

# **Supporting Information**

## **A General Approach for Machine Learning-Aided Design of DNA-Stabilized Silver Clusters**

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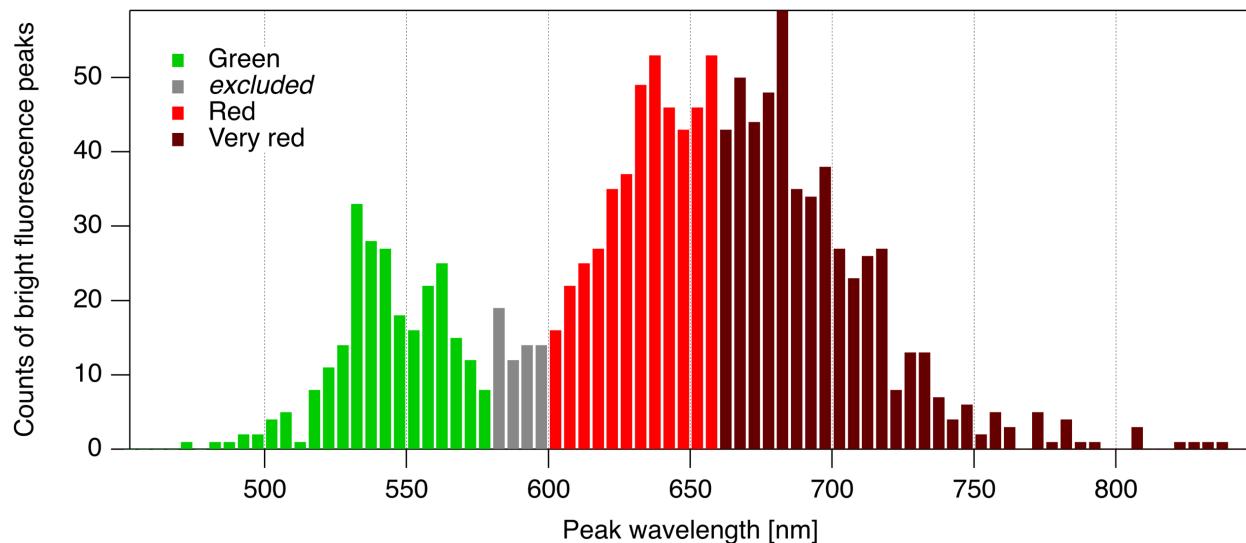
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## I. Experimental details

*Ag<sub>N</sub>-DNA synthesis:* DNA was ordered from Integrated DNA Technologies with standard desalting, suspended in water at 40  $\mu$ M in 384 well plates. Solutions were stored at -20°C until use and thawed by placing plates in a shallow water bath at 50°C. A Biomek 2000 pipetting robot (Beckman Coulter) was used to synthesize Ag<sub>N</sub>-DNA in 384 flat, clear bottom well plates (Corning 3540) using low-retention pipet tips. 20  $\mu$ L of DNA was mixed with 10  $\mu$ L of a solution of AgNO<sub>3</sub> and NH<sub>4</sub>OAc, pH 7, by repeated pipetting. Then, after 17-18 minutes, NaBH<sub>4</sub> was added to reduce the mixture and form silver clusters. The final concentration in each well was 20  $\mu$ M DNA, 10 mM NH<sub>4</sub>OAc, 100  $\mu$ M AgNO<sub>3</sub> (unless otherwise indicated for Figure 4), and 50  $\mu$ M NaBH<sub>4</sub>. Well plates were stored at 4°C and protected from light until measurement. Each 384 well plate contained a control DNA strand TTCCCCACCCACCCCCGGGCCGTT used to normalize fluorescence intensity with past experiments.<sup>1-3</sup>



**Figure S1: Color class definitions.** Histogram of all brightly fluorescent peaks  $\lambda_p$  measured for Ag<sub>N</sub>-DNA stabilized by the 2161 different 10-base DNA templates in the training data. The bimodal nature of the distribution results from the magic number behavior of these clusters,<sup>1</sup> forming the basis for the physically motivated class definitions. Green peaks are defined as  $\lambda_p < 580$  nm, red peaks are defined as  $600$  nm  $< \lambda_p < 660$  nm, and very red peaks are defined as  $\lambda_p > 660$  nm.

