
160	-4.838	0.738	-1.82
172	-4.842	0.733	-1.83
301	-4.842	0.733	-1.83
142	-4.849	0.686	-1.83
188	-4.877	0.538	-1.86
126	-4.890	0.793	-1.88
178	-4.898	0.575	-1.88
133	-4.907	0.766	-1.89
134	-4.917	0.750	-1.90
144	-4.917	0.750	-1.90
205	-4.917	0.561	-1.90
303	-4.917	0.637	-1.90
491	-4.917	0.637	-1.90
150	-4.929	0.523	-1.91
159	-4.929	0.626	-1.91
164	-4.929	0.523	-1.91
168	-4.929	0.626	-1.91
179	-4.929	0.622	-1.91
193	-4.929	0.732	-1.91
194	-4.929	0.622	-1.91
212	-4.929	0.626	-1.91
228	-4.929	0.523	-1.91
369	-4.929	0.626	-1.91
146	-4.945	0.614	-1.93
265	-4.945	0.614	-1.93
130	-4.966	0.684	-1.95
148	-4.966	0.684	-1.95
151	-4.966	0.684	-1.95
152	-4.966	0.684	-1.95
166	-4.966	0.602	-1.95
177	-4.966	0.602	-1.95
185	-4.966	0.684	-1.95
190	-4.966	0.602	-1.95
216	-4.966	0.549	-1.95
288	-4.966	0.602	-1.95
299	-4.966	0.602	-1.95
370	-4.966	0.602	-1.95
145	-4.998	0.652	-1.98
154	-4.998	0.594	-1.98
156	-4.998	0.558	-1.98
157	-4.998	0.594	-1.98
163	-4.998	0.594	-1.98
165	-4.998	0.652	-1.98
167	-4.998	0.594	-1.98
170	-4.998	0.558	-1.98
173	-4.998	0.594	-1.98
176	-4.998	0.558	-1.98
181	-4.998	0.594	-1.98
191	-4.998	0.652	-1.98
195	-4.998	0.558	-1.98
199	-4.998	0.594	-1.98
202	-4.998	0.558	-1.98
217	-4.998	0.558	-1.98
231	-4.998	0.558	-1.98
233	-4.998	0.594	-1.98
245	-4.998	0.558	-1.98
247	-4.998	0.558	-1.98
268	-4.998	0.558	-1.98

141	15
135	14
121	11
184	11
124	10
129	10
126	8
162	8
128	7
138	7
147	7
132	6
133	6
142	6
143	6
131	5
134	5
144	5
149	5
205	5
303	5
491	5
159	4
168	4
188	4
193	4
212	4
369	4
146	3
178	3
265	3
130	2
148	2
150	2
151	2
152	2
164	2
166	2
177	2
179	2
185	2
190	2
194	2
216	2
228	2
288	2
299	2
370	2
145	1
154	1
156	1
157	1
163	1
165	1
167	1
170	1
173	1
176	1
181	1
191	1
195	1
199	1
202	1
217	1
231	1
233	1
245	1
247	1
268	1

271	-4.998	0.558	-1.98
272	-4.998	0.594	-1.98
277	-4.998	0.594	-1.98
294	-4.998	0.558	-1.98
321	-4.998	0.594	-1.98
485	-4.998	0.594	-1.98
153	-5.066	0.616	-2.05
155	-5.066	0.616	-2.05
158	-5.066	0.616	-2.05
161	-5.066	0.616	-2.05
171	-5.066	0.616	-2.05
174	-5.066	0.616	-2.05
175	-5.066	0.616	-2.05
180	-5.066	0.616	-2.05
182	-5.066	0.616	-2.05
183	-5.066	0.616	-2.05
186	-5.066	0.616	-2.05
187	-5.066	0.616	-2.05
189	-5.066	0.616	-2.05
192	-5.066	0.616	-2.05
196	-5.066	0.616	-2.05
197	-5.066	0.616	-2.05
198	-5.066	0.616	-2.05
200	-5.066	0.616	-2.05
201	-5.066	0.616	-2.05
203	-5.066	0.616	-2.05
204	-5.066	0.616	-2.05
206	-5.066	0.616	-2.05
207	-5.066	0.616	-2.05
208	-5.066	0.616	-2.05
209	-5.066	0.616	-2.05
210	-5.066	0.616	-2.05
211	-5.066	0.616	-2.05
213	-5.066	0.616	-2.05
214	-5.066	0.616	-2.05
215	-5.066	0.616	-2.05
218	-5.066	0.616	-2.05
219	-5.066	0.616	-2.05
220	-5.066	0.616	-2.05
221	-5.066	0.616	-2.05
222	-5.066	0.616	-2.05
223	-5.066	0.616	-2.05
224	-5.066	0.616	-2.05
225	-5.066	0.616	-2.05
226	-5.066	0.616	-2.05
227	-5.066	0.616	-2.05
229	-5.066	0.616	-2.05
230	-5.066	0.616	-2.05
232	-5.066	0.616	-2.05
234	-5.066	0.616	-2.05
235	-5.066	0.616	-2.05
236	-5.066	0.616	-2.05
237	-5.066	0.616	-2.05
238	-5.066	0.616	-2.05
239	-5.066	0.616	-2.05
240	-5.066	0.616	-2.05
241	-5.066	0.616	-2.05
242	-5.066	0.616	-2.05
243	-5.066	0.616	-2.05
244	-5.066	0.616	-2.05
246	-5.066	0.616	-2.05
248	-5.066	0.616	-2.05
249	-5.066	0.616	-2.05
250	-5.066	0.616	-2.05
251	-5.066	0.616	-2.05
252	-5.066	0.616	-2.05
253	-5.066	0.616	-2.05
254	-5.066	0.616	-2.05
255	-5.066	0.616	-2.05

271	1
272	1
277	1
294	1
321	1
485	1
153	0
155	0
158	0
161	0
171	0
174	0
175	0
180	0
182	0
183	0
186	0
187	0
189	0
192	0
196	0
197	0
198	0
200	0
201	0
203	0
204	0
206	0
207	0
208	0
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210	0
211	0
213	0
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215	0
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219	0
220	0
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222	0
223	0
224	0
225	0
226	0
227	0
229	0
230	0
232	0
234	0
235	0
236	0
237	0
238	0
239	0
240	0
241	0
242	0
243	0
244	0
246	0
248	0
249	0
250	0
251	0
252	0
253	0
254	0
255	0

Range 4.534 * Median = max score - range/2
Median -2.442 * Centered score = score - range

Bulge size	Score	SD	Centered Score
1	-0.175	0.141	2.27
2	-0.889	0.337	1.55
3	-1.298	0.530	1.14
4	-2.202	1.033	0.24
5	-2.316	0.629	0.13
6	-2.625	1.192	-0.18
7	-2.832	0.638	-0.39
9	-3.106	0.355	-0.66
8	-3.179	0.905	-0.74
10	-3.245	0.606	-0.80
11	-3.563	0.639	-1.12
13	-3.647	0.588	-1.20
12	-3.668	0.611	-1.23
14	-3.755	0.723	-1.31
15	-3.794	0.640	-1.35
16	-3.931	0.616	-1.49
20	-3.969	0.813	-1.53
18	-4.041	0.590	-1.60
17	-4.136	0.585	-1.69
25	-4.147	0.556	-1.71
26	-4.175	0.747	-1.73
24	-4.255	0.712	-1.81
22	-4.263	0.651	-1.82
28	-4.264	0.659	-1.82
47	-4.272	1.246	-1.83
23	-4.310	0.650	-1.87
21	-4.334	0.666	-1.89
38	-4.341	0.678	-1.90
27	-4.346	0.583	-1.90
37	-4.358	0.658	-1.92
29	-4.375	0.659	-1.93
35	-4.388	0.664	-1.95
34	-4.392	0.673	-1.95
32	-4.410	0.681	-1.97
19	-4.432	0.774	-1.99
30	-4.433	0.663	-1.99
40	-4.433	0.757	-1.99
31	-4.450	0.893	-2.01
33	-4.452	0.753	-2.01
44	-4.458	0.738	-2.02
39	-4.473	0.740	-2.03
41	-4.492	0.746	-2.05
46	-4.500	1.044	-2.06
48	-4.520	0.848	-2.08
43	-4.541	0.777	-2.10
49	-4.541	0.777	-2.10
51	-4.541	0.777	-2.10
52	-4.541	0.829	-2.10
63	-4.541	0.989	-2.10
74	-4.541	0.732	-2.10
36	-4.550	0.733	-2.11
50	-4.550	0.978	-2.11
121	-4.550	0.733	-2.11
73	-4.560	0.736	-2.12
65	-4.573	0.807	-2.13
61	-4.588	0.748	-2.15
72	-4.588	0.748	-2.15
76	-4.588	0.748	-2.15
99	-4.588	0.748	-2.15
117	-4.588	0.748	-2.15
119	-4.588	0.748	-2.15
56	-4.609	0.762	-2.17
58	-4.609	0.762	-2.17
116	-4.609	0.762	-2.17
42	-4.641	0.790	-2.20

Bulge size	Total bulge count
1	355822
2	87253
3	74274
4	22261
6	4941
5	3906
8	1265
7	1137
10	1026
9	578
15	249
11	233
47	191
14	182
12	167
13	166
18	104
20	89
16	86
24	73
17	64
26	51
19	43
25	40
22	29
21	27
32	21
28	20
35	19
29	18
23	16
27	14
46	14
37	12
38	11
30	10
40	10
44	10
31	8
34	8
39	8
63	7
74	7
36	6
41	6
50	6
121	6
33	5
73	5
48	4
43	3
49	3
51	3
52	3
61	3
72	3
76	3
99	3
117	3
119	3
56	2
58	2
65	2
116	2
42	1

Category	Total bulge count
antisense	44465
CD-box	23212
CRISPR	1121
Gene	312059
HACA-box	86487
miRNA	84506
scaRNA	2714

45	-4.641	0.896	-2.20
53	-4.641	0.790	-2.20
55	-4.641	0.790	-2.20
57	-4.641	0.896	-2.20
59	-4.641	0.790	-2.20
60	-4.641	0.896	-2.20
62	-4.641	0.790	-2.20
66	-4.641	0.896	-2.20
69	-4.641	0.896	-2.20
70	-4.641	0.790	-2.20
77	-4.641	0.790	-2.20
78	-4.641	0.790	-2.20
79	-4.641	0.790	-2.20
98	-4.641	0.790	-2.20
109	-4.641	0.790	-2.20
145	-4.641	0.790	-2.20
181	-4.641	0.790	-2.20
54	-4.709	0.874	-2.27
64	-4.709	0.874	-2.27
67	-4.709	0.874	-2.27
68	-4.709	0.874	-2.27
71	-4.709	0.874	-2.27
75	-4.709	0.874	-2.27
80	-4.709	0.874	-2.27
81	-4.709	0.874	-2.27
82	-4.709	0.874	-2.27
83	-4.709	0.874	-2.27
84	-4.709	0.874	-2.27
85	-4.709	0.874	-2.27
86	-4.709	0.874	-2.27
87	-4.709	0.874	-2.27
88	-4.709	0.874	-2.27
89	-4.709	0.874	-2.27
90	-4.709	0.874	-2.27
91	-4.709	0.874	-2.27
92	-4.709	0.874	-2.27
93	-4.709	0.874	-2.27
94	-4.709	0.874	-2.27
95	-4.709	0.874	-2.27
96	-4.709	0.874	-2.27
97	-4.709	0.874	-2.27
100	-4.709	0.874	-2.27
101	-4.709	0.874	-2.27
102	-4.709	0.874	-2.27
103	-4.709	0.874	-2.27
104	-4.709	0.874	-2.27
105	-4.709	0.874	-2.27
106	-4.709	0.874	-2.27
107	-4.709	0.874	-2.27
108	-4.709	0.874	-2.27
110	-4.709	0.874	-2.27
111	-4.709	0.874	-2.27
112	-4.709	0.874	-2.27
113	-4.709	0.874	-2.27
114	-4.709	0.874	-2.27
115	-4.709	0.874	-2.27
118	-4.709	0.874	-2.27
120	-4.709	0.874	-2.27
122	-4.709	0.874	-2.27
123	-4.709	0.874	-2.27
124	-4.709	0.874	-2.27
125	-4.709	0.874	-2.27
126	-4.709	0.874	-2.27
127	-4.709	0.874	-2.27
128	-4.709	0.874	-2.27
129	-4.709	0.874	-2.27
130	-4.709	0.874	-2.27
131	-4.709	0.874	-2.27
132	-4.709	0.874	-2.27

45	1
53	1
55	1
57	1
59	1
60	1
62	1
66	1
69	1
70	1
77	1
78	1
79	1
98	1
109	1
145	1
181	1
54	0
64	0
67	0
68	0
71	0
75	0
80	0
81	0
82	0
83	0
84	0
85	0
86	0
87	0
88	0
89	0
90	0
91	0
92	0
93	0
94	0
95	0
96	0
97	0
100	0
101	0
102	0
103	0
104	0
105	0
106	0
107	0
108	0
110	0
111	0
112	0
113	0
114	0
115	0
118	0
120	0
122	0
123	0
124	0
125	0
126	0
127	0
128	0
129	0
130	0
131	0
132	0

Range 4.298 * Median = max score - range/2
Median -2.954 * Centered score = score - range

5' size	3 'size	Score	SD	Centered Score
1	1	-0.806	0.489	2.15
2	2	-1.432	0.391	1.52
1	2	-1.464	0.614	1.49
2	1	-1.641	0.329	1.31
1	3	-1.651	0.651	1.30
2	3	-1.828	0.783	1.13
4	4	-1.835	0.748	1.12
3	3	-1.986	0.806	0.97
4	1	-2.226	0.800	0.73
3	1	-2.294	1.101	0.66
3	2	-2.457	0.957	0.50
3	4	-2.527	0.617	0.43
4	3	-2.604	1.114	0.35
5	5	-2.678	1.067	0.28
1	4	-2.678	0.631	0.28
2	5	-2.693	0.542	0.26
1	5	-2.827	0.828	0.13
4	2	-2.845	0.837	0.11
5	3	-2.901	0.914	0.05
5	4	-2.973	0.733	-0.02
2	4	-3.062	0.806	-0.11
5	6	-3.082	0.708	-0.13
5	2	-3.107	1.171	-0.15
3	5	-3.111	0.709	-0.16
6	6	-3.181	1.158	-0.23
6	4	-3.186	1.178	-0.23
4	5	-3.202	1.029	-0.25
8	8	-3.212	1.342	-0.26
7	8	-3.214	1.094	-0.26
6	3	-3.227	1.248	-0.27
7	7	-3.253	1.286	-0.30
5	1	-3.307	0.767	-0.35
6	1	-3.314	1.019	-0.36
6	5	-3.340	0.822	-0.39
7	6	-3.355	1.137	-0.40
5	8	-3.391	1.701	-0.44
7	5	-3.406	1.069	-0.45
7	9	-3.420	1.162	-0.47
6	7	-3.422	1.141	-0.47
5	7	-3.423	0.881	-0.47
8	4	-3.458	1.119	-0.50
7	4	-3.509	1.068	-0.55
4	6	-3.512	1.051	-0.56
6	8	-3.519	0.903	-0.56
8	7	-3.529	1.042	-0.57
11	7	-3.602	0.941	-0.65
7	2	-3.622	0.876	-0.67
9	4	-3.637	1.317	-0.68
8	9	-3.637	1.027	-0.68
6	2	-3.653	1.139	-0.70
3	7	-3.654	0.718	-0.70
2	7	-3.684	0.841	-0.73
7	3	-3.715	0.808	-0.76
10	10	-3.717	0.900	-0.76
9	9	-3.730	0.818	-0.78
11	9	-3.738	1.025	-0.78
2	6	-3.765	0.639	-0.81
3	6	-3.765	0.553	-0.81
11	8	-3.769	1.224	-0.81
10	8	-3.783	1.123	-0.83
1	7	-3.793	0.760	-0.84
8	6	-3.820	1.082	-0.87
9	7	-3.845	1.277	-0.89
9	3	-3.848	0.927	-0.89
8	3	-3.875	0.790	-0.92

5' size	3 'size	Total i-loop count
1	1	255654
1	2	77725
4	4	60735
2	2	55200
2	3	54785
3	3	46820
3	1	39325
1	3	35500
2	1	29803
4	1	27881
5	5	23502
9	4	18196
3	2	11146
4	3	10765
6	3	8568
50	26	6848
5	8	5740
8	8	4746
5	2	4442
3	4	4243
4	2	4241
1	4	4099
2	4	3474
5	11	3418
4	6	3297
5	4	3030
7	4	2945
1	5	2512
4	5	2445
6	6	2219
8	9	2214
5	3	2150
7	7	2093
7	9	2033
5	1	2004
4	9	1878
11	8	1837
2	5	1791
14	7	1767
8	7	1709
6	4	1698
6	1	1558
5	6	1526
9	3	1459
7	6	1332
21	11	1322
10	8	1256
3	5	1210
6	11	1172
9	7	1148
6	7	1070
13	1	1059
7	5	1045
11	11	1044
4	11	1028
7	11	1005
7	8	995
5	7	985
6	8	977
6	5	953
11	9	902
29	2	898
3	7	871
10	7	837
6	2	829

Category	Total i-loop count
antisense	85788
CD-box	49637
CRISPR	8561
Gene	266299
HACA-box	201422
miRNA	284383
scaRNA	7408

13	14	-3.876	1.136	-0.92
4	8	-3.882	0.918	-0.93
11	10	-3.882	1.056	-0.93
1	6	-3.886	0.807	-0.93
8	1	-3.899	0.465	-0.94
7	1	-3.899	0.686	-0.94
9	1	-3.907	0.805	-0.95
10	7	-3.924	1.346	-0.97
3	8	-3.945	0.909	-0.99
10	9	-3.947	0.758	-0.99
9	8	-3.952	0.933	-1.00
7	11	-3.987	0.995	-1.03
8	5	-3.987	0.734	-1.03
9	5	-3.993	0.802	-1.04
9	6	-4.000	0.894	-1.05
9	2	-4.019	0.925	-1.06
6	9	-4.019	0.703	-1.06
8	10	-4.022	0.872	-1.07
4	7	-4.045	0.846	-1.09
11	4	-4.075	1.017	-1.12
8	2	-4.081	0.671	-1.13
11	6	-4.088	0.620	-1.13
6	10	-4.091	0.577	-1.14
14	10	-4.100	0.595	-1.15
7	10	-4.106	0.842	-1.15
2	8	-4.115	0.661	-1.16
11	2	-4.118	0.607	-1.16
7	12	-4.123	0.725	-1.17
13	1	-4.129	0.900	-1.17
3	10	-4.134	0.738	-1.18
14	14	-4.135	0.854	-1.18
15	2	-4.135	0.879	-1.18
14	8	-4.143	1.012	-1.19
13	13	-4.149	0.620	-1.19
17	14	-4.158	1.013	-1.20
12	7	-4.159	0.969	-1.20
4	9	-4.168	0.980	-1.21
10	3	-4.175	0.661	-1.22
11	11	-4.176	0.936	-1.22
10	4	-4.188	0.892	-1.23
15	13	-4.193	0.871	-1.24
4	11	-4.198	0.911	-1.24
14	2	-4.200	0.428	-1.25
12	9	-4.201	0.832	-1.25
11	5	-4.202	0.576	-1.25
10	1	-4.207	0.528	-1.25
3	11	-4.207	0.807	-1.25
14	7	-4.213	1.307	-1.26
1	8	-4.215	0.709	-1.26
12	10	-4.219	0.927	-1.26
10	6	-4.223	1.157	-1.27
12	8	-4.232	0.899	-1.28
13	10	-4.232	0.754	-1.28
12	4	-4.234	0.963	-1.28
5	9	-4.244	0.603	-1.29
13	2	-4.257	0.757	-1.30
13	4	-4.258	1.050	-1.30
2	9	-4.267	0.496	-1.31
15	11	-4.272	0.725	-1.32
10	5	-4.272	0.810	-1.32
10	2	-4.273	0.786	-1.32
14	13	-4.273	0.773	-1.32
12	1	-4.274	0.492	-1.32
10	11	-4.274	0.784	-1.32
4	10	-4.275	0.677	-1.32
14	15	-4.279	0.815	-1.32
5	11	-4.286	1.127	-1.33
8	11	-4.287	0.696	-1.33
11	1	-4.294	0.481	-1.34

8	4	781
10	10	777
8	6	712
9	1	706
4	8	686
8	10	663
1	6	630
20	33	609
17	11	561
9	9	552
15	2	547
2	7	543
7	3	534
7	2	524
9	8	514
10	9	494
3	8	477
10	6	464
8	3	456
9	11	445
3	11	422
12	10	419
1	7	410
4	7	400
11	10	375
11	7	362
14	13	360
50	28	356
3	6	348
7	1	329
19	11	326
14	16	325
9	6	322
10	12	322
10	4	315
14	14	286
8	5	283
20	32	274
7	12	271
2	6	267
9	5	262
1	8	248
2	8	241
13	2	241
12	11	233
19	22	232
10	11	231
1	24	229
3	10	224
13	12	223
15	11	223
79	25	219
14	10	217
8	2	216
50	27	214
6	9	213
14	8	212
8	1	211
13	14	209
21	12	207
20	11	203
9	2	202
16	13	202
50	25	199
12	9	195
15	13	195
17	13	192
13	4	191
14	12	190

14	12	-4.295	0.624	-1.34
2	11	-4.308	0.579	-1.35
13	7	-4.311	0.861	-1.36
14	9	-4.314	0.684	-1.36
3	9	-4.319	0.553	-1.36
17	11	-4.319	1.102	-1.36
1	13	-4.324	0.420	-1.37
9	11	-4.329	1.044	-1.37
1	11	-4.331	0.567	-1.38
1	9	-4.332	0.578	-1.38
1	10	-4.335	0.497	-1.38
2	10	-4.335	0.472	-1.38
10	12	-4.345	1.023	-1.39
13	8	-4.347	0.925	-1.39
19	20	-4.353	0.432	-1.40
3	12	-4.355	0.646	-1.40
15	14	-4.357	0.692	-1.40
17	7	-4.362	0.693	-1.41
13	11	-4.363	0.683	-1.41
11	12	-4.369	0.787	-1.41
12	2	-4.375	1.117	-1.42
9	10	-4.377	0.854	-1.42
14	11	-4.388	0.682	-1.43
12	11	-4.390	0.759	-1.44
14	4	-4.398	0.760	-1.44
12	6	-4.402	0.804	-1.45
17	17	-4.411	0.492	-1.46
15	10	-4.422	0.487	-1.47
8	13	-4.426	0.885	-1.47
16	7	-4.434	1.063	-1.48
13	15	-4.439	0.943	-1.48
12	12	-4.441	0.595	-1.49
15	8	-4.447	0.857	-1.49
14	5	-4.451	0.603	-1.50
8	12	-4.453	0.541	-1.50
6	11	-4.463	1.089	-1.51
11	14	-4.466	0.897	-1.51
16	2	-4.468	0.692	-1.51
1	12	-4.471	0.525	-1.52
13	12	-4.472	0.920	-1.52
16	13	-4.477	0.919	-1.52
16	11	-4.479	0.814	-1.52
14	16	-4.484	0.956	-1.53
17	15	-4.487	0.843	-1.53
12	3	-4.493	0.572	-1.54
4	12	-4.495	0.666	-1.54
6	12	-4.502	0.732	-1.55
17	1	-4.509	0.512	-1.55
16	8	-4.511	0.447	-1.56
5	10	-4.512	0.726	-1.56
12	5	-4.512	0.523	-1.56
50	26	-4.512	1.745	-1.56
18	11	-4.519	0.702	-1.56
20	23	-4.519	0.675	-1.56
13	5	-4.529	0.494	-1.57
17	13	-4.531	0.829	-1.58
14	6	-4.533	0.880	-1.58
16	10	-4.538	0.478	-1.58
16	14	-4.541	0.742	-1.59
15	4	-4.543	0.596	-1.59
15	7	-4.543	0.864	-1.59
13	16	-4.543	0.980	-1.59
21	11	-4.546	1.178	-1.59
14	1	-4.552	0.662	-1.60
3	13	-4.561	0.718	-1.61
15	12	-4.564	0.720	-1.61
1	14	-4.567	0.566	-1.61
16	12	-4.569	0.510	-1.62
7	13	-4.573	0.420	-1.62

12	6	188
17	14	178
10	5	172
3	12	170
13	10	170
13	16	170
16	11	168
9	10	165
14	4	165
5	9	164
4	10	163
11	4	163
11	16	163
5	10	161
13	7	160
12	7	158
8	13	154
15	14	147
8	11	145
10	1	140
16	7	139
11	14	138
13	11	136
11	12	131
7	10	129
3	41	123
6	10	122
12	8	122
13	13	119
12	12	116
3	9	114
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28	2	67

12	14	-4.577	0.565	-1.62
13	9	-4.578	0.648	-1.62
12	13	-4.583	0.668	-1.63
13	3	-4.584	0.586	-1.63
22	21	-4.586	0.744	-1.63
1	24	-4.587	0.858	-1.63
11	3	-4.596	0.545	-1.64
20	5	-4.596	0.640	-1.64
19	7	-4.600	0.646	-1.65
32	30	-4.601	1.400	-1.65
4	19	-4.601	0.931	-1.65
19	11	-4.602	0.926	-1.65
4	13	-4.603	0.435	-1.65
20	18	-4.603	0.656	-1.65
16	16	-4.606	0.527	-1.65
11	13	-4.613	0.745	-1.66
18	7	-4.615	0.452	-1.66
5	12	-4.618	0.732	-1.66
12	16	-4.622	0.711	-1.67
11	16	-4.624	0.870	-1.67
19	12	-4.626	0.652	-1.67
21	21	-4.626	0.720	-1.67
11	15	-4.627	0.754	-1.67
29	2	-4.638	1.192	-1.68
19	17	-4.652	0.655	-1.70
9	12	-4.657	0.677	-1.70
7	18	-4.657	0.726	-1.70
16	1	-4.658	0.401	-1.70
17	9	-4.659	0.447	-1.70
1	17	-4.659	0.380	-1.70
11	17	-4.660	0.668	-1.71
20	33	-4.662	1.387	-1.71
8	16	-4.667	0.676	-1.71
17	6	-4.667	0.428	-1.71
24	20	-4.669	0.569	-1.71
17	10	-4.670	0.669	-1.72
32	26	-4.676	1.052	-1.72
22	11	-4.678	0.840	-1.72
10	14	-4.679	0.781	-1.72
7	17	-4.682	0.528	-1.73
16	15	-4.682	0.821	-1.73
1	18	-4.687	0.540	-1.73
5	18	-4.687	0.829	-1.73
16	4	-4.693	0.691	-1.74
18	16	-4.694	0.598	-1.74
50	28	-4.696	1.310	-1.74
16	9	-4.701	0.752	-1.75
28	15	-4.703	0.951	-1.75
3	42	-4.703	0.854	-1.75
19	19	-4.704	0.874	-1.75
8	19	-4.705	0.690	-1.75
1	16	-4.707	0.688	-1.75
18	14	-4.707	0.592	-1.75
2	16	-4.709	0.431	-1.75
1	19	-4.710	0.720	-1.76
19	21	-4.710	0.677	-1.76
1	21	-4.711	0.645	-1.76
20	32	-4.712	1.274	-1.76
13	6	-4.715	0.606	-1.76
15	1	-4.718	0.630	-1.76
31	27	-4.721	1.135	-1.77
1	27	-4.722	0.574	-1.77
19	22	-4.722	1.012	-1.77
14	3	-4.723	0.478	-1.77
10	13	-4.725	0.635	-1.77
15	9	-4.725	0.521	-1.77
79	25	-4.726	1.243	-1.77
1	23	-4.726	0.732	-1.77
13	17	-4.726	0.690	-1.77

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6	13	-4.730	0.618	-1.78
20	11	-4.730	0.940	-1.78
15	16	-4.731	0.651	-1.78
20	21	-4.731	0.621	-1.78
30	21	-4.731	0.975	-1.78
50	25	-4.732	1.230	-1.78
25	2	-4.738	0.602	-1.78
21	23	-4.738	0.787	-1.78
4	15	-4.740	0.603	-1.79
9	13	-4.740	0.603	-1.79
32	15	-4.741	1.241	-1.79
6	14	-4.746	0.628	-1.79
22	7	-4.746	0.752	-1.79
21	9	-4.747	0.786	-1.79
3	15	-4.749	0.864	-1.79
20	10	-4.749	0.595	-1.80
22	20	-4.752	0.608	-1.80
18	1	-4.755	0.648	-1.80
19	8	-4.755	0.606	-1.80
20	22	-4.755	0.568	-1.80
25	1	-4.755	0.709	-1.80
3	18	-4.758	0.715	-1.80
21	33	-4.759	0.971	-1.80
4	17	-4.761	0.587	-1.81
3	41	-4.761	1.164	-1.81
28	1	-4.761	0.755	-1.81
3	16	-4.762	0.845	-1.81
6	19	-4.762	0.845	-1.81
20	8	-4.765	0.570	-1.81
1	25	-4.767	0.724	-1.81
18	15	-4.767	0.719	-1.81
20	4	-4.767	0.597	-1.81
20	17	-4.771	0.752	-1.82
3	20	-4.772	1.183	-1.82
7	16	-4.772	0.575	-1.82
20	14	-4.774	0.747	-1.82
23	11	-4.774	0.747	-1.82
2	12	-4.776	0.648	-1.82
2	18	-4.776	0.877	-1.82
49	26	-4.776	1.133	-1.82
8	31	-4.777	1.132	-1.82
30	2	-4.777	0.904	-1.82
1	22	-4.778	0.646	-1.82
22	32	-4.778	1.129	-1.82
32	23	-4.779	1.063	-1.82
54	31	-4.779	1.127	-1.82
4	16	-4.780	0.866	-1.83
17	5	-4.783	0.412	-1.83
19	18	-4.783	0.720	-1.83
21	16	-4.783	0.720	-1.83
25	35	-4.783	0.850	-1.83
14	17	-4.784	0.589	-1.83
21	17	-4.784	0.595	-1.83
18	19	-4.786	0.860	-1.83
19	14	-4.786	0.604	-1.83
3	19	-4.788	0.863	-1.83
23	32	-4.788	1.108	-1.83
5	13	-4.791	0.573	-1.84
32	29	-4.791	1.077	-1.84
80	25	-4.791	1.101	-1.84
4	18	-4.794	0.670	-1.84
6	17	-4.794	0.579	-1.84
2	19	-4.798	1.330	-1.84
28	2	-4.799	0.863	-1.84
32	34	-4.799	0.792	-1.84
21	7	-4.799	0.719	-1.84

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37	16	-4.799	0.719	-1.84
3	17	-4.800	0.575	-1.85
51	26	-4.804	1.075	-1.85
10	16	-4.805	0.672	-1.85
31	29	-4.805	1.314	-1.85
36	47	-4.806	1.071	-1.85
7	14	-4.808	0.747	-1.85
9	14	-4.808	0.570	-1.85
17	32	-4.808	0.877	-1.85
25	18	-4.808	0.877	-1.85
21	10	-4.810	0.793	-1.86
26	32	-4.810	1.062	-1.86
24	19	-4.811	0.629	-1.86
18	29	-4.812	1.058	-1.86
25	32	-4.812	1.058	-1.86
3	14	-4.814	0.625	-1.86
9	17	-4.814	0.659	-1.86
22	17	-4.814	0.615	-1.86
33	36	-4.814	1.053	-1.86
2	13	-4.818	0.516	-1.86
7	46	-4.818	0.779	-1.86
38	29	-4.818	0.858	-1.86
84	25	-4.819	1.043	-1.86
19	4	-4.821	0.596	-1.87
19	10	-4.821	0.576	-1.87
26	41	-4.821	0.775	-1.87
25	34	-4.823	0.743	-1.87
42	25	-4.823	1.035	-1.87
4	28	-4.825	0.769	-1.87
22	12	-4.826	0.612	-1.87
28	27	-4.826	1.029	-1.87
31	20	-4.826	0.979	-1.87
1	15	-4.828	0.539	-1.87
9	15	-4.828	0.571	-1.87
12	17	-4.828	0.571	-1.87
21	22	-4.828	0.560	-1.87
6	18	-4.831	0.638	-1.88
15	3	-4.831	0.559	-1.88
22	2	-4.831	0.463	-1.88
32	33	-4.831	0.972	-1.88
16	5	-4.834	0.516	-1.88
25	11	-4.834	0.755	-1.88
39	21	-4.834	1.014	-1.88
5	19	-4.835	0.756	-1.88
3	40	-4.835	0.827	-1.88
13	41	-4.835	1.011	-1.88
30	33	-4.835	1.011	-1.88
36	39	-4.837	1.008	-1.88
15	6	-4.842	0.790	-1.89
40	35	-4.842	0.997	-1.89
12	15	-4.844	0.561	-1.89
21	2	-4.844	0.576	-1.89
30	28	-4.844	1.017	-1.89
18	2	-4.846	0.558	-1.89
24	2	-4.846	0.558	-1.89
24	15	-4.846	0.872	-1.89
17	29	-4.846	0.949	-1.89
31	11	-4.846	0.669	-1.89
50	24	-4.848	0.986	-1.89
1	26	-4.852	0.655	-1.90
9	20	-4.852	0.775	-1.90
18	18	-4.852	0.795	-1.90
23	33	-4.852	0.978	-1.90
25	15	-4.852	0.940	-1.90
29	15	-4.852	1.200	-1.90
4	14	-4.855	0.557	-1.90
17	12	-4.855	0.724	-1.90

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6	51	-4.859	0.965	-1.90
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19	33	-4.859	0.965	-1.90
21	28	-4.859	0.706	-1.90
26	21	-4.859	0.706	-1.90
30	31	-4.859	0.931	-1.90
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18	30	-4.862	0.960	-1.91
24	32	-4.862	0.960	-1.91
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40	25	-4.864	0.955	-1.91
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17	16	-4.867	0.709	-1.91
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22	6	-4.867	0.556	-1.91
25	19	-4.867	0.581	-1.91
26	29	-4.867	0.825	-1.91
37	34	-4.867	0.714	-1.91
3	49	-4.870	0.704	-1.92
9	46	-4.870	0.704	-1.92
27	27	-4.870	0.945	-1.92
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64	44	-4.873	0.939	-1.92
17	2	-4.876	0.593	-1.92
18	22	-4.876	0.684	-1.92
20	2	-4.876	0.593	-1.92
21	14	-4.876	0.760	-1.92
24	44	-4.876	0.651	-1.92
24	46	-4.876	0.933	-1.92
27	2	-4.876	0.741	-1.92
28	28	-4.876	0.738	-1.92
32	80	-4.876	0.696	-1.92
39	19	-4.876	0.933	-1.92
5	20	-4.879	0.736	-1.92
9	53	-4.879	0.692	-1.92
28	81	-4.879	0.927	-1.92
42	32	-4.879	0.927	-1.92
42	35	-4.879	0.927	-1.92
86	7	-4.879	0.927	-1.92
1	20	-4.883	0.519	-1.93
4	20	-4.883	0.845	-1.93
5	15	-4.883	0.552	-1.93
9	45	-4.883	0.688	-1.93
11	19	-4.883	0.557	-1.93
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19	15	-4.883	0.557	-1.93
24	24	-4.883	0.662	-1.93
32	28	-4.883	0.940	-1.93
40	30	-4.883	0.921	-1.93
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3	23	-4.886	0.741	-1.93
8	15	-4.886	0.727	-1.93

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15	19	-4.886	0.915	-1.93
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20	31	-4.886	0.915	-1.93
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40	36	-4.886	0.915	-1.93
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79	23	-4.886	0.915	-1.93
19	9	-4.890	0.679	-1.94
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31	36	-4.890	0.908	-1.94
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42	29	-4.890	0.908	-1.94
44	23	-4.890	0.908	-1.94
19	30	-4.894	0.900	-1.94
24	8	-4.894	0.674	-1.94
30	35	-4.894	0.900	-1.94
31	21	-4.894	0.900	-1.94
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85	7	-4.894	0.900	-1.94
1	28	-4.899	0.635	-1.94
3	38	-4.899	0.893	-1.94
5	14	-4.899	0.643	-1.94
17	18	-4.899	0.593	-1.94
18	13	-4.899	0.670	-1.94
18	20	-4.899	0.727	-1.94
18	34	-4.899	0.893	-1.94
23	12	-4.899	0.643	-1.94
25	30	-4.899	0.893	-1.94
27	11	-4.899	0.670	-1.94
35	20	-4.899	0.712	-1.94
35	29	-4.899	0.764	-1.94
37	35	-4.899	0.893	-1.94
39	25	-4.899	0.893	-1.94
42	21	-4.899	0.893	-1.94
42	33	-4.899	0.893	-1.94
5	306	-4.903	0.665	-1.95
7	20	-4.903	0.706	-1.95
20	9	-4.903	0.522	-1.95
21	15	-4.903	0.670	-1.95
21	29	-4.903	0.901	-1.95
22	22	-4.903	0.655	-1.95
23	7	-4.903	0.670	-1.95
29	14	-4.903	1.080	-1.95
30	26	-4.903	0.884	-1.95
34	36	-4.903	0.884	-1.95
35	2	-4.903	0.706	-1.95
36	42	-4.903	0.884	-1.95
40	26	-4.903	0.884	-1.95
42	34	-4.903	0.884	-1.95
47	26	-4.903	0.884	-1.95
48	26	-4.903	0.884	-1.95
53	31	-4.903	0.884	-1.95
54	34	-4.903	0.884	-1.95
64	42	-4.903	0.884	-1.95
70	74	-4.903	0.884	-1.95
72	25	-4.903	0.884	-1.95
1	33	-4.909	0.875	-1.95
8	25	-4.909	0.875	-1.95