*Fluorimetry and spectral fitting:* A Tecan Infinite M200 Pro was used to measure fluorescence spectra from 450 nm to 800 nm in 2 nm steps, with excitation centered at 280 nm to universally excited all Ag<sub>N</sub>-DNA products.<sup>4</sup> Due to the poor sensitivity of the fluorimeter beyond ~800 nm, we excluded fluorescence measured above this range. To extract the peak wavelength(s) of products formed for a given DNA sequence, emission spectra were fitted to a set of Gaussians as a function of energy, using a custom Igor Pro

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(Wavemetrics) script and a screening method to remove bad fits, described in detail elsewhere.<sup>3</sup> The fluorescence brightness of each Ag<sub>N</sub>-DNA product is defined as the product of the peak amplitude and the peak width (a proxy of peak area). Peaks whose brightness is above a defined threshold that is normalized across experiments using control DNA strands<sup>1–3</sup> are defined to be brightly fluorescent and are assigned to a color class (see main text and Figure S1). Peaks whose total integrated intensity are below a separate defined threshold are defined to be Dark. For a detailed description of this process, see the Supporting Information of past work.<sup>3</sup>

## **II. Computational Details**

*Classification problem and training data:* Here, we seek to discriminate among the four color classes described above: Green, Red, Very Red, and Dark. (Wavelength definitions for Green, Red, and Very Red are shown in Figure S1.) Training data consists only of sequences associated with a single bright fluorescence peak falling within the Green, Red, or Very Red color class and of Dark sequences (defined above). Sequences associated with brightly fluorescent Ag<sub>N</sub>-DNA of multiple color classes, *i.e.* those that exhibit multiple bright peaks in multiple wavelength regions (*e.g.* a bright Green peak and a bright Red peak), and sequences associated with no brightly fluorescent peaks but with total integrated intensity above the Dark threshold are excluded from training data. Of the 2,161 10-base DNA sequences experimentally tested, 1,124 meet the criteria for inclusion within training data.

*Motif mining:* The algorithm MERCI<sup>5,6</sup> is used to mine for DNA base motifs that occur frequently in one set of sequences but not another. We assign one of the four color classes (Green, Red, Very Red, Dark) as the “positive set” and combine the other three into a “negative set”. Then, MERCI searches for motifs that occur in at least 5% of positive sequences and at most 5% of negative sequences (these frequencies were found to maximize machine learning classification accuracies). This process is repeated with each color class assigned as “positive.”

*Specific MERCI parameters:* -fp and -fn scaled as 5% rates, -g 1 (allowing one wildcard gap that represents either one of the four canonical bases or no base), default settings for other parameters.

*Feature selection and additional features:* We use greedy feature selection<sup>7</sup> within the Weka open source software package.<sup>7,8</sup> This iterative process selects features using Correlational Feature Selection<sup>9</sup> to reduce the feature set to only those most important for machine learning classification. Feature selection is performed on the MERCI-identified motifs to reduce the set of thousands of motifs to the top ~120 most important motifs, corresponding to  $\geq 8$  or 9 selections among 60 total runs, 10 runs for each of the six possible pairs of color classes. Then, the following are also added to the feature vectors: total counts of color class-specific motifs per sequence; counts of all 2-base and 3-base subsequences (base-to-base and base-to-pair transitions); total class-specific

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likelihoods of base-base transitions. This process is described in detail in the Supporting Information of past work.<sup>3</sup>

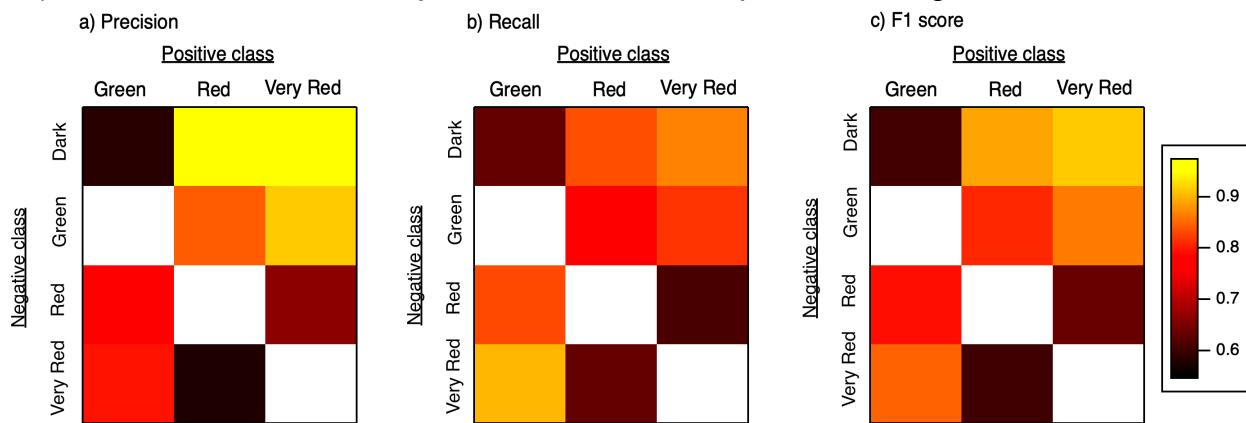
**Machine learning classification:** Support vector machines (SVMs) are used from the Weka library,<sup>7,8</sup> with a radial basis function (rbf) kernel with gamma equal to  $N^{-1}$  and cost parameter  $C = 1$ . Because SVMs are pairwise classifiers, we use one-versus-one (OvO) classification and train classifiers for each of the six pairs of Green, Red, Very Red, and Dark classes. Classifier performance is tested using 10-fold cross-validation. For a given classifier, a sequence may be correctly classified as positive (“true positive,” TP) or negative (“true negative,” TN) or incorrectly classified as positive (“false positive,” FP) or negative (“false negative,” FN). Classifier *accuracy* is defined as:

$$\text{accuracy} = \frac{TP+TN}{TP+TN+FP+FN} \quad (\text{displayed in Figure 1c})$$

Additional commonly used metrics of success include:

$$\text{precision} = \frac{TP}{TP+FP} \quad \text{recall} = \frac{TP}{TP+FN}$$

*Precision* is the fraction of sequences correctly predicted as positive out of all positive predictions made and is sensitive to FP. *Recall* is the fraction of positive sequences the classifier correctly identifies and is sensitive to FN. The “F1 score” is the harmonic mean of *precision* and *recall*. When precision and recall are equal,  $FP = FN$ ; thus, precision and recall together indicate whether a classifier is more biased towards the positive or negative class. When *precision* and *recall* are approximately equal (thus both matching F1), a classifier is not severely biased toward either positive or negative class.