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18	33	-4.909	0.875	-1.95
22	34	-4.909	0.875	-1.95
23	10	-4.909	0.660	-1.95
24	31	-4.909	0.875	-1.95
26	2	-4.909	0.700	-1.95
29	21	-4.909	0.875	-1.95
40	33	-4.909	0.875	-1.95
46	26	-4.909	0.875	-1.95
50	1	-4.909	0.875	-1.95
74	25	-4.909	0.875	-1.95
194	92	-4.909	0.875	-1.95
3	21	-4.914	0.856	-1.96
6	49	-4.914	0.866	-1.96
8	17	-4.914	0.666	-1.96
8	18	-4.914	0.694	-1.96
8	33	-4.914	0.866	-1.96
10	20	-4.914	0.569	-1.96
11	32	-4.914	0.634	-1.96
13	38	-4.914	0.866	-1.96
16	22	-4.914	0.694	-1.96
17	8	-4.914	0.573	-1.96
17	20	-4.914	0.694	-1.96
20	7	-4.914	0.720	-1.96
21	4	-4.914	0.535	-1.96
21	34	-4.914	0.866	-1.96
22	30	-4.914	0.866	-1.96
23	31	-4.914	0.866	-1.96
25	17	-4.914	0.707	-1.96
25	31	-4.914	0.866	-1.96
30	32	-4.914	0.866	-1.96
31	23	-4.914	0.921	-1.96
35	21	-4.914	0.707	-1.96
39	33	-4.914	0.866	-1.96
44	35	-4.914	0.866	-1.96
50	18	-4.914	0.866	-1.96
52	33	-4.914	0.866	-1.96
53	33	-4.914	0.866	-1.96
83	7	-4.914	0.866	-1.96
5	17	-4.920	0.688	-1.97
6	45	-4.920	0.856	-1.97
13	25	-4.920	0.856	-1.97
15	23	-4.920	0.856	-1.97
16	29	-4.920	1.041	-1.97
24	33	-4.920	0.856	-1.97
28	19	-4.920	0.856	-1.97
30	29	-4.920	1.041	-1.97
31	10	-4.920	0.649	-1.97
32	2	-4.920	0.688	-1.97
38	21	-4.920	0.856	-1.97
41	32	-4.920	0.856	-1.97
43	22	-4.920	0.856	-1.97
44	48	-4.920	0.856	-1.97
46	30	-4.920	0.856	-1.97
49	25	-4.920	0.856	-1.97
50	11	-4.920	0.856	-1.97
50	21	-4.920	0.856	-1.97
1	71	-4.927	0.643	-1.97
16	19	-4.927	0.844	-1.97
16	33	-4.927	0.844	-1.97
16	40	-4.927	0.844	-1.97
19	13	-4.927	0.643	-1.97
19	31	-4.927	0.844	-1.97
19	34	-4.927	0.844	-1.97
21	8	-4.927	0.643	-1.97
21	35	-4.927	0.844	-1.97
22	33	-4.927	0.844	-1.97
30	22	-4.927	0.844	-1.97
31	6	-4.927	0.643	-1.97
33	23	-4.927	0.844	-1.97

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44	29	-4.927	0.844	-1.97
50	14	-4.927	0.844	-1.97
54	33	-4.927	0.844	-1.97
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81	25	-4.927	0.844	-1.97
16	17	-4.935	0.539	-1.98
18	4	-4.935	0.555	-1.98
20	13	-4.935	0.561	-1.98
20	20	-4.935	0.629	-1.98
22	1	-4.935	0.561	-1.98
23	2	-4.935	0.569	-1.98
23	23	-4.935	0.629	-1.98
24	21	-4.935	0.555	-1.98
24	22	-4.935	0.537	-1.98
32	83	-4.935	0.638	-1.98
3	43	-4.935	0.682	-1.98
8	30	-4.935	0.832	-1.98
12	21	-4.935	0.636	-1.98
14	20	-4.935	0.636	-1.98
15	18	-4.935	0.679	-1.98
16	3	-4.935	0.641	-1.98
17	21	-4.935	0.696	-1.98
18	21	-4.935	0.696	-1.98
20	6	-4.935	0.641	-1.98
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20	30	-4.935	0.832	-1.98
22	16	-4.935	0.696	-1.98
22	23	-4.935	0.832	-1.98
22	29	-4.935	0.844	-1.98
23	17	-4.935	0.641	-1.98
25	21	-4.935	0.696	-1.98
28	20	-4.935	0.832	-1.98
28	35	-4.935	0.832	-1.98
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32	25	-4.935	0.880	-1.98
32	36	-4.935	0.832	-1.98
33	20	-4.935	0.880	-1.98
34	26	-4.935	0.844	-1.98
36	33	-4.935	0.832	-1.98
36	37	-4.935	0.682	-1.98
37	17	-4.935	0.682	-1.98
40	21	-4.935	0.832	-1.98
42	19	-4.935	0.832	-1.98
44	49	-4.935	0.832	-1.98
46	29	-4.935	0.832	-1.98
50	8	-4.935	0.832	-1.98
50	17	-4.935	0.832	-1.98
50	33	-4.935	0.682	-1.98
55	31	-4.935	0.832	-1.98
79	24	-4.935	0.832	-1.98
6	50	-4.944	0.819	-1.99
17	19	-4.944	0.819	-1.99
18	32	-4.944	0.819	-1.99
20	34	-4.944	0.819	-1.99
25	33	-4.944	0.819	-1.99
25	41	-4.944	0.632	-1.99
26	10	-4.944	0.632	-1.99
30	30	-4.944	0.819	-1.99
31	15	-4.944	0.988	-1.99
32	11	-4.944	0.632	-1.99
32	14	-4.944	0.988	-1.99

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43	26	-4.944	0.819	-1.99
44	26	-4.944	0.819	-1.99
45	52	-4.944	0.819	-1.99
49	27	-4.944	0.819	-1.99
50	20	-4.944	0.819	-1.99
51	27	-4.944	0.819	-1.99
53	32	-4.944	0.819	-1.99
54	16	-4.944	0.819	-1.99
68	7	-4.944	0.819	-1.99
78	25	-4.944	0.819	-1.99
9	16	-4.954	0.659	-2.00
17	22	-4.954	0.659	-2.00
22	31	-4.954	0.803	-2.00
23	20	-4.954	0.618	-2.00
24	11	-4.954	0.626	-2.00
28	5	-4.954	0.618	-2.00
28	82	-4.954	0.803	-2.00
29	18	-4.954	0.803	-2.00
30	15	-4.954	0.965	-2.00
30	27	-4.954	0.965	-2.00
31	22	-4.954	0.803	-2.00
35	31	-4.954	0.803	-2.00
37	21	-4.954	0.803	-2.00
38	26	-4.954	0.803	-2.00
39	17	-4.954	0.803	-2.00
39	20	-4.954	0.803	-2.00
39	38	-4.954	0.803	-2.00
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43	35	-4.954	0.803	-2.00
44	52	-4.954	0.803	-2.00
46	31	-4.954	0.803	-2.00
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79	15	-4.954	0.803	-2.00
1	35	-4.967	0.552	-2.01
1	44	-4.967	0.621	-2.01
6	30	-4.967	0.613	-2.01
14	22	-4.967	0.651	-2.01
15	5	-4.967	0.569	-2.01
18	3	-4.967	0.573	-2.01
18	8	-4.967	0.621	-2.01
18	10	-4.967	0.621	-2.01
19	24	-4.967	0.651	-2.01
20	16	-4.967	0.621	-2.01
21	13	-4.967	0.621	-2.01
21	24	-4.967	0.613	-2.01
22	4	-4.967	0.573	-2.01
23	5	-4.967	0.613	-2.01
23	8	-4.967	0.621	-2.01
23	49	-4.967	0.621	-2.01
25	10	-4.967	0.552	-2.01
26	1	-4.967	0.613	-2.01
27	15	-4.967	0.938	-2.01
29	1	-4.967	0.651	-2.01
29	13	-4.967	0.938	-2.01

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30	1	-4.967	0.651	-2.01
30	6	-4.967	0.552	-2.01
30	10	-4.967	0.552	-2.01
30	13	-4.967	0.938	-2.01
32	4	-4.967	0.746	-2.01
32	82	-4.967	0.621	-2.01
32	84	-4.967	0.621	-2.01
34	2	-4.967	0.651	-2.01
3	35	-4.967	0.786	-2.01
3	47	-4.967	0.652	-2.01
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13	18	-4.967	0.667	-2.01
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13	30	-4.967	0.786	-2.01
14	19	-4.967	0.667	-2.01
16	6	-4.967	0.667	-2.01
18	12	-4.967	0.652	-2.01
20	15	-4.967	0.652	-2.01
20	24	-4.967	0.786	-2.01
20	25	-4.967	0.786	-2.01
21	32	-4.967	0.786	-2.01
22	15	-4.967	0.820	-2.01
24	111	-4.967	0.786	-2.01
25	29	-4.967	0.820	-2.01
26	20	-4.967	0.649	-2.01
26	30	-4.967	0.820	-2.01
27	20	-4.967	0.786	-2.01
27	24	-4.967	0.820	-2.01
28	21	-4.967	0.786	-2.01
28	31	-4.967	0.652	-2.01
29	27	-4.967	0.820	-2.01
30	20	-4.967	0.649	-2.01
31	17	-4.967	0.652	-2.01
32	20	-4.967	0.652	-2.01
34	16	-4.967	0.652	-2.01
34	21	-4.967	0.786	-2.01
34	27	-4.967	0.786	-2.01
35	1	-4.967	0.652	-2.01
36	40	-4.967	0.786	-2.01
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37	32	-4.967	0.786	-2.01
37	36	-4.967	0.652	-2.01
37	58	-4.967	0.786	-2.01
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46	63	-4.967	0.786	-2.01
49	22	-4.967	0.786	-2.01
50	2	-4.967	0.786	-2.01
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54	14	-4.967	0.786	-2.01
54	24	-4.967	0.786	-2.01
56	16	-4.967	0.786	-2.01
56	32	-4.967	0.786	-2.01
57	7	-4.967	0.786	-2.01
58	7	-4.967	0.786	-2.01
66	26	-4.967	0.786	-2.01

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80	15	-4.967	0.786	-2.01
80	23	-4.967	0.786	-2.01
84	7	-4.967	0.786	-2.01
186	93	-4.967	0.786	-2.01
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2	20	-4.982	0.904	-2.03
2	23	-4.982	0.610	-2.03
2	25	-4.982	0.610	-2.03
5	312	-4.982	0.616	-2.03
6	16	-4.982	0.616	-2.03
6	22	-4.982	0.643	-2.03
7	22	-4.982	0.643	-2.03
8	20	-4.982	0.643	-2.03
10	22	-4.982	0.643	-2.03
11	24	-4.982	0.610	-2.03
12	173	-4.982	0.616	-2.03
13	20	-4.982	0.643	-2.03
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38	32	-4.982	0.765	-2.03
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27	41	-5.003	0.615	-2.05
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31	28	-5.003	0.860	-2.05
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32	32	-5.003	0.860	-2.05
32	81	-5.003	0.615	-2.05
32	86	-5.003	0.615	-2.05
33	29	-5.003	0.860	-2.05
34	1	-5.003	0.615	-2.05

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72	1	-5.003	0.615	-2.05
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208	93	-5.003	0.740	-2.05
209	90	-5.003	0.740	-2.05
1	30	-5.035	0.618	-2.08
1	42	-5.035	0.622	-2.08
1	66	-5.035	0.622	-2.08
2	15	-5.035	0.622	-2.08
2	17	-5.035	0.637	-2.08
2	24	-5.035	0.618	-2.08
2	27	-5.035	0.622	-2.08
2	48	-5.035	0.622	-2.08
2	66	-5.035	0.622	-2.08
3	30	-5.035	0.618	-2.08
3	51	-5.035	0.622	-2.08
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5	349	-5.035	0.622	-2.08
6	21	-5.035	0.796	-2.08
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6	120	-5.035	0.622	-2.08
6	169	-5.035	0.622	-2.08
6	174	-5.035	0.622	-2.08
6	181	-5.035	0.622	-2.08
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6	306	-5.035	0.622	-2.08
7	24	-5.035	0.796	-2.08
7	39	-5.035	0.618	-2.08
7	47	-5.035	0.622	-2.08
9	22	-5.035	0.637	-2.08
10	15	-5.035	0.637	-2.08
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10	111	-5.035	0.622	-2.08
11	20	-5.035	0.637	-2.08
12	18	-5.035	0.637	-2.08
12	23	-5.035	0.618	-2.08
12	191	-5.035	0.622	-2.08
12	200	-5.035	0.622	-2.08
13	53	-5.035	0.618	-2.08
14	18	-5.035	0.637	-2.08
14	40	-5.035	0.618	-2.08
14	56	-5.035	0.618	-2.08
15	20	-5.035	0.637	-2.08
15	22	-5.035	0.637	-2.08
17	3	-5.035	0.622	-2.08
17	53	-5.035	0.622	-2.08
18	5	-5.035	0.622	-2.08
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19	3	-5.035	0.622	-2.08
19	6	-5.035	0.622	-2.08
20	1	-5.035	0.622	-2.08
20	27	-5.035	0.618	-2.08
20	39	-5.035	0.622	-2.08
21	1	-5.035	0.622	-2.08
21	26	-5.035	0.618	-2.08
21	44	-5.035	0.622	-2.08
22	5	-5.035	0.622	-2.08
22	9	-5.035	0.618	-2.08
22	18	-5.035	0.637	-2.08
22	25	-5.035	0.618	-2.08
22	45	-5.035	0.622	-2.08
23	4	-5.035	0.637	-2.08
23	22	-5.035	0.618	-2.08
23	24	-5.035	0.618	-2.08
23	41	-5.035	0.622	-2.08
23	78	-5.035	0.622	-2.08
24	4	-5.035	0.622	-2.08
24	17	-5.035	0.637	-2.08
24	18	-5.035	0.622	-2.08
24	42	-5.035	0.622	-2.08
24	51	-5.035	0.622	-2.08
25	9	-5.035	0.618	-2.08
25	25	-5.035	0.622	-2.08
25	44	-5.035	0.622	-2.08
26	4	-5.035	0.622	-2.08
26	9	-5.035	0.622	-2.08
26	17	-5.035	0.637	-2.08
26	43	-5.035	0.622	-2.08
26	44	-5.035	0.622	-2.08
26	50	-5.035	0.622	-2.08
26	51	-5.035	0.622	-2.08
27	1	-5.035	0.622	-2.08

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27	46	-5.035	0.622	-2.08
27	50	-5.035	0.622	-2.08
28	4	-5.035	0.622	-2.08
28	13	-5.035	0.796	-2.08
28	14	-5.035	0.796	-2.08
28	17	-5.035	0.618	-2.08
28	39	-5.035	0.622	-2.08
28	41	-5.035	0.622	-2.08
29	3	-5.035	0.637	-2.08
29	6	-5.035	0.637	-2.08
29	8	-5.035	0.622	-2.08
29	11	-5.035	0.622	-2.08
29	37	-5.035	0.622	-2.08
29	47	-5.035	0.622	-2.08
30	8	-5.035	0.622	-2.08
30	11	-5.035	0.622	-2.08
30	44	-5.035	0.622	-2.08
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32	27	-5.035	0.622	-2.08
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33	16	-5.035	0.622	-2.08
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35	26	-5.035	0.796	-2.08
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36	12	-5.035	0.622	-2.08
36	16	-5.035	0.622	-2.08
37	1	-5.035	0.622	-2.08
37	13	-5.035	0.622	-2.08
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38	11	-5.035	0.622	-2.08
40	11	-5.035	0.622	-2.08
42	11	-5.035	0.622	-2.08
44	11	-5.035	0.622	-2.08
44	12	-5.035	0.622	-2.08
46	11	-5.035	0.622	-2.08
47	43	-5.035	0.622	-2.08
49	11	-5.035	0.622	-2.08
57	11	-5.035	0.622	-2.08
59	11	-5.035	0.622	-2.08
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108	2	-5.035	0.622	-2.08
117	3	-5.035	0.622	-2.08
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44	32	1
44	33	1
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45	11	1
45	22	1
45	25	1
45	50	1
46	11	1
46	20	1
46	52	1
46	55	1
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52	34	1
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54	15	1
54	17	1
54	26	1
55	44	1
56	31	1
57	11	1
57	20	1

54	26	-5.035	0.709	-2.08
55	44	-5.035	0.709	-2.08
56	31	-5.035	0.709	-2.08
57	20	-5.035	0.709	-2.08
58	3	-5.035	0.709	-2.08
58	44	-5.035	0.709	-2.08
58	45	-5.035	0.709	-2.08
60	30	-5.035	0.709	-2.08
61	7	-5.035	0.709	-2.08
66	7	-5.035	0.709	-2.08
69	7	-5.035	0.709	-2.08
69	41	-5.035	0.709	-2.08
70	8	-5.035	0.709	-2.08
71	27	-5.035	0.709	-2.08
71	31	-5.035	0.709	-2.08
72	7	-5.035	0.709	-2.08
75	25	-5.035	0.709	-2.08
77	17	-5.035	0.709	-2.08
79	7	-5.035	0.709	-2.08
79	22	-5.035	0.709	-2.08
80	26	-5.035	0.709	-2.08
83	25	-5.035	0.709	-2.08
84	23	-5.035	0.709	-2.08
112	7	-5.035	0.709	-2.08
114	7	-5.035	0.709	-2.08
130	16	-5.035	0.709	-2.08
155	88	-5.035	0.709	-2.08
180	91	-5.035	0.709	-2.08
180	93	-5.035	0.709	-2.08
183	97	-5.035	0.709	-2.08
186	60	-5.035	0.709	-2.08
187	94	-5.035	0.709	-2.08
188	28	-5.035	0.709	-2.08
188	92	-5.035	0.709	-2.08
188	102	-5.035	0.709	-2.08
191	92	-5.035	0.709	-2.08
194	95	-5.035	0.709	-2.08
196	93	-5.035	0.709	-2.08
197	92	-5.035	0.709	-2.08
200	93	-5.035	0.709	-2.08
211	90	-5.035	0.709	-2.08
211	93	-5.035	0.709	-2.08
228	93	-5.035	0.709	-2.08
1	32	-5.103	0.673	-2.15
1	36	-5.103	0.673	-2.15
1	38	-5.103	0.673	-2.15
1	39	-5.103	0.673	-2.15
1	40	-5.103	0.673	-2.15
1	41	-5.103	0.673	-2.15
1	43	-5.103	0.673	-2.15
1	45	-5.103	0.673	-2.15
1	46	-5.103	0.673	-2.15
1	48	-5.103	0.673	-2.15
1	49	-5.103	0.673	-2.15
1	50	-5.103	0.673	-2.15
1	51	-5.103	0.673	-2.15
1	52	-5.103	0.673	-2.15
1	53	-5.103	0.673	-2.15
1	54	-5.103	0.673	-2.15
1	55	-5.103	0.673	-2.15
1	56	-5.103	0.673	-2.15
1	57	-5.103	0.673	-2.15
1	58	-5.103	0.673	-2.15
1	59	-5.103	0.673	-2.15
1	60	-5.103	0.673	-2.15
1	61	-5.103	0.673	-2.15
1	62	-5.103	0.673	-2.15
1	63	-5.103	0.673	-2.15
1	64	-5.103	0.673	-2.15

58	3	1
58	44	1
58	45	1
59	11	1
60	30	1
61	7	1
66	7	1
68	4	1
69	7	1
69	41	1
70	8	1
71	27	1
71	31	1
72	7	1
75	25	1
77	17	1
79	7	1
79	22	1
80	26	1
83	25	1
84	23	1
108	2	1
112	7	1
114	7	1
117	3	1
130	16	1
155	88	1
180	91	1
180	93	1
183	97	1
186	60	1
187	94	1
188	28	1
188	92	1
188	102	1
191	92	1
194	95	1
196	93	1
197	92	1
200	93	1
211	90	1
211	93	1
228	93	1
1	32	0
1	36	0
1	38	0
1	39	0
1	40	0
1	41	0
1	43	0
1	45	0
1	46	0
1	48	0
1	49	0
1	50	0
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1	52	0
1	53	0
1	54	0
1	55	0
1	56	0
1	57	0
1	58	0
1	59	0
1	60	0
1	61	0
1	62	0
1	63	0
1	64	0

Table S24. Terminal loops

Biloops		
Range	1.254	
Median	-1.544	
Loop	**Score**	**Centered score**
UA	-0.917	0.63
UU	-1.058	0.49
AA	-1.149	0.39
CA	-1.200	0.34
AG	-1.238	0.31
UG	-1.309	0.23
GA	-1.313	0.23
CU	-1.370	0.17
AC	-1.405	0.14
GG	-1.418	0.13
UC	-1.462	0.08
AU	-1.548	0.00
GU	-1.570	-0.03
CC	-1.627	-0.08
GC	-2.100	-0.56
CG	-2.171	-0.63

Triloops		
Range	1.843	
Median	-2.649	
Loop	**Score**	**Centered score**
UAA	-1.728	0.92
UAU	-1.782	0.87
UUU	-1.803	0.85
ACC	-1.804	0.85
CAU	-1.834	0.82
CAA	-1.874	0.78
UCA	-1.941	0.71
AAA	-1.944	0.71
UGU	-1.964	0.69
CCA	-1.968	0.68
ACA	-2.003	0.65
CUA	-2.074	0.58
CUC	-2.114	0.54
AUA	-2.118	0.53
GAU	-2.128	0.52
GAA	-2.136	0.51
UCU	-2.149	0.50
AUU	-2.214	0.43
AUC	-2.232	0.42
UUC	-2.272	0.38
AGC	-2.291	0.36
UUA	-2.316	0.33
AAC	-2.351	0.30
AAU	-2.357	0.29
UAG	-2.358	0.29
UGA	-2.392	0.26
CUU	-2.455	0.19
GCU	-2.460	0.19
AUG	-2.503	0.15
UCC	-2.505	0.14
GGC	-2.509	0.14
CAC	-2.517	0.13
UGG	-2.524	0.13
CCU	-2.528	0.12
GUU	-2.541	0.11
UUG	-2.543	0.11
CUG	-2.552	0.10
ACU	-2.554	0.10
UAC	-2.565	0.08
GAG	-2.607	0.04
GCA	-2.625	0.02
AGU	-2.647	0.00
GGU	-2.655	-0.01
AGA	-2.657	-0.01
UGC	-2.666	-0.02
AAG	-2.674	-0.03
GUA	-2.685	-0.04
CCC	-2.734	-0.08
CAG	-2.777	-0.13
GUG	-2.891	-0.24
UCG	-2.931	-0.28
GAC	-3.022	-0.37
GUC	-3.027	-0.38
CGU	-3.034	-0.39
GGA	-3.112	-0.46
ACG	-3.187	-0.54
CGA	-3.268	-0.62
AGG	-3.332	-0.68
GCC	-3.401	-0.75
CGC	-3.438	-0.79
GGG	-3.457	-0.81
GCG	-3.497	-0.85
CCG	-3.536	-0.89
CGG	-3.571	-0.92

Tetraloops		
Range	2.910	
Median	-2.963	
Loop	**Score**	**Centered score**
UUUU	-1.508	1.45
GAAA	-1.656	1.31
AAAG	-1.793	1.17
UUCG	-1.853	1.11
GGAA	-1.903	1.06
GUAA	-1.968	1.00
GCAA	-2.010	0.95
AAAA	-2.062	0.90
GGAG	-2.109	0.85
GAGU	-2.170	0.79
UUAU	-2.185	0.78
AUUU	-2.199	0.76
GUCA	-2.201	0.76
UCAU	-2.204	0.76
UAUA	-2.210	0.75
UGGC	-2.219	0.74
UGGU	-2.264	0.70
UAGU	-2.278	0.69
UCCA	-2.278	0.68
UUGC	-2.303	0.66
ACGU	-2.364	0.60
CUUG	-2.379	0.58
ACCA	-2.382	0.58
UUUG	-2.391	0.57
AAGU	-2.404	0.56
AGAA	-2.404	0.56
GAAU	-2.409	0.55
CUUU	-2.410	0.55
UUGU	-2.418	0.55
AAAU	-2.422	0.54
GCCA	-2.437	0.53
UAUC	-2.439	0.52
GAGA	-2.449	0.51
UAAA	-2.472	0.49
UCUU	-2.472	0.49
UUCA	-2.481	0.48
GUGA	-2.490	0.47
UACA	-2.518	0.45
UGCU	-2.521	0.44
GAUC	-2.535	0.43
CAGU	-2.537	0.43
GAAG	-2.555	0.41
CUCU	-2.556	0.41
GACA	-2.560	0.40
AACA	-2.569	0.39
UUUC	-2.569	0.39
UGUU	-2.572	0.39
UGAU	-2.577	0.39
UUUA	-2.590	0.37
AAAC	-2.591	0.37
AGCU	-2.592	0.37
AGAG	-2.597	0.37
UAAU	-2.605	0.36
AUGU	-2.605	0.36
UUCU	-2.606	0.36
UCCG	-2.611	0.35
CUGC	-2.616	0.35
CUGU	-2.618	0.35
ACCC	-2.619	0.34
UAUU	-2.625	0.34
AUCA	-2.627	0.34
GGGC	-2.638	0.33
UCAA	-2.638	0.32
AGCA	-2.639	0.32

Pentaloops		
Range	2.339	
Median	-3.658	
Loop	**Score**	**Centered score**
UGCAU	-2.488	1.17
UCCAG	-2.496	1.16
UGGGC	-2.540	1.12
UGGGU	-2.571	1.09
UGUGU	-2.733	0.92
UUGCC	-2.747	0.91
UUUAU	-2.786	0.87
UUUUG	-2.816	0.84
CUUGU	-2.832	0.83
AGAAA	-2.842	0.82
UGGUA	-2.864	0.79
UUCUU	-2.886	0.77
CCUGU	-2.892	0.77
UUUAG	-2.909	0.75
UAUGU	-2.912	0.75
UUCGU	-2.921	0.74
UUUUA	-2.924	0.73
UGUGC	-2.930	0.73
UGAGU	-2.931	0.73
UUUCG	-2.934	0.72
UGGAU	-2.953	0.70
UUGUG	-2.954	0.70
UAUAG	-2.967	0.69
UCCUG	-3.013	0.64
CUUUG	-3.013	0.64
UGCUU	-3.026	0.63
UGCAA	-3.036	0.62
AAUUU	-3.059	0.60
UCUAA	-3.065	0.59
CUUCG	-3.075	0.58
UCCAU	-3.093	0.56
AUUUG	-3.105	0.55
UACUG	-3.107	0.55
UGUGG	-3.121	0.54
UGAAU	-3.131	0.53
UUACC	-3.138	0.52
UUGCU	-3.139	0.52
UACAU	-3.142	0.52
UCUGA	-3.142	0.52
UAUAU	-3.146	0.51
UAUUU	-3.181	0.48
UGCAC	-3.182	0.48
UUUUC	-3.185	0.47
UUUCC	-3.186	0.47
UGCAG	-3.188	0.47
UGGAC	-3.190	0.47
UUCUC	-3.195	0.46
CCCAG	-3.208	0.45
UGGCC	-3.213	0.44
GCGCA	-3.224	0.43
UUCGC	-3.228	0.43
AGUGU	-3.235	0.42
AUAAU	-3.240	0.42
UGCGC	-3.249	0.41
AUAUA	-3.253	0.40
UUCAU	-3.254	0.40
UAUAA	-3.256	0.40
CAUGC	-3.262	0.40
AUUAA	-3.267	0.39
UUUGC	-3.273	0.38
UUUUU	-3.273	0.38
UGACC	-3.277	0.38
UUGGC	-3.284	0.37
GCAUA	-3.292	0.37

CUCG	-2.649	0.31
UCAC	-2.649	0.31
ACAU	-2.679	0.28
ACAC	-2.705	0.26
GAUU	-2.721	0.24
UCAG	-2.737	0.23
UAUG	-2.739	0.22
GUUA	-2.740	0.22
GCGA	-2.742	0.22
AUUA	-2.743	0.22
GAAC	-2.748	0.22
UCGC	-2.751	0.21
GGCA	-2.753	0.21
CCAG	-2.756	0.21
GUAG	-2.765	0.20
ACAA	-2.771	0.19
CCAU	-2.782	0.18
ACAG	-2.784	0.18
UGCC	-2.784	0.18
CAAG	-2.785	0.18
AUGG	-2.788	0.18
AUGC	-2.799	0.16
UUAG	-2.804	0.16
UGUG	-2.817	0.15
AAUA	-2.825	0.14
GGGU	-2.831	0.13
GGGG	-2.834	0.13
GAUG	-2.834	0.13
CAAA	-2.835	0.13
GGUA	-2.837	0.13
UCCU	-2.840	0.12
UCCC	-2.847	0.12
UUAA	-2.855	0.11
UAAC	-2.862	0.10
CAAU	-2.871	0.09
CUCA	-2.880	0.08
CCAC	-2.881	0.08
CCCC	-2.891	0.07
ACUA	-2.892	0.07
UUAC	-2.898	0.07
AUAA	-2.899	0.06
AGUA	-2.903	0.06
CUAU	-2.904	0.06
UAGC	-2.905	0.06
GUCC	-2.909	0.05
AUCU	-2.910	0.05
UGUC	-2.911	0.05
AAUC	-2.915	0.05
GGAU	-2.917	0.05
AAGC	-2.925	0.04
GUCU	-2.933	0.03
CAGC	-2.939	0.02
UGAA	-2.947	0.02
UUCC	-2.948	0.01
GAUA	-2.952	0.01
UGAG	-2.964	0.00
CCCA	-2.967	0.00
UCUG	-2.970	-0.01
CAAC	-2.970	-0.01
AUGA	-2.970	-0.01
AUAU	-2.972	-0.01
AGGU	-2.986	-0.02
AGAU	-2.987	-0.02
AGUG	-2.987	-0.02
GUGU	-2.997	-0.03
CCAA	-3.000	-0.04
GCAG	-3.010	-0.05
UGCA	-3.014	-0.05
GCGU	-3.026	-0.06

UGUAU	-3.293	0.36
GUGGA	-3.299	0.36
UUUGU	-3.305	0.35
GAAUA	-3.305	0.35
UUAUA	-3.311	0.35
UGCGU	-3.321	0.34
CAUGU	-3.322	0.34
UCCCU	-3.324	0.33
UCCUC	-3.329	0.33
AUUCG	-3.330	0.33
UUGGU	-3.334	0.32
AUGUG	-3.342	0.32
UCUGU	-3.344	0.31
UCAAG	-3.348	0.31
UCCAA	-3.349	0.31
CUAGU	-3.350	0.31
UGUUU	-3.352	0.31
UCAUG	-3.356	0.30
UCCAC	-3.361	0.30
AUUAG	-3.362	0.30
UUGUC	-3.368	0.29
UGCCU	-3.369	0.29
ACUGU	-3.369	0.29
UCUCG	-3.372	0.29
UUCCC	-3.373	0.28
ACUUG	-3.381	0.28
GUAUA	-3.383	0.27
CAUCA	-3.384	0.27
CUCGU	-3.388	0.27
GUUUU	-3.389	0.27
GCUCA	-3.390	0.27
UGUGA	-3.390	0.27
UUCAG	-3.392	0.27
UUCCU	-3.401	0.26
UAUUG	-3.407	0.25
CUAUA	-3.407	0.25
UUUAA	-3.409	0.25
UCCUU	-3.411	0.25
AUUGU	-3.415	0.24
UUGGG	-3.417	0.24
UCUUU	-3.423	0.23
UGUAA	-3.433	0.22
GCUGU	-3.434	0.22
UUCUG	-3.441	0.22
GGUUU	-3.444	0.21
UGACU	-3.444	0.21
UGAGC	-3.450	0.21
CUUCU	-3.455	0.20
GACAA	-3.455	0.20
UGCCA	-3.458	0.20
GGACA	-3.458	0.20
UUGUU	-3.458	0.20
GAUUA	-3.459	0.20
CUUAU	-3.461	0.20
AAAAA	-3.466	0.19
CGUCG	-3.470	0.19
UGUUC	-3.471	0.19
CUUGA	-3.474	0.18
UCGUG	-3.476	0.18
UCAUA	-3.482	0.18
CUCUU	-3.489	0.17
ACUGA	-3.491	0.17
UUUGG	-3.495	0.16
AGGAA	-3.497	0.16
CGUGU	-3.498	0.16
AUUUA	-3.505	0.15
CCCCA	-3.506	0.15
AUACA	-3.515	0.14
GAUGA	-3.518	0.14

GGUU	-3.028	-0.06
AGUU	-3.029	-0.07
GCAU	-3.029	-0.07
GGGA	-3.030	-0.07
GUUU	-3.032	-0.07
AAGG	-3.034	-0.07
CACU	-3.034	-0.07
CCUG	-3.036	-0.07
AACU	-3.067	-0.10
GCCU	-3.069	-0.11
ACUC	-3.076	-0.11
UGUA	-3.079	-0.12
CCUC	-3.079	-0.12
CAUA	-3.082	-0.12
GCUU	-3.086	-0.12
AUUG	-3.093	-0.13
GCAC	-3.096	-0.13
GUUC	-3.097	-0.13
CACG	-3.102	-0.14
CACA	-3.104	-0.14
GACU	-3.110	-0.15
GGUG	-3.118	-0.15
GGUC	-3.120	-0.16
CCGU	-3.126	-0.16
UCUC	-3.127	-0.16
AUAG	-3.137	-0.17
AUUC	-3.139	-0.18
CUCC	-3.152	-0.19
GUAU	-3.154	-0.19
AAUG	-3.160	-0.20
UAAG	-3.167	-0.20
UGGA	-3.174	-0.21
UACC	-3.177	-0.21
GGCU	-3.177	-0.21
CCUU	-3.178	-0.21
UCGU	-3.194	-0.23
AAGA	-3.195	-0.23
CACC	-3.201	-0.24
GUGG	-3.212	-0.25
UGCG	-3.212	-0.25
GCUA	-3.219	-0.26
ACUG	-3.221	-0.26
UGGG	-3.221	-0.26
GACC	-3.227	-0.26
AGGC	-3.232	-0.27
UCUA	-3.234	-0.27
AGGA	-3.235	-0.27
GACG	-3.236	-0.27
GUAC	-3.237	-0.27
CUAG	-3.238	-0.27
GUUG	-3.238	-0.27
ACCU	-3.238	-0.28
GCUG	-3.238	-0.28
UUGG	-3.242	-0.28
ACGC	-3.245	-0.28
UCGG	-3.248	-0.29
CUUC	-3.251	-0.29
CUAC	-3.259	-0.30
AAUU	-3.263	-0.30
GAGG	-3.273	-0.31
CAUU	-3.276	-0.31
UGAC	-3.276	-0.31
CCCU	-3.279	-0.32
UAGA	-3.284	-0.32
AGUC	-3.293	-0.33
CUGG	-3.297	-0.33
GUGC	-3.312	-0.35
GGAC	-3.330	-0.37
UUGA	-3.333	-0.37

UCCGA	-3.521	0.14
UGAGG	-3.524	0.13
UGGGA	-3.525	0.13
ACCAG	-3.530	0.13
AUGCC	-3.531	0.13
CUUUU	-3.532	0.13
ACAUA	-3.535	0.12
CAGGA	-3.538	0.12
CUCAG	-3.543	0.11
CUUCA	-3.544	0.11
GCUUG	-3.545	0.11
UUUAC	-3.547	0.11
AUCAU	-3.548	0.11
AACUU	-3.550	0.11
CACAG	-3.551	0.11
AAGUC	-3.553	0.10
UCCCC	-3.554	0.10
UUCCG	-3.555	0.10
AGAAC	-3.557	0.10
UGUAC	-3.558	0.10
UCUCU	-3.558	0.10
UGAAA	-3.561	0.10
CAAAA	-3.561	0.10
UCCGU	-3.561	0.10
AUUUC	-3.564	0.09
UUGAU	-3.564	0.09
UAGGC	-3.566	0.09
UAUAC	-3.566	0.09
CUCCA	-3.569	0.09
UUCCA	-3.569	0.09
UUUGA	-3.569	0.09
UACAG	-3.572	0.09
CCUUU	-3.573	0.08
UACAA	-3.576	0.08
UUCAA	-3.577	0.08
UUAAU	-3.579	0.08
AUGUC	-3.582	0.08
CUGGU	-3.582	0.08
UAUGC	-3.582	0.08
CUUAA	-3.584	0.07
UUCAC	-3.586	0.07
CUCUG	-3.587	0.07
AUGAA	-3.591	0.07
CAGCC	-3.592	0.07
UGAGA	-3.598	0.06
UCUGG	-3.605	0.05
UUGAC	-3.607	0.05
GUCAU	-3.615	0.04
UGAAG	-3.615	0.04
UGCUA	-3.616	0.04
UGUAG	-3.616	0.04
AUCAG	-3.617	0.04
GGAGA	-3.619	0.04
AUUCC	-3.619	0.04
UGGUC	-3.619	0.04
UCAAA	-3.622	0.04
CAUUU	-3.623	0.03
ACAUC	-3.633	0.02
GAAUG	-3.633	0.02
AAUAC	-3.636	0.02
GCCAG	-3.636	0.02
CCUAG	-3.639	0.02
GAGGA	-3.639	0.02
GUACA	-3.639	0.02
CUGGC	-3.645	0.01
GGAUA	-3.645	0.01
UUACA	-3.647	0.01
GCACA	-3.648	0.01
UCUAC	-3.648	0.01

AGAC	-3.337	-0.37
GAGC	-3.339	-0.38
UACU	-3.343	-0.38
AACC	-3.345	-0.38
CUUA	-3.351	-0.39
GUCG	-3.353	-0.39
ACGA	-3.358	-0.39
UACG	-3.361	-0.40
UAGG	-3.361	-0.40
GCGC	-3.381	-0.42
CCUA	-3.387	-0.42
CGGC	-3.389	-0.43
CCGG	-3.397	-0.43
CAUC	-3.412	-0.45
AGCC	-3.414	-0.45
AUCC	-3.422	-0.46
AGGG	-3.424	-0.46
GCCC	-3.426	-0.46
CAGA	-3.431	-0.47
CUGA	-3.441	-0.48
CGGU	-3.448	-0.48
GGCG	-3.460	-0.50
ACUU	-3.463	-0.50
CAGG	-3.471	-0.51
CUAA	-3.479	-0.52
CGAU	-3.502	-0.54
CGUG	-3.507	-0.54
CAUG	-3.526	-0.56
GCUC	-3.541	-0.58
CGAA	-3.556	-0.59
ACCG	-3.556	-0.59
CGCU	-3.622	-0.66
CCCG	-3.634	-0.67
AUAC	-3.639	-0.68
GGCC	-3.639	-0.68
CGAC	-3.715	-0.75
CGAG	-3.739	-0.78
CGGA	-3.759	-0.80
CCGC	-3.762	-0.80
CGUU	-3.776	-0.81
AACG	-3.782	-0.82
UCGA	-3.789	-0.83
ACGG	-3.793	-0.83
CCGA	-3.818	-0.86
CGGG	-3.818	-0.86
AUCG	-3.838	-0.87
AGCG	-3.867	-0.90
GCGG	-3.973	-1.01
CGUA	-3.978	-1.01
CGCA	-4.026	-1.06
GCCG	-4.071	-1.11
CGUC	-4.185	-1.22
CGCC	-4.344	-1.38
CGCG	-4.418	-1.45

AUAUG	-3.650	0.01
GACUG	-3.653	0.00
UUAGU	-3.653	0.00
UAGCC	-3.654	0.00
CUUGC	-3.655	0.00
GCUAU	-3.655	0.00
AUCAA	-3.656	0.00
UCCCA	-3.659	0.00
AGCUA	-3.662	0.00
AUGGA	-3.663	-0.01
UAAUA	-3.664	-0.01
UAGUC	-3.664	-0.01
AUCCA	-3.668	-0.01
CAAUG	-3.671	-0.01
AAUAA	-3.672	-0.01
UAUGA	-3.674	-0.02
UGGCU	-3.674	-0.02
UCUUC	-3.676	-0.02
AAUGG	-3.679	-0.02
GCUCU	-3.679	-0.02
AAAUC	-3.681	-0.02
CUUGG	-3.684	-0.03
UUCUA	-3.684	-0.03
GCUAA	-3.685	-0.03
AUAUU	-3.688	-0.03
UACCU	-3.688	-0.03
UGAUG	-3.690	-0.03
GAAUU	-3.690	-0.03
UCGCC	-3.690	-0.03
UCUAU	-3.692	-0.03
UAAAA	-3.697	-0.04
GUGUA	-3.698	-0.04
CUUAG	-3.701	-0.04
CUGCC	-3.703	-0.05
CUUCC	-3.704	-0.05
GUAGU	-3.705	-0.05
GCUGA	-3.707	-0.05
CCAGA	-3.707	-0.05
GCAUU	-3.708	-0.05
CUACC	-3.708	-0.05
UGCUG	-3.710	-0.05
AUGAG	-3.713	-0.06
GGUGA	-3.713	-0.06
UCAGU	-3.713	-0.06
AGCAU	-3.714	-0.06
UGCUC	-3.723	-0.07
AAAUA	-3.723	-0.07
CUAGA	-3.727	-0.07
UAUUC	-3.727	-0.07
UUAAA	-3.727	-0.07
AGCAG	-3.730	-0.07
UUCGG	-3.731	-0.07
CUAUC	-3.732	-0.07
CCCGU	-3.733	-0.08
UAAUG	-3.734	-0.08
CUGGA	-3.735	-0.08
AAAAG	-3.736	-0.08
AAGUA	-3.737	-0.08
UCUUG	-3.739	-0.08
UGGUG	-3.740	-0.08
GCUGG	-3.741	-0.08
CCAGU	-3.741	-0.08
ACACA	-3.743	-0.09
AUCUG	-3.746	-0.09
UGGUU	-3.746	-0.09
AUAGU	-3.747	-0.09
UAUCA	-3.748	-0.09
AGGGU	-3.749	-0.09
GAAAA	-3.750	-0.09

UUGCA	-3.750	-0.09
AUGUA	-3.751	-0.09
CUAUG	-3.752	-0.09
ACUUU	-3.753	-0.10
CAGAA	-3.754	-0.10
UCAUU	-3.756	-0.10
CCUGA	-3.757	-0.10
UUUCU	-3.758	-0.10
UACUU	-3.760	-0.10
GUAAU	-3.765	-0.11
UUAAC	-3.768	-0.11
UUGCG	-3.768	-0.11
UUGUA	-3.769	-0.11
ACUCU	-3.770	-0.11
UGGAG	-3.774	-0.12
UUAGA	-3.774	-0.12
UGUCU	-3.776	-0.12
CAUAA	-3.778	-0.12
CUCUA	-3.779	-0.12
UAGGG	-3.781	-0.12
UGAUU	-3.781	-0.12
UAGAU	-3.782	-0.12
ACUAA	-3.782	-0.12
UCUAG	-3.785	-0.13
AGUUU	-3.786	-0.13
AGUUC	-3.788	-0.13
UCCGG	-3.791	-0.13
AAACC	-3.796	-0.14
GGCAG	-3.797	-0.14
CGCGA	-3.799	-0.14
UGCCG	-3.799	-0.14
UCGGC	-3.804	-0.15
UAAGU	-3.804	-0.15
UCUCC	-3.806	-0.15
CUAGC	-3.806	-0.15
CUGUG	-3.806	-0.15
AUAAA	-3.809	-0.15
AUUAU	-3.809	-0.15
CUAAG	-3.810	-0.15
CUCAU	-3.810	-0.15
UGACG	-3.813	-0.16
ACUAG	-3.813	-0.16
AAACA	-3.815	-0.16
CAGGU	-3.815	-0.16
AUUUU	-3.816	-0.16
CCUGC	-3.817	-0.16
AUGGG	-3.818	-0.16
ACCAU	-3.820	-0.16
AGAAU	-3.823	-0.17
CUCAA	-3.824	-0.17
UAUCG	-3.824	-0.17
GCCUU	-3.827	-0.17
UAAAU	-3.833	-0.18
AGCAC	-3.834	-0.18
ACAGU	-3.835	-0.18
ACCUG	-3.835	-0.18
CCCUU	-3.835	-0.18
CCUAU	-3.835	-0.18
UCCUA	-3.835	-0.18
UGCGG	-3.835	-0.18
UCCGC	-3.839	-0.18
UGUCG	-3.839	-0.18
GAAAU	-3.840	-0.18
ACAGC	-3.841	-0.18
GCAUG	-3.842	-0.18
GGUUA	-3.847	-0.19
UGCGA	-3.847	-0.19
AUGUU	-3.849	-0.19
UGUCC	-3.849	-0.19

ACUAU	-3.850	-0.19
AAACU	-3.852	-0.19
GUUCU	-3.853	-0.20
CAGAU	-3.854	-0.20
GGCUA	-3.855	-0.20
UAGUG	-3.855	-0.20
UUACG	-3.855	-0.20
UGACA	-3.856	-0.20
UAAAG	-3.856	-0.20
UAAUU	-3.856	-0.20
UUAUC	-3.859	-0.20
CGACA	-3.861	-0.20
AGGGC	-3.863	-0.21
CCCAC	-3.863	-0.21
CUUUC	-3.863	-0.21
CCCUG	-3.864	-0.21
GUCAA	-3.866	-0.21
GUGUC	-3.866	-0.21
AGAGC	-3.866	-0.21
AAAAU	-3.867	-0.21
ACGUG	-3.871	-0.21
AGCUC	-3.871	-0.21
GGAAG	-3.872	-0.21
UGGGG	-3.873	-0.22
AAGUG	-3.874	-0.22
CCAUU	-3.876	-0.22
UAACA	-3.876	-0.22
GCCAA	-3.877	-0.22
UAUCC	-3.878	-0.22
UCGGU	-3.878	-0.22
UUACU	-3.878	-0.22
AUGGC	-3.880	-0.22
UGGCA	-3.880	-0.22
AAUGU	-3.884	-0.23
CUCAC	-3.892	-0.23
UAGGU	-3.895	-0.24
AAAUU	-3.895	-0.24
UAUGG	-3.895	-0.24
UCUGC	-3.898	-0.24
AUUGG	-3.899	-0.24
AGACA	-3.900	-0.24
AUCGA	-3.900	-0.24
UAGAA	-3.902	-0.24
CACUG	-3.904	-0.25
CCUGG	-3.907	-0.25
CUGAU	-3.907	-0.25
GCCUA	-3.907	-0.25
UAACC	-3.909	-0.25
ACCCA	-3.911	-0.25
AUCCC	-3.913	-0.26
GUCUU	-3.918	-0.26
CCUCU	-3.919	-0.26
AAAGA	-3.921	-0.26
CUACA	-3.921	-0.26
CUCGC	-3.921	-0.26
UUGAA	-3.921	-0.26
CAUCG	-3.924	-0.27
CGACC	-3.924	-0.27
ACAUG	-3.927	-0.27
AAAAC	-3.929	-0.27
ACAAA	-3.929	-0.27
GUUAU	-3.929	-0.27
UUAUG	-3.929	-0.27
GAAGG	-3.930	-0.27
CCACC	-3.933	-0.28
CGCAU	-3.933	-0.28
GGAGU	-3.934	-0.28
AGCGU	-3.935	-0.28
UAUCU	-3.935	-0.28

AUCAC	-3.936	-0.28
AUGCG	-3.937	-0.28
AGAAG	-3.938	-0.28
UACCC	-3.940	-0.28
CUCCG	-3.941	-0.28
AGAGA	-3.946	-0.29
AUACG	-3.946	-0.29
GCUUA	-3.946	-0.29
CACGC	-3.947	-0.29
GUAAA	-3.948	-0.29
UUCGA	-3.950	-0.29
AAUUC	-3.951	-0.29
CCUAA	-3.952	-0.29
AUGAC	-3.958	-0.30
GGCCU	-3.958	-0.30
GUGCC	-3.958	-0.30
UCAAU	-3.958	-0.30
UCAGG	-3.960	-0.30
UGUUA	-3.960	-0.30
AAAUG	-3.962	-0.30
AGUAA	-3.965	-0.31
CACAA	-3.965	-0.31
AUAGC	-3.965	-0.31
AUUGA	-3.965	-0.31
AGGUG	-3.969	-0.31
GACUC	-3.971	-0.31
CAAGA	-3.973	-0.32
GAAAC	-3.974	-0.32
GUGGC	-3.976	-0.32
GUUGU	-3.976	-0.32
GUCUA	-3.979	-0.32
GUUGA	-3.979	-0.32
UACUC	-3.979	-0.32
GCUAG	-3.981	-0.32
UACAC	-3.981	-0.32
GUGCG	-3.982	-0.32
ACUCA	-3.983	-0.33
GGAGG	-3.988	-0.33
CAACC	-3.989	-0.33
CCAUG	-3.991	-0.33
ACCUC	-3.994	-0.34
AUGAU	-3.994	-0.34
CCAAU	-3.994	-0.34
CGCUC	-3.994	-0.34
UCAUC	-3.994	-0.34
ACAUU	-4.003	-0.35
AGUAC	-4.003	-0.35
CAAAU	-4.003	-0.35
GGGGC	-4.003	-0.35
GUUAA	-4.003	-0.35
AAGUU	-4.009	-0.35
AUAAG	-4.009	-0.35
CAUGA	-4.009	-0.35
GAGCA	-4.009	-0.35
GCCCA	-4.009	-0.35
UGAAC	-4.009	-0.35
UGUUG	-4.009	-0.35
CCCAA	-4.012	-0.35
AACUA	-4.014	-0.36
ACUGG	-4.014	-0.36
AGGUC	-4.015	-0.36
CAGUA	-4.015	-0.36
GUUCG	-4.015	-0.36
AGUCC	-4.022	-0.36
AGUUA	-4.022	-0.36
CCCGG	-4.029	-0.37
AGUGA	-4.031	-0.37
CCCGC	-4.031	-0.37
GAUGG	-4.032	-0.37

GGGUC	-4.032	-0.37
UCCCG	-4.034	-0.38
AUUCU	-4.039	-0.38
CACUU	-4.039	-0.38
UGCCC	-4.039	-0.38
AAUUA	-4.043	-0.39
AGGUA	-4.043	-0.39
AUGGU	-4.043	-0.39
CAAGG	-4.043	-0.39
CUUUA	-4.043	-0.39
GUGCA	-4.043	-0.39
GAUGU	-4.046	-0.39
AGCCA	-4.047	-0.39
CGCGC	-4.055	-0.40
GACCU	-4.055	-0.40
GGAUC	-4.055	-0.40
GACCA	-4.058	-0.40
GCCUG	-4.058	-0.40
GACUA	-4.062	-0.40
AAAGG	-4.064	-0.41
CGUAA	-4.064	-0.41
GUGGU	-4.064	-0.41
UAUUA	-4.064	-0.41
UGGAA	-4.064	-0.41
UGUCA	-4.064	-0.41
ACGAG	-4.068	-0.41
ACUUC	-4.068	-0.41
AUCUU	-4.068	-0.41
GAUCU	-4.068	-0.41
GCCGG	-4.068	-0.41
UCAGC	-4.068	-0.41
UCGAG	-4.068	-0.41
UUAGC	-4.068	-0.41
UUGAG	-4.068	-0.41
AUAGA	-4.070	-0.41
CAACA	-4.072	-0.41
CCCGA	-4.072	-0.41
AGAUG	-4.073	-0.42
CACAU	-4.073	-0.42
GAGAA	-4.073	-0.42
CGUAU	-4.080	-0.42
CUAUU	-4.080	-0.42
GAAUC	-4.080	-0.42
UAACU	-4.080	-0.42
UAGUA	-4.080	-0.42
AGUUG	-4.083	-0.43
AUCUA	-4.083	-0.43
GCUCG	-4.083	-0.43
AACAC	-4.088	-0.43
AAUAG	-4.088	-0.43
ACAGA	-4.088	-0.43
GAAAG	-4.088	-0.43
GAGUG	-4.088	-0.43
GUUUA	-4.088	-0.43
GUUUG	-4.088	-0.43
UCACU	-4.088	-0.43
UUGGA	-4.088	-0.43
UUUCA	-4.088	-0.43
CUGCA	-4.092	-0.43
AAGAA	-4.093	-0.44
AACGC	-4.099	-0.44
ACUCC	-4.099	-0.44
GGAGC	-4.099	-0.44
GGCGC	-4.099	-0.44
GGCUG	-4.099	-0.44
AAUGA	-4.105	-0.45
GUAGA	-4.105	-0.45
GUCCU	-4.105	-0.45
UAGUU	-4.105	-0.45

UCAAC	-4.105	-0.45
AACAA	-4.117	-0.46
AACAG	-4.117	-0.46
AACAU	-4.117	-0.46
AAUAU	-4.117	-0.46
AAUCU	-4.117	-0.46
AUGCA	-4.117	-0.46
CAACU	-4.117	-0.46
CAGUC	-4.117	-0.46
CCAAC	-4.117	-0.46
CUCCU	-4.117	-0.46
GGAAA	-4.117	-0.46
GUUGG	-4.117	-0.46
UACUA	-4.117	-0.46
UCUCA	-4.117	-0.46
AAGGC	-4.119	-0.46
GUGAC	-4.119	-0.46
GCGUA	-4.121	-0.46
CGUGC	-4.124	-0.47
CUCGA	-4.124	-0.47
GCAGG	-4.124	-0.47
GGUUC	-4.126	-0.47
ACUAC	-4.128	-0.47
CUCUC	-4.128	-0.47
AAGAG	-4.131	-0.47
GGGAA	-4.131	-0.47
GAACA	-4.135	-0.48
CCAAA	-4.138	-0.48
GAAGA	-4.138	-0.48
GACAC	-4.138	-0.48
AGUGG	-4.140	-0.48
CAAGC	-4.140	-0.48
GUUCA	-4.140	-0.48
CAUUG	-4.145	-0.49
UGAUC	-4.145	-0.49
CGACG	-4.148	-0.49
AACUG	-4.154	-0.50
AAGGU	-4.154	-0.50
AAUGC	-4.154	-0.50
ACACC	-4.154	-0.50
AGCUU	-4.154	-0.50
AUCGG	-4.154	-0.50
CACGG	-4.154	-0.50
CCCCG	-4.154	-0.50
CGAGC	-4.154	-0.50
CUAAU	-4.154	-0.50
CUGAA	-4.154	-0.50
GAAGU	-4.154	-0.50
GCGUG	-4.154	-0.50
GGGCA	-4.154	-0.50
GUUAG	-4.154	-0.50
UGAUA	-4.154	-0.50
GCGAU	-4.159	-0.50
AGGAC	-4.162	-0.50
CCGUG	-4.162	-0.50
CUGAC	-4.162	-0.50
GGAAC	-4.162	-0.50
GGAUG	-4.162	-0.50
GUAGC	-4.162	-0.50
UCUUA	-4.162	-0.50
UUAUU	-4.162	-0.50
CAAAC	-4.168	-0.51
CAGCU	-4.168	-0.51
UAAGC	-4.168	-0.51
GGUGU	-4.171	-0.51
UUAGG	-4.171	-0.51
ACCCU	-4.174	-0.52
CUAAA	-4.174	-0.52
CACAC	-4.177	-0.52

AUAGG	-4.181	-0.52
CCUCA	-4.181	-0.52
AUAUC	-4.184	-0.53
CACCU	-4.184	-0.53
CACUC	-4.184	-0.53
AGUCU	-4.191	-0.53
CUCGG	-4.191	-0.53
CUUAC	-4.191	-0.53
AAUCA	-4.191	-0.53
AGUAG	-4.191	-0.53
GGGGU	-4.191	-0.53
UACGU	-4.191	-0.53
GUGUG	-4.195	-0.54
CCAGC	-4.198	-0.54
UACCG	-4.198	-0.54
ACUGC	-4.202	-0.54
AGGCC	-4.202	-0.54
AUUGC	-4.202	-0.54
CAUCU	-4.202	-0.54
GGGGG	-4.202	-0.54
GUCAC	-4.202	-0.54
GUGAA	-4.202	-0.54
GUGUU	-4.202	-0.54
GUUCC	-4.202	-0.54
UAAGA	-4.202	-0.54
UAAGG	-4.202	-0.54
AGGAG	-4.210	-0.55
AACCU	-4.214	-0.56
AUGCU	-4.214	-0.56
CAAGU	-4.214	-0.56
CACGU	-4.214	-0.56
CGAGA	-4.214	-0.56
GAGGG	-4.214	-0.56
GGACU	-4.214	-0.56
GGGAG	-4.219	-0.56
CAGUU	-4.223	-0.57
CCCCU	-4.223	-0.57
CCUCC	-4.223	-0.57
CGCAC	-4.223	-0.57
GGUGG	-4.223	-0.57
UACGC	-4.223	-0.57
UACGG	-4.223	-0.57
AAGCA	-4.227	-0.57
ACCAA	-4.227	-0.57
ACGGC	-4.227	-0.57
AGCCC	-4.227	-0.57
AGGUU	-4.227	-0.57
CAAUC	-4.227	-0.57
CUACU	-4.227	-0.57
CUAGG	-4.227	-0.57
GAUAC	-4.227	-0.57
GCAGC	-4.227	-0.57
GUAUG	-4.227	-0.57
GUUUC	-4.227	-0.57
UAGCU	-4.227	-0.57
UCGUC	-4.227	-0.57
UCGUU	-4.227	-0.57
CCGAA	-4.237	-0.58
GAGUA	-4.237	-0.58
AUAAC	-4.242	-0.58
CACCA	-4.242	-0.58
CAUUC	-4.242	-0.58
CCCCC	-4.242	-0.58
CCGGC	-4.242	-0.58
CGUGA	-4.242	-0.58
GCUUU	-4.242	-0.58
GGCGA	-4.242	-0.58
AACCC	-4.247	-0.59
AAGGA	-4.247	-0.59

ACACU	-4.247	-0.59
AGAUA	-4.247	-0.59
CAUAC	-4.247	-0.59
CCAAG	-4.247	-0.59
CCUUA	-4.247	-0.59
CGGGC	-4.247	-0.59
GGAUU	-4.247	-0.59
GGGGA	-4.247	-0.59
CGAUG	-4.252	-0.59
CAUAU	-4.258	-0.60
GCAAG	-4.258	-0.60
AACGU	-4.264	-0.61
AAGGG	-4.264	-0.61
ACGUA	-4.264	-0.61
AGACG	-4.264	-0.61
CAGCA	-4.264	-0.61
CUGUC	-4.264	-0.61
CUGUU	-4.264	-0.61
GAUAA	-4.264	-0.61
GUCCA	-4.264	-0.61
ACCUU	-4.276	-0.62
ACGCA	-4.276	-0.62
ACUUA	-4.276	-0.62
AGAUU	-4.276	-0.62
AGCAA	-4.276	-0.62
AGGGA	-4.276	-0.62
CCACU	-4.276	-0.62
CCAUA	-4.276	-0.62
CCCUC	-4.276	-0.62
CCUUC	-4.276	-0.62
CGGGG	-4.276	-0.62
CUGCU	-4.276	-0.62
GAACC	-4.276	-0.62
GAGAU	-4.276	-0.62
GAUUU	-4.276	-0.62
GGCUU	-4.276	-0.62
GUUAC	-4.276	-0.62
UCACA	-4.276	-0.62
UCGAA	-4.276	-0.62
UUAAG	-4.276	-0.62
CAGGG	-4.283	-0.63
CCCAU	-4.283	-0.63
CGGCC	-4.283	-0.63
GAGAG	-4.290	-0.63
AACCA	-4.297	-0.64
CAAAG	-4.297	-0.64
CAGGC	-4.297	-0.64
CCUCG	-4.297	-0.64
CGCAG	-4.297	-0.64
GAUGC	-4.297	-0.64
GGCAU	-4.297	-0.64
GGGUA	-4.297	-0.64
UAAUC	-4.297	-0.64
GGUAA	-4.305	-0.65
ACGCU	-4.313	-0.66
ACGGU	-4.313	-0.66
AUCCU	-4.313	-0.66
CCGCC	-4.313	-0.66
CGAAC	-4.313	-0.66
CGGUG	-4.313	-0.66
CGUCA	-4.313	-0.66
GCCAC	-4.313	-0.66
GUACU	-4.313	-0.66
GUGAU	-4.313	-0.66
UAACG	-4.313	-0.66
UCAGA	-4.313	-0.66
GGUAG	-4.321	-0.66
GUGGG	-4.321	-0.66
AACUC	-4.321	-0.66

ACACG	-4.321	-0.66
ACGAA	-4.321	-0.66
ACGUU	-4.321	-0.66
AGACC	-4.321	-0.66
GCCCG	-4.321	-0.66
GGCAC	-4.321	-0.66
UAGAC	-4.321	-0.66
AGUGC	-4.330	-0.67
CACGA	-4.330	-0.67
CGAAA	-4.330	-0.67
GGUGC	-4.330	-0.67
UAAAC	-4.330	-0.67
GCAAC	-4.340	-0.68
GUACC	-4.340	-0.68
AAGCC	-4.350	-0.69
ACCAC	-4.350	-0.69
ACGGG	-4.350	-0.69
ACUCG	-4.350	-0.69
AGCCU	-4.350	-0.69
AGCUG	-4.350	-0.69
AUUAC	-4.350	-0.69
CAACG	-4.350	-0.69
CGAAU	-4.350	-0.69
CGGGU	-4.350	-0.69
CGUCC	-4.350	-0.69
CUGAG	-4.350	-0.69
CUGUA	-4.350	-0.69
GAUUC	-4.350	-0.69
GGGUG	-4.350	-0.69
GUAAC	-4.350	-0.69
GUCUC	-4.350	-0.69
AAGAU	-4.361	-0.70
ACAAG	-4.361	-0.70
CCACA	-4.361	-0.70
CCAGG	-4.361	-0.70
CGAGU	-4.361	-0.70
CGUUU	-4.361	-0.70
GAUAU	-4.361	-0.70
GCACG	-4.361	-0.70
GCUCC	-4.361	-0.70
GUAUU	-4.361	-0.70
CAAUA	-4.373	-0.72
CAGAG	-4.373	-0.72
CCGGA	-4.373	-0.72
CGACU	-4.373	-0.72
GAAGC	-4.373	-0.72
GGUCA	-4.373	-0.72
AAUUG	-4.387	-0.73
ACCGA	-4.387	-0.73
ACGAU	-4.387	-0.73
AGGAU	-4.387	-0.73
AUACC	-4.387	-0.73
AUACU	-4.387	-0.73
AUCGU	-4.387	-0.73
AUCUC	-4.387	-0.73
AUUCA	-4.387	-0.73
CGAGG	-4.387	-0.73
CGGAC	-4.387	-0.73
CUAAC	-4.387	-0.73
GAGUU	-4.387	-0.73
GCAGA	-4.387	-0.73
GCGCG	-4.387	-0.73
GCGGG	-4.387	-0.73
GGUAC	-4.387	-0.73
GUCGU	-4.387	-0.73
UACCA	-4.387	-0.73
UAGAG	-4.387	-0.73
AGAGU	-4.401	-0.74
CGCGU	-4.401	-0.74

CGCUG	-4.401	-0.74
GAACU	-4.401	-0.74
GAGAC	-4.401	-0.74
UACGA	-4.401	-0.74
AAUCG	-4.417	-0.76
ACAAU	-4.417	-0.76
ACCUA	-4.417	-0.76
AGCGC	-4.417	-0.76
CAUAG	-4.417	-0.76
CGGGA	-4.417	-0.76
GAUAG	-4.417	-0.76
GGACC	-4.417	-0.76
AAAGU	-4.435	-0.78
ACGGA	-4.435	-0.78
AGCGG	-4.435	-0.78
AGGCU	-4.435	-0.78
AGUCA	-4.435	-0.78
CAGAC	-4.435	-0.78
CAGUG	-4.435	-0.78
CAUGG	-4.435	-0.78
CCGAG	-4.435	-0.78
CUCCC	-4.435	-0.78
GACAU	-4.435	-0.78
GACCG	-4.435	-0.78
GAGGC	-4.435	-0.78
GCAGU	-4.435	-0.78
GCCAU	-4.435	-0.78
GGAAU	-4.435	-0.78
GGCGU	-4.435	-0.78
GUAAG	-4.435	-0.78
GUGCU	-4.435	-0.78
UAGGA	-4.435	-0.78
UCGAC	-4.435	-0.78
UCGAU	-4.435	-0.78
ACAGG	-4.456	-0.80
ACGCC	-4.456	-0.80
AGACU	-4.456	-0.80
GAUCA	-4.456	-0.80
GGUAU	-4.456	-0.80
GUCAG	-4.456	-0.80
UAGCG	-4.456	-0.80
AAAGC	-4.480	-0.82
ACCCG	-4.480	-0.82
ACCGU	-4.480	-0.82
CGCCU	-4.480	-0.82
CGGUA	-4.480	-0.82
CGUGG	-4.480	-0.82
CUGCG	-4.480	-0.82
CUGGG	-4.480	-0.82
AACGA	-4.509	-0.85
AAGAC	-4.509	-0.85
AAGCG	-4.509	-0.85
AAUCC	-4.509	-0.85
ACGAC	-4.509	-0.85
ACGUC	-4.509	-0.85
AGAGG	-4.509	-0.85
AGCCG	-4.509	-0.85
AGGCA	-4.509	-0.85
AGGCG	-4.509	-0.85
CACCC	-4.509	-0.85
CCGUU	-4.509	-0.85
CCUUG	-4.509	-0.85
CGCCC	-4.509	-0.85
CGGCA	-4.509	-0.85
CGGCU	-4.509	-0.85
GACGA	-4.509	-0.85
GCAAA	-4.509	-0.85
GCGGU	-4.509	-0.85
GCUGC	-4.509	-0.85

GGCAA	-4.509	-0.85
GGCGG	-4.509	-0.85
GUAGG	-4.509	-0.85
GUUGC	-4.509	-0.85
UCACC	-4.509	-0.85
ACGCG	-4.546	-0.89
AGAUC	-4.546	-0.89
AGCGA	-4.546	-0.89
AGGGG	-4.546	-0.89
AGUAU	-4.546	-0.89
CACUA	-4.546	-0.89
CAUUA	-4.546	-0.89
CCGAC	-4.546	-0.89
CGGAU	-4.546	-0.89
CGGUC	-4.546	-0.89
CUACG	-4.546	-0.89
GACGU	-4.546	-0.89
GACUU	-4.546	-0.89
GAGCC	-4.546	-0.89
GAUUG	-4.546	-0.89
GCAUC	-4.546	-0.89
GGUCC	-4.546	-0.89
UAGCA	-4.546	-0.89
UCGCA	-4.546	-0.89
UCGGG	-4.546	-0.89
UGGCG	-4.546	-0.89
AAACG	-4.594	-0.94
AACCG	-4.594	-0.94
ACCGG	-4.594	-0.94
CAAUU	-4.594	-0.94
CCGCU	-4.594	-0.94
CCGUC	-4.594	-0.94
CGCCA	-4.594	-0.94
CGCCG	-4.594	-0.94
CGGAG	-4.594	-0.94
CGGUU	-4.594	-0.94
CGUAG	-4.594	-0.94
GAGGU	-4.594	-0.94
GAUCG	-4.594	-0.94
GCACC	-4.594	-0.94
GCGUU	-4.594	-0.94
GGCCG	-4.594	-0.94
GGCUC	-4.594	-0.94
GGGAC	-4.594	-0.94
GGGUU	-4.594	-0.94
GGUUG	-4.594	-0.94
GUACG	-4.594	-0.94
GUAUC	-4.594	-0.94
GUCGA	-4.594	-0.94
GUCUG	-4.594	-0.94
GUGAG	-4.594	-0.94
UCGCU	-4.594	-0.94
UCGUA	-4.594	-0.94
AACGG	-4.668	-1.01
AAGCU	-4.668	-1.01
ACAAC	-4.668	-1.01
ACCCC	-4.668	-1.01
AUCCG	-4.668	-1.01
CAGCG	-4.668	-1.01
CAUCC	-4.668	-1.01
CCACG	-4.668	-1.01
CCAUC	-4.668	-1.01
CCGCG	-4.668	-1.01
CCGGG	-4.668	-1.01
CCGGU	-4.668	-1.01
CCUAC	-4.668	-1.01
CGAAG	-4.668	-1.01
CGAUA	-4.668	-1.01
CGAUC	-4.668	-1.01

CGAUU	-4.668	-1.01
CGCAA	-4.668	-1.01
CGCGG	-4.668	-1.01
CGCUA	-4.668	-1.01
CGCUU	-4.668	-1.01
CGGAA	-4.668	-1.01
CGUAC	-4.668	-1.01
CGUCU	-4.668	-1.01
CGUUC	-4.668	-1.01
CGUUG	-4.668	-1.01
GACAG	-4.668	-1.01
GACGG	-4.668	-1.01
GAGCG	-4.668	-1.01
GAGCU	-4.668	-1.01
GAGUC	-4.668	-1.01
GCACU	-4.668	-1.01
GCCCU	-4.668	-1.01
GCGAA	-4.668	-1.01
GCGAG	-4.668	-1.01
GCUUC	-4.668	-1.01
GGACG	-4.668	-1.01
GGCCA	-4.668	-1.01
GGCCC	-4.668	-1.01
GGGAU	-4.668	-1.01
GGGCU	-4.668	-1.01
GGUCG	-4.668	-1.01
GGUCU	-4.668	-1.01
GUCCC	-4.668	-1.01
GUCGC	-4.668	-1.01
UCACG	-4.668	-1.01
UCGGA	-4.668	-1.01
ACCGC	-4.827	-1.17
AGUCG	-4.827	-1.17
AUCGC	-4.827	-1.17
CACCG	-4.827	-1.17
CCCUA	-4.827	-1.17
CCGAU	-4.827	-1.17
CCGCA	-4.827	-1.17
CCGUA	-4.827	-1.17
CGGCG	-4.827	-1.17
CGUUA	-4.827	-1.17
GAACG	-4.827	-1.17
GACCC	-4.827	-1.17
GACGC	-4.827	-1.17
GAUCC	-4.827	-1.17
GCAAU	-4.827	-1.17
GCCCC	-4.827	-1.17
GCCGA	-4.827	-1.17
GCCGC	-4.827	-1.17
GCCGU	-4.827	-1.17
GCCUC	-4.827	-1.17
GCGAC	-4.827	-1.17
GCGCC	-4.827	-1.17
GCGCU	-4.827	-1.17
GCGGA	-4.827	-1.17
GCGGC	-4.827	-1.17
GCGUC	-4.827	-1.17
GCUAC	-4.827	-1.17
GGGCC	-4.827	-1.17
GGGCG	-4.827	-1.17
GUCCG	-4.827	-1.17
GUCGG	-4.827	-1.17
UCGCG	-4.827	-1.17

Table S25. Biloops

Loop	Score	SD
UA	-0.917	0.830
UU	-1.058	0.461
AA	-1.149	0.077
CA	-1.200	0.176
AG	-1.238	0.076
UG	-1.309	0.335
GA	-1.313	0.262
CU	-1.370	0.355
AC	-1.405	0.468
GG	-1.418	0.255
UC	-1.462	0.444
AU	-1.548	0.140
GU	-1.570	0.536
CC	-1.627	0.428
GC	-2.100	0.324
CG	-2.171	0.211

Loop	Total loop count
AA	1095
AC	304
AG	863
AU	308
CA	1274
CC	213
CG	67
CU	361
GA	605
GC	92
GG	349
GU	228
UA	6474
UC	350
UG	841
UU	654

Supercategory	Total loop count
Antisense	926
Gene	11897
SnoRNA	1255

Antisense scores

Table S26. Triloops

Loop	Score	SD
UAA	-1.728	1.655
UAU	-1.782	0.188
UUU	-1.803	1.004
ACC	-1.804	1.458
CAU	-1.834	0.698
CAA	-1.874	0.529
UCA	-1.941	1.377
AAA	-1.944	0.523
UGU	-1.964	0.654
CCA	-1.968	0.499
ACA	-2.003	0.022
CUA	-2.074	0.177
CUC	-2.114	0.115
AUA	-2.118	0.955
GAU	-2.128	0.458
GAA	-2.136	0.518
UCU	-2.149	0.913
AUU	-2.214	0.602
AUC	-2.232	0.372
UUC	-2.272	0.717
AGC	-2.291	0.672
UUA	-2.316	0.817
AAC	-2.351	0.700
AAU	-2.357	0.247
UAG	-2.358	0.545
UGA	-2.392	0.897
CUU	-2.455	0.488
GCU	-2.460	0.720
AUG	-2.503	0.177
UCC	-2.505	0.517
GGC	-2.509	0.661
CAC	-2.517	0.322
UGG	-2.524	0.617
CCU	-2.528	0.150
GUU	-2.541	0.518
UUG	-2.543	0.829
CUG	-2.552	0.160
ACU	-2.554	0.419
UAC	-2.565	0.949
GAG	-2.607	1.226
GCA	-2.625	0.179
AGU	-2.647	0.268
GGU	-2.655	0.255
AGA	-2.657	0.673
UGC	-2.666	0.762
AAG	-2.674	0.531
GUA	-2.685	0.389
CCC	-2.734	0.493
CAG	-2.777	0.901
GUG	-2.891	0.981
UCG	-2.931	1.068
GAC	-3.022	0.639
GUC	-3.027	0.441
CGU	-3.034	0.865
GGA	-3.112	1.223
ACG	-3.187	0.353
CGA	-3.268	1.051
AGG	-3.332	0.854
GCC	-3.401	1.409
CGC	-3.438	0.466
GGG	-3.457	1.337
GCG	-3.497	0.380
CCG	-3.536	0.355
CGG	-3.571	0.469