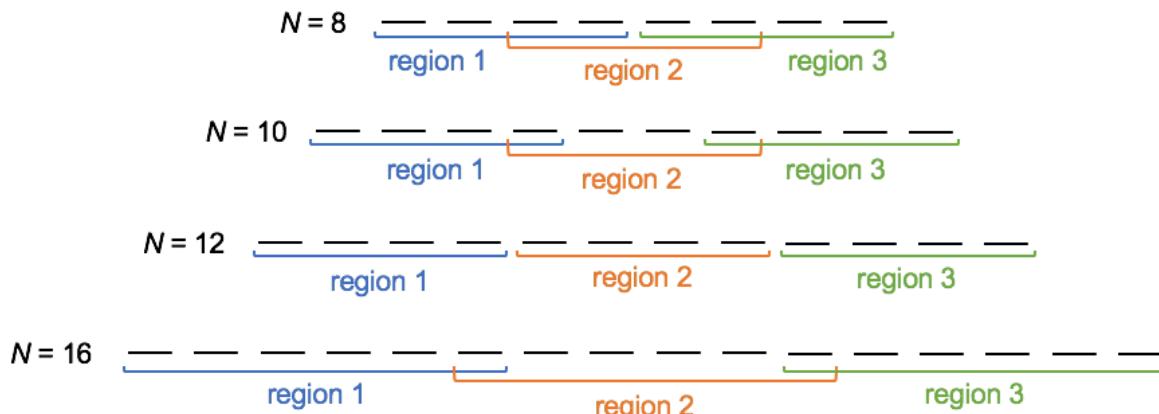


**Figure S2: Performance metrics for one-versus-one classifiers.** Heat maps of **a)** precision, **b)** recall, and **c)** F1 score. Values indicated by the color bar to the right. The similarities of precision, recall, and F1 score indicate that classifiers do not strongly prefer any class. Slightly higher precision than recall for positive Red and Very Red classes and negative Green and Dark classes indicate a slight preference for Red and Very Red for those classifiers. Note: Matrices are 4x3 because Dark was not treated as a positive class.

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*Sequence generation:* 2,000 new sequences for Red Ag<sub>N</sub>-DNA were generated by sampling the motifs identified for the Red class by MERCI and further identified by feature selection (the top 40 most prevalent are shown in Table S2). Motifs were sampled from a probability distribution and placed within an empty N-base template. Specifically, the probability distribution describes the frequency of motifs in each overlapping third of the 10-base training templates (Figure S3). For sequence generation, these regions are generalized to the overlapping thirds of an N-base sequence, as shown for the N = 8, 12, and 16 base templates tested here. Motifs are sampled for each region based on the probability distribution and placed in the empty N-base template (unless incompatible with already-placed motifs) until at most 3 bases remain unassigned (these could be gap “wildcards” used by MERCI or simply unfilled bases). Any unassigned base is filled by randomly selecting A, C, G, T. Feature vectors are then generated for each candidate sequence based on the motifs selected by feature selection and the additional features described in Section II, and these candidate Red sequences are screened using the trained SVMs. Candidate sequences are then screened using the trained OvO SVMs. The probability that a given sequence will be Red is estimated by each of the three SVMs specific to the Red class, and candidates are ranked by the minimum probability assigned by these three SVMs. The top 187 sequences for each sequence length are chosen for experimental testing using the conditions described in Section I.



**Figure S3:** Schematic of sequence regions 1, 2, and 3 used during sequence generation.

**Table S1:** Mean edit distances of designed sequences from training data. Edit distance is measured in the number of single base mutations needed to transform a designed sequence into the training sequence that is most similar to the designed sequence. For sequences N ≠ 10, edit distance also includes the number of bases added or removed to transform from one sequence to a training sequence.

Strand length	Mean edit distance
8 bases	3.09
10 bases	2.41
12 bases	3.78
16 bases	5.43

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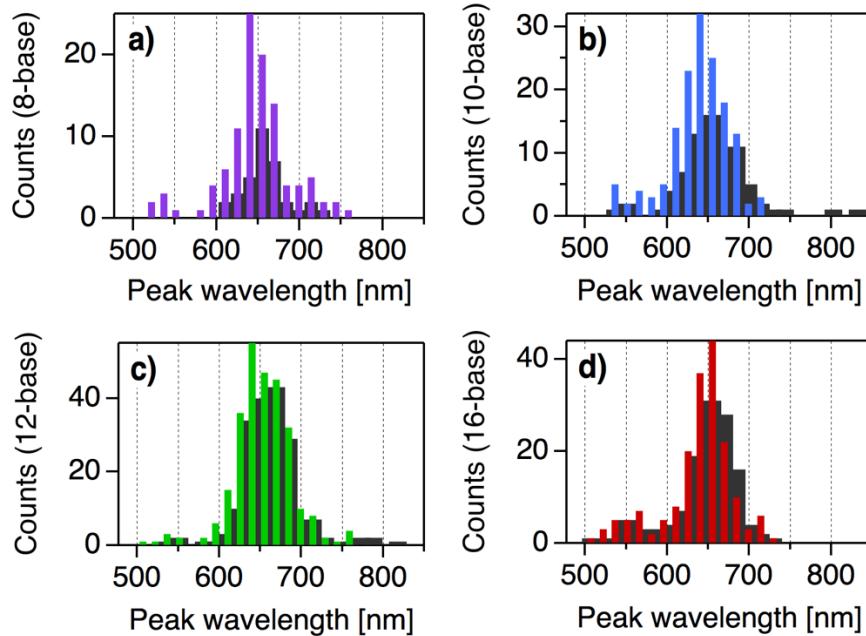
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**Table S2:** Top 40 red motifs. Motifs are listed in order of average occurrence as selected by ten separate rounds of the feature selection process described in Methods. Because subsampling is used to balance class size during feature selection, there is some variation in the list of feature selected motifs between separate runs; thus, we report an average of ten separate lists. Readers are reminded that the gap “\_” represents either one of the four canonical bases or no base, *i.e.* C\_C = CAC, CCC, CGC, CTC, or CC.

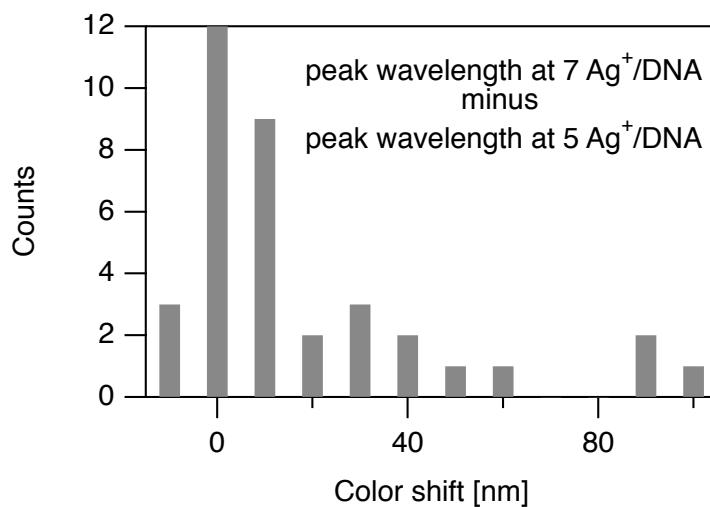
	<b>Motif</b>	<b>Average occurrence</b>
1	CCG_C	35.6 ± 1.6
2	CGCG	28.1 ± 2.3
3	GCCG	26.9 ± 1.6
4	GCC	21.3 ± 1.2
5	CC_GGA	20.6 ± 1.2
6	GCCC	20.3 ± 1.9
7	CCGC	19.1 ± 2.1
8	GCGC	18.9 ± 2.1
9	CGGGA	18.6 ± 2.0
10	C_CGA	17.7 ± 1.7
11	CC_GC	17.2 ± 1.9
12	CG_CC	16.4 ± 1.9
13	GC_AC	16.1 ± 2.0
14	GCGG	15.8 ± 1.6
15	C_AGC	15.3 ± 2.4
16	CG_GAG	15.3 ± 2.2
17	CA_GC	15.2 ± 2.0
18	CC_CGA	15.2 ± 1.5
19	A_CCG	14.9 ± 1.5
20	CCGC_A	13.4 ± 1.2

	<b>Motif</b>	<b>Average occurrence</b>
21	CGGGC	13.4 ± 2.3
22	CCGG_A	13.1 ± 1.9
23	GCG_C	13.1 ± 0.9
24	C_GCC	12.7 ± 1.7
25	GC_GC	12.6 ± 2.1
26	G_CGC	11.6 ± 1.2
27	C_CGC	11.4 ± 1.3
28	AC_CG	11.3 ± 1.6
29	GCC_CA	11.3 ± 1.2
30	GGGC_C	11.2 ± 1.7
31	CCGA_C	11.1 ± 4.3
32	CG_CG	11.0 ± 4.2
33	CGGC	10.9 ± 0.9
34	CAC_C	10.7 ± 0.7
35	CCCAC	10.7 ± 4.7
36	CGC_A	10.7 ± 0.7
37	GGGCG	10.7 ± 4.2
38	CGGG_A	10.6 ± 4.1
39	C_GGAG	10.4 ± 4.1
40	ACGC	10.3 ± 0.5