Loop	Total loop count
AAA	1484
AAC	366
AAG	238
AAU	363
ACA	787
ACC	32916
ACG	42
ACU	383
AGA	299
AGC	563
AGG	67
AGU	158
AUA	2257
AUC	737
AUG	277
AUU	1525
CAA	1371
CAC	194
CAG	295
CAU	3111
CCA	2047
CCC	126
CCG	18
CCU	210
CGA	197
CGC	36
CGG	28
CGU	84
CUA	851
CUC	658
CUG	203
CUU	229
GAA	574
GAC	92
GAG	434
GAU	477
GCA	172
GCC	798
GCG	21
GCU	393
GGA	178
GGC	607
GGG	94
GGU	144
GUA	190
GUC	84
GUG	166
GUU	193
UAA	12585
UAC	294
UAG	593
UAU	1447
UCA	2103
UCC	215
UCG	141
UCU	756
UGA	820
UGC	214
UGG	357
UGU	803
UUA	554
UUC	449
UUG	245
UUU	2009

Supercategory	Total loop count
Antisense	47410
Gene	24766
SnoRNA	8146

Loop	Score	SD
UUUU	-1.508	0.430
GAAA	-1.656	0.957
AAAG	-1.793	0.716
UUCG	-1.853	0.605
GGAA	-1.903	0.723
GUAA	-1.968	0.247
GCAA	-2.010	0.263
AAAA	-2.062	0.349
GGAG	-2.109	1.098
GAGU	-2.170	0.736
UUAU	-2.185	0.346
AUUU	-2.199	0.206
GUCA	-2.201	0.745
UCAU	-2.204	0.786
UAUA	-2.210	0.862
UGGC	-2.219	1.245
UGGU	-2.264	0.961
UAGU	-2.278	0.285
UCCA	-2.278	0.674
UUGC	-2.303	0.441
ACGU	-2.364	0.792
CUUG	-2.379	0.217
ACCA	-2.382	1.002
UUUG	-2.391	0.609
AAGU	-2.404	0.553
AGAA	-2.404	0.423
GAAU	-2.409	0.204
CUUU	-2.410	0.431
UUGU	-2.418	0.926
AAAU	-2.422	0.429
GCCA	-2.437	1.152
UAUC	-2.439	0.556
GAGA	-2.449	0.536
UAAA	-2.472	0.347
UCUU	-2.472	1.047
UUCA	-2.481	0.458
GUGA	-2.490	0.312
UACA	-2.518	0.454
UGCU	-2.521	0.233
GAUC	-2.535	0.529
CAGU	-2.537	0.577
GAAG	-2.555	0.795
CUCU	-2.556	0.586
GACA	-2.560	0.243
AACA	-2.569	0.384
UUUC	-2.569	0.414
UGUU	-2.572	0.280
UGAU	-2.577	0.559
UUUA	-2.590	0.392
AAAC	-2.591	0.422
AGCU	-2.592	0.436
AGAG	-2.597	0.676
UAAU	-2.605	0.299
AUGU	-2.605	0.583
UUCU	-2.606	0.884
UCCG	-2.611	0.528
CUGC	-2.616	1.102
CUGU	-2.618	0.724
ACCC	-2.619	0.418
UAUU	-2.625	0.392
AUCA	-2.627	0.298
GGGC	-2.638	0.371
UCAA	-2.638	0.152
AGCA	-2.639	0.672
CUCG	-2.649	0.326
UCAC	-2.649	0.501
ACAU	-2.679	0.540
ACAC	-2.705	0.412

Loop	Total loop count
AAAA	1291
AAAC	168
AAAG	1367
AAAU	213
AACA	211
AACC	81
AACG	9
AACU	81
AAGA	91
AAGC	73
AAGG	51
AAGU	233
AAUA	140
AAUC	108
AAUG	40
AAUU	98
ACAA	140
ACAC	131
ACAG	107
ACAU	167
ACCA	734
ACCC	142
ACCG	41
ACCU	37
ACGA	25
ACGC	40
ACGG	8
ACGU	398
ACUA	95
ACUC	48
ACUG	34
ACUU	24
AGAA	402
AGAC	104
AGAG	810
AGAU	110
AGCA	208
AGCC	35
AGCG	11
AGCU	250
AGGA	209
AGGC	205
AGGG	69
AGGU	152
AGUA	88
AGUC	40
AGUG	110
AGUU	75
AUAA	118
AUAC	19
AUAG	88
AUAU	89
AUCA	139
AUCC	22
AUCG	18
AUCU	119
AUGA	62
AUGC	96
AUGG	106
AUGU	149
AUUA	111
AUUC	65
AUUG	46
AUUU	457
CAAA	302
CAAC	72
CAAG	253
CAAU	204

Supercategory	Total loop count
Antisense	12307
Gene	58879
SnoRNA	9305

GAUU	-2.721	1.230
UCAG	-2.737	0.369
UAUG	-2.739	0.409
GUUA	-2.740	0.571
GCGA	-2.742	0.432
AUUA	-2.743	0.300
GAAC	-2.748	0.213
UCGC	-2.751	1.233
GGCA	-2.753	0.175
CCAG	-2.756	1.052
GUAG	-2.765	0.412
ACAA	-2.771	0.299
CCAU	-2.782	0.958
ACAG	-2.784	0.195
UGCC	-2.784	0.362
CAAG	-2.785	0.329
AUGG	-2.788	0.738
AUGC	-2.799	0.353
UUAG	-2.804	0.255
UGUG	-2.817	0.345
AAUA	-2.825	0.253
GGGU	-2.831	0.302
GGGG	-2.834	0.555
GAUG	-2.834	0.277
CAAA	-2.835	0.517
GGUA	-2.837	0.204
UCCU	-2.840	0.867
UCCC	-2.847	0.717
UUAA	-2.855	0.505
UAAC	-2.862	0.404
CAAU	-2.871	1.000
CUCA	-2.880	0.559
CCAC	-2.881	0.378
CCCC	-2.891	0.565
ACUA	-2.892	0.678
UUAC	-2.898	0.452
AUAA	-2.899	0.281
AGUA	-2.903	0.298
CUAU	-2.904	0.709
UAGC	-2.905	1.185
GUCC	-2.909	0.536
AUCU	-2.910	0.907
UGUC	-2.911	0.350
AAUC	-2.915	0.304
GGAU	-2.917	1.178
AAGC	-2.925	0.237
GUCU	-2.933	0.754
CAGC	-2.939	0.382
UGAA	-2.947	0.513
UUCC	-2.948	0.843
GAUA	-2.952	0.265
UGAG	-2.964	0.693
CCCA	-2.967	0.525
UCUG	-2.970	0.781
CAAC	-2.970	0.170
AUGA	-2.970	0.275
AUAU	-2.972	0.299
AGGU	-2.986	0.836
AGAU	-2.987	0.211
AGUG	-2.987	0.505
GUGU	-2.997	0.315
CCAA	-3.000	0.686
GCAG	-3.010	0.831
UGCA	-3.014	0.525
GCGU	-3.026	0.383
GGUU	-3.028	0.383
AGUU	-3.029	0.577
GCAU	-3.029	0.668
GGGA	-3.030	0.387

CACA	66
CACC	47
CACG	72
CACU	54
CAGA	61
CAGC	166
CAGG	43
CAGU	250
CAUA	82
CAUC	21
CAUG	22
CAUU	36
CCAA	106
CCAC	77
CCAG	317
CCAU	232
CCCA	65
CCCC	86
CCCG	13
CCCU	31
CCGA	14
CCGC	17
CCGG	38
CCGU	43
CCUA	36
CCUC	69
CCUG	52
CCUU	50
CGAA	26
CGAC	30
CGAG	55
CGAU	40
CGCA	4
CGCC	2
CGCG	1
CGCU	13
CGGA	30
CGGC	91
CGGG	14
CGGU	73
CGUA	11
CGUC	7
CGUG	20
CGUU	16
CUAA	49
CUAC	30
CUAG	62
CUAU	85
CUCA	103
CUCC	61
CUCG	129
CUCU	222
CUGA	32
CUGC	571
CUGG	35
CUGU	155
CUUA	26
CUUC	33
CUUG	260
CUUU	219
GAAA	12446
GAAC	201
GAAG	1352
GAAU	426
GACA	269
GACC	37
GACG	40
GACU	56
GAGA	855

GUUU	-3.032	0.472
AAGG	-3.034	0.452
CACU	-3.034	0.444
CCUG	-3.036	0.349
AACU	-3.067	0.787
GCCU	-3.069	0.490
ACUC	-3.076	0.588
UGUA	-3.079	0.331
CCUC	-3.079	0.597
CAUA	-3.082	0.684
GCUU	-3.086	0.437
AUUG	-3.093	0.354
GCAC	-3.096	0.570
GUUC	-3.097	0.775
CACG	-3.102	0.987
CACA	-3.104	0.097
GACU	-3.110	0.504
GGUG	-3.118	0.766
GGUC	-3.120	0.259
CCGU	-3.126	0.521
UCUC	-3.127	0.399
AUAG	-3.137	0.281
AUUC	-3.139	0.734
CUCC	-3.152	0.384
GUAU	-3.154	0.246
AAUG	-3.160	0.278
UAAG	-3.167	0.544
UGGA	-3.174	0.769
UACC	-3.177	0.516
GGCU	-3.177	0.351
CCUU	-3.178	0.563
UCGU	-3.194	0.389
AAGA	-3.195	0.625
CACC	-3.201	0.151
GUGG	-3.212	0.623
UGCG	-3.212	0.800
GCUA	-3.219	0.495
ACUG	-3.221	0.372
UGGG	-3.221	0.705
GACC	-3.227	0.312
AGGC	-3.232	0.727
UCUA	-3.234	0.572
AGGA	-3.235	1.017
GACG	-3.236	0.287
GUAC	-3.237	0.356
CUAG	-3.238	0.642
GUUG	-3.238	0.346
ACCU	-3.238	0.359
GCUG	-3.238	0.246
UUGG	-3.242	0.391
ACGC	-3.245	0.427
UCGG	-3.248	1.172
CUUC	-3.251	0.512
CUAC	-3.259	0.477
AAUU	-3.263	1.119
GAGG	-3.273	0.256
CAUU	-3.276	0.247
UGAC	-3.276	1.196
CCCU	-3.279	0.341
UAGA	-3.284	0.476
AGUC	-3.293	0.141
CUGG	-3.297	0.808
GUGC	-3.312	0.382
GGAC	-3.330	0.909
UUGA	-3.333	0.399
AGAC	-3.337	0.913
GAGC	-3.339	0.342
UACU	-3.343	0.992
AACC	-3.345	1.088

GAGC	63
GAGG	45
GAGU	439
GAUA	136
GAUC	222
GAUG	97
GAUU	410
GCAA	738
GCAC	173
GCAG	324
GCAU	269
GCCA	874
GCCC	23
GCCG	6
GCCU	51
GCGA	166
GCGC	102
GCGG	8
GCGU	143
GCUA	39
GCUC	15
GCUG	43
GCUU	49
GGAA	5092
GGAC	309
GGAG	8001
GGAU	500
GGCA	142
GGCC	49
GGCG	57
GGCU	45
GGGA	164
GGGC	330
GGGG	366
GGGU	188
GGUA	110
GGUC	44
GGUG	312
GGUU	86
GUAA	690
GUAC	90
GUAG	315
GUAU	67
GUCA	478
GUCC	71
GUCG	29
GUCU	88
GUGA	187
GUGC	75
GUGG	77
GUGU	77
GUUA	106
GUUC	76
GUUG	38
GUUU	93
UAAA	379
UAAC	218
UAAG	92
UAAU	223
UACA	219
UACC	48
UACG	39
UACU	70
UAGA	113
UAGC	484
UAGG	31
UAGU	483
UAUA	570
UAUC	272

CUUA	-3.351	0.223
GUCG	-3.353	0.675
ACGA	-3.358	0.564
UACG	-3.361	1.075
UAGG	-3.361	0.115
GCGC	-3.381	1.236
CCUA	-3.387	0.805
CGGC	-3.389	0.501
CCGG	-3.397	0.902
CAUC	-3.412	0.329
AGCC	-3.414	0.727
AUCC	-3.422	0.635
AGGG	-3.424	0.840
GCCC	-3.426	0.212
CAGA	-3.431	0.844
CUGA	-3.441	0.462
CGGU	-3.448	0.817
GGCG	-3.460	0.437
ACUU	-3.463	0.699
CAGG	-3.471	0.389
CUAA	-3.479	0.811
CGAU	-3.502	0.878
CGUG	-3.507	0.205
CAUG	-3.526	0.479
GCUC	-3.541	0.375
CGAA	-3.556	0.316
ACCG	-3.556	1.041
CGCU	-3.622	0.244
CCCG	-3.634	0.235
AUAC	-3.639	0.250
GGCC	-3.639	0.589
CGAC	-3.715	0.492
CGAG	-3.739	0.680
CGGA	-3.759	0.481
CCGC	-3.762	0.169
CGUU	-3.776	0.584
AACG	-3.782	0.706
UCGA	-3.789	0.715
ACGG	-3.793	0.535
CCGA	-3.818	0.767
CGGG	-3.818	0.654
AUCG	-3.838	0.479
AGCG	-3.867	0.538
GCGG	-3.973	0.410
CGUA	-3.978	0.359
CGCA	-4.026	0.521
GCCG	-4.071	0.645
CGUC	-4.185	0.259
CGCC	-4.344	0.065
CGCG	-4.418	0.164

UAUG	104
UAUU	146
UCAA	150
UCAC	210
UCAG	125
UCAU	657
UCCA	410
UCCC	90
UCCG	140
UCCU	183
UCGA	9
UCGC	566
UCGG	143
UCGU	40
UCUA	33
UCUC	67
UCUG	73
UCUU	467
UGAA	240
UGAC	575
UGAG	374
UGAU	441
UGCA	86
UGCC	152
UGCG	67
UGCU	198
UGGA	251
UGGC	6867
UGGG	222
UGGU	3056
UGUA	63
UGUC	190
UGUG	104
UGUU	183
UUAA	125
UUAC	76
UUAG	113
UUAU	404
UUCA	192
UUCC	127
UUCG	874
UUCU	234
UUGA	30
UUGC	356
UUGG	64
UUGU	505
UUUA	211
UUUC	152
UUUG	291
UUUU	1835

Loop	Score	SD
UGCAU	-2.488	1.185
UCCAG	-2.496	1.946
UGGGC	-2.540	0.765
UGGGU	-2.571	0.105
UGUGU	-2.733	1.466
UUGCC	-2.747	1.370
UUUAU	-2.786	0.305
UUUUG	-2.816	0.143
CUUGU	-2.832	0.622
AGAAA	-2.842	0.061
UGGUA	-2.864	1.187
UUCUU	-2.886	0.273
CCUGU	-2.892	0.902
UUUAG	-2.909	0.727
UAUGU	-2.912	0.561
UUCGU	-2.921	0.575
UUUUA	-2.924	0.328
UGUGC	-2.930	1.493
UGAGU	-2.931	0.653
UUUCG	-2.934	2.340
UGGAU	-2.953	0.416
UUGUG	-2.954	0.273
UAUAG	-2.967	0.531
UCCUG	-3.013	0.831
CUUUG	-3.013	0.305
UGCUU	-3.026	0.535
UGCAA	-3.036	0.801
AAUUU	-3.059	0.662
UCUAA	-3.065	0.427
CUUCG	-3.075	1.111
UCCAU	-3.093	0.949
AUUUG	-3.105	0.330
UACUG	-3.107	0.656
UGUGG	-3.121	0.614
UGAAU	-3.131	0.478
UUACC	-3.138	0.475
UUGCU	-3.139	0.588
UACAU	-3.142	0.782
UCUGA	-3.142	0.318
UAUAU	-3.146	0.256
UAUUU	-3.181	0.219
UGCAC	-3.182	1.701
UUUUC	-3.185	0.447
UUUCC	-3.186	0.334
UGCAG	-3.188	1.655
UGGAC	-3.190	0.274
UUCUC	-3.195	0.158
CCCAG	-3.208	1.772
UGGCC	-3.213	0.660
GCGCA	-3.224	0.915
UUCGC	-3.228	0.783
AGUGU	-3.235	0.674
AUAAU	-3.240	0.476
UGCGC	-3.249	1.758
AUAUA	-3.253	0.345
UUCAU	-3.254	1.195
UAUAA	-3.256	0.825
CAUGC	-3.262	0.382
AUUAA	-3.267	0.522
UUUGC	-3.273	0.594
UUUUU	-3.273	0.836
UGACC	-3.277	1.062
UUGGC	-3.284	0.208
GCAUA	-3.292	1.760
UGUAU	-3.293	0.985
GUGGA	-3.299	0.913
UUUGU	-3.305	1.592
GAAUA	-3.305	0.495

Loop	Total loop count
AAAAA	51
AAAAC	19
AAAAG	34
AAAAU	27
AAACA	22
AAACC	33
AAACG	2
AAACU	14
AAAGA	54
AAAGC	5
AAAGG	9
AAAGU	3
AAAUA	71
AAAUC	61
AAAUG	66
AAAUU	64
AACAA	23
AACAC	12
AACAG	7
AACAU	11
AACCA	7
AACCC	7
AACCG	2
AACCU	12
AACGA	2
AACGC	12
AACGG	1
AACGU	6
AACUA	17
AACUC	6
AACUG	12
AACUU	42
AAGAA	27
AAGAC	2
AAGAG	21
AAGAU	12
AAGCA	11
AAGCC	5
AAGCG	2
AAGCU	1
AAGGA	7
AAGGC	12
AAGGG	6
AAGGU	6
AAGUA	25
AAGUC	68
AAGUG	74
AAGUU	16
AAUAA	70
AAUAC	64
AAUAG	8
AAUAU	9
AAUCA	8
AAUCC	2
AAUCG	8
AAUCU	11
AAUGA	13
AAUGC	12
AAUGG	34
AAUGU	25
AAUUA	10
AAUUC	20
AAUUG	10
AAUUU	111
ACAAA	19
ACAAC	1
ACAAG	12
ACAAU	8

Supercategory	Total loop count
Antisense	62660
Gene	21365
SnoRNA	28312

UUAUA	-3.311	1.182
UGCGU	-3.321	1.593
CAUGU	-3.322	0.937
UCCCU	-3.324	0.698
UCCUC	-3.329	0.381
AUUCG	-3.330	1.533
UUGGU	-3.334	0.504
AUGUG	-3.342	1.637
UCUGU	-3.344	1.525
UCAAG	-3.348	1.516
UCCAA	-3.349	1.643
CUAGU	-3.350	0.707
UGUUU	-3.352	0.860
UCAUG	-3.356	0.772
UCCAC	-3.361	1.575
AUUAG	-3.362	0.803
UUGUC	-3.368	0.734
UGCCU	-3.369	0.850
ACUGU	-3.369	0.166
UCUCG	-3.372	1.705
UUCCC	-3.373	0.133
ACUUG	-3.381	0.496
GUAUA	-3.383	1.058
CAUCA	-3.384	0.826
CUCGU	-3.388	0.116
GUUUU	-3.389	1.037
GCUCA	-3.390	0.280
UGUGA	-3.390	1.114
UUCAG	-3.392	1.771
UUCCU	-3.401	0.469
UAUUG	-3.407	0.403
CUAUA	-3.407	0.223
UUUAA	-3.409	0.279
UCCUU	-3.411	0.602
AUUGU	-3.415	0.700
UUGGG	-3.417	0.838
UCUUU	-3.423	0.797
UGUAA	-3.433	0.311
GCUGU	-3.434	0.545
UUCUG	-3.441	0.830
GGUUU	-3.444	0.404
UGACU	-3.444	0.816
UGAGC	-3.450	1.321
CUUCU	-3.455	0.319
GACAA	-3.455	0.673
UGCCA	-3.458	0.803
GGACA	-3.458	1.169
UUGUU	-3.458	0.343
GAUUA	-3.459	1.135
CUUAU	-3.461	0.282
AAAAA	-3.466	0.707
CGUCG	-3.470	1.729
UGUUC	-3.471	0.604
CUUGA	-3.474	0.619
UCGUG	-3.476	0.677
UCAUA	-3.482	0.771
CUCUU	-3.489	0.398
ACUGA	-3.491	0.371
UUUGG	-3.495	0.341
AGGAA	-3.497	0.798
CGUGU	-3.498	0.600
AUUUA	-3.505	0.481
CCCCA	-3.506	0.490
AUACA	-3.515	0.198
GAUGA	-3.518	0.335
UCCGA	-3.521	0.580
UGAGG	-3.524	0.652
UGGGA	-3.525	0.651
ACCAG	-3.530	0.879

ACACA	60
ACACC	6
ACACG	6
ACACU	27
ACAGA	12
ACAGC	52
ACAGG	6
ACAGU	26
ACAUA	60
ACAUC	24
ACAUG	84
ACAUU	10
ACCAA	31
ACCAC	5
ACCAG	85
ACCAU	20
ACCCA	14
ACCCC	1
ACCCG	5
ACCCU	9
ACCGA	4
ACCGC	0
ACCGG	2
ACCGU	5
ACCUA	8
ACCUC	11
ACCUG	26
ACCUU	6
ACGAA	6
ACGAC	2
ACGAG	8
ACGAU	4
ACGCA	6
ACGCC	6
ACGCG	3
ACGCU	17
ACGGA	7
ACGGC	5
ACGGG	13
ACGGU	5
ACGUA	6
ACGUC	2
ACGUG	124
ACGUU	6
ACUAA	37
ACUAC	14
ACUAG	16
ACUAU	17
ACUCA	20
ACUCC	26
ACUCG	5
ACUCU	24
ACUGA	35
ACUGC	9
ACUGG	9
ACUGU	42
ACUUA	8
ACUUC	8
ACUUG	58
ACUUU	24
AGAAA	159
AGAAC	44
AGAAG	22
AGAAU	28
AGACA	12
AGACC	16
AGACG	6
AGACU	6
AGAGA	14

AUGCC	-3.531	0.331
CUUUU	-3.532	0.338
ACAUA	-3.535	0.643
CAGGA	-3.538	0.337
CUCAG	-3.543	0.778
CUUCA	-3.544	0.069
GCUUG	-3.545	0.215
UUUAC	-3.547	0.616
AUCAU	-3.548	0.495
AACUU	-3.550	0.782
CACAG	-3.551	0.531
AAGUC	-3.553	0.984
UCCCC	-3.554	0.734
UUCCG	-3.555	0.425
AGAAC	-3.557	0.332
UGUAC	-3.558	1.345
UCUCU	-3.558	0.518
UGAAA	-3.561	1.568
CAAAA	-3.561	0.674
UCCGU	-3.561	1.375
AUUUC	-3.564	0.925
UUGAU	-3.564	0.317
UAGGC	-3.566	0.785
UAUAC	-3.566	0.426
CUCCA	-3.569	0.719
UUCCA	-3.569	0.719
UUUGA	-3.569	0.731
UACAG	-3.572	1.058
CCUUU	-3.573	0.834
UACAA	-3.576	0.368
UUCAA	-3.577	1.327
UUAAU	-3.579	0.757
AUGUC	-3.582	0.962
CUGGU	-3.582	0.426
UAUGC	-3.582	0.994
CUUAA	-3.584	1.336
UUCAC	-3.586	1.357
CUCUG	-3.587	0.780
AUGAA	-3.591	0.276
CAGCC	-3.592	0.879
UGAGA	-3.598	1.112
UCUGG	-3.605	1.117
UUGAC	-3.607	0.393
GUCAU	-3.615	0.308
UGAAG	-3.615	0.323
UGCUA	-3.616	0.876
UGUAG	-3.616	0.709
AUCAG	-3.617	0.287
GGAGA	-3.619	0.748
AUUCC	-3.619	0.715
UGGUC	-3.619	0.443
UCAAA	-3.622	0.629
CAUUU	-3.623	0.877
ACAUC	-3.633	0.096
GAAUG	-3.633	0.787
AAUAC	-3.636	1.042
GCCAG	-3.636	1.482
CCUAG	-3.639	1.276
GAGGA	-3.639	0.608
GUACA	-3.639	1.421
CUGGC	-3.645	0.950
GGAUA	-3.645	1.276
UUACA	-3.647	0.445
GCACA	-3.648	1.810
UCUAC	-3.648	0.695
AUAUG	-3.650	1.413
GACUG	-3.653	0.242
UUAGU	-3.653	0.838
UAGCC	-3.654	0.953

AGAGC	46
AGAGG	4
AGAGU	9
AGAUA	7
AGAUC	3
AGAUG	31
AGAUU	8
AGCAA	8
AGCAC	20
AGCAG	50
AGCAU	30
AGCCA	37
AGCCC	5
AGCCG	2
AGCCU	13
AGCGA	3
AGCGC	8
AGCGG	3
AGCGU	21
AGCUA	27
AGCUC	16
AGCUG	5
AGCUU	12
AGGAA	56
AGGAC	9
AGGAG	35
AGGAU	4
AGGCA	2
AGGCC	5
AGGCG	4
AGGCU	3
AGGGA	4
AGGGC	27
AGGGG	3
AGGGU	29
AGGUA	10
AGGUC	10
AGGUG	39
AGGUU	5
AGUAA	65
AGUAC	10
AGUAG	8
AGUAU	3
AGUCA	3
AGUCC	18
AGUCG	0
AGUCU	6
AGUGA	20
AGUGC	15
AGUGG	13
AGUGU	96
AGUUA	18
AGUUC	56
AGUUG	11
AGUUU	15
AUAAA	56
AUAAC	10
AUAAG	12
AUAAU	70
AUACA	30
AUACC	4
AUACG	10
AUACU	4
AUAGA	13
AUAGC	10
AUAGG	15
AUAGU	45
AUAUA	59
AUAUC	10

CUUGC	-3.655	0.361
GCUAU	-3.655	0.075
AUCAA	-3.656	0.644
UCCCA	-3.659	0.775
AGCUA	-3.662	0.358
AUGGA	-3.663	0.964
UAAUA	-3.664	0.202
UAGUC	-3.664	0.514
AUCCA	-3.668	0.528
CAAUG	-3.671	0.652
AAUAA	-3.672	1.297
UAUGA	-3.674	0.971
UGGCU	-3.674	0.294
UCUUC	-3.676	0.426
AAUGG	-3.679	0.717
GCUCU	-3.679	0.428
AAAUC	-3.681	1.051
CUUGG	-3.684	0.148
UUCUA	-3.684	0.813
GCUAA	-3.685	0.822
AUAUU	-3.688	0.418
UACCU	-3.688	0.373
UGAUG	-3.690	0.633
GAAUU	-3.690	1.057
UCGCC	-3.690	0.921
UCUAU	-3.692	0.517
UAAAA	-3.697	1.045
GUGUA	-3.698	0.724
CUUAG	-3.701	0.555
CUGCC	-3.703	0.234
CUUCC	-3.704	0.433
GUAGU	-3.705	0.494
GCUGA	-3.707	0.664
CCAGA	-3.707	1.081
GCAUU	-3.708	0.108
CUACC	-3.708	0.514
UGCUG	-3.710	0.691
AUGAG	-3.713	0.971
GGUGA	-3.713	0.670
UCAGU	-3.713	0.669
AGCAU	-3.714	0.829
UGCUC	-3.723	1.269
AAAUA	-3.723	1.066
CUAGA	-3.727	0.782
UAUUC	-3.727	0.381
UUAAA	-3.727	0.354
AGCAG	-3.730	0.925
UUCGG	-3.731	0.828
CUAUC	-3.732	0.510
CCCGU	-3.733	0.370
UAAUG	-3.734	1.336
CUGGA	-3.735	0.617
AAAAG	-3.736	0.873
AAGUA	-3.737	0.507
UCUUG	-3.739	0.780
UGGUG	-3.740	0.509
GCUGG	-3.741	0.597
CCAGU	-3.741	1.386
ACACA	-3.743	0.889
AUCUG	-3.746	0.681
UGGUU	-3.746	0.475
AUAGU	-3.747	0.894
UAUCA	-3.748	0.178
AGGGU	-3.749	0.742
GAAAA	-3.750	1.221
UUGCA	-3.750	0.073
AUGUA	-3.751	1.055
CUAUG	-3.752	0.757
ACUUU	-3.753	0.669

AUAUG	120
AUAUU	24
AUCAA	27
AUCAC	26
AUCAG	23
AUCAU	34
AUCCA	38
AUCCC	42
AUCCG	1
AUCCU	5
AUCGA	37
AUCGC	0
AUCGG	18
AUCGU	4
AUCUA	13
AUCUC	10
AUCUG	25
AUCUU	14
AUGAA	32
AUGAC	10
AUGAG	48
AUGAU	11
AUGCA	23
AUGCC	43
AUGCG	36
AUGCU	12
AUGGA	55
AUGGC	16
AUGGG	38
AUGGU	16
AUGUA	59
AUGUC	62
AUGUG	683
AUGUU	64
AUUAA	76
AUUAC	3
AUUAG	126
AUUAU	21
AUUCA	4
AUUCC	40
AUUCG	1720
AUUCU	15
AUUGA	192
AUUGC	9
AUUGG	18
AUUGU	63
AUUUA	33
AUUUC	50
AUUUG	90
AUUUU	37
CAAAA	37
CAAAC	11
CAAAG	7
CAAAU	18
CAACA	20
CAACC	55
CAACG	13
CAACU	15
CAAGA	38
CAAGC	13
CAAGG	38
CAAGU	12
CAAUA	11
CAAUC	11
CAAUG	26
CAAUU	2
CACAA	23
CACAC	44
CACAG	34

CAGAA	-3.754	1.182
UCAUU	-3.756	1.202
CCUGA	-3.757	1.363
UUUCU	-3.758	0.773
UACUU	-3.760	0.881
GUAAU	-3.765	0.742
UUAAC	-3.768	0.263
UUGCG	-3.768	0.295
UUGUA	-3.769	0.469
ACUCU	-3.770	0.443
UGGAG	-3.774	0.453
UUAGA	-3.774	0.381
UGUCU	-3.776	0.540
CAUAA	-3.778	0.843
CUCUA	-3.779	0.735
UAGGG	-3.781	0.543
UGAUU	-3.781	0.745
UAGAU	-3.782	0.835
ACUAA	-3.782	1.140
UCUAG	-3.785	1.884
AGUUU	-3.786	0.242
AGUUC	-3.788	1.198
UCCGG	-3.791	1.874
AAACC	-3.796	0.474
GGCAG	-3.797	0.541
CGCGA	-3.799	0.715
UGCCG	-3.799	0.221
UCGGC	-3.804	0.752
UAAGU	-3.804	0.719
UCUCC	-3.806	1.120
CUAGC	-3.806	0.238
CUGUG	-3.806	1.194
AUAAA	-3.809	1.089
AUUAU	-3.809	0.298
CUAAG	-3.810	0.211
CUCAU	-3.810	0.704
UGACG	-3.813	0.691
ACUAG	-3.813	0.508
AAACA	-3.815	0.618
CAGGU	-3.815	0.635
AUUUU	-3.816	1.125
CCUGC	-3.817	1.111
AUGGG	-3.818	0.902
ACCAU	-3.820	0.728
AGAAU	-3.823	0.764
CUCAA	-3.824	1.222
UAUCG	-3.824	1.504
GCCUU	-3.827	0.833
UAAAU	-3.833	1.249
AGCAC	-3.834	0.586
ACAGU	-3.835	0.762
ACCUG	-3.835	0.824
CCCUU	-3.835	0.703
CCUAU	-3.835	0.689
UCCUA	-3.835	0.543
UGCGG	-3.835	1.117
UCCGC	-3.839	1.091
UGUCG	-3.839	1.105
GAAAU	-3.840	1.038
ACAGC	-3.841	1.066
GCAUG	-3.842	0.409
GGUUA	-3.847	1.276
UGCGA	-3.847	1.283
AUGUU	-3.849	1.280
UGUCC	-3.849	0.720
ACUAU	-3.850	0.677
AAACU	-3.852	0.292
GUUCU	-3.853	1.419
CAGAU	-3.854	0.370

CACAU	31
CACCA	10
CACCC	4
CACCG	0
CACCU	10
CACGA	15
CACGC	20
CACGG	10
CACGU	12
CACUA	3
CACUC	10
CACUG	24
CACUU	9
CAGAA	42
CAGAC	3
CAGAG	11
CAGAU	14
CAGCA	6
CAGCC	62
CAGCG	1
CAGCU	11
CAGGA	29
CAGGC	7
CAGGG	21
CAGGU	20
CAGUA	10
CAGUC	15
CAGUG	7
CAGUU	8
CAUAA	37
CAUAC	7
CAUAG	8
CAUAU	9
CAUCA	69
CAUCC	1
CAUCG	14
CAUCU	5
CAUGA	12
CAUGC	67
CAUGG	3
CAUGU	87
CAUUA	3
CAUUC	10
CAUUG	19
CAUUU	51
CCAAA	10
CCAAC	7
CCAAG	7
CCAAU	13
CCACA	4
CCACC	21
CCACG	1
CCACU	8
CCAGA	64
CCAGC	8
CCAGG	4
CCAGU	104
CCAUA	4
CCAUC	1
CCAUG	17
CCAUU	13
CCCAA	47
CCCAC	19
CCCAG	759
CCCAU	21
CCCCA	59
CCCCC	10
CCCCG	12
CCCCU	8

GGCUA	-3.855	0.369
UAGUG	-3.855	1.099
UUACG	-3.855	0.249
UGACA	-3.856	1.214
UAAAG	-3.856	0.371
UAAUU	-3.856	0.317
UUAUC	-3.859	0.171
CGACA	-3.861	0.960
AGGGC	-3.863	0.801
CCCAC	-3.863	0.495
CUUUC	-3.863	1.073
CCCUG	-3.864	1.069
GUCAA	-3.866	0.660
GUGUC	-3.866	0.406
AGAGC	-3.866	1.054
AAAAU	-3.867	1.075
ACGUG	-3.871	1.415
AGCUC	-3.871	0.665
GGAAG	-3.872	0.855
UGGGG	-3.873	0.349
AAGUG	-3.874	1.324
CCAUU	-3.876	0.454
UAACA	-3.876	0.311
GCCAA	-3.877	1.381
UAUCC	-3.878	0.758
UCGGU	-3.878	0.701
UUACU	-3.878	0.701
AUGGC	-3.880	0.507
UGGCA	-3.880	0.755
AAUGU	-3.884	1.054
CUCAC	-3.892	1.162
UAGGU	-3.895	0.367
AAAUU	-3.895	1.289
UAUGG	-3.895	0.523
UCUGC	-3.898	1.076
AUUGG	-3.899	0.335
AGACA	-3.900	0.436
AUCGA	-3.900	0.766
UAGAA	-3.902	0.446
CACUG	-3.904	1.048
CCUGG	-3.907	1.034
CUGAU	-3.907	1.203
GCCUA	-3.907	0.504
UAACC	-3.909	0.525
ACCCA	-3.911	0.345
AUCCC	-3.913	1.052
GUCUU	-3.918	0.622
CCUCU	-3.919	0.844
AAAGA	-3.921	1.250
CUACA	-3.921	0.012
CUCGC	-3.921	0.776
UUGAA	-3.921	0.472
CAUCG	-3.924	0.199
CGACC	-3.924	1.165
ACAUG	-3.927	1.378
AAAAC	-3.929	0.762
ACAAA	-3.929	0.710
GUUAU	-3.929	0.221
UUAUG	-3.929	1.042
GAAGG	-3.930	1.013
CCACC	-3.933	0.754
CGCAU	-3.933	1.153
GGAGU	-3.934	0.907
AGCGU	-3.935	1.007
UAUCU	-3.935	0.816
AUCAC	-3.936	1.034
AUGCG	-3.937	1.012
AGAAG	-3.938	1.028
UACCC	-3.940	1.358

CCCGA	20
CCCGC	8
CCCGG	42
CCCGU	19
CCCUA	0
CCCUC	4
CCCUG	27
CCCUU	38
CCGAA	29
CCGAC	3
CCGAG	3
CCGAU	0
CCGCA	0
CCGCC	5
CCGCG	1
CCGCU	2
CCGGA	11
CCGGC	10
CCGGG	1
CCGGU	1
CCGUA	0
CCGUC	2
CCGUG	9
CCGUU	2
CCUAA	27
CCUAC	1
CCUAG	69
CCUAU	32
CCUCA	15
CCUCC	8
CCUCG	7
CCUCU	31
CCUGA	94
CCUGC	33
CCUGG	23
CCUGU	234
CCUUA	7
CCUUC	8
CCUUG	2
CCUUU	59
CGAAA	15
CGAAC	5
CGAAG	1
CGAAU	3
CGACA	36
CGACC	39
CGACG	54
CGACU	11
CGAGA	34
CGAGC	12
CGAGG	4
CGAGU	4
CGAUA	1
CGAUC	1
CGAUG	26
CGAUU	1
CGCAA	1
CGCAC	32
CGCAG	7
CGCAU	37
CGCCA	2
CGCCC	2
CGCCG	2
CGCCU	5
CGCGA	21
CGCGC	13
CGCGG	1
CGCGU	9
CGCUA	1

CUCCG	-3.941	0.039
AGAGA	-3.946	0.657
AUACG	-3.946	0.182
GCUUA	-3.946	0.286
CACGC	-3.947	1.002
GUAAA	-3.948	0.732
UUCGA	-3.950	0.589
AAUUC	-3.951	0.994
CCUAA	-3.952	1.078
AUGAC	-3.958	0.387
GGCCU	-3.958	0.599
GUGCC	-3.958	0.305
UCAAU	-3.958	1.191
UCAGG	-3.960	1.061
UGUUA	-3.960	0.527
AAAUG	-3.962	1.320
AGUAA	-3.965	1.317
CACAA	-3.965	0.855
AUAGC	-3.965	0.341
AUUGA	-3.965	1.260
AGGUG	-3.969	1.173
GACUC	-3.971	0.708
CAAGA	-3.973	1.167
GAAAC	-3.974	1.302
GUGGC	-3.976	0.946
GUUGU	-3.976	0.573
GUCUA	-3.979	0.177
GUUGA	-3.979	0.675
UACUC	-3.979	0.574
GCUAG	-3.981	1.116
UACAC	-3.981	1.289
GUGCG	-3.982	1.032
ACUCA	-3.983	0.667
GGAGG	-3.988	1.072
CAACC	-3.989	1.277
CCAUG	-3.991	0.960
ACCUC	-3.994	0.588
AUGAU	-3.994	0.588
CCAAU	-3.994	0.597
CGCUC	-3.994	1.023
UCAUC	-3.994	0.503
ACAUU	-4.003	0.545
AGUAC	-4.003	0.545
CAAAU	-4.003	0.958
GGGGC	-4.003	0.372
GUUAA	-4.003	1.009
AAGUU	-4.009	0.943
AUAAG	-4.009	0.572
CAUGA	-4.009	0.636
GAGCA	-4.009	0.238
GCCCA	-4.009	1.244
UGAAC	-4.009	0.998
UGUUG	-4.009	0.577
CCCAA	-4.012	1.163
AACUA	-4.014	0.642
ACUGG	-4.014	0.351
AGGUC	-4.015	0.560
CAGUA	-4.015	0.530
GUUCG	-4.015	1.033
AGUCC	-4.022	0.952
AGUUA	-4.022	0.984
CCCGG	-4.029	1.137
AGUGA	-4.031	1.011
CCCGC	-4.031	0.235
GAUGG	-4.032	0.315
GGGUC	-4.032	0.322
UCCCG	-4.034	1.456
AUUCU	-4.039	0.939
CACUU	-4.039	0.528

CGCUC	33
CGCUG	9
CGCUU	1
CGGAA	1
CGGAC	4
CGGAG	2
CGGAU	3
CGGCA	2
CGGCC	21
CGGCG	0
CGGCU	4
CGGGA	8
CGGGC	7
CGGGG	6
CGGGU	13
CGGUA	5
CGGUC	3
CGGUG	5
CGGUU	2
CGUAA	21
CGUAC	1
CGUAG	2
CGUAU	7
CGUCA	5
CGUCC	5
CGUCG	1968
CGUCU	1
CGUGA	10
CGUGC	22
CGUGG	5
CGUGU	38
CGUUA	0
CGUUC	1
CGUUG	1
CGUUU	4
CUAAA	9
CUAAC	4
CUAAG	18
CUAAU	6
CUACA	12
CUACC	21
CUACG	3
CUACU	7
CUAGA	26
CUAGC	21
CUAGG	7
CUAGU	78
CUAUA	57
CUAUC	20
CUAUG	25
CUAUU	7
CUCAA	51
CUCAC	39
CUCAG	48
CUCAU	20
CUCCA	36
CUCCC	3
CUCCG	11
CUCCU	7
CUCGA	22
CUCGC	20
CUCGG	8
CUCGU	47
CUCUA	23
CUCUC	14
CUCUG	48
CUCUU	47
CUGAA	6
CUGAC	49

UGCCC	-4.039	1.544
AAUUA	-4.043	0.583
AGGUA	-4.043	0.513
AUGGU	-4.043	0.615
CAAGG	-4.043	1.188
CUUUA	-4.043	1.004
GUGCA	-4.043	0.202
GAUGU	-4.046	0.637
AGCCA	-4.047	1.182
CGCGC	-4.055	0.702
GACCU	-4.055	0.702
GGAUC	-4.055	0.702
GACCA	-4.058	0.606
GCCUG	-4.058	0.810
GACUA	-4.062	1.092
AAAGG	-4.064	0.552
CGUAA	-4.064	0.904
GUGGU	-4.064	1.029
UAUUA	-4.064	0.085
UGGAA	-4.064	0.630
UGUCA	-4.064	0.552
ACGAG	-4.068	0.340
ACUUC	-4.068	0.478
AUCUU	-4.068	0.925
GAUCU	-4.068	0.239
GCCGG	-4.068	0.600
UCAGC	-4.068	0.680
UCGAG	-4.068	1.075
UUAGC	-4.068	0.478
UUGAG	-4.068	0.600
AUAGA	-4.070	0.608
CAACA	-4.072	1.018
CCCGA	-4.072	1.018
AGAUG	-4.073	1.065
CACAU	-4.073	1.140
GAGAA	-4.073	1.486
CGUAU	-4.080	0.308
CUAUU	-4.080	0.277
GAAUC	-4.080	1.475
UAACU	-4.080	0.908
UAGUA	-4.080	0.162
AGUUG	-4.083	0.656
AUCUA	-4.083	0.702
GCUCG	-4.083	0.581
AACAC	-4.088	0.875
AAUAG	-4.088	0.174
ACAGA	-4.088	0.650
GAAAG	-4.088	1.116
GAGUG	-4.088	0.517
GUUUA	-4.088	0.875
GUUUG	-4.088	0.875
UCACU	-4.088	0.474
UUGGA	-4.088	0.057
UUUCA	-4.088	0.474
CUGCA	-4.092	0.894
AAGAA	-4.093	1.030
AACGC	-4.099	0.888
ACUCC	-4.099	1.098
GGAGC	-4.099	1.442
GGCGC	-4.099	0.869
GGCUG	-4.099	0.629
AAUGA	-4.105	0.734
GUAGA	-4.105	0.561
GUCCU	-4.105	0.911
UAGUU	-4.105	0.451
UCAAC	-4.105	0.178
AACAA	-4.117	0.989
AACAG	-4.117	0.441
AACAU	-4.117	0.867

CUGAG	5
CUGAU	59
CUGCA	14
CUGCC	28
CUGCG	5
CUGCU	8
CUGGA	27
CUGGC	59
CUGGG	5
CUGGU	28
CUGUA	5
CUGUC	6
CUGUG	45
CUGUU	6
CUUAA	182
CUUAC	8
CUUAG	32
CUUAU	35
CUUCA	33
CUUCC	28
CUUCG	959
CUUCU	57
CUUGA	41
CUUGC	22
CUUGG	21
CUUGU	182
CUUUA	24
CUUUC	27
CUUUG	124
CUUUU	29
GAAAA	96
GAAAC	61
GAAAG	28
GAAAU	46
GAACA	11
GAACC	8
GAACG	0
GAACU	9
GAAGA	20
GAAGC	11
GAAGG	22
GAAGU	6
GAAUA	111
GAAUC	87
GAAUG	46
GAAUU	65
GACAA	57
GACAC	8
GACAG	1
GACAU	3
GACCA	17
GACCC	0
GACCG	3
GACCU	13
GACGA	2
GACGC	0
GACGG	1
GACGU	3
GACUA	98
GACUC	29
GACUG	33
GACUU	3
GAGAA	91
GAGAC	9
GAGAG	20
GAGAU	6
GAGCA	12
GAGCC	3
GAGCG	1

AAUAU	-4.117	0.599
AAUCU	-4.117	0.564
AUGCA	-4.117	0.989
CAACU	-4.117	0.951
CAGUC	-4.117	0.814
CCAAC	-4.117	0.302
CUCCU	-4.117	0.441
GGAAA	-4.117	0.989
GUUGG	-4.117	0.302
UACUA	-4.117	0.441
UCUCA	-4.117	0.302
AAGGC	-4.119	0.862
GUGAC	-4.119	0.862
GCGUA	-4.121	0.990
CGUGC	-4.124	1.059
CUCGA	-4.124	1.059
GCAGG	-4.124	1.059
GGUUC	-4.126	0.982
ACUAC	-4.128	0.680
CUCUC	-4.128	0.935
AAGAG	-4.131	1.048
GGGAA	-4.131	0.966
GAACA	-4.135	0.536
CCAAA	-4.138	0.832
GAAGA	-4.138	0.953
GACAC	-4.138	0.565
AGUGG	-4.140	0.918
CAAGC	-4.140	0.918
GUUCA	-4.140	0.918
CAUUG	-4.145	1.024
UGAUC	-4.145	1.024
CGACG	-4.148	1.358
AACUG	-4.154	0.899
AAGGU	-4.154	0.426
AAUGC	-4.154	0.899
ACACC	-4.154	0.246
AGCUU	-4.154	0.899
AUCGG	-4.154	0.600
CACGG	-4.154	0.849
CCCCG	-4.154	0.855
CGAGC	-4.154	0.753
CUAAU	-4.154	0.099
CUGAA	-4.154	0.405
GAAGU	-4.154	0.426
GCGUG	-4.154	0.899
GGGCA	-4.154	0.324
GUUAG	-4.154	0.324
UGAUA	-4.154	0.655
GCGAU	-4.159	0.925
AGGAC	-4.162	0.546
CCGUG	-4.162	0.817
CUGAC	-4.162	1.239
GGAAC	-4.162	0.998
GGAUG	-4.162	0.912
GUAGC	-4.162	0.912
UCUUA	-4.162	0.460
UUAUU	-4.162	0.455
CAAAC	-4.168	0.879
CAGCU	-4.168	0.729
UAAGC	-4.168	0.729
GGUGU	-4.171	0.984
UUAGG	-4.171	0.984
ACCCU	-4.174	0.824
CUAAA	-4.174	0.824
CACAC	-4.177	1.307
AUAGG	-4.181	0.879
CCUCA	-4.181	0.904
AUAUC	-4.184	0.817
CACCU	-4.184	0.856

GAGCU	1
GAGGA	33
GAGGC	3
GAGGG	12
GAGGU	2
GAGUA	29
GAGUC	1
GAGUG	8
GAGUU	4
GAUAA	6
GAUAC	7
GAUAG	8
GAUAU	4
GAUCA	6
GAUCC	0
GAUCG	2
GAUCU	8
GAUGA	31
GAUGC	7
GAUGG	9
GAUGU	14
GAUUA	113
GAUUC	3
GAUUG	3
GAUUU	8
GCAAA	2
GCAAC	14
GCAAG	9
GCAAU	0
GCACA	1728
GCACC	2
GCACG	4
GCACU	1
GCAGA	10
GCAGC	5
GCAGG	22
GCAGU	3
GCAUA	2882
GCAUC	3
GCAUG	25
GCAUU	20
GCCAA	119
GCCAC	5
GCCAG	211
GCCAU	7
GCCCA	48
GCCCC	0
GCCCG	6
GCCCU	1
GCCGA	0
GCCGC	0
GCCGG	12
GCCGU	0
GCCUA	15
GCCUC	0
GCCUG	17
GCCUU	50
GCGAA	1
GCGAC	0
GCGAG	1
GCGAU	50
GCGCA	187
GCGCC	0
GCGCG	10
GCGCU	0
GCGGA	0
GCGGC	0
GCGGG	10
GCGGU	2

CACUC	-4.184	0.856
AGUCU	-4.191	0.478
CUCGG	-4.191	0.788
CUUAC	-4.191	0.788
AAUCA	-4.191	0.418
AGUAG	-4.191	0.540
GGGGU	-4.191	0.418
UACGU	-4.191	1.284
GUGUG	-4.195	1.277
CCAGC	-4.198	0.584
UACCG	-4.198	0.462
ACUGC	-4.202	0.796
AGGCC	-4.202	0.242
AUUGC	-4.202	0.832
CAUCU	-4.202	0.178
GGGGG	-4.202	0.832
GUCAC	-4.202	0.368
GUGAA	-4.202	0.842
GUGUU	-4.202	0.242
GUUCC	-4.202	0.796
UAAGA	-4.202	0.242
UAAGG	-4.202	0.935
AGGAG	-4.210	1.251
AACCU	-4.214	0.916
AUGCU	-4.214	0.821
CAAGU	-4.214	0.855
CACGU	-4.214	0.916
CGAGA	-4.214	1.244
GAGGG	-4.214	0.450
GGACU	-4.214	0.916
GGGAG	-4.219	1.237
CAGUU	-4.223	0.772
CCCCU	-4.223	0.772
CCUCC	-4.223	0.772
CGCAC	-4.223	1.229
GGUGG	-4.223	0.804
UACGC	-4.223	1.229
UACGG	-4.223	0.772
AAGCA	-4.227	0.836
ACCAA	-4.227	1.128
ACGGC	-4.227	0.420
AGCCC	-4.227	0.420
AGGUU	-4.227	0.420
CAAUC	-4.227	0.896
CUACU	-4.227	0.539
CUAGG	-4.227	0.539
GAUAC	-4.227	0.754
GCAGC	-4.227	0.420
GUAUG	-4.227	0.896
GUUUC	-4.227	0.836
UAGCU	-4.227	0.754
UCGUC	-4.227	0.065
UCGUU	-4.227	0.362
CCGAA	-4.237	1.205
GAGUA	-4.237	0.790
AUAAC	-4.242	0.774
CACCA	-4.242	0.874
CAUUC	-4.242	0.815
CCCCC	-4.242	0.815
CCGGC	-4.242	0.874
CGUGA	-4.242	0.874
GCUUU	-4.242	0.665
GGCGA	-4.242	0.665
AACCC	-4.247	0.773
AAGGA	-4.247	0.597
ACACU	-4.247	1.188
AGAUA	-4.247	0.773
CAUAC	-4.247	0.745
CCAAG	-4.247	0.745

GCGUA	65
GCGUC	0
GCGUG	12
GCGUU	2
GCUAA	33
GCUAC	0
GCUAG	58
GCUAU	22
GCUCA	52
GCUCC	4
GCUCG	13
GCUCU	27
GCUGA	31
GCUGC	2
GCUGG	23
GCUGU	43
GCUUA	14
GCUUC	1
GCUUG	38
GCUUU	10
GGAAA	23
GGAAC	17
GGAAG	27
GGAAU	7
GGACA	221
GGACC	8
GGACG	1
GGACU	12
GGAGA	44
GGAGC	76
GGAGG	26
GGAGU	28
GGAUA	354
GGAUC	13
GGAUG	17
GGAUU	7
GGCAA	4
GGCAC	16
GGCAG	17
GGCAU	19
GGCCA	1
GGCCC	1
GGCCG	2
GGCCU	12
GGCGA	10
GGCGC	12
GGCGG	2
GGCGU	3
GGCUA	18
GGCUC	2
GGCUG	10
GGCUU	4
GGGAA	21
GGGAC	2
GGGAG	33
GGGAU	1
GGGCA	6
GGGCC	0
GGGCG	0
GGGCU	1
GGGGA	7
GGGGC	18
GGGGG	9
GGGGU	8
GGGUA	7
GGGUC	15
GGGUG	5
GGGUU	2
GGUAA	18

CCUUA	-4.247	0.773
CGGGC	-4.247	0.443
GGAUU	-4.247	0.773
GGGGA	-4.247	0.773
CGAUG	-4.252	1.178
CAUAU	-4.258	0.849
GCAAG	-4.258	0.746
AACGU	-4.264	0.725
AAGGG	-4.264	0.484
ACGUA	-4.264	0.725
AGACG	-4.264	0.725
CAGCA	-4.264	0.725
CUGUC	-4.264	0.484
CUGUU	-4.264	0.725
GAUAA	-4.264	0.725
GUCCA	-4.264	0.725
ACCUU	-4.276	0.549
ACGCA	-4.276	0.549
ACUUA	-4.276	0.822
AGAUU	-4.276	0.822
AGCAA	-4.276	0.715
AGGGA	-4.276	0.345
CCACU	-4.276	0.715
CCAUA	-4.276	0.345
CCCUC	-4.276	0.345
CCUUC	-4.276	0.768
CGGGG	-4.276	0.549
CUGCU	-4.276	0.606
GAACC	-4.276	0.822
GAGAU	-4.276	0.549
GAUUU	-4.276	0.606
GGCUU	-4.276	0.345
GUUAC	-4.276	0.303
UCACA	-4.276	0.345
UCGAA	-4.276	0.303
UUAAG	-4.276	0.715
CAGGG	-4.283	1.127
CCCAU	-4.283	1.034
CGGCC	-4.283	1.127
GAGAG	-4.290	1.115
AACCA	-4.297	0.679
CAAAG	-4.297	0.791
CAGGC	-4.297	0.791
CCUCG	-4.297	0.324
CGCAG	-4.297	0.740
GAUGC	-4.297	0.570
GGCAU	-4.297	1.102
GGGUA	-4.297	0.404
UAAUC	-4.297	0.679
GGUAA	-4.305	1.089
ACGCU	-4.313	1.076
ACGGU	-4.313	0.693
AUCCU	-4.313	0.414
CCGCC	-4.313	0.293
CGAAC	-4.313	0.489
CGGUG	-4.313	0.489
CGUCA	-4.313	0.414
GCCAC	-4.313	0.693
GUACU	-4.313	0.369
GUGAU	-4.313	0.489
UAACG	-4.313	0.680
UCAGA	-4.313	0.369
GGUAG	-4.321	0.755
GUGGG	-4.321	0.755
AACUC	-4.321	0.637
ACACG	-4.321	0.637
ACGAA	-4.321	0.377
ACGUU	-4.321	0.637
AGACC	-4.321	1.061

GGUAC	4
GGUAG	6
GGUAU	6
GGUCA	11
GGUCC	3
GGUCG	1
GGUCU	1
GGUGA	30
GGUGC	15
GGUGG	8
GGUGU	16
GGUUA	89
GGUUC	63
GGUUG	2
GGUUU	40
GUAAA	17
GUAAC	5
GUAAG	3
GUAAU	23
GUACA	611
GUACC	14
GUACG	2
GUACU	5
GUAGA	13
GUAGC	17
GUAGG	2
GUAGU	24
GUAUA	434
GUAUC	2
GUAUG	11
GUAUU	4
GUCAA	16
GUCAC	5
GUCAG	6
GUCAU	41
GUCCA	6
GUCCC	1
GUCCG	0
GUCCU	13
GUCGA	2
GUCGC	1
GUCGG	0
GUCGU	4
GUCUA	11
GUCUC	5
GUCUG	2
GUCUU	26
GUGAA	13
GUGAC	12
GUGAG	2
GUGAU	5
GUGCA	10
GUGCC	16
GUGCG	27
GUGCU	3
GUGGA	357
GUGGC	28
GUGGG	6
GUGGU	21
GUGUA	84
GUGUC	14
GUGUG	39
GUGUU	5
GUUAA	20
GUUAC	4
GUUAG	6
GUUAU	13
GUUCA	13
GUUCC	9

GCCCG	-4.321	0.528
GGCAC	-4.321	1.061
UAGAC	-4.321	0.637
AGUGC	-4.330	1.046
CACGA	-4.330	1.046
CGAAA	-4.330	1.046
GGUGC	-4.330	1.046
UAAAC	-4.330	1.046
GCAAC	-4.340	1.029
GUACC	-4.340	0.613
AAGCC	-4.350	0.714
ACCAC	-4.350	0.672
ACGGG	-4.350	1.011
ACUCG	-4.350	0.349
AGCCU	-4.350	1.011
AGCUG	-4.350	0.587
AUUAC	-4.350	0.242
CAACG	-4.350	1.011
CGAAU	-4.350	0.242
CGGGU	-4.350	0.595
CGUCC	-4.350	0.714
CUGAG	-4.350	0.672
CUGUA	-4.350	0.714
GAUUC	-4.350	0.242
GGGUG	-4.350	0.714
GUAAC	-4.350	0.587
GUCUC	-4.350	0.672
AAGAU	-4.361	0.992
ACAAG	-4.361	0.992
CCACA	-4.361	0.641
CCAGG	-4.361	0.641
CGAGU	-4.361	0.641
CGUUU	-4.361	0.641
GAUAU	-4.361	0.412
GCACG	-4.361	0.412
GCUCC	-4.361	0.290
GUAUU	-4.361	0.290
CAAUA	-4.373	0.972
CAGAG	-4.373	0.972
CCGGA	-4.373	0.972
CGACU	-4.373	0.972
GAAGC	-4.373	0.972
GGUCA	-4.373	0.972
AAUUG	-4.387	0.949
ACCGA	-4.387	0.415
ACGAU	-4.387	0.628
AGGAU	-4.387	0.663
AUACC	-4.387	0.628
AUACU	-4.387	0.663
AUCGU	-4.387	0.628
AUCUC	-4.387	0.949
AUUCA	-4.387	0.525
CGAGG	-4.387	0.663
CGGAC	-4.387	0.212
CUAAC	-4.387	0.321
GAGUU	-4.387	0.415
GCAGA	-4.387	0.532
GCGCG	-4.387	0.949
GCGGG	-4.387	0.949
GGUAC	-4.387	0.628
GUCGU	-4.387	0.628
UACCA	-4.387	0.525
UAGAG	-4.387	0.628
AGAGU	-4.401	0.925
CGCGU	-4.401	0.925
CGCUG	-4.401	0.925
GAACU	-4.401	0.925
GAGAC	-4.401	0.925
UACGA	-4.401	0.925

GUUCG	22
GUUCU	140
GUUGA	19
GUUGC	2
GUUGG	7
GUUGU	12
GUUUA	12
GUUUC	11
GUUUG	12
GUUUU	170
UAAAA	62
UAAAC	15
UAAAG	13
UAAAU	57
UAACA	13
UAACC	15
UAACG	5
UAACU	15
UAAGA	5
UAAGC	11
UAAGG	13
UAAGU	20
UAAUA	23
UAAUC	7
UAAUG	109
UAAUU	13
UACAA	26
UACAC	58
UACAG	94
UACAU	132
UACCA	4
UACCC	77
UACCG	8
UACCU	24
UACGA	9
UACGC	32
UACGG	8
UACGU	40
UACUA	7
UACUC	11
UACUG	146
UACUU	34
UAGAA	13
UAGAC	6
UAGAG	4
UAGAU	36
UAGCA	3
UAGCC	68
UAGCG	6
UAGCU	7
UAGGA	3
UAGGC	53
UAGGG	22
UAGGU	15
UAGUA	7
UAGUC	23
UAGUG	34
UAGUU	7
UAUAA	257
UAUAC	28
UAUAG	292
UAUAU	78
UAUCA	20
UAUCC	30
UAUCG	510
UAUCU	49
UAUGA	92
UAUGC	82
UAUGG	16

AAUCG	-4.417	0.480
ACAAU	-4.417	0.897
ACCUA	-4.417	0.897
AGCGC	-4.417	0.897
CAUAG	-4.417	0.480
CGGGA	-4.417	0.897
GAUAG	-4.417	0.809
GGACC	-4.417	0.897
AAAGU	-4.435	0.576
ACGGA	-4.435	0.449
AGCGG	-4.435	0.441
AGGCU	-4.435	0.441
AGUCA	-4.435	0.441
CAGAC	-4.435	0.441
CAGUG	-4.435	0.867
CAUGG	-4.435	0.599
CCGAG	-4.435	0.576
CUCCC	-4.435	0.599
GACAU	-4.435	0.441
GACCG	-4.435	0.301
GAGGC	-4.435	0.441
GCAGU	-4.435	0.330
GCCAU	-4.435	0.779
GGAAU	-4.435	0.867
GGCGU	-4.435	0.599
GUAAG	-4.435	0.441
GUGCU	-4.435	0.599
UAGGA	-4.435	0.599
UCGAC	-4.435	0.330
UCGAU	-4.435	0.330
ACAGG	-4.456	0.831
ACGCC	-4.456	0.745
AGACU	-4.456	0.831
GAUCA	-4.456	0.413
GGUAU	-4.456	0.831
GUCAG	-4.456	0.745
UAGCG	-4.456	0.831
AAAGC	-4.480	0.790
ACCCG	-4.480	0.790
ACCGU	-4.480	0.705
CGCCU	-4.480	0.790
CGGUA	-4.480	0.372
CGUGG	-4.480	0.790
CUGCG	-4.480	0.790
CUGGG	-4.480	0.790
AACGA	-4.509	0.202
AAGAC	-4.509	0.202
AAGCG	-4.509	0.514
AAUCC	-4.509	0.514
ACGAC	-4.509	0.514
ACGUC	-4.509	0.514
AGAGG	-4.509	0.741
AGCCG	-4.509	0.514
AGGCA	-4.509	0.315
AGGCG	-4.509	0.741
CACCC	-4.509	0.741
CCGUU	-4.509	0.202
CCUUG	-4.509	0.514
CGCCC	-4.509	0.514
CGGCA	-4.509	0.514
CGGCU	-4.509	0.741
GACGA	-4.509	0.315
GCAAA	-4.509	0.315
GCGGU	-4.509	0.315
GCUGC	-4.509	0.202
GGCAA	-4.509	0.741
GGCGG	-4.509	0.514
GUAGG	-4.509	0.514
GUUGC	-4.509	0.315

UAUGU	165
UAUUA	9
UAUUC	21
UAUUG	41
UAUUU	69
UCAAA	33
UCAAC	7
UCAAG	165
UCAAU	42
UCACA	4
UCACC	2
UCACG	1
UCACU	8
UCAGA	5
UCAGC	12
UCAGG	31
UCAGU	30
UCAUA	160
UCAUC	13
UCAUG	70
UCAUU	46
UCCAA	910
UCCAC	289
UCCAG	15696
UCCAU	246
UCCCA	54
UCCCC	59
UCCCG	119
UCCCU	99
UCCGA	49
UCCGC	30
UCCGG	643
UCCGU	96
UCCUA	22
UCCUC	58
UCCUG	271
UCCUU	53
UCGAA	4
UCGAC	3
UCGAG	32
UCGAU	3
UCGCA	3
UCGCC	58
UCGCG	0
UCGCU	2
UCGGA	1
UCGGC	27
UCGGG	3
UCGGU	26
UCGUA	2
UCGUC	5
UCGUG	131
UCGUU	5
UCUAA	93
UCUAC	34
UCUAG	670
UCUAU	24
UCUCA	7
UCUCC	34
UCUCG	2317
UCUCU	42
UCUGA	72
UCUGC	27
UCUGG	114
UCUGU	184
UCUUA	9
UCUUC	21
UCUUG	28
UCUUU	73

UCACC	-4.509	0.514
ACGCG	-4.546	0.680
AGAUC	-4.546	0.680
AGCGA	-4.546	0.680
AGGGG	-4.546	0.680
AGUAU	-4.546	0.680
CACUA	-4.546	0.680
CAUUA	-4.546	0.680
CCGAC	-4.546	0.600
CGGAU	-4.546	0.680
CGGUC	-4.546	0.680
CUACG	-4.546	0.600
GACGU	-4.546	0.680
GACUU	-4.546	0.261
GAGCC	-4.546	0.680
GAUUG	-4.546	0.261
GCAUC	-4.546	0.261
GGUCC	-4.546	0.680
UAGCA	-4.546	0.680
UCGCA	-4.546	0.261
UCGGG	-4.546	0.600
UGGCG	-4.546	0.680
AAACG	-4.594	0.599
AACCG	-4.594	0.599
ACCGG	-4.594	0.523
CAAUU	-4.594	0.599
CCGCU	-4.594	0.523
CCGUC	-4.594	0.523
CGCCA	-4.594	0.599
CGCCG	-4.594	0.599
CGGAG	-4.594	0.180
CGGUU	-4.594	0.599
CGUAG	-4.594	0.523
GAGGU	-4.594	0.599
GAUCG	-4.594	0.180
GCACC	-4.594	0.599
GCGUU	-4.594	0.180
GGCCG	-4.594	0.599
GGCUC	-4.594	0.180
GGGAC	-4.594	0.599
GGGUU	-4.594	0.180
GGUUG	-4.594	0.180
GUACG	-4.594	0.599
GUAUC	-4.594	0.523
GUCGA	-4.594	0.180
GUCUG	-4.594	0.180
GUGAG	-4.594	0.599
UCGCU	-4.594	0.523
UCGUA	-4.594	0.180
AACGG	-4.668	0.074
AAGCU	-4.668	0.478
ACAAC	-4.668	0.478
ACCCC	-4.668	0.412
AUCCG	-4.668	0.074
CAGCG	-4.668	0.478
CAUCC	-4.668	0.412
CCACG	-4.668	0.478
CCAUC	-4.668	0.478
CCGCG	-4.668	0.478
CCGGG	-4.668	0.478
CCGGU	-4.668	0.412
CCUAC	-4.668	0.074
CGAAG	-4.668	0.074
CGAUA	-4.668	0.478
CGAUC	-4.668	0.478
CGAUU	-4.668	0.478
CGCAA	-4.668	0.074
CGCGG	-4.668	0.478
CGCUA	-4.668	0.412

UGAAA	354
UGAAC	30
UGAAG	27
UGAAU	97
UGACA	49
UGACC	165
UGACG	25
UGACU	70
UGAGA	81
UGAGC	185
UGAGG	37
UGAGU	168
UGAUA	10
UGAUC	19
UGAUG	30
UGAUU	22
UGCAA	179
UGCAC	1238
UGCAG	288
UGCAU	1483
UGCCA	69
UGCCC	115
UGCCG	19
UGCCU	97
UGCGA	65
UGCGC	1294
UGCGG	32
UGCGU	616
UGCUA	38
UGCUC	116
UGCUG	27
UGCUU	120
UGGAA	13
UGGAC	67
UGGAG	18
UGGAU	128
UGGCA	20
UGGCC	102
UGGCG	3
UGGCU	20
UGGGA	61
UGGGC	882
UGGGG	18
UGGGU	316
UGGUA	2004
UGGUC	30
UGGUG	21
UGGUU	21
UGUAA	36
UGUAC	178
UGUAG	32
UGUAU	159
UGUCA	9
UGUCC	24
UGUCG	154
UGUCU	18
UGUGA	145
UGUGC	1052
UGUGG	113
UGUGU	1073
UGUUA	13
UGUUC	40
UGUUG	12
UGUUU	79
UUAAA	21
UUAAC	26
UUAAG	6
UUAAU	38
UUACA	35

CGCUU	-4.668	0.478
CGGAA	-4.668	0.478
CGUAC	-4.668	0.478
CGUCU	-4.668	0.412
CGUUC	-4.668	0.074
CGUUG	-4.668	0.074
GACAG	-4.668	0.412
GACGG	-4.668	0.074
GAGCG	-4.668	0.074
GAGCU	-4.668	0.478
GAGUC	-4.668	0.478
GCACU	-4.668	0.412
GCCCU	-4.668	0.478
GCGAA	-4.668	0.478
GCGAG	-4.668	0.478
GCUUC	-4.668	0.412
GGACG	-4.668	0.478
GGCCA	-4.668	0.074
GGCCC	-4.668	0.478
GGGAU	-4.668	0.478
GGGCU	-4.668	0.074
GGUCG	-4.668	0.478
GGUCU	-4.668	0.478
GUCCC	-4.668	0.412
GUCGC	-4.668	0.412
UCACG	-4.668	0.412
UCGGA	-4.668	0.074
ACCGC	-4.827	0.242
AGUCG	-4.827	0.242
AUCGC	-4.827	0.242
CACCG	-4.827	0.242
CCCUA	-4.827	0.242
CCGAU	-4.827	0.242
CCGCA	-4.827	0.242
CCGUA	-4.827	0.242
CGGCG	-4.827	0.242
CGUUA	-4.827	0.242
GAACG	-4.827	0.242
GACCC	-4.827	0.242
GACGC	-4.827	0.242
GAUCC	-4.827	0.242
GCAAU	-4.827	0.242
GCCCC	-4.827	0.242
GCCGA	-4.827	0.242
GCCGC	-4.827	0.242
GCCGU	-4.827	0.242
GCCUC	-4.827	0.242
GCGAC	-4.827	0.242
GCGCC	-4.827	0.242
GCGCU	-4.827	0.242
GCGGA	-4.827	0.242
GCGGC	-4.827	0.242
GCGUC	-4.827	0.242
GCUAC	-4.827	0.242
GGGCC	-4.827	0.242
GGGCG	-4.827	0.242
GUCCG	-4.827	0.242
GUCGG	-4.827	0.242
UCGCG	-4.827	0.242

UUACC	175
UUACG	14
UUACU	26
UUAGA	22
UUAGC	8
UUAGG	16
UUAGU	34
UUAUA	710
UUAUC	16
UUAUG	27
UUAUU	7
UUCAA	84
UUCAC	89
UUCAG	781
UUCAU	136
UUCCA	36
UUCCC	48
UUCCG	58
UUCCU	45
UUCGA	12
UUCGC	116
UUCGG	35
UUCGU	150
UUCUA	31
UUCUC	71
UUCUG	56
UUCUU	140
UUGAA	12
UUGAC	39
UUGAG	12
UUGAU	29
UUGCA	20
UUGCC	3576
UUGCG	26
UUGCU	131
UUGGA	8
UUGGC	63
UUGGG	80
UUGGU	57
UUGUA	39
UUGUC	168
UUGUG	168
UUGUU	42
UUUAA	61
UUUAC	35
UUUAG	175
UUUAU	170
UUUCA	8
UUUCC	117
UUUCG	34091
UUUCU	42
UUUGA	36
UUUGC	64
UUUGG	40
UUUGU	283
UUUUA	160
UUUUC	151
UUUUG	164
UUUUU	111

Table S29. Bulges

Bulge size 1		
Range	0.559	
Median	-0.692	
Bulge	**Score**	**Centered score**
A	-0.412	0.28
U	-0.616	0.08
C	-0.668	0.02
G	-0.971	-0.28

Bulge size 2		
Range	1.091	
Median	-1.478	
Bulge	**Score**	**Centered score**
UU	-0.932	0.55
CU	-1.030	0.45
AA	-1.140	0.34
CA	-1.194	0.28
GA	-1.202	0.28
UA	-1.255	0.22
AG	-1.301	0.18
UG	-1.314	0.16
AU	-1.342	0.14
AC	-1.362	0.12
UC	-1.384	0.09
CC	-1.411	0.07
GU	-1.557	-0.08
GG	-1.818	-0.34
GC	-1.909	-0.43
CG	-2.023	-0.55

Bulge size 3		
Range	1.775	
Median	-2.235	
Bulge	**Score**	**Centered score**
ACU	-1.347	0.89
AUU	-1.351	0.88
UCU	-1.448	0.79
AUC	-1.492	0.74
ACC	-1.498	0.74
UUU	-1.524	0.71
CAA	-1.551	0.68
GUU	-1.724	0.51
GCU	-1.728	0.51
UCA	-1.744	0.49
UAG	-1.857	0.38
GAU	-1.868	0.37
CAG	-1.880	0.36
AGU	-1.910	0.32
AAA	-1.945	0.29
AAC	-1.984	0.25
CUU	-2.000	0.23
AAU	-2.032	0.20
UAA	-2.034	0.20
GGG	-2.037	0.20
CCU	-2.039	0.20
CUA	-2.055	0.18
UUA	-2.074	0.16
GUG	-2.077	0.16
UGA	-2.107	0.13
CUC	-2.114	0.12
GUC	-2.124	0.11
AUA	-2.124	0.11
UCC	-2.129	0.11
ACA	-2.132	0.10
GAC	-2.151	0.08
CCA	-2.156	0.08
AUG	-2.165	0.07
GCA	-2.216	0.02
GAG	-2.229	0.01
UUC	-2.241	-0.01
AGA	-2.255	-0.02
AAG	-2.260	-0.03
UGU	-2.282	-0.05
GCC	-2.298	-0.06
CCC	-2.331	-0.10
CAC	-2.338	-0.10
GGU	-2.339	-0.10
CUG	-2.374	-0.14
UAU	-2.382	-0.15
UUG	-2.383	-0.15
CGA	-2.384	-0.15
AGG	-2.389	-0.15
CAU	-2.400	-0.17
AGC	-2.402	-0.17
GAA	-2.415	-0.18
GUA	-2.432	-0.20
GGA	-2.460	-0.23
UGG	-2.471	-0.24
UGC	-2.536	-0.30
UAC	-2.696	-0.46
UCG	-2.733	-0.50
CGU	-2.826	-0.59
CCG	-2.857	-0.62
GGC	-2.886	-0.65
CGG	-2.922	-0.69
ACG	-3.064	-0.83
GCG	-3.089	-0.85
CGC	-3.122	-0.89

Bulge size 4		
Range	2.395	
Median	-2.646	
Bulge	**Score**	**Centered score**
AUUU	-1.448	1.20
ACUU	-1.719	0.93
AAUU	-1.784	0.86
UAUU	-1.898	0.75
UCAA	-1.964	0.68
UGUU	-2.079	0.57
UUUU	-2.085	0.56
AGUC	-2.122	0.52
AGAA	-2.155	0.49
UGUA	-2.172	0.47
UUGU	-2.177	0.47
AGUU	-2.193	0.45
AAAA	-2.230	0.42
CAGG	-2.244	0.40
AGCU	-2.272	0.37
AUAU	-2.291	0.35
CAUU	-2.303	0.34
GACA	-2.307	0.34
AGGA	-2.319	0.33
UAAA	-2.336	0.31
CUGU	-2.340	0.31
AAGA	-2.347	0.30
AUAA	-2.360	0.29
GUUU	-2.361	0.28
UUAU	-2.373	0.27
GUGU	-2.393	0.25
GCUU	-2.413	0.23
UUCU	-2.424	0.22
CUCA	-2.429	0.22
ACUA	-2.439	0.21
UUAA	-2.440	0.21
CUAA	-2.440	0.21
CUUU	-2.445	0.20
GAUC	-2.450	0.20
CGAA	-2.456	0.19
AAUA	-2.466	0.18
AUCU	-2.469	0.18
GGCA	-2.475	0.17
AAAU	-2.487	0.16
AUGU	-2.488	0.16
AUUG	-2.495	0.15
GACU	-2.496	0.15
AGCA	-2.497	0.15
UCUU	-2.508	0.14
UGAU	-2.519	0.13
UUAC	-2.537	0.11
AGCC	-2.546	0.10
GGAA	-2.557	0.09
CUGG	-2.561	0.08
UUCA	-2.566	0.08
UAGA	-2.568	0.08
ACAA	-2.577	0.07
GUAU	-2.580	0.07
AGGU	-2.585	0.06
UGGU	-2.601	0.05
CAGA	-2.603	0.04
CAAA	-2.606	0.04
UCUG	-2.607	0.04
AAUG	-2.619	0.03
CCAA	-2.621	0.02
AUCA	-2.629	0.02
AACU	-2.632	0.01
GCAC	-2.638	0.01
CAUG	-2.640	0.01

AACC	-2.648	0.00
AAGC	-2.648	0.00
GAAA	-2.654	-0.01
UUGG	-2.654	-0.01
CCAU	-2.660	-0.01
AAUC	-2.665	-0.02
UUGC	-2.670	-0.02
AUGA	-2.678	-0.03
UUUG	-2.678	-0.03
AGAU	-2.680	-0.03
AAGU	-2.685	-0.04
UGCU	-2.686	-0.04
GAGU	-2.693	-0.05
CUUA	-2.701	-0.06
GAUU	-2.702	-0.06
AUAC	-2.712	-0.07
CCCA	-2.712	-0.07
GUCU	-2.713	-0.07
UAGU	-2.716	-0.07
CGUU	-2.720	-0.07
UGAA	-2.723	-0.08
CAGU	-2.729	-0.08
AUUA	-2.741	-0.10
CCUU	-2.742	-0.10
AUCC	-2.744	-0.10
GAGA	-2.761	-0.11
UAAG	-2.767	-0.12
GGUU	-2.768	-0.12
AUGG	-2.768	-0.12
ACCA	-2.771	-0.13
GGCC	-2.774	-0.13
UUUC	-2.778	-0.13
GCAU	-2.781	-0.14
AUGC	-2.783	-0.14
AGGC	-2.785	-0.14
AAGG	-2.792	-0.15
UAAU	-2.797	-0.15
AGUG	-2.802	-0.16
GGUC	-2.802	-0.16
UUUA	-2.803	-0.16
GUCA	-2.807	-0.16
CUAU	-2.809	-0.16
GGGC	-2.815	-0.17
CUUC	-2.816	-0.17
CAAG	-2.823	-0.18
GCUC	-2.826	-0.18
GCUG	-2.828	-0.18
AUAG	-2.831	-0.19
AGAG	-2.834	-0.19
GUUG	-2.840	-0.19
UAGG	-2.843	-0.20
CUAG	-2.850	-0.20
AAAC	-2.852	-0.21
UCAU	-2.852	-0.21
CGAG	-2.853	-0.21
AUUC	-2.856	-0.21
GCUA	-2.856	-0.21
AGGG	-2.859	-0.21
UGGG	-2.859	-0.21
AACA	-2.861	-0.22
GCAG	-2.863	-0.22
UGUG	-2.866	-0.22
CCGU	-2.873	-0.23
UGCC	-2.873	-0.23
GGAG	-2.877	-0.23
AAAG	-2.879	-0.23
CACU	-2.882	-0.24
GAAU	-2.887	-0.24
ACUC	-2.890	-0.24

UUAG	-2.897	-0.25
UGAG	-2.901	-0.26
ACAU	-2.906	-0.26
ACCU	-2.907	-0.26
GGCU	-2.907	-0.26
GAUA	-2.908	-0.26
UAUA	-2.908	-0.26
ACCC	-2.911	-0.27
UGUC	-2.911	-0.27
GGGG	-2.926	-0.28
GUCC	-2.926	-0.28
CAUA	-2.926	-0.28
ACAC	-2.935	-0.29
GGAC	-2.937	-0.29
CACA	-2.945	-0.30
UCAG	-2.956	-0.31
UUGA	-2.956	-0.31
GAGG	-2.962	-0.32
GUAC	-2.962	-0.32
ACUG	-2.968	-0.32
CCAG	-2.977	-0.33
UGAC	-2.977	-0.33
CUGA	-2.993	-0.35
UCAC	-2.995	-0.35
AGCG	-2.998	-0.35
CCUA	-3.006	-0.36
CUAC	-3.006	-0.36
UCCA	-3.007	-0.36
GAUG	-3.028	-0.38
UAGC	-3.032	-0.39
UAUC	-3.032	-0.39
GCAA	-3.047	-0.40
UACA	-3.047	-0.40
ACGA	-3.048	-0.40
CCUG	-3.056	-0.41
UCGU	-3.056	-0.41
GGGA	-3.060	-0.41
GUGA	-3.065	-0.42
AGUA	-3.069	-0.42
CUCC	-3.070	-0.42
CUGC	-3.070	-0.42
UACU	-3.072	-0.43
CAUC	-3.079	-0.43
UAUG	-3.080	-0.43
GCCU	-3.085	-0.44
GUCG	-3.085	-0.44
CACC	-3.096	-0.45
GAGC	-3.096	-0.45
GGUA	-3.099	-0.45
ACGU	-3.108	-0.46
UCUA	-3.115	-0.47
UGGA	-3.121	-0.48
UCCC	-3.123	-0.48
GAAC	-3.134	-0.49
CCCG	-3.145	-0.50
CACG	-3.149	-0.50
GUGC	-3.149	-0.50
CAAU	-3.154	-0.51
CUCU	-3.157	-0.51
GUUC	-3.157	-0.51
AGAC	-3.176	-0.53
AACG	-3.184	-0.54
GCCA	-3.184	-0.54
GUUA	-3.184	-0.54
GAAG	-3.197	-0.55
CAAC	-3.207	-0.56
CCCC	-3.215	-0.57
CGGC	-3.219	-0.57
CUUG	-3.219	-0.57

UACC	-3.219	-0.57
UUCC	-3.239	-0.59
CGUC	-3.244	-0.60
ACAG	-3.258	-0.61
CCGA	-3.264	-0.62
GGCG	-3.264	-0.62
GGGU	-3.264	-0.62
CCAC	-3.274	-0.63
CCCU	-3.274	-0.63
CCGG	-3.280	-0.63
CGGG	-3.293	-0.65
GACG	-3.293	-0.65
GCCC	-3.293	-0.65
GUGG	-3.293	-0.65
UCGA	-3.293	-0.65
UGGC	-3.293	-0.65
GGAU	-3.313	-0.67
UACG	-3.313	-0.67
UGCA	-3.313	-0.67
CAGC	-3.321	-0.67
GACC	-3.321	-0.67
CGCU	-3.337	-0.69
UAAC	-3.337	-0.69
UCCU	-3.337	-0.69
GUAA	-3.356	-0.71
CGAC	-3.367	-0.72
UCCG	-3.367	-0.72
UCGG	-3.367	-0.72
UCUC	-3.367	-0.72
CCUC	-3.378	-0.73
CGAU	-3.378	-0.73
GGUG	-3.378	-0.73
CGUG	-3.390	-0.74
GCGC	-3.403	-0.76
GUAG	-3.433	-0.79
CGUA	-3.452	-0.81
ACGG	-3.452	-0.81
ACCG	-3.496	-0.85
CCGC	-3.496	-0.85
CGGA	-3.496	-0.85
CGCA	-3.526	-0.88
CUCG	-3.526	-0.88
UUCG	-3.526	-0.88
AUCG	-3.562	-0.92
GCCG	-3.562	-0.92
CGGU	-3.611	-0.96
ACGC	-3.685	-1.04
CGCC	-3.685	-1.04
GCGG	-3.685	-1.04
UCGC	-3.685	-1.04
CGCG	-3.844	-1.20
GCGA	-3.844	-1.20
GCGU	-3.844	-1.20
UGCG	-3.844	-1.20

Table S30. Bulges size 1

Bulge	Score	SD
A	-0.412	0.142
U	-0.616	0.111
C	-0.668	0.058
G	-0.971	0.357

Bulge	Total bulge count
A	134631
C	74689
G	57779
U	88689

Supercategory	Total bulge count
Antisense	99714
Gene	163161
SnoRNA	92913

Table S31. Bulges size 2

Bulge	Score	SD
UU	-0.932	0.237
CU	-1.030	0.455
AA	-1.140	0.089
CA	-1.194	0.336
GA	-1.202	0.053
UA	-1.255	0.299
AG	-1.301	0.685
UG	-1.314	0.210
AU	-1.342	0.215
AC	-1.362	0.579
UC	-1.384	0.368
CC	-1.411	0.305
GU	-1.557	0.082
GG	-1.818	0.102
GC	-1.909	0.105
CG	-2.023	0.059

Bulge	Total bulge count
AA	7376
AC	4092
AG	4307
AU	3616
CA	10445
CC	2990
CG	816
CU	17673
GA	5296
GC	1149
GG	1544
GU	2741
UA	4831
UC	2923
UG	3537
UU	13909

Supercategory	Total bulge count
Antisense	14108
Gene	64028
SnoRNA	9109

Table S32. Bulges size 3

Bulge	Score	SD
ACU	-1.347	0.353
AUU	-1.351	0.800
UCU	-1.448	0.754
AUC	-1.492	0.391
ACC	-1.498	0.460
UUU	-1.524	0.626
CAA	-1.551	0.385
GUU	-1.724	0.776
GCU	-1.728	0.806
UCA	-1.744	0.312
UAG	-1.857	0.594
GAU	-1.868	0.769
CAG	-1.880	0.242
AGU	-1.910	0.285
AAA	-1.945	0.384
AAC	-1.984	0.422
CUU	-2.000	0.480
AAU	-2.032	0.363
UAA	-2.034	0.129
GGG	-2.037	0.750
CCU	-2.039	0.316
CUA	-2.055	0.089
UUA	-2.074	0.308
GUG	-2.077	0.159
UGA	-2.107	0.921
CUC	-2.114	0.215
GUC	-2.124	0.147
AUA	-2.124	0.510
UCC	-2.129	0.516
ACA	-2.132	0.167
GAC	-2.151	0.357
CCA	-2.156	0.323
AUG	-2.165	0.467
GCA	-2.216	0.560
GAG	-2.229	0.269
UUC	-2.241	0.495
AGA	-2.255	0.358
AAG	-2.260	0.279
UGU	-2.282	0.264
GCC	-2.298	0.308
CCC	-2.331	0.376
CAC	-2.338	0.263
GGU	-2.339	0.129
CUG	-2.374	0.246
UAU	-2.382	0.245
UUG	-2.383	0.072
CGA	-2.384	0.851
AGG	-2.389	0.183
CAU	-2.400	0.099
AGC	-2.402	0.161
GAA	-2.415	0.171
GUA	-2.432	0.201
GGA	-2.460	0.286
UGG	-2.471	0.086
UGC	-2.536	1.000
UAC	-2.696	0.333
UCG	-2.733	0.262
CGU	-2.826	0.261
CCG	-2.857	0.141
GGC	-2.886	0.601
CGG	-2.922	0.096
ACG	-3.064	0.351
GCG	-3.089	0.992
CGC	-3.122	0.500

Bulge	Total bulge count
AAA	776
AAC	1938
AAG	332
AAU	843
ACA	532
ACC	1723
ACG	93
ACU	5544
AGA	882
AGC	250
AGG	397
AGU	804
AUA	1291
AUC	5541
AUG	909
AUU	4962
CAA	3662
CAC	370
CAG	969
CAU	265
CCA	967
CCC	254
CCG	91
CCU	581
CGA	2121
CGC	157
CGG	88
CGU	102
CUA	720
CUC	533
CUG	408
CUU	505
GAA	304
GAC	365
GAG	620
GAU	1283
GCA	524
GCC	399
GCG	499
GCU	7892
GGA	460
GGC	210
GGG	889
GGU	433
GUA	366
GUC	622
GUG	710
GUU	1662
UAA	809
UAC	284
UAG	2391
UAU	216
UCA	884
UCC	475
UCG	170
UCU	3132
UGA	4621
UGC	2207
UGG	294
UGU	368
UUA	449
UUC	348
UUG	282
UUU	1469

Supercategory	Total bulge count
Antisense	10305
Gene	58255
SnoRNA	5687

Bulge	Score	SD
AUUU	-1.448	0.395
ACUU	-1.719	0.299
AAUU	-1.784	0.603
UAUU	-1.898	0.708
UCAA	-1.964	0.936
UGUU	-2.079	0.520
UUUU	-2.085	0.417
AGUC	-2.122	0.638
AGAA	-2.155	0.618
UGUA	-2.172	0.610
UUGU	-2.177	0.817
AGUU	-2.193	1.635
AAAA	-2.230	0.170
CAGG	-2.244	0.431
AGCU	-2.272	0.846
AUAU	-2.291	0.348
CAUU	-2.303	0.534
GACA	-2.307	0.589
AGGA	-2.319	0.384
UAAA	-2.336	0.743
CUGU	-2.340	0.513
AAGA	-2.347	0.634
AUAA	-2.360	0.468
GUUU	-2.361	0.429
UUAU	-2.373	0.351
GUGU	-2.393	0.821
GCUU	-2.413	0.307
UUCU	-2.424	0.585
CUCA	-2.429	0.838
ACUA	-2.439	0.337
UUAA	-2.440	0.808
CUAA	-2.440	0.631
CUUU	-2.445	0.952
GAUC	-2.450	0.358
CGAA	-2.456	0.388
AAUA	-2.466	0.129
AUCU	-2.469	0.134
GGCA	-2.475	1.043
AAAU	-2.487	0.182
AUGU	-2.488	0.507
AUUG	-2.495	0.309
GACU	-2.496	0.546
AGCA	-2.497	0.263
UCUU	-2.508	0.589
UGAU	-2.519	0.294
UUAC	-2.537	0.440
AGCC	-2.546	0.462
GGAA	-2.557	0.505
CUGG	-2.561	0.193
UUCA	-2.566	0.607
UAGA	-2.568	0.886
ACAA	-2.577	0.272
GUAU	-2.580	0.526
AGGU	-2.585	0.520
UGGU	-2.601	0.688
CAGA	-2.603	0.413
CAAA	-2.606	0.577
UCUG	-2.607	0.402
AAUG	-2.619	0.142
CCAA	-2.621	0.299
AUCA	-2.629	0.641
AACU	-2.632	0.249
GCAC	-2.638	0.497
CAUG	-2.640	0.175
AACC	-2.648	0.665
AAGC	-2.648	0.505
GAAA	-2.654	0.323
UUGG	-2.654	0.675

Bulge	Total bulge count
AAAA	107
AAAC	18
AAAG	19
AAAU	87
AACA	36
AACC	29
AACG	47
AACU	71
AAGA	182
AAGC	26
AAGG	18
AAGU	60
AAUA	58
AAUC	85
AAUG	72
AAUU	1124
ACAA	37
ACAC	33
ACAG	10
ACAU	34
ACCA	43
ACCC	15
ACCG	5
ACCU	108
ACGA	9
ACGC	1
ACGG	3
ACGU	14
ACUA	173
ACUC	26
ACUG	27
ACUU	323
AGAA	145
AGAC	50
AGAG	39
AGAU	224
AGCA	127
AGCC	124
AGCG	14
AGCU	794
AGGA	72
AGGC	85
AGGG	40
AGGU	201
AGUA	105
AGUC	435
AGUG	98
AGUU	8964
AUAA	75
AUAC	29
AUAG	22
AUAU	62
AUCA	247
AUCC	61
AUCG	3
AUCU	57
AUGA	27
AUGC	53
AUGG	17
AUGU	39
AUUA	42
AUUC	33
AUUG	41
AUUU	441
CAAA	27
CAAC	14
CAAG	33
CAAU	20

Supercategory	Total bulge count
Antisense	1243
Gene	19236
SnoRNA	1775

CCAU	-2.660	0.680
AAUC	-2.665	0.364
UUGC	-2.670	0.312
AUGA	-2.678	0.398
UUUG	-2.678	0.499
AGAU	-2.680	0.729
AAGU	-2.685	0.340
UGCU	-2.686	0.537
GAGU	-2.693	0.573
CUUA	-2.701	0.206
GAUU	-2.702	0.368
AUAC	-2.712	0.313
CCCA	-2.712	0.205
GUCU	-2.713	1.247
UAGU	-2.716	0.205
CGUU	-2.720	0.288
UGAA	-2.723	0.418
CAGU	-2.729	0.250
AUUA	-2.741	0.163
CCUU	-2.742	0.543
AUCC	-2.744	0.733
GAGA	-2.761	0.081
UAAG	-2.767	0.336
GGUU	-2.768	0.867
AUGG	-2.768	0.767
ACCA	-2.771	0.639
GGCC	-2.774	1.181
UUUC	-2.778	0.450
GCAU	-2.781	0.461
AUGC	-2.783	0.179
AGGC	-2.785	0.374
AAGG	-2.792	0.473
UAAU	-2.797	0.627
AGUG	-2.802	0.552
GGUC	-2.802	0.531
UUUA	-2.803	0.313
GUCA	-2.807	0.576
CUAU	-2.809	0.185
GGGC	-2.815	0.970
CUUC	-2.816	0.463
CAAG	-2.823	0.726
GCUC	-2.826	0.761
GCUG	-2.828	0.739
AUAG	-2.831	0.413
AGAG	-2.834	0.539
GUUG	-2.840	0.865
UAGG	-2.843	0.080
CUAG	-2.850	0.430
AAAC	-2.852	0.302
UCAU	-2.852	0.448
CGAG	-2.853	0.689
AUUC	-2.856	0.059
GCUA	-2.856	0.195
AGGG	-2.859	0.490
UGGG	-2.859	0.506
AACA	-2.861	0.512
GCAG	-2.863	0.871
UGUG	-2.866	0.433
CCGU	-2.873	0.659
UGCC	-2.873	0.519
GGAG	-2.877	0.666
AAAG	-2.879	0.266
CACU	-2.882	0.211
GAAU	-2.887	0.436
ACUC	-2.890	0.848
UUAG	-2.897	0.740
UGAG	-2.901	0.452
ACAU	-2.906	1.110
ACCU	-2.907	0.589

CACA	31
CACC	19
CACG	10
CACU	44
CAGA	102
CAGC	18
CAGG	105
CAGU	30
CAUA	58
CAUC	98
CAUG	39
CAUU	198
CCAA	54
CCAC	9
CCAG	67
CCAU	28
CCCA	43
CCCC	8
CCCG	14
CCCU	9
CCGA	27
CCGC	5
CCGG	6
CCGU	13
CCUA	18
CCUC	12
CCUG	9
CCUU	19
CGAA	167
CGAC	3
CGAG	15
CGAU	12
CGCA	2
CGCC	1
CGCG	0
CGCU	6
CGGA	5
CGGC	37
CGGG	4
CGGU	2
CGUA	7
CGUC	7
CGUG	11
CGUU	81
CUAA	38
CUAC	18
CUAG	20
CUAU	28
CUCA	58
CUCC	14
CUCG	2
CUCU	13
CUGA	28
CUGC	104
CUGG	43
CUGU	152
CUUA	46
CUUC	22
CUUG	13
CUUU	96
GAAA	36
GAAC	9
GAAG	15
GAAU	16
GACA	53
GACC	18
GACG	8
GACU	48
GAGA	39

GGCU	-2.907	0.512
GAUA	-2.908	0.427
UAUA	-2.908	0.170
ACCC	-2.911	0.496
UGUC	-2.911	0.496
GGGG	-2.926	0.625
GUCC	-2.926	0.701
CAUA	-2.926	0.437
ACAC	-2.935	1.136
GGAC	-2.937	0.879
CACA	-2.945	0.409
UCAG	-2.956	0.381
UUGA	-2.956	0.564
GAGG	-2.962	0.281
GUAC	-2.962	0.674
ACUG	-2.968	0.557
CCAG	-2.977	0.475
UGAC	-2.977	0.387
CUGA	-2.993	0.510
UCAC	-2.995	0.519
AGCG	-2.998	0.198
CCUA	-3.006	0.505
CUAC	-3.006	0.505
UCCA	-3.007	0.597
GAUG	-3.028	0.404
UAGC	-3.032	0.462
UAUC	-3.032	0.347
GCAA	-3.047	0.345
UACA	-3.047	0.345
ACGA	-3.048	0.595
CCUG	-3.056	0.436
UCGU	-3.056	0.627
GGGA	-3.060	0.305
GUGA	-3.065	0.346
AGUA	-3.069	0.704
CUCC	-3.070	0.632
CUGC	-3.070	0.702
UACU	-3.072	0.153
CAUC	-3.079	0.687
UAUG	-3.080	0.282
GCCU	-3.085	0.428
GUCG	-3.085	0.485
CACC	-3.096	0.429
GAGC	-3.096	0.506
GGUA	-3.099	0.195
ACGU	-3.108	0.935
UCUA	-3.115	0.221
UGGA	-3.121	0.372
UCCC	-3.123	0.272
GAAC	-3.134	0.251
CCCG	-3.145	0.894
CACG	-3.149	0.560
GUGC	-3.149	0.689
CAAU	-3.154	0.213
CUCU	-3.157	0.431
GUUC	-3.157	0.553
AGAC	-3.176	0.521
AACG	-3.184	1.615
GCCA	-3.184	0.292
GUUA	-3.184	0.292
GAAG	-3.197	0.174
CAAC	-3.207	0.319
CCCC	-3.215	0.448
CGGC	-3.219	0.447
CUUG	-3.219	0.317
UACC	-3.219	0.579
UUCC	-3.239	0.338
CGUC	-3.244	0.702
ACAG	-3.258	0.166

GAGC	15
GAGG	14
GAGU	32
GAUA	39
GAUC	99
GAUG	19
GAUU	91
GCAA	20
GCAC	24
GCAG	17
GCAU	17
GCCA	11
GCCC	6
GCCG	3
GCCU	14
GCGA	0
GCGC	4
GCGG	1
GCGU	0
GCUA	33
GCUC	35
GCUG	36
GCUU	162
GGAA	32
GGAC	16
GGAG	33
GGAU	19
GGCA	104
GGCC	30
GGCG	7
GGCU	28
GGGA	10
GGGC	27
GGGG	11
GGGU	7
GGUA	11
GGUC	51
GGUG	12
GGUU	281
GUAA	14
GUAC	10
GUAG	8
GUAU	27
GUCA	15
GUCC	15
GUCG	8
GUCU	100
GUGA	18
GUGC	10
GUGG	22
GUGU	50
GUUA	11
GUUC	57
GUUG	31
GUUU	84
UAAA	66
UAAC	6
UAAG	20
UAAU	22
UACA	20
UACC	5
UACG	7
UACU	13
UAGA	108
UAGC	10
UAGG	36
UAGU	42
UAUA	37
UAUC	22

CCGA	-3.264	0.371
GGCG	-3.264	0.365
GGGU	-3.264	0.365
CCAC	-3.274	0.176
CCCU	-3.274	0.176
CCGG	-3.280	0.527
CGGG	-3.293	0.520
GACG	-3.293	0.190
GCCC	-3.293	0.400
GUGG	-3.293	0.322
UCGA	-3.293	0.400
UGGC	-3.293	0.332
GGAU	-3.313	0.287
UACG	-3.313	0.936
UGCA	-3.313	0.211
CAGC	-3.321	0.274
GACC	-3.321	0.274
CGCU	-3.337	0.363
UAAC	-3.337	0.801
UCCU	-3.337	0.363
GUAA	-3.356	0.216
CGAC	-3.367	0.647
UCCG	-3.367	0.647
UCGG	-3.367	0.756
UCUC	-3.367	0.200
CCUC	-3.378	0.182
CGAU	-3.378	0.182
GGUG	-3.378	0.182
CGUG	-3.390	0.163
GCGC	-3.403	0.430
GUAG	-3.433	0.103
CGUA	-3.452	0.086
ACGG	-3.452	0.630
ACCG	-3.496	0.088
CCGC	-3.496	0.088
CGGA	-3.496	0.088
CGCA	-3.526	0.530
CUCG	-3.526	0.595
UUCG	-3.526	0.921
AUCG	-3.562	0.173
GCCG	-3.562	0.173
CGGU	-3.611	0.251
ACGC	-3.685	0.796
CGCC	-3.685	0.796
GCGG	-3.685	0.375
UCGC	-3.685	0.375
CGCG	-3.844	0.647
GCGA	-3.844	0.647
GCGU	-3.844	0.647
UGCG	-3.844	0.647

UAUG	21
UAUU	230
UCAA	182
UCAC	11
UCAG	13
UCAU	18
UCCA	17
UCCC	16
UCCG	3
UCCU	6
UCGA	6
UCGC	1
UCGG	5
UCGU	9
UCUA	10
UCUC	13
UCUG	32
UCUU	47
UGAA	23
UGAC	13
UGAG	35
UGAU	40
UGCA	7
UGCC	13
UGCG	0
UGCU	34
UGGA	25
UGGC	8
UGGG	18
UGGU	29
UGUA	89
UGUC	15
UGUG	15
UGUU	196
UUAA	61
UUAC	34
UUAG	12
UUAU	56
UUCA	28
UUCC	8
UUCG	2
UUCU	45
UUGA	21
UUGC	41
UUGG	30
UUGU	129
UUUA	19
UUUC	19
UUUG	37
UUUU	97

iLoop size 1x1			
Range		0.494	
Median		-1.295	
5'	**3'**	**Score**	**Centered score**
U	U	-1.048	0.25
A	A	-1.112	0.18
C	A	-1.132	0.16
U	G	-1.139	0.16
A	U	-1.163	0.13
U	A	-1.175	0.12
C	U	-1.210	0.08
A	C	-1.269	0.03
G	C	-1.322	-0.03
U	C	-1.324	-0.03
C	G	-1.392	-0.10
G	G	-1.424	-0.13
C	C	-1.465	-0.17
G	A	-1.466	-0.17
G	U	-1.486	-0.19
A	G	-1.541	-0.25

iLoop size 1x2			
Range		1.730	
Median		-2.360	
5'	**3'**	**Score**	**Centered score**
U	CC	-1.495	0.87
A	CA	-1.515	0.84
U	CU	-1.517	0.84
U	UU	-1.566	0.79
C	CU	-1.600	0.76
A	AU	-1.707	0.65
U	UC	-1.738	0.62
A	UU	-1.910	0.45
C	UU	-1.913	0.45
G	UU	-1.963	0.40
A	AA	-1.978	0.38
A	GA	-1.985	0.38
A	UG	-1.998	0.36
A	UA	-2.033	0.33
C	CC	-2.101	0.26
A	CU	-2.103	0.26
A	CC	-2.121	0.24
A	AG	-2.176	0.18
A	AC	-2.179	0.18
U	CA	-2.179	0.18
U	AA	-2.192	0.17
G	CC	-2.196	0.16
U	UG	-2.196	0.16
C	UC	-2.197	0.16
A	UC	-2.202	0.16
U	AU	-2.236	0.12
G	AA	-2.266	0.09
A	GU	-2.283	0.08
G	AC	-2.293	0.07
G	UC	-2.294	0.07
C	AU	-2.295	0.06
A	CG	-2.301	0.06
U	UA	-2.314	0.05
A	GG	-2.315	0.04
C	GC	-2.420	-0.06
C	AA	-2.425	-0.07
G	CU	-2.433	-0.07
U	AG	-2.433	-0.07
U	GU	-2.440	-0.08
U	AC	-2.442	-0.08
C	UG	-2.453	-0.09
G	AG	-2.462	-0.10
U	GC	-2.473	-0.11
C	AC	-2.487	-0.13
C	CA	-2.495	-0.13
G	UG	-2.496	-0.14
A	GC	-2.509	-0.15
C	GU	-2.518	-0.16
C	GA	-2.524	-0.16
G	GA	-2.528	-0.17
C	AG	-2.553	-0.19
U	GA	-2.597	-0.24
G	CA	-2.654	-0.29
U	GG	-2.658	-0.30
G	AU	-2.674	-0.31
C	UA	-2.681	-0.32
G	GC	-2.685	-0.32
G	UA	-2.760	-0.40
G	GU	-2.763	-0.40
C	CG	-2.827	-0.47
C	GG	-2.830	-0.47
G	GG	-2.899	-0.54
U	CG	-3.075	-0.72
G	CG	-3.225	-0.87

iLoop size 2x1			
Range		2.169	
Median		-2.366	
5'	**3'**	**Score**	**Centered score**
GG	A	-1.281	1.08
UU	C	-1.483	0.88
AA	A	-1.498	0.87
UU	U	-1.532	0.83
GA	A	-1.573	0.79
AG	A	-1.621	0.75
AA	U	-1.807	0.56
CU	U	-1.809	0.56
UC	U	-1.826	0.54
AC	A	-1.909	0.46
CA	U	-1.913	0.45
GC	A	-1.917	0.45
AA	C	-1.925	0.44
UU	A	-1.928	0.44
AC	C	-1.928	0.44
CA	A	-1.974	0.39
CC	A	-1.986	0.38
AU	U	-2.007	0.36
AA	G	-2.039	0.33
CU	C	-2.063	0.30
UC	C	-2.105	0.26
GU	U	-2.110	0.26
UA	A	-2.122	0.24
GA	G	-2.135	0.23
GA	U	-2.154	0.21
AG	G	-2.156	0.21
UG	A	-2.166	0.20
CA	G	-2.170	0.20
GU	C	-2.171	0.19
AC	U	-2.220	0.15
GC	C	-2.222	0.14
AU	A	-2.230	0.14
CU	A	-2.253	0.11
CC	G	-2.274	0.09
AU	C	-2.315	0.05
GU	A	-2.327	0.04
UU	G	-2.333	0.03
UG	U	-2.353	0.01
UA	U	-2.372	-0.01
UC	A	-2.386	-0.02
GG	C	-2.390	-0.02
UG	C	-2.408	-0.04
AG	C	-2.419	-0.05
AG	U	-2.422	-0.06
CC	U	-2.450	-0.08
GG	G	-2.469	-0.10
UG	G	-2.473	-0.11
CA	C	-2.483	-0.12
CU	G	-2.484	-0.12
CC	C	-2.495	-0.13
UA	C	-2.507	-0.14
GA	C	-2.510	-0.14
UC	G	-2.550	-0.18
GG	U	-2.574	-0.21
AC	G	-2.650	-0.28
UA	G	-2.681	-0.31
GC	U	-2.717	-0.35
AU	G	-2.739	-0.37
GU	G	-2.785	-0.42
GC	G	-2.842	-0.48
CG	U	-2.891	-0.53
CG	C	-2.897	-0.53
CG	A	-2.954	-0.59
CG	G	-3.451	-1.08

iLoop size 1x3			
Range	2.536		
Median	-2.893		
5'	**3'**	**Score**	**Centered score**
U	CUC	-1.625	1.27
U	UGU	-1.964	0.93
C	CUC	-2.115	0.78
U	CAU	-2.149	0.74
A	CUU	-2.168	0.72
A	CUA	-2.178	0.72
U	CAC	-2.183	0.71
U	CCC	-2.184	0.71
U	UGC	-2.198	0.69
U	AUU	-2.257	0.64
A	CCU	-2.270	0.62
U	UGA	-2.288	0.60
U	UUC	-2.347	0.55
A	UGA	-2.367	0.53
U	CGC	-2.385	0.51
A	CCC	-2.387	0.51
C	CUU	-2.441	0.45
A	CUC	-2.443	0.45
G	ACU	-2.465	0.43
A	CAA	-2.490	0.40
A	CAU	-2.507	0.39
U	AUC	-2.517	0.38
A	UUA	-2.521	0.37
A	GUC	-2.525	0.37
C	CCU	-2.540	0.35
U	UUU	-2.542	0.35
C	CAC	-2.552	0.34
G	CCC	-2.557	0.34
U	CGA	-2.568	0.32
G	AAA	-2.576	0.32
A	GCU	-2.597	0.30
G	CUC	-2.599	0.29
A	UGU	-2.604	0.29
U	UAG	-2.614	0.28
A	AAU	-2.628	0.26
C	AAU	-2.637	0.26
A	CAC	-2.639	0.25
A	UCA	-2.640	0.25
C	CAU	-2.641	0.25
U	CUU	-2.646	0.25
U	CCU	-2.653	0.24
C	UUU	-2.672	0.22
G	UGU	-2.677	0.22
C	UCC	-2.684	0.21
A	UCU	-2.685	0.21
A	UAU	-2.694	0.20
A	AUC	-2.697	0.20
G	UCC	-2.699	0.19
G	AAG	-2.715	0.18
U	AAU	-2.717	0.18
C	UGC	-2.723	0.17
C	ACA	-2.729	0.16
A	UUU	-2.730	0.16
C	CCC	-2.730	0.16
U	UAU	-2.735	0.16
A	CCA	-2.751	0.14
A	ACU	-2.761	0.13
G	CAA	-2.765	0.13
A	UAA	-2.788	0.10
U	UCC	-2.796	0.10
A	UCC	-2.799	0.09
G	AAC	-2.803	0.09
U	AAG	-2.805	0.09
U	CAA	-2.813	0.08
G	CAC	-2.817	0.08

iLoop size 2x2			
Range	2.457		
Median	-2.908		
5'	**3'**	**Score**	**Centered score**
UU	UU	-1.680	1.23
UG	UG	-1.849	1.06
GU	AC	-1.893	1.01
CU	UU	-1.908	1.00
AG	AC	-1.993	0.92
AA	UU	-2.056	0.85
AG	AA	-2.080	0.83
UU	UC	-2.120	0.79
AA	AC	-2.154	0.75
GU	AU	-2.169	0.74
UU	CU	-2.190	0.72
AG	AG	-2.221	0.69
AG	CC	-2.223	0.69
UG	AU	-2.235	0.67
AG	AU	-2.261	0.65
CC	UU	-2.266	0.64
UG	CU	-2.276	0.63
AA	GC	-2.315	0.59
AG	UC	-2.361	0.55
GG	AA	-2.370	0.54
AA	CA	-2.379	0.53
UA	AU	-2.384	0.52
CC	GG	-2.392	0.52
UG	CC	-2.394	0.51
UG	AC	-2.397	0.51
CA	AC	-2.399	0.51
AU	AC	-2.409	0.50
GU	AA	-2.421	0.49
GU	UU	-2.423	0.49
GU	UC	-2.423	0.48
AA	AU	-2.443	0.46
AU	UU	-2.446	0.46
UG	CA	-2.453	0.45
AA	GA	-2.464	0.44
UU	AA	-2.469	0.44
UA	UU	-2.471	0.44
CA	UG	-2.474	0.43
AA	AA	-2.477	0.43
CU	CU	-2.478	0.43
UU	AU	-2.479	0.43
CA	AU	-2.495	0.41
UG	AA	-2.500	0.41
UC	AU	-2.501	0.41
UG	UU	-2.504	0.40
AU	AU	-2.505	0.40
AC	CC	-2.516	0.39
AU	AA	-2.530	0.38
GA	UC	-2.532	0.38
UC	UU	-2.538	0.37
CA	UC	-2.540	0.37
CA	UU	-2.544	0.36
GA	AC	-2.546	0.36
CC	CU	-2.549	0.36
UA	UA	-2.554	0.35
CU	UA	-2.567	0.34
CU	AG	-2.574	0.33
AG	CU	-2.582	0.33
CA	AA	-2.587	0.32
GG	CC	-2.592	0.32
UA	AC	-2.602	0.31
UU	GA	-2.628	0.28
AG	GU	-2.640	0.27
CU	UC	-2.654	0.25
GG	AC	-2.658	0.25
AC	CU	-2.667	0.24

iLoop size 3x1			
Range	2.525		
Median	-2.726		
5'	**3'**	**Score**	**Centered score**
UCU	U	-1.464	1.26
UUU	U	-1.668	1.06
AAA	G	-1.847	0.88
AAC	A	-1.930	0.80
CAC	C	-2.065	0.66
UCA	U	-2.109	0.62
AUU	C	-2.220	0.51
UGU	U	-2.239	0.49
ACA	A	-2.256	0.47
CCU	U	-2.273	0.45
UUC	U	-2.275	0.45
GCU	U	-2.296	0.43
AUU	U	-2.335	0.39
UCU	C	-2.338	0.39
UCU	A	-2.368	0.36
AAC	G	-2.389	0.34
AAA	A	-2.445	0.28
CUC	C	-2.460	0.27
UAU	U	-2.541	0.19
CUU	U	-2.554	0.17
AAU	U	-2.557	0.17
UGA	U	-2.564	0.16
UUU	C	-2.578	0.15
GCU	C	-2.579	0.15
GCA	U	-2.589	0.14
UAU	A	-2.656	0.07
AUC	C	-2.662	0.06
AGA	C	-2.674	0.05
UUG	U	-2.709	0.02
GCC	U	-2.714	0.01
UAC	U	-2.715	0.01
ACU	C	-2.720	0.01
UGA	A	-2.726	0.00
UCC	C	-2.728	0.00
UUA	G	-2.729	0.00
UGG	U	-2.734	-0.01
AUA	G	-2.738	-0.01
AAA	U	-2.750	-0.02
UCC	U	-2.753	-0.03
CUC	U	-2.761	-0.03
UGU	A	-2.765	-0.04
UUG	A	-2.769	-0.04
AUA	A	-2.778	-0.05
CAU	U	-2.780	-0.05
UAU	C	-2.783	-0.06
UUU	A	-2.787	-0.06
CAU	C	-2.791	-0.06
GUU	U	-2.793	-0.07
AAC	U	-2.796	-0.07
CAC	A	-2.797	-0.07
CAG	A	-2.805	-0.08
CUG	U	-2.806	-0.08
AAU	C	-2.808	-0.08
ACA	G	-2.818	-0.09
CAC	U	-2.825	-0.10
CCU	G	-2.837	-0.11
GCA	C	-2.841	-0.11
GCC	A	-2.845	-0.12
AAU	A	-2.849	-0.12
CUC	A	-2.852	-0.13
GUG	C	-2.859	-0.13
AAA	C	-2.868	-0.14
ACA	U	-2.881	-0.15
GUA	A	-2.882	-0.16
AUG	G	-2.885	-0.16

A	AUA	-2.835	0.06
U	UAC	-2.838	0.05
G	UAC	-2.839	0.05
G	CAU	-2.842	0.05
A	GUU	-2.848	0.05
G	AAU	-2.850	0.04
C	UUA	-2.855	0.04
U	UUA	-2.862	0.03
C	UGU	-2.863	0.03
G	UAU	-2.867	0.03
A	UGG	-2.891	0.00
A	GAU	-2.892	0.00
C	AAC	-2.893	0.00
C	UCU	-2.907	-0.01
U	GGC	-2.918	-0.03
A	AAA	-2.919	-0.03
U	GUA	-2.919	-0.03
C	CUA	-2.922	-0.03
U	AAA	-2.928	-0.04
C	UAG	-2.929	-0.04
A	CAG	-2.929	-0.04
A	CGC	-2.947	-0.05
G	AUU	-2.952	-0.06
A	CUG	-2.962	-0.07
C	AUU	-2.963	-0.07
G	UUA	-2.963	-0.07
U	CGU	-2.966	-0.07
C	CAA	-2.973	-0.08
G	UCA	-2.981	-0.09
U	AGC	-2.983	-0.09
A	GUA	-2.984	-0.09
A	AUU	-2.987	-0.09
C	UUC	-2.987	-0.09
U	CAG	-2.993	-0.10
U	CUG	-2.993	-0.10
U	AUG	-2.995	-0.10
G	AGA	-3.001	-0.11
A	UGC	-3.004	-0.11
G	GCC	-3.006	-0.11
G	AUG	-3.008	-0.12
U	GUC	-3.017	-0.12
A	GGC	-3.021	-0.13
U	ACC	-3.025	-0.13
G	UGC	-3.026	-0.13
U	UCU	-3.029	-0.14
G	CUA	-3.032	-0.14
A	UAC	-3.035	-0.14
G	CUU	-3.035	-0.14
A	UUG	-3.043	-0.15
G	UGA	-3.054	-0.16
A	UUC	-3.073	-0.18
C	ACU	-3.083	-0.19
G	GGA	-3.088	-0.20
C	UGA	-3.103	-0.21
C	UAC	-3.107	-0.21
A	AGA	-3.111	-0.22
A	GAA	-3.123	-0.23
C	UAU	-3.124	-0.23
G	UUU	-3.126	-0.23
G	CCU	-3.132	-0.24
A	CGA	-3.134	-0.24
A	CCG	-3.140	-0.25
C	CAG	-3.140	-0.25
U	AGU	-3.140	-0.25
U	UUG	-3.151	-0.26
U	CUA	-3.163	-0.27
C	UAA	-3.169	-0.28
U	CCA	-3.172	-0.28
G	UUC	-3.177	-0.28

GA	GA	-2.682	0.23
AA	CC	-2.692	0.22
AG	UU	-2.693	0.22
GU	CU	-2.702	0.21
UU	AC	-2.706	0.20
UA	AA	-2.713	0.20
CG	UU	-2.723	0.19
AC	UC	-2.726	0.18
AG	CA	-2.729	0.18
GC	GC	-2.730	0.18
UC	UG	-2.734	0.17
AA	UC	-2.734	0.17
UC	CU	-2.736	0.17
UU	UG	-2.740	0.17
AU	GA	-2.740	0.17
GU	CC	-2.749	0.16
CU	AC	-2.749	0.16
AC	GG	-2.750	0.16
UC	GG	-2.756	0.15
AG	GC	-2.757	0.15
UC	GA	-2.770	0.14
AG	GA	-2.771	0.14
CA	AG	-2.771	0.14
UG	CG	-2.779	0.13
CA	GA	-2.786	0.12
CU	AU	-2.795	0.11
GU	GC	-2.795	0.11
GA	UU	-2.796	0.11
GC	AU	-2.801	0.11
GG	UG	-2.806	0.10
AU	CA	-2.812	0.10
GC	AC	-2.818	0.09
UC	AC	-2.824	0.08
GA	CC	-2.827	0.08
AU	UA	-2.830	0.08
GA	AA	-2.831	0.08
GC	GA	-2.834	0.07
UC	AA	-2.839	0.07
UU	UA	-2.840	0.07
GG	CU	-2.842	0.07
CU	UG	-2.843	0.06
CC	AU	-2.844	0.06
AA	GU	-2.847	0.06
UC	GU	-2.853	0.06
CA	UA	-2.854	0.05
AC	AU	-2.857	0.05
AG	UG	-2.859	0.05
AU	UC	-2.859	0.05
AU	CU	-2.862	0.05
CU	CA	-2.869	0.04
CC	GU	-2.869	0.04
UA	UG	-2.869	0.04
AU	CC	-2.871	0.04
AA	GG	-2.876	0.03
CC	UC	-2.876	0.03
AA	CU	-2.879	0.03
AG	UA	-2.880	0.03
AA	UA	-2.887	0.02
GG	AU	-2.887	0.02
GC	CC	-2.889	0.02
UG	GU	-2.889	0.02
AC	GU	-2.892	0.02
AU	GU	-2.894	0.01
GC	CU	-2.897	0.01
AC	AG	-2.899	0.01
GU	GU	-2.900	0.01
GG	UC	-2.904	0.00
UU	AG	-2.904	0.00
CA	CU	-2.906	0.00

UAA	U	-2.895	-0.17
AAG	A	-2.899	-0.17
UAC	A	-2.900	-0.17
AUG	A	-2.905	-0.18
AUA	C	-2.908	-0.18
GCG	U	-2.911	-0.18
CCC	U	-2.914	-0.19
AGG	G	-2.914	-0.19
GAU	A	-2.915	-0.19
ACU	U	-2.923	-0.20
UAC	C	-2.923	-0.20
AGA	G	-2.925	-0.20
AGU	A	-2.929	-0.20
ACU	A	-2.931	-0.20
UCA	A	-2.937	-0.21
CAG	U	-2.945	-0.22
GUU	C	-2.950	-0.22
CUA	U	-2.950	-0.22
UGA	C	-2.950	-0.22
AUA	U	-2.952	-0.23
AAU	G	-2.956	-0.23
CAA	U	-2.958	-0.23
UCU	G	-2.959	-0.23
UAA	A	-2.975	-0.25
UGU	C	-2.977	-0.25
CAG	C	-3.012	-0.29
GUG	G	-3.012	-0.29
CUG	G	-3.013	-0.29
UUA	U	-3.027	-0.30
GUG	A	-3.032	-0.31
AUC	A	-3.033	-0.31
AGU	U	-3.042	-0.32
GCA	A	-3.048	-0.32
GAA	A	-3.051	-0.32
GUG	U	-3.052	-0.33
CAA	G	-3.056	-0.33
CCA	C	-3.066	-0.34
UGC	C	-3.066	-0.34
UUC	C	-3.069	-0.34
AUU	A	-3.073	-0.35
UUA	A	-3.073	-0.35
AAG	G	-3.082	-0.36
CUG	C	-3.082	-0.36
CAA	C	-3.088	-0.36
GGC	A	-3.090	-0.36
CCU	C	-3.091	-0.36
GCC	C	-3.104	-0.38
CUU	C	-3.111	-0.38
GUA	U	-3.120	-0.39
GCA	G	-3.122	-0.40
AGA	A	-3.127	-0.40
ACC	U	-3.131	-0.40
UAG	A	-3.145	-0.42
CAC	G	-3.150	-0.42
GCC	G	-3.152	-0.43
GAA	U	-3.154	-0.43
CAA	A	-3.155	-0.43
GAU	C	-3.156	-0.43
GUC	U	-3.165	-0.44
AGA	U	-3.174	-0.45
CAU	A	-3.177	-0.45
CUC	G	-3.177	-0.45
AGC	A	-3.181	-0.45
CUG	A	-3.183	-0.46
UGC	U	-3.191	-0.46
AAC	C	-3.203	-0.48
GCU	A	-3.205	-0.48
ACC	A	-3.206	-0.48
GCG	C	-3.210	-0.48

U	ACU	-3.194	-0.30
A	AGC	-3.199	-0.31
A	UAG	-3.201	-0.31
A	ACA	-3.203	-0.31
C	AAA	-3.205	-0.31
G	ACA	-3.205	-0.31
U	GUU	-3.205	-0.31
C	CCG	-3.209	-0.32
A	GAC	-3.218	-0.32
A	GCC	-3.218	-0.32
U	UCA	-3.224	-0.33
G	GAG	-3.230	-0.34
U	AAC	-3.232	-0.34
G	AUC	-3.238	-0.35
U	AUA	-3.238	-0.35
G	UGG	-3.243	-0.35
C	AAG	-3.252	-0.36
G	GUU	-3.257	-0.36
G	GUA	-3.259	-0.37
C	GAA	-3.267	-0.37
C	AGU	-3.268	-0.38
G	AUA	-3.268	-0.38
C	AGG	-3.273	-0.38
A	GAG	-3.275	-0.38
A	UCG	-3.285	-0.39
C	CUG	-3.288	-0.40
A	AUG	-3.291	-0.40
G	CCA	-3.295	-0.40
C	GAU	-3.298	-0.41
G	ACC	-3.298	-0.41
A	GUG	-3.299	-0.41
U	GAC	-3.299	-0.41
U	GCA	-3.305	-0.41
G	UCG	-3.312	-0.42
U	UGG	-3.312	-0.42
G	UAA	-3.322	-0.43
U	GAA	-3.323	-0.43
A	ACC	-3.328	-0.44
C	ACC	-3.328	-0.44
C	GUC	-3.328	-0.44
U	GAU	-3.336	-0.44
G	GGG	-3.345	-0.45
U	UCG	-3.345	-0.45
C	CGA	-3.349	-0.46
A	GCA	-3.355	-0.46
C	GGC	-3.355	-0.46
U	GGA	-3.362	-0.47
G	AGC	-3.364	-0.47
G	AGU	-3.365	-0.47
U	UAA	-3.365	-0.47
G	UUG	-3.370	-0.48
G	GGC	-3.373	-0.48
C	CGC	-3.375	-0.48
U	GCU	-3.377	-0.48
G	CGU	-3.377	-0.48
U	GAG	-3.379	-0.49
U	GCC	-3.385	-0.49
G	GCU	-3.397	-0.50
G	AGG	-3.402	-0.51
G	GAA	-3.402	-0.51
G	GUC	-3.402	-0.51
C	AUA	-3.407	-0.51
A	AAG	-3.422	-0.53
G	UAG	-3.422	-0.53
U	ACA	-3.422	-0.53
C	GCU	-3.425	-0.53
C	AGC	-3.427	-0.53
A	AGG	-3.432	-0.54
C	GCC	-3.451	-0.56

CC	UA	-2.911	0.00
CA	GU	-2.912	0.00
AA	UG	-2.921	-0.01
GU	AG	-2.924	-0.02
CU	GG	-2.925	-0.02
AU	UG	-2.932	-0.02
GU	UG	-2.932	-0.02
UA	GA	-2.943	-0.03
CG	CA	-2.943	-0.04
AC	GA	-2.948	-0.04
GC	GU	-2.949	-0.04
CG	CG	-2.960	-0.05
UG	UA	-2.963	-0.06
GC	UC	-2.969	-0.06
GU	GA	-2.972	-0.06
AC	UU	-2.976	-0.07
GC	UG	-2.978	-0.07
GU	UA	-2.980	-0.07
UU	CC	-2.982	-0.07
CG	UA	-2.996	-0.09
GA	AU	-3.001	-0.09
AA	AG	-3.004	-0.10
UG	UC	-3.008	-0.10
GA	CA	-3.014	-0.11
GA	CU	-3.014	-0.11
CU	GA	-3.015	-0.11
UA	AG	-3.019	-0.11
UC	UC	-3.020	-0.11
UC	CA	-3.021	-0.11
CG	AA	-3.022	-0.11
GC	CA	-3.022	-0.11
UU	GU	-3.026	-0.12
CC	CC	-3.028	-0.12
UA	GU	-3.031	-0.12
GA	GC	-3.031	-0.12
GC	UU	-3.032	-0.12
CU	AA	-3.032	-0.12
CC	UG	-3.032	-0.12
AC	AC	-3.034	-0.13
CU	CC	-3.035	-0.13
UC	UA	-3.039	-0.13
CG	GG	-3.063	-0.15
GG	AG	-3.068	-0.16
UG	AG	-3.075	-0.17
AG	CG	-3.078	-0.17
CA	CC	-3.079	-0.17
CU	CG	-3.079	-0.17
GG	CA	-3.087	-0.18
CG	CU	-3.087	-0.18
GU	CA	-3.090	-0.18
CA	CA	-3.101	-0.19
UA	CU	-3.102	-0.19
UC	AG	-3.108	-0.20
CC	CA	-3.124	-0.22
AC	UG	-3.127	-0.22
UU	GG	-3.132	-0.22
UC	GC	-3.147	-0.24
GC	UA	-3.160	-0.25
GG	UU	-3.162	-0.25
AU	GC	-3.165	-0.26
GG	CG	-3.167	-0.26
UA	CA	-3.171	-0.26
GA	GG	-3.175	-0.27
CC	AC	-3.180	-0.27
AU	AG	-3.185	-0.28
AC	AA	-3.190	-0.28
CA	GG	-3.193	-0.29
AG	GG	-3.201	-0.29
GC	AA	-3.208	-0.30

GGG	A	-3.213	-0.49
UAA	G	-3.221	-0.49
GGU	C	-3.223	-0.50
UCA	G	-3.226	-0.50
UCC	A	-3.226	-0.50
GAU	U	-3.230	-0.50
GUA	C	-3.232	-0.51
GAC	A	-3.232	-0.51
UGC	A	-3.241	-0.51
CCG	C	-3.241	-0.51
AUG	C	-3.262	-0.54
GAG	A	-3.263	-0.54
CUU	G	-3.266	-0.54
UAU	G	-3.266	-0.54
CCA	A	-3.279	-0.55
UUC	A	-3.279	-0.55
GGU	U	-3.284	-0.56
CGG	U	-3.297	-0.57
ACU	G	-3.298	-0.57
AUC	G	-3.299	-0.57
UCG	U	-3.302	-0.58
UUA	C	-3.311	-0.58
AAG	C	-3.315	-0.59
AUC	U	-3.315	-0.59
UGG	C	-3.315	-0.59
GGA	C	-3.323	-0.60
AAG	U	-3.324	-0.60
UAG	U	-3.324	-0.60
UGG	A	-3.330	-0.60
CGC	C	-3.335	-0.61
GGA	A	-3.339	-0.61
CUA	G	-3.346	-0.62
GAA	G	-3.347	-0.62
GUC	C	-3.349	-0.62
GCU	G	-3.353	-0.63
UGG	G	-3.353	-0.63
GAC	U	-3.360	-0.63
UUG	C	-3.360	-0.63
UAG	C	-3.375	-0.65
GGG	C	-3.379	-0.65
ACC	G	-3.389	-0.66
GGC	U	-3.389	-0.66
ACC	C	-3.400	-0.67
AUG	U	-3.404	-0.68
UGA	G	-3.404	-0.68
GGG	G	-3.412	-0.69
CCA	U	-3.414	-0.69
AGG	A	-3.414	-0.69
GAC	G	-3.416	-0.69
AUU	G	-3.420	-0.69
GGA	U	-3.420	-0.69
GAG	C	-3.427	-0.70
CUA	A	-3.438	-0.71
UUU	G	-3.438	-0.71
GGG	U	-3.444	-0.72
AGC	G	-3.449	-0.72
UAC	G	-3.451	-0.72
CUU	A	-3.456	-0.73
UGU	G	-3.456	-0.73
CGA	C	-3.459	-0.73
AGU	C	-3.466	-0.74
UCA	C	-3.474	-0.75
CCC	C	-3.474	-0.75
GGC	G	-3.477	-0.75
GCG	A	-3.480	-0.75
CGA	A	-3.486	-0.76
GGU	A	-3.492	-0.77
AGC	U	-3.501	-0.77
CCC	A	-3.501	-0.77

A	AAC	-3.453	-0.56
C	GAG	-3.462	-0.57
U	AGG	-3.462	-0.57
U	GGG	-3.464	-0.57
G	UCU	-3.469	-0.58
A	CGU	-3.471	-0.58
U	GUG	-3.471	-0.58
U	GGU	-3.476	-0.58
C	UCG	-3.487	-0.59
C	AUC	-3.511	-0.62
G	CAG	-3.514	-0.62
G	CGA	-3.514	-0.62
C	UCA	-3.518	-0.62
C	ACG	-3.525	-0.63
C	GUU	-3.525	-0.63
C	CCA	-3.528	-0.64
A	GGU	-3.536	-0.64
C	AUG	-3.536	-0.64
A	AGU	-3.561	-0.67
G	CUG	-3.570	-0.68
A	GCG	-3.575	-0.68
C	AGA	-3.581	-0.69
G	GAC	-3.581	-0.69
G	GGU	-3.581	-0.69
G	GCA	-3.591	-0.70
U	ACG	-3.591	-0.70
U	AGA	-3.603	-0.71
C	GUG	-3.610	-0.72
G	CGC	-3.616	-0.72
U	CGG	-3.616	-0.72
C	GCA	-3.630	-0.74
G	CGG	-3.630	-0.74
A	GGA	-3.638	-0.75
A	GGG	-3.684	-0.79
C	CGU	-3.684	-0.79
C	GUA	-3.695	-0.80
U	CCG	-3.707	-0.81
C	CGG	-3.720	-0.83
C	GAC	-3.769	-0.88
C	GGA	-3.769	-0.88
A	CGG	-3.789	-0.90
C	UGG	-3.789	-0.90
C	UUG	-3.789	-0.90
G	GAU	-3.843	-0.95
C	GGU	-3.879	-0.99
G	CCG	-3.879	-0.99
G	GUG	-3.879	-0.99
C	GCG	-3.928	-1.03
G	ACG	-3.928	-1.03
A	ACG	-4.002	-1.11
U	GCG	-4.002	-1.11
C	GGG	-4.161	-1.27
G	GCG	-4.161	-1.27

GA	UG	-3.215	-0.31
GA	GU	-3.224	-0.32
CU	GC	-3.229	-0.32
CG	AU	-3.229	-0.32
CG	GA	-3.232	-0.32
CG	UG	-3.242	-0.33
UA	CC	-3.254	-0.35
CA	GC	-3.261	-0.35
AU	GG	-3.263	-0.36
UA	GG	-3.263	-0.36
UC	CC	-3.264	-0.36
CC	AA	-3.280	-0.37
UA	CG	-3.316	-0.41
AC	UA	-3.329	-0.42
CC	AG	-3.339	-0.43
GG	GC	-3.360	-0.45
CA	CG	-3.362	-0.45
CU	GU	-3.367	-0.46
UG	GC	-3.373	-0.47
UU	CA	-3.398	-0.49
CC	GA	-3.410	-0.50
CG	UC	-3.419	-0.51
CG	CC	-3.420	-0.51
CC	CG	-3.433	-0.52
GA	UA	-3.433	-0.52
UU	GC	-3.445	-0.54
AC	GC	-3.447	-0.54
GU	GG	-3.453	-0.55
GC	AG	-3.456	-0.55
UA	GC	-3.456	-0.55
UA	UC	-3.466	-0.56
GC	GG	-3.489	-0.58
AC	CA	-3.493	-0.58
UG	GG	-3.519	-0.61
GG	GG	-3.537	-0.63
UU	CG	-3.551	-0.64
CG	AC	-3.556	-0.65
CC	GC	-3.556	-0.65
GG	GU	-3.585	-0.68
GU	CG	-3.592	-0.68
GG	GA	-3.609	-0.70
UG	GA	-3.622	-0.71
GC	CG	-3.630	-0.72
GG	UA	-3.631	-0.72
GA	AG	-3.659	-0.75
AA	CG	-3.710	-0.80
CG	AG	-3.818	-0.91
UC	CG	-3.855	-0.95
CG	GU	-3.903	-1.00
AU	CG	-3.959	-1.05
CG	GC	-4.014	-1.11
AC	CG	-4.118	-1.21
GA	CG	-4.136	-1.23

ACG	U	-3.512	-0.79
CCG	G	-3.523	-0.80
CCU	A	-3.523	-0.80
CGA	U	-3.523	-0.80
CGC	G	-3.544	-0.82
GAC	C	-3.544	-0.82
GCG	G	-3.548	-0.82
GUU	G	-3.548	-0.82
CGG	A	-3.563	-0.84
GAG	G	-3.563	-0.84
CGU	G	-3.568	-0.84
CAG	G	-3.579	-0.85
AGG	C	-3.579	-0.85
CGA	G	-3.597	-0.87
GAG	U	-3.597	-0.87
UCC	G	-3.597	-0.87
GAU	G	-3.610	-0.88
CCA	G	-3.618	-0.89
CGU	U	-3.618	-0.89
GUC	A	-3.618	-0.89
UAG	G	-3.618	-0.89
AGC	C	-3.625	-0.90
UCG	C	-3.625	-0.90
CUA	C	-3.633	-0.91
GUU	A	-3.642	-0.92
UCG	A	-3.642	-0.92
GUA	G	-3.671	-0.94
UAA	C	-3.671	-0.94
ACA	C	-3.682	-0.96
AGU	G	-3.682	-0.96
GGA	G	-3.694	-0.97
CCC	G	-3.707	-0.98
GAA	C	-3.738	-1.01
UUG	G	-3.738	-1.01
ACG	C	-3.756	-1.03
ACG	G	-3.756	-1.03
CAU	G	-3.756	-1.03
CGU	C	-3.756	-1.03
GUC	G	-3.756	-1.03
CGG	G	-3.777	-1.05
ACG	A	-3.801	-1.07
CGC	A	-3.801	-1.07
AGG	U	-3.830	-1.10
CCG	U	-3.830	-1.10
CGC	U	-3.830	-1.10
UUC	G	-3.830	-1.10
CCG	A	-3.866	-1.14
CGU	A	-3.866	-1.14
UGC	G	-3.866	-1.14
GGC	C	-3.915	-1.19
GGU	G	-3.915	-1.19
CGG	C	-3.989	-1.26
UCG	G	-3.989	-1.26

Table S35. Internal loops 1x1

5'	3'	Score	SD
U	U	-1.048	0.315
A	A	-1.112	0.164
C	A	-1.132	0.238
U	G	-1.139	0.611
A	U	-1.163	0.292
U	A	-1.175	0.025
C	U	-1.210	0.142
A	C	-1.269	0.167
G	C	-1.322	0.346
U	C	-1.324	0.145
C	G	-1.392	0.176
G	G	-1.424	0.185
C	C	-1.465	0.338
G	A	-1.466	0.016
G	U	-1.486	0.103
A	G	-1.541	0.150

5'	3'	Total count
A	A	22993
A	C	16235
A	G	6878
A	U	25785
C	A	17038
C	C	12047
C	G	11946
C	U	14547
G	A	8658
G	C	19467
G	G	11627
G	U	8672
U	A	16733
U	C	12632
U	G	29672
U	U	20697

Supercategory	Total count
Antisense	135819
Gene	39410
SnoRNA	80398

5'	3'	Score	SD
U	CC	-1.495	0.515
A	CA	-1.515	1.225
U	CU	-1.517	0.683
U	UU	-1.566	0.187
C	CU	-1.600	0.809
A	AU	-1.707	0.487
U	UC	-1.738	0.499
A	UU	-1.910	0.515
C	UU	-1.913	0.176
G	UU	-1.963	0.916
A	AA	-1.978	0.347
A	GA	-1.985	0.560
A	UG	-1.998	1.137
A	UA	-2.033	0.310
C	CC	-2.101	0.677
A	CU	-2.103	0.616
A	CC	-2.121	0.210
A	AG	-2.176	0.508
A	AC	-2.179	0.883
U	CA	-2.179	0.426
U	AA	-2.192	0.336
G	CC	-2.196	0.581
U	UG	-2.196	0.566
C	UC	-2.197	0.626
A	UC	-2.202	0.673
U	AU	-2.236	0.524
G	AA	-2.266	0.845
A	GU	-2.283	0.276
G	AC	-2.293	0.415
G	UC	-2.294	0.520
C	AU	-2.295	0.341
A	CG	-2.301	0.210
U	UA	-2.314	0.548
A	GG	-2.315	0.387
C	GC	-2.420	0.303
C	AA	-2.425	0.416
G	CU	-2.433	0.554
U	AG	-2.433	0.686
U	GU	-2.440	0.387
U	AC	-2.442	0.574
C	UG	-2.453	0.602
G	AG	-2.462	0.898
U	GC	-2.473	0.617
C	AC	-2.487	0.248
C	CA	-2.495	0.362
G	UG	-2.496	1.148
A	GC	-2.509	0.331
C	GU	-2.518	0.589
C	GA	-2.524	0.306
G	GA	-2.528	0.150
C	AG	-2.553	0.548
U	GA	-2.597	0.632
G	CA	-2.654	0.441
U	GG	-2.658	0.519
G	AU	-2.674	0.565
C	UA	-2.681	0.495
G	GC	-2.685	0.344
G	UA	-2.760	0.657
G	GU	-2.763	0.107
C	CG	-2.827	0.490
C	GG	-2.830	0.522
G	GG	-2.899	0.747
U	CG	-3.075	0.581
G	CG	-3.225	0.442

5'	3'	Total count
A	AA	630
A	AC	451
A	AG	351
A	AU	3612
A	CA	37007
A	CC	507
A	CG	316
A	CU	944
A	GA	559
A	GC	232
A	GG	273
A	GU	307
A	UA	725
A	UC	589
A	UG	896
A	UU	853
C	AA	305
C	AC	201
C	AG	154
C	AU	314
C	CA	244
C	CC	484
C	CG	116
C	CU	6044
C	GA	182
C	GC	225
C	GG	176
C	GU	403
C	UA	284
C	UC	356
C	UG	212
C	UU	969
G	AA	391
G	AC	288
G	AG	227
G	AU	145
G	CA	256
G	CC	337
G	CG	31
G	CU	402
G	GA	200
G	GC	167
G	GG	90
G	GU	128
G	UA	206
G	UC	377
G	UG	295
G	UU	1295
U	AA	497
U	AC	323
U	AG	247
U	AU	543
U	CA	528
U	CC	1711
U	CG	60
U	CU	4342
U	GA	216
U	GC	198
U	GG	173
U	GU	241
U	UA	622
U	UC	1501
U	UG	440
U	UU	2220

Supercategory	Total count
Antisense	47372
Gene	25825
SnoRNA	4421

5'	3'	Score	SD
GG	A	-1.281	0.781
UU	C	-1.483	0.884
AA	A	-1.498	0.969
UU	U	-1.532	0.884
GA	A	-1.573	0.403
AG	A	-1.621	0.238
AA	U	-1.807	0.851
CU	U	-1.809	0.710
UC	U	-1.826	0.627
AC	A	-1.909	0.107
CA	U	-1.913	0.095
GC	A	-1.917	0.195
AA	C	-1.925	0.593
UU	A	-1.928	0.412
AC	C	-1.928	0.318
CA	A	-1.974	0.255
CC	A	-1.986	0.185
AU	U	-2.007	0.229
AA	G	-2.039	0.725
CU	C	-2.063	0.170
UC	C	-2.105	0.010
GU	U	-2.110	0.137
UA	A	-2.122	0.225
GA	G	-2.135	0.376
GA	U	-2.154	0.187
AG	G	-2.156	0.182
UG	A	-2.166	0.106
CA	G	-2.170	0.057
GU	C	-2.171	0.098
AC	U	-2.220	0.197
GC	C	-2.222	0.148
AU	A	-2.230	0.263
CU	A	-2.253	0.331
CC	G	-2.274	0.552
AU	C	-2.315	0.275
GU	A	-2.327	0.179
UU	G	-2.333	0.357
UG	U	-2.353	0.437
UA	U	-2.372	0.107
UC	A	-2.386	0.357
GG	C	-2.390	0.474
UG	C	-2.408	0.645
AG	C	-2.419	0.343
AG	U	-2.422	0.422
CC	U	-2.450	0.205
GG	G	-2.469	0.269
UG	G	-2.473	0.697
CA	C	-2.483	0.160
CU	G	-2.484	0.454
CC	C	-2.495	0.374
UA	C	-2.507	0.438
GA	C	-2.510	0.452
UC	G	-2.550	0.575
GG	U	-2.574	0.199
AC	G	-2.650	0.199
UA	G	-2.681	0.324
GC	U	-2.717	0.668
AU	G	-2.739	0.312
GU	G	-2.785	0.171
GC	G	-2.842	0.456
CG	U	-2.891	0.655
CG	C	-2.897	0.413
CG	A	-2.954	0.174
CG	G	-3.451	0.477

5'	3'	Total count
AA	A	4127
AA	C	654
AA	G	607
AA	U	1605
AC	A	396
AC	C	322
AC	G	61
AC	U	162
AG	A	648
AG	C	152
AG	G	207
AG	U	125
AU	A	163
AU	C	175
AU	G	48
AU	U	300
CA	A	367
CA	C	89
CA	G	210
CA	U	352
CC	A	371
CC	C	134
CC	G	289
CC	U	96
CG	A	38
CG	C	47
CG	G	11
CG	U	103
CU	A	150
CU	C	301
CU	G	145
CU	U	632
GA	A	756
GA	C	88
GA	G	281
GA	U	208
GC	A	369
GC	C	165
GC	G	49
GC	U	67
GG	A	4831
GG	C	192
GG	G	115
GG	U	96
GU	A	127
GU	C	198
GU	G	44
GU	U	221
UA	A	254
UA	C	170
UA	G	80
UA	U	133
UC	A	188
UC	C	234
UC	G	187
UC	U	664
UG	A	222
UG	C	165
UG	G	210
UG	U	129
UU	A	339
UU	C	4211
UU	G	126
UU	U	1592

Supercategory	Total count
Antisense	14687
Gene	10431
SnoRNA	4680

5'	3'	Score	SD
U	CUC	-1.625	0.169
U	UGU	-1.964	0.181
C	CUC	-2.115	0.786
U	CAU	-2.149	0.920
A	CUU	-2.168	0.170
A	CUA	-2.178	1.427
U	CAC	-2.183	1.066
U	CCC	-2.184	0.462
U	UGC	-2.198	1.025
U	AUU	-2.257	1.304
A	CCU	-2.270	0.735
U	UGA	-2.288	0.544
U	UUC	-2.347	0.330
A	UGA	-2.367	0.427
U	CGC	-2.385	1.379
A	CCC	-2.387	0.372
C	CUU	-2.441	0.768
A	CUC	-2.443	0.512
G	ACU	-2.465	1.776
A	CAA	-2.490	0.458
A	CAU	-2.507	0.608
U	AUC	-2.517	0.049
A	UUA	-2.521	0.703
A	GUC	-2.525	0.479
C	CCU	-2.540	0.314
U	UUU	-2.542	0.748
C	CAC	-2.552	0.736
G	CCC	-2.557	0.535
U	CGA	-2.568	0.405
G	AAA	-2.576	0.942
A	GCU	-2.597	0.893
G	CUC	-2.599	0.597
A	UGU	-2.604	0.040
U	UAG	-2.614	1.071
A	AAU	-2.628	0.895
C	AAU	-2.637	1.892
A	CAC	-2.639	0.467
A	UCA	-2.640	0.342
C	CAU	-2.641	0.654
U	CUU	-2.646	0.356
U	CCU	-2.653	0.045
C	UUU	-2.672	0.657
G	UGU	-2.677	0.717
C	UCC	-2.684	0.524
A	UCU	-2.685	0.131
A	UAU	-2.694	1.057
A	AUC	-2.697	0.490
G	UCC	-2.699	0.587
G	AAG	-2.715	0.218
U	AAU	-2.717	0.775
C	UGC	-2.723	0.518
C	ACA	-2.729	0.689
A	UUU	-2.730	0.149
C	CCC	-2.730	0.521
U	UAU	-2.735	0.582
A	CCA	-2.751	1.020
A	ACU	-2.761	0.336
G	CAA	-2.765	0.488
A	UAA	-2.788	0.274
U	UCC	-2.796	0.360
A	UCC	-2.799	0.194
G	AAC	-2.803	0.513
U	AAG	-2.805	1.027
U	CAA	-2.813	0.270
G	CAC	-2.817	0.167
A	AUA	-2.835	0.664
U	UAC	-2.838	0.773
G	UAC	-2.839	0.093

5'	3'	Total count
A	AAA	86
A	AAC	12
A	AAG	18
A	AAU	75
A	ACA	56
A	ACC	13
A	ACG	1
A	ACU	41
A	AGA	80
A	AGC	35
A	AGG	12
A	AGU	7
A	AUA	229
A	AUC	78
A	AUG	23
A	AUU	60
A	CAA	286
A	CAC	172
A	CAG	70
A	CAU	117
A	CCA	412
A	CCC	96
A	CCG	31
A	CCU	198
A	CGA	122
A	CGC	79
A	CGG	6
A	CGU	10
A	CUA	8094
A	CUC	227
A	CUG	659
A	CUU	269
A	GAA	23
A	GAC	17
A	GAG	35
A	GAU	30
A	GCA	44
A	GCC	17
A	GCG	10
A	GCU	123
A	GGA	18
A	GGC	26
A	GGG	5
A	GGU	5
A	GUA	192
A	GUC	68
A	GUG	40
A	GUU	135
A	UAA	52
A	UAC	34
A	UAG	27
A	UAU	143
A	UCA	64
A	UCC	41
A	UCG	20
A	UCU	58
A	UGA	177
A	UGC	168
A	UGG	37
A	UGU	89
A	UUA	548
A	UUC	47
A	UUG	74
A	UUU	57
C	AAA	15
C	AAC	44
C	AAG	26
C	AAU	1248

Supercategory	Total count
Antisense	3788
Gene	28021
SnoRNA	3573

G	CAU	-2.842	0.191
A	GUU	-2.848	1.232
G	AAU	-2.850	0.912
C	UUA	-2.855	0.511
U	UUA	-2.862	0.187
C	UGU	-2.863	0.508
G	UAU	-2.867	0.927
A	UGG	-2.891	0.481
A	GAU	-2.892	0.384
C	AAC	-2.893	0.304
C	UCU	-2.907	0.814
U	GGC	-2.918	0.817
A	AAA	-2.919	0.440
U	GUA	-2.919	0.231
C	CUA	-2.922	0.839
U	AAA	-2.928	0.079
C	UAG	-2.929	0.603
A	CAG	-2.929	0.883
A	CGC	-2.947	0.801
G	AUU	-2.952	0.436
A	CUG	-2.962	1.176
C	AUU	-2.963	0.465
G	UUA	-2.963	0.197
U	CGU	-2.966	0.555
C	CAA	-2.973	0.482
G	UCA	-2.981	0.202
U	AGC	-2.983	0.994
A	GUA	-2.984	0.857
A	AUU	-2.987	0.829
C	UUC	-2.987	0.225
U	CAG	-2.993	0.505
U	CUG	-2.993	0.051
U	AUG	-2.995	0.925
G	AGA	-3.001	0.987
A	UGC	-3.004	0.814
G	GCC	-3.006	0.980
G	AUG	-3.008	0.517
U	GUC	-3.017	0.546
A	GGC	-3.021	0.276
U	ACC	-3.025	0.135
G	UGC	-3.026	0.752
U	UCU	-3.029	0.740
G	CUA	-3.032	0.915
A	UAC	-3.035	0.362
G	CUU	-3.035	0.407
A	UUG	-3.043	0.703
G	UGA	-3.054	0.396
A	UUC	-3.073	0.302
C	ACU	-3.083	0.761
G	GGA	-3.088	0.723
C	UGA	-3.103	0.295
C	UAC	-3.107	0.676
A	AGA	-3.111	0.483
A	GAA	-3.123	0.099
C	UAU	-3.124	0.446
G	UUU	-3.126	0.074
G	CCU	-3.132	0.812
A	CGA	-3.134	0.745
A	CCG	-3.140	0.206
C	CAG	-3.140	0.099
U	AGU	-3.140	0.668
U	UUG	-3.151	0.457
U	CUA	-3.163	0.845
C	UAA	-3.169	0.677
U	CCA	-3.172	0.378
G	UUC	-3.177	0.230
U	ACU	-3.194	0.177
A	AGC	-3.199	0.577
A	UAG	-3.201	0.669

C	ACA	57
C	ACC	11
C	ACG	6
C	ACU	42
C	AGA	7
C	AGC	27
C	AGG	29
C	AGU	21
C	AUA	31
C	AUC	44
C	AUG	9
C	AUU	97
C	CAA	28
C	CAC	230
C	CAG	21
C	CAU	86
C	CCA	39
C	CCC	47
C	CCG	120
C	CCU	73
C	CGA	16
C	CGC	113
C	CGG	4
C	CGU	13
C	CUA	145
C	CUC	311
C	CUG	43
C	CUU	131
C	GAA	24
C	GAC	3
C	GAG	14
C	GAU	25
C	GCA	19
C	GCC	7
C	GCG	2
C	GCU	14
C	GGA	7
C	GGC	16
C	GGG	0
C	GGU	3
C	GUA	12
C	GUC	13
C	GUG	22
C	GUU	6
C	UAA	32
C	UAC	50
C	UAG	34
C	UAU	15
C	UCA	10
C	UCC	64
C	UCG	6
C	UCU	51
C	UGA	28
C	UGC	216
C	UGG	6
C	UGU	56
C	UUA	62
C	UUC	33
C	UUG	6
C	UUU	47
G	AAA	94
G	AAC	33
G	AAG	49
G	AAU	37
G	ACA	15
G	ACC	25
G	ACG	2
G	ACU	1324
G	AGA	61

A	ACA	-3.203	0.586
C	AAA	-3.205	0.201
G	ACA	-3.205	0.210
U	GUU	-3.205	0.210
C	CCG	-3.209	0.769
A	GAC	-3.218	0.803
A	GCC	-3.218	0.254
U	UCA	-3.224	0.156
G	GAG	-3.230	0.264
U	AAC	-3.232	0.550
G	AUC	-3.238	0.121
U	AUA	-3.238	0.262
G	UGG	-3.243	0.297
C	AAG	-3.252	0.578
G	GUU	-3.257	0.622
G	GUA	-3.259	0.871
C	GAA	-3.267	0.858
C	AGU	-3.268	0.733
G	AUA	-3.268	0.175
C	AGG	-3.273	0.530
A	GAG	-3.275	0.504
A	UCG	-3.285	0.715
C	CUG	-3.288	0.537
A	AUG	-3.291	0.517
G	CCA	-3.295	0.511
C	GAU	-3.298	0.515
G	ACC	-3.298	0.912
A	GUG	-3.299	0.524
U	GAC	-3.299	0.524
U	GCA	-3.305	0.511
G	UCG	-3.312	0.376
U	UGG	-3.312	0.602
G	UAA	-3.322	0.462
U	GAA	-3.323	0.570
A	ACC	-3.328	0.150
C	ACC	-3.328	0.272
C	GUC	-3.328	0.879
U	GAU	-3.336	0.534
G	GGG	-3.345	0.942
U	UCG	-3.345	0.496
C	CGA	-3.349	0.574
A	GCA	-3.355	0.524
C	GGC	-3.355	0.061
U	GGA	-3.362	0.514
G	AGC	-3.364	0.449
G	AGU	-3.365	0.448
U	UAA	-3.365	0.448
G	UUG	-3.370	0.443
G	GGC	-3.373	0.428
C	CGC	-3.375	0.851
U	GCU	-3.377	0.436
G	CGU	-3.377	0.599
U	GAG	-3.379	0.582
U	GCC	-3.385	0.479
G	GCU	-3.397	0.589
G	AGG	-3.402	0.381
G	GAA	-3.402	0.025
G	GUC	-3.402	0.465
C	AUA	-3.407	0.459
A	AAG	-3.422	0.375
G	UAG	-3.422	0.375
U	ACA	-3.422	0.398
C	GCU	-3.425	0.436
C	AGC	-3.427	0.415
A	AGG	-3.432	0.470
C	GCC	-3.451	0.322
A	AAC	-3.453	0.410
C	GAG	-3.462	0.375
U	AGG	-3.462	0.350

G	AGC	26
G	AGG	8
G	AGU	9
G	AUA	13
G	AUC	22
G	AUG	31
G	AUU	44
G	CAA	49
G	CAC	74
G	CAG	15
G	CAU	41
G	CCA	41
G	CCC	63
G	CCG	3
G	CCU	27
G	CGA	15
G	CGC	21
G	CGG	7
G	CGU	8
G	CUA	244
G	CUC	54
G	CUG	29
G	CUU	23
G	GAA	12
G	GAC	7
G	GAG	16
G	GAU	2
G	GCA	9
G	GCC	46
G	GCG	0
G	GCU	13
G	GGA	42
G	GGC	19
G	GGG	17
G	GGU	27
G	GUA	25
G	GUC	14
G	GUG	3
G	GUU	14
G	UAA	26
G	UAC	49
G	UAG	18
G	UAU	71
G	UCA	26
G	UCC	53
G	UCG	11
G	UCU	11
G	UGA	29
G	UGC	103
G	UGG	15
G	UGU	65
G	UUA	30
G	UUC	21
G	UUG	25
G	UUU	29
U	AAA	46
U	AAC	46
U	AAG	107
U	AAU	85
U	ACA	18
U	ACC	41
U	ACG	9
U	ACU	29
U	AGA	23
U	AGC	343
U	AGG	14
U	AGU	85
U	AUA	34
U	AUC	116

U	GGG	-3.464	0.363
G	UCU	-3.469	0.437
A	CGU	-3.471	0.510
U	GUG	-3.471	0.510
U	GGU	-3.476	0.676
C	UCG	-3.487	0.381
C	AUC	-3.511	0.617
G	CAG	-3.514	0.300
G	CGA	-3.514	0.320
C	UCA	-3.518	0.362
C	ACG	-3.525	0.694
C	GUU	-3.525	0.234
C	CCA	-3.528	0.587
A	GGU	-3.536	0.637
C	AUG	-3.536	0.338
A	AGU	-3.561	0.573
G	CUG	-3.570	0.513
A	GCG	-3.575	0.244
C	AGA	-3.581	0.354
G	GAC	-3.581	0.354
G	GGU	-3.581	0.496
G	GCA	-3.591	0.259
U	ACG	-3.591	0.259
U	AGA	-3.603	0.456
C	GUG	-3.610	0.446
G	CGC	-3.616	0.434
U	CGG	-3.616	0.434
C	GCA	-3.630	0.410
G	CGG	-3.630	0.251
A	GGA	-3.638	0.397
A	GGG	-3.684	0.245
C	CGU	-3.684	0.318
C	GUA	-3.695	0.298
U	CCG	-3.707	0.277
C	CGG	-3.720	0.646
C	GAC	-3.769	0.350
C	GGA	-3.769	0.170
A	CGG	-3.789	0.135
C	UGG	-3.789	0.135
C	UUG	-3.789	0.135
G	GAU	-3.843	0.448
C	GGU	-3.879	0.025
G	CCG	-3.879	0.025
G	GUG	-3.879	0.025
C	GCG	-3.928	0.106
G	ACG	-3.928	0.106
A	ACG	-4.002	0.234
U	GCG	-4.002	0.234
C	GGG	-4.161	0.509
G	GCG	-4.161	0.509

U	AUG	57
U	AUU	641
U	CAA	94
U	CAC	2459
U	CAG	109
U	CAU	533
U	CCA	53
U	CCC	288
U	CCG	11
U	CCU	74
U	CGA	142
U	CGC	1958
U	CGG	21
U	CGU	130
U	CUA	165
U	CUC	643
U	CUG	38
U	CUU	94
U	GAA	18
U	GAC	40
U	GAG	14
U	GAU	18
U	GCA	24
U	GCC	36
U	GCG	1
U	GCU	24
U	GGA	42
U	GGC	298
U	GGG	21
U	GGU	56
U	GUA	29
U	GUC	30
U	GUG	10
U	GUU	15
U	UAA	9
U	UAC	312
U	UAG	178
U	UAU	112
U	UCA	24
U	UCC	103
U	UCG	19
U	UCU	89
U	UGA	216
U	UGC	2716
U	UGG	59
U	UGU	525
U	UUA	69
U	UUC	149
U	UUG	19
U	UUU	111

5'	3'	Score	SD
UU	UU	-1.680	0.802
UG	UG	-1.849	0.427
GU	AC	-1.893	1.098
CU	UU	-1.908	0.709
AG	AC	-1.993	1.157
AA	UU	-2.056	0.822
AG	AA	-2.080	0.268
UU	UC	-2.120	0.220
AA	AC	-2.154	0.510
GU	AU	-2.169	0.588
UU	CU	-2.190	0.552
AG	AG	-2.221	0.492
AG	CC	-2.223	0.356
UG	AU	-2.235	1.162
AG	AU	-2.261	0.538
CC	UU	-2.266	0.690
UG	CU	-2.276	0.236
AA	GC	-2.315	0.557
AG	UC	-2.361	0.176
GG	AA	-2.370	0.565
AA	CA	-2.379	0.325
UA	AU	-2.384	0.472
CC	GG	-2.392	0.945
UG	CC	-2.394	0.718
UG	AC	-2.397	0.397
CA	AC	-2.399	0.526
AU	AC	-2.409	0.770
GU	AA	-2.421	0.523
GU	UU	-2.423	0.355
GU	UC	-2.423	0.095
AA	AU	-2.443	0.471
AU	UU	-2.446	0.480
UG	CA	-2.453	0.241
AA	GA	-2.464	0.715
UU	AA	-2.469	0.642
UA	UU	-2.471	0.185
CA	UG	-2.474	0.662
AA	AA	-2.477	0.302
CU	CU	-2.478	0.972
UU	AU	-2.479	0.266
CA	AU	-2.495	0.223
UG	AA	-2.500	0.223
UC	AU	-2.501	0.783
UG	UU	-2.504	0.624
AU	AU	-2.505	0.367
AC	CC	-2.516	0.945
AU	AA	-2.530	0.612
GA	UC	-2.532	0.461
UC	UU	-2.538	1.318
CA	UC	-2.540	0.602
CA	UU	-2.544	0.281
GA	AC	-2.546	0.432
CC	CU	-2.549	0.571
UA	UA	-2.554	0.687
CU	UA	-2.567	0.390
CU	AG	-2.574	0.344
AG	CU	-2.582	0.227
CA	AA	-2.587	0.777
GG	CC	-2.592	0.534
UA	AC	-2.602	0.773
UU	GA	-2.628	0.460
AG	GU	-2.640	0.190
CU	UC	-2.654	0.465
GG	AC	-2.658	0.682
AC	CU	-2.667	0.096
GA	GA	-2.682	0.376
AA	CC	-2.692	0.073
AG	UU	-2.693	0.447

5'	3'	Total count
AA	AA	192
AA	AC	442
AA	AG	62
AA	AU	382
AA	CA	244
AA	CC	118
AA	CG	30
AA	CU	194
AA	GA	296
AA	GC	369
AA	GG	329
AA	GU	196
AA	UA	275
AA	UC	235
AA	UG	81
AA	UU	2239
AC	AA	41
AC	AC	106
AC	AG	265
AC	AU	69
AC	CA	34
AC	CC	959
AC	CG	8
AC	CU	126
AC	GA	117
AC	GC	29
AC	GG	287
AC	GU	98
AC	UA	42
AC	UC	126
AC	UG	166
AC	UU	99
AG	AA	490
AG	AC	3647
AG	AG	344
AG	AU	459
AG	CA	162
AG	CC	316
AG	CG	49
AG	CU	153
AG	GA	99
AG	GC	344
AG	GG	44
AG	GU	136
AG	UA	112
AG	UC	262
AG	UG	186
AG	UU	172
AU	AA	250
AU	AC	518
AU	AG	33
AU	AU	230
AU	CA	95
AU	CC	226
AU	CG	9
AU	CU	76
AU	GA	245
AU	GC	43
AU	GG	48
AU	GU	121
AU	UA	82
AU	UC	151
AU	UG	79
AU	UU	375
CA	AA	255
CA	AC	254
CA	AG	257
CA	AU	209

Supercategory	Total count
Antisense	28325
Gene	16246
SnoRNA	10457

GU	CU	-2.702	0.077
UU	AC	-2.706	0.430
UA	AA	-2.713	0.696
CG	UU	-2.723	0.031
AC	UC	-2.726	0.461
AG	CA	-2.729	0.647
GC	GC	-2.730	0.551
UC	UG	-2.734	0.526
AA	UC	-2.734	0.530
UC	CU	-2.736	1.133
UU	UG	-2.740	0.858
AU	GA	-2.740	1.027
GU	CC	-2.749	0.426
CU	AC	-2.749	0.195
AC	GG	-2.750	0.629
UC	GG	-2.756	0.679
AG	GC	-2.757	0.930
UC	GA	-2.770	0.392
AG	GA	-2.771	0.193
CA	AG	-2.771	0.740
UG	CG	-2.779	0.188
CA	GA	-2.786	0.327
CU	AU	-2.795	0.202
GU	GC	-2.795	0.779
GA	UU	-2.796	0.386
GC	AU	-2.801	0.332
GG	UG	-2.806	0.070
AU	CA	-2.812	0.209
GC	AC	-2.818	0.551
UC	AC	-2.824	0.711
GA	CC	-2.827	0.266
AU	UA	-2.830	0.234
GA	AA	-2.831	0.569
GC	GA	-2.834	0.701
UC	AA	-2.839	0.480
UU	UA	-2.840	0.645
GG	CU	-2.842	0.301
CU	UG	-2.843	0.444
CC	AU	-2.844	0.560
AA	GU	-2.847	0.678
UC	GU	-2.853	0.517
CA	UA	-2.854	0.849
AC	AU	-2.857	0.207
AG	UG	-2.859	0.731
AU	UC	-2.859	0.625
AU	CU	-2.862	0.071
CU	CA	-2.869	0.539
CC	GU	-2.869	0.171
UA	UG	-2.869	0.428
AU	CC	-2.871	0.664
AA	GG	-2.876	0.929
CC	UC	-2.876	1.182
AA	CU	-2.879	0.616
AG	UA	-2.880	0.345
AA	UA	-2.887	0.818
GG	AU	-2.887	0.556
GC	CC	-2.889	0.517
UG	GU	-2.889	0.284
AC	GU	-2.892	0.625
AU	GU	-2.894	0.412
GC	CU	-2.897	0.606
AC	AG	-2.899	0.738
GU	GU	-2.900	0.456
GG	UC	-2.904	0.246
UU	AG	-2.904	0.327
CA	CU	-2.906	0.705
CC	UA	-2.911	0.593
CA	GU	-2.912	0.590
AA	UG	-2.921	0.254

CA	CA	359
CA	CC	151
CA	CG	47
CA	CU	105
CA	GA	137
CA	GC	28
CA	GG	70
CA	GU	133
CA	UA	316
CA	UC	246
CA	UG	351
CA	UU	212
CC	AA	84
CC	AC	35
CC	AG	173
CC	AU	169
CC	CA	133
CC	CC	73
CC	CG	67
CC	CU	197
CC	GA	78
CC	GC	30
CC	GG	1168
CC	GU	79
CC	UA	92
CC	UC	616
CC	UG	116
CC	UU	626
CG	AA	81
CG	AC	18
CG	AG	7
CG	AU	56
CG	CA	157
CG	CC	29
CG	CG	69
CG	CU	55
CG	GA	77
CG	GC	5
CG	GG	93
CG	GU	5
CG	UA	64
CG	UC	35
CG	UG	46
CG	UU	101
CU	AA	95
CU	AC	108
CU	AG	230
CU	AU	80
CU	CA	130
CU	CC	101
CU	CG	121
CU	CU	418
CU	GA	282
CU	GC	69
CU	GG	186
CU	GU	97
CU	UA	143
CU	UC	175
CU	UG	84
CU	UU	1055
GA	AA	112
GA	AC	227
GA	AG	16
GA	AU	64
GA	CA	75
GA	CC	77
GA	CG	3
GA	CU	176
GA	GA	112

GU	AG	-2.924	0.577
CU	GG	-2.925	0.808
AU	UG	-2.932	0.407
GU	UG	-2.932	0.500
UA	GA	-2.943	0.343
CG	CA	-2.943	0.685
AC	GA	-2.948	0.855
GC	GU	-2.949	0.602
CG	CG	-2.960	0.509
UG	UA	-2.963	1.342
GC	UC	-2.969	0.456
GU	GA	-2.972	0.462
AC	UU	-2.976	0.601
GC	UG	-2.978	0.556
GU	UA	-2.980	0.624
UU	CC	-2.982	0.639
CG	UA	-2.996	0.454
GA	AU	-3.001	0.244
AA	AG	-3.004	0.183
UG	UC	-3.008	0.581
GA	CA	-3.014	0.660
GA	CU	-3.014	0.682
CU	GA	-3.015	0.881
UA	AG	-3.019	0.478
UC	UC	-3.020	0.884
UC	CA	-3.021	0.273
CG	AA	-3.022	0.710
GC	CA	-3.022	0.462
UU	GU	-3.026	0.392
CC	CC	-3.028	0.460
UA	GU	-3.031	1.020
GA	GC	-3.031	0.112
GC	UU	-3.032	0.710
CU	AA	-3.032	0.430
CC	UG	-3.032	0.702
AC	AC	-3.034	0.748
CU	CC	-3.035	0.883
UC	UA	-3.039	0.655
CG	GG	-3.063	0.527
GG	AG	-3.068	0.390
UG	AG	-3.075	0.115
AG	CG	-3.078	0.411
CA	CC	-3.079	0.876
CU	CG	-3.079	0.590
GG	CA	-3.087	0.631
CG	CU	-3.087	0.559
GU	CA	-3.090	0.655
CA	CA	-3.101	1.090
UA	CU	-3.102	0.813
UC	AG	-3.108	1.240
CC	CA	-3.124	0.733
AC	UG	-3.127	0.805
UU	GG	-3.132	0.520
UC	GC	-3.147	0.535
GC	UA	-3.160	0.756
GG	UU	-3.162	0.572
AU	GC	-3.165	0.160
GG	CG	-3.167	0.624
UA	CA	-3.171	0.699
GA	GG	-3.175	0.437
CC	AC	-3.180	0.148
AU	AG	-3.185	0.189
AC	AA	-3.190	0.319
CA	GG	-3.193	0.475
AG	GG	-3.201	0.618
GC	AA	-3.208	0.493
GA	UG	-3.215	0.543
GA	GU	-3.224	0.158
CU	GC	-3.229	0.711

GA	GC	52
GA	GG	44
GA	GU	32
GA	UA	27
GA	UC	318
GA	UG	43
GA	UU	120
GC	AA	36
GC	AC	134
GC	AG	24
GC	AU	107
GC	CA	53
GC	CC	81
GC	CG	19
GC	CU	170
GC	GA	168
GC	GC	175
GC	GG	21
GC	GU	160
GC	UA	64
GC	UC	93
GC	UG	134
GC	UU	122
GG	AA	349
GG	AC	244
GG	AG	71
GG	AU	115
GG	CA	79
GG	CC	165
GG	CG	103
GG	CU	92
GG	GA	59
GG	GC	72
GG	GG	16
GG	GU	17
GG	UA	22
GG	UC	74
GG	UG	81
GG	UU	89
GU	AA	390
GU	AC	3911
GU	AG	110
GU	AU	640
GU	CA	96
GU	CC	135
GU	CG	24
GU	CU	108
GU	GA	96
GU	GC	228
GU	GG	17
GU	GU	124
GU	UA	119
GU	UC	200
GU	UG	79
GU	UU	218
UA	AA	256
UA	AC	242
UA	AG	82
UA	AU	342
UA	CA	126
UA	CC	57
UA	CG	85
UA	CU	101
UA	GA	73
UA	GC	24
UA	GG	60
UA	GU	130
UA	UA	316
UA	UC	33

CG	AU	-3.229	0.596
CG	GA	-3.232	0.549
CG	UG	-3.242	0.496
UA	CC	-3.254	0.679
CA	GC	-3.261	0.268
AU	GG	-3.263	0.757
UA	GG	-3.263	0.679
UC	CC	-3.264	0.714
CC	AA	-3.280	0.653
UA	CG	-3.316	0.745
AC	UA	-3.329	0.461
CC	AG	-3.339	1.144
GG	GC	-3.360	0.943
CA	CG	-3.362	0.610
CU	GU	-3.367	1.034
UG	GC	-3.373	0.217
UU	CA	-3.398	0.178
CC	GA	-3.410	0.753
CG	UC	-3.419	0.425
CG	CC	-3.420	0.668
CC	CG	-3.433	0.685
GA	UA	-3.433	0.351
UU	GC	-3.445	0.346
AC	GC	-3.447	0.512
GU	GG	-3.453	0.152
GC	AG	-3.456	0.397
UA	GC	-3.456	0.589
UA	UC	-3.466	0.526
GC	GG	-3.489	0.317
AC	CA	-3.493	0.463
UG	GG	-3.519	0.150
GG	GG	-3.537	0.097
UU	CG	-3.551	0.497
CG	AC	-3.556	0.389
CC	GC	-3.556	0.514
GG	GU	-3.585	0.615
GU	CG	-3.592	0.409
GG	GA	-3.609	0.910
UG	GA	-3.622	0.890
GC	CG	-3.630	0.562
GG	UA	-3.631	0.832
GA	AG	-3.659	0.293
AA	CG	-3.710	0.761
CG	AG	-3.818	0.249
UC	CG	-3.855	0.212
CG	GU	-3.903	0.244
AU	CG	-3.959	0.404
CG	GC	-4.014	0.329
AC	CG	-4.118	0.525
GA	CG	-4.136	0.342

UA	UG	114
UA	UU	222
UC	AA	141
UC	AC	105
UC	AG	217
UC	AU	322
UC	CA	72
UC	CC	46
UC	CG	6
UC	CU	287
UC	GA	162
UC	GC	41
UC	GG	296
UC	GU	92
UC	UA	134
UC	UC	135
UC	UG	194
UC	UU	560
UG	AA	172
UG	AC	267
UG	AG	49
UG	AU	2126
UG	CA	244
UG	CC	352
UG	CG	106
UG	CU	275
UG	GA	54
UG	GC	20
UG	GG	15
UG	GU	81
UG	UA	239
UG	UC	76
UG	UG	865
UG	UU	247
UU	AA	567
UU	AC	145
UU	AG	81
UU	AU	168
UU	CA	20
UU	CC	81
UU	CG	17
UU	CU	451
UU	GA	165
UU	GC	30
UU	GG	85
UU	GU	61
UU	UA	117
UU	UC	404
UU	UG	188
UU	UU	2035

5'	3'	Score	SD
UCU	U	-1.464	0.766
UUU	U	-1.668	0.608
AAA	G	-1.847	1.377
AAC	A	-1.930	1.322
CAC	C	-2.065	0.571
UCA	U	-2.109	0.793
AUU	C	-2.220	0.823
UGU	U	-2.239	0.260
ACA	A	-2.256	0.388
CCU	U	-2.273	0.456
UUC	U	-2.275	0.855
GCU	U	-2.296	0.600
AUU	U	-2.335	0.617
UCU	C	-2.338	0.598
UCU	A	-2.368	0.385
AAC	G	-2.389	0.858
AAA	A	-2.445	0.726
CUC	C	-2.460	1.240
UAU	U	-2.541	0.458
CUU	U	-2.554	0.760
AAU	U	-2.557	0.325
UGA	U	-2.564	0.415
UUU	C	-2.578	0.343
GCU	C	-2.579	0.943
GCA	U	-2.589	1.400
UAU	A	-2.656	0.281
AUC	C	-2.662	1.083
AGA	C	-2.674	0.622
UUG	U	-2.709	0.865
GCC	U	-2.714	1.525
UAC	U	-2.715	0.656
ACU	C	-2.720	0.634
UGA	A	-2.726	0.264
UCC	C	-2.728	0.286
UUA	G	-2.729	0.530
UGG	U	-2.734	0.396
AUA	G	-2.738	1.259
AAA	U	-2.750	0.493
UCC	U	-2.753	1.067
CUC	U	-2.761	0.624
UGU	A	-2.765	0.352
UUG	A	-2.769	0.611
AUA	A	-2.778	0.621
CAU	U	-2.780	0.333
UAU	C	-2.783	0.851
UUU	A	-2.787	0.386
CAU	C	-2.791	0.436
GUU	U	-2.793	0.222
AAC	U	-2.796	1.027
CAC	A	-2.797	0.797
CAG	A	-2.805	0.170
CUG	U	-2.806	0.482
AAU	C	-2.808	0.604
ACA	G	-2.818	0.580
CAC	U	-2.825	1.044
CCU	G	-2.837	0.728
GCA	C	-2.841	1.067
GCC	A	-2.845	0.227
AAU	A	-2.849	1.265
CUC	A	-2.852	0.597
GUG	C	-2.859	0.150
AAA	C	-2.868	0.751
ACA	U	-2.881	0.726
GUA	A	-2.882	0.729
AUG	G	-2.885	0.875
UAA	U	-2.895	0.117
AAG	A	-2.899	1.110
UAC	A	-2.900	0.774

5'	3'	Total count
AAA	A	628
AAA	C	84
AAA	G	2725
AAA	U	43
AAC	A	9290
AAC	C	342
AAC	G	1099
AAC	U	223
AAG	A	558
AAG	C	53
AAG	G	50
AAG	U	20
AAU	A	1314
AAU	C	111
AAU	G	118
AAU	U	74
ACA	A	154
ACA	C	4
ACA	G	32
ACA	U	47
ACC	A	112
ACC	C	15
ACC	G	12
ACC	U	34
ACG	A	5
ACG	C	3
ACG	G	3
ACG	U	14
ACU	A	42
ACU	C	43
ACU	G	37
ACU	U	160
AGA	A	31
AGA	C	94
AGA	G	71
AGA	U	20
AGC	A	397
AGC	C	18
AGC	G	62
AGC	U	15
AGG	A	27
AGG	C	9
AGG	G	39
AGG	U	2
AGU	A	74
AGU	C	19
AGU	G	12
AGU	U	27
AUA	A	45
AUA	C	48
AUA	G	69
AUA	U	26
AUC	A	124
AUC	C	89
AUC	G	11
AUC	U	9
AUG	A	34
AUG	C	11
AUG	G	32
AUG	U	29
AUU	A	40
AUU	C	174
AUU	G	12
AUU	U	101
CAA	A	159
CAA	C	53
CAA	G	22
CAA	U	36

Supercategory	Total count
Antisense	4794
Gene	32276
SnoRNA	2244

AUG	A	-2.905	0.712
AUA	C	-2.908	1.080
GCG	U	-2.911	0.549
CCC	U	-2.914	0.243
AGG	G	-2.914	0.444
GAU	A	-2.915	0.652
ACU	U	-2.923	0.597
UAC	C	-2.923	0.838
AGA	G	-2.925	0.685
AGU	A	-2.929	0.499
ACU	A	-2.931	0.374
UCA	A	-2.937	0.269
CAG	U	-2.945	0.302
GUU	C	-2.950	0.505
CUA	U	-2.950	0.294
UGA	C	-2.950	0.546
AUA	U	-2.952	0.655
AAU	G	-2.956	0.619
CAA	U	-2.958	0.093
UCU	G	-2.959	0.679
UAA	A	-2.975	0.313
UGU	C	-2.977	0.925
CAG	C	-3.012	0.342
GUG	G	-3.012	0.804
CUG	G	-3.013	0.250
UUA	U	-3.027	0.483
GUG	A	-3.032	0.537
AUC	A	-3.033	0.556
AGU	U	-3.042	0.626
GCA	A	-3.048	0.396
GAA	A	-3.051	0.745
GUG	U	-3.052	0.807
CAA	G	-3.056	0.256
CCA	C	-3.066	0.675
UGC	C	-3.066	0.137
UUC	C	-3.069	0.402
AUU	A	-3.073	0.965
UUA	A	-3.073	0.680
AAG	G	-3.082	0.503
CUG	C	-3.082	0.538
CAA	C	-3.088	0.250
GGC	A	-3.090	0.832
CCU	C	-3.091	0.486
GCC	C	-3.104	0.454
CUU	C	-3.111	0.650
GUA	U	-3.120	0.881
GCA	G	-3.122	0.354
AGA	A	-3.127	0.352
ACC	U	-3.131	0.864
UAG	A	-3.145	0.595
CAC	G	-3.150	0.349
GCC	G	-3.152	0.273
GAA	U	-3.154	0.477
CAA	A	-3.155	0.737
GAU	C	-3.156	0.306
GUC	U	-3.165	0.910
AGA	U	-3.174	0.422
CAU	A	-3.177	0.736
CUC	G	-3.177	0.518
AGC	A	-3.181	1.113
CUG	A	-3.183	0.993
UGC	U	-3.191	0.805
AAC	C	-3.203	1.077
GCU	A	-3.205	0.683
ACC	A	-3.206	0.761
GCG	C	-3.210	0.669
GGG	A	-3.213	0.400
UAA	G	-3.221	0.581
GGU	C	-3.223	0.390

CAC	A	378
CAC	C	232
CAC	G	27
CAC	U	68
CAG	A	59
CAG	C	24
CAG	G	25
CAG	U	29
CAU	A	37
CAU	C	43
CAU	G	3
CAU	U	70
CCA	A	12
CCA	C	41
CCA	G	7
CCA	U	27
CCC	A	15
CCC	C	12
CCC	G	4
CCC	U	31
CCG	A	3
CCG	C	16
CCG	G	9
CCG	U	4
CCU	A	37
CCU	C	56
CCU	G	56
CCU	U	547
CGA	A	48
CGA	C	10
CGA	G	8
CGA	U	13
CGC	A	5
CGC	C	9
CGC	G	8
CGC	U	4
CGG	A	10
CGG	C	1
CGG	G	6
CGG	U	12
CGU	A	3
CGU	C	7
CGU	G	7
CGU	U	7
CUA	A	11
CUA	C	5
CUA	G	11
CUA	U	33
CUC	A	32
CUC	C	442
CUC	G	17
CUC	U	60
CUG	A	47
CUG	C	43
CUG	G	24
CUG	U	39
CUU	A	11
CUU	C	35
CUU	G	10
CUU	U	118
GAA	A	197
GAA	C	8
GAA	G	16
GAA	U	20
GAC	A	279
GAC	C	32
GAC	G	78
GAC	U	19
GAG	A	76

UCA	G	-3.226	0.447
UCC	A	-3.226	0.054
GAU	U	-3.230	0.653
GUA	C	-3.232	0.373
GAC	A	-3.232	1.026
UGC	A	-3.241	0.379
CCG	C	-3.241	0.693
AUG	C	-3.262	0.387
GAG	A	-3.263	0.680
CUU	G	-3.266	0.536
UAU	G	-3.266	0.654
CCA	A	-3.279	0.316
UUC	A	-3.279	0.579
GGU	U	-3.284	0.793
CGG	U	-3.297	0.792
ACU	G	-3.298	0.592
AUC	G	-3.299	0.351
UCG	U	-3.302	0.589
UUA	C	-3.311	0.372
AAG	C	-3.315	0.609
AUC	U	-3.315	0.525
UGG	C	-3.315	0.445
GGA	C	-3.323	0.609
AAG	U	-3.324	0.643
UAG	U	-3.324	0.643
UGG	A	-3.330	0.326
CGC	C	-3.335	0.751
GGA	A	-3.339	0.578
CUA	G	-3.346	0.856
GAA	G	-3.347	0.367
GUC	C	-3.349	1.165
GCU	G	-3.353	0.313
UGG	G	-3.353	0.442
GAC	U	-3.360	0.590
UUG	C	-3.360	0.373
UAG	C	-3.375	0.874
GGG	C	-3.379	0.761
ACC	G	-3.389	0.186
GGC	U	-3.389	0.641
ACC	C	-3.400	0.587
AUG	U	-3.404	0.504
UGA	G	-3.404	0.312
GGG	G	-3.412	0.260
CCA	U	-3.414	0.494
AGG	A	-3.414	0.294
GAC	G	-3.416	0.714
AUU	G	-3.420	0.657
GGA	U	-3.420	0.215
GAG	C	-3.427	0.197
CUA	A	-3.438	0.835
UUU	G	-3.438	0.664
GGG	U	-3.444	0.243
AGC	G	-3.449	0.658
UAC	G	-3.451	0.232
CUU	A	-3.456	0.279
UGU	G	-3.456	0.279
CGA	C	-3.459	0.522
AGU	C	-3.466	0.208
UCA	C	-3.474	0.514
CCC	C	-3.474	0.742
GGC	G	-3.477	0.611
GCG	A	-3.480	0.607
CGA	A	-3.486	0.597
GGU	A	-3.492	0.430
AGC	U	-3.501	0.425
CCC	A	-3.501	0.152
ACG	U	-3.512	0.137
CCG	G	-3.523	0.523
CCU	A	-3.523	0.535

GAG	C	16
GAG	G	10
GAG	U	22
GAU	A	85
GAU	C	18
GAU	G	20
GAU	U	43
GCA	A	51
GCA	C	98
GCA	G	32
GCA	U	227
GCC	A	46
GCC	C	26
GCC	G	19
GCC	U	236
GCG	A	50
GCG	C	49
GCG	G	11
GCG	U	126
GCU	A	41
GCU	C	182
GCU	G	17
GCU	U	250
GGA	A	45
GGA	C	17
GGA	G	11
GGA	U	10
GGC	A	151
GGC	C	2
GGC	G	51
GGC	U	8
GGG	A	30
GGG	C	17
GGG	G	14
GGG	U	22
GGU	A	16
GGU	C	13
GGU	G	2
GGU	U	19
GUA	A	27
GUA	C	30
GUA	G	5
GUA	U	35
GUC	A	19
GUC	C	42
GUC	G	3
GUC	U	21
GUG	A	67
GUG	C	65
GUG	G	30
GUG	U	80
GUU	A	6
GUU	C	24
GUU	G	5
GUU	U	51
UAA	A	82
UAA	C	13
UAA	G	12
UAA	U	52
UAC	A	257
UAC	C	32
UAC	G	21
UAC	U	50
UAG	A	31
UAG	C	14
UAG	G	7
UAG	U	20
UAU	A	56
UAU	C	54

CGA	U	-3.523	0.415
CGC	G	-3.544	0.873
GAC	C	-3.544	0.501
GCG	G	-3.548	0.407
GUU	G	-3.548	0.680
CGG	A	-3.563	0.079
GAG	G	-3.563	0.079
CGU	G	-3.568	0.543
CAG	G	-3.579	0.444
AGG	C	-3.579	0.074
CGA	G	-3.597	0.080
GAG	U	-3.597	0.415
UCC	G	-3.597	0.080
GAU	G	-3.610	0.394
CCA	G	-3.618	0.409
CGU	U	-3.618	0.409
GUC	A	-3.618	0.383
UAG	G	-3.618	0.409
AGC	C	-3.625	0.371
UCG	C	-3.625	0.371
CUA	C	-3.633	0.341
GUU	A	-3.642	0.418
UCG	A	-3.642	0.418
GUA	G	-3.671	0.861
UAA	C	-3.671	0.302
ACA	C	-3.682	0.415
AGU	G	-3.682	0.286
GGA	G	-3.694	0.269
CCC	G	-3.707	0.235
GAA	C	-3.738	0.214
UUG	G	-3.738	0.214
ACG	C	-3.756	0.507
ACG	G	-3.756	0.717
CAU	G	-3.756	0.507
CGU	C	-3.756	1.006
GUC	G	-3.756	0.507
CGG	G	-3.777	0.179
ACG	A	-3.801	0.167
CGC	A	-3.801	0.167
AGG	U	-3.830	0.594
CCG	U	-3.830	0.166
CGC	U	-3.830	0.166
UUC	G	-3.830	0.166
CCG	A	-3.866	0.186
CGU	A	-3.866	0.186
UGC	G	-3.866	0.186
GGC	C	-3.915	0.237
GGU	G	-3.915	0.237
CGG	C	-3.989	0.818
UCG	G	-3.989	0.340

UAU	G	28
UAU	U	256
UCA	A	32
UCA	C	12
UCA	G	14
UCA	U	304
UCC	A	22
UCC	C	47
UCC	G	8
UCC	U	214
UCG	A	6
UCG	C	18
UCG	G	1
UCG	U	36
UCU	A	296
UCU	C	596
UCU	G	206
UCU	U	8551
UGA	A	127
UGA	C	23
UGA	G	29
UGA	U	60
UGC	A	16
UGC	C	25
UGC	G	3
UGC	U	28
UGG	A	12
UGG	C	11
UGG	G	9
UGG	U	44
UGU	A	43
UGU	C	67
UGU	G	11
UGU	U	316
UUA	A	28
UUA	C	10
UUA	G	78
UUA	U	36
UUC	A	10
UUC	C	18
UUC	G	4
UUC	U	166
UUG	A	46
UUG	C	15
UUG	G	8
UUG	U	84
UUU	A	57
UUU	C	69
UUU	G	11
UUU	U	706