### III. Effects of stoichiometry on Ag<sub>N</sub>-DNA color distribution

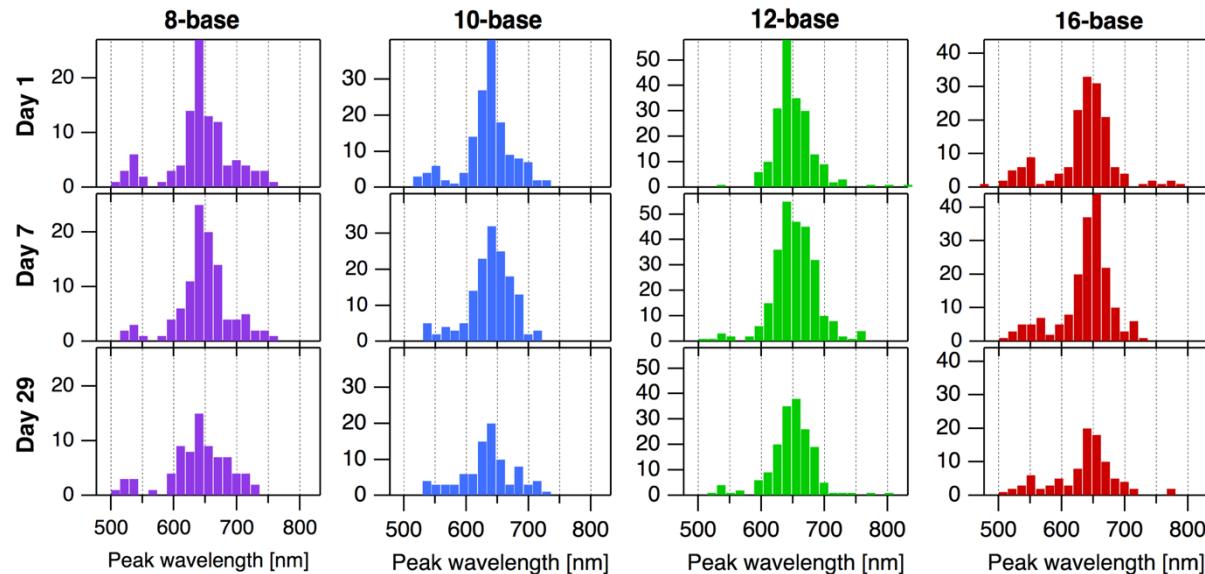


**Figure S4:** Role of synthesis stoichiometry on Ag<sub>N</sub>-DNA products. Histograms of brightly fluorescent peak wavelengths for Ag<sub>N</sub>-DNA synthesis performed at 5 Ag<sup>+</sup>/DNA (colored bars, same data as Figure 1b) and at 7 Ag<sup>+</sup>/DNA (black bars). a) 8 bases (5 Ag<sup>+</sup>/DNA is purple), b) 10 bases (5 Ag<sup>+</sup>/DNA is blue), c) 12 bases (5 Ag<sup>+</sup>/DNA is green), and d) 16 bases (5 Ag<sup>+</sup>/DNA is red). Higher silver:DNA ratios reduce the numbers of brightly fluorescent peaks and slightly shift color distributions to higher wavelengths.



**Figure S5:** Histogram of peak wavelength shifts for synthesis at Ag<sup>+</sup>/DNA = 7 as compared to Ag<sup>+</sup>/DNA = 5.

#### IV. Effects of aging on Ag<sub>N</sub>-DNA color distribution



**Figure S6:** Variation of Ag<sub>N</sub>-DNA color distribution over time. Measurements are taken at varying times after synthesis of Ag<sub>N</sub>-DNA clusters. Histograms of brightly fluorescent peaks for varying DNA strand lengths (indicated at the top) and at varying times after synthesis (indicated to the left).

#### V. References

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## VI. Training data and designed sequence data

Data libraries for all 10-base training data and Red designed sequences with lengths N = 8, 10, 12, 16 bases. The column labeled “Dark” indicates whether sequences were in the Dark class due to complete spectral intensities below a defined threshold (See Section I above). Peak wavelengths are given in nanometers, and peak areas indicate relative brightness, as normalized to the brightness threshold of 1.0. Note to readers: Only peaks with areas 1.0 or above were classified as bright peaks; peaks below this threshold were excluded from analysis and training.

**Table S3: Training data.** Sequences and spectral properties of the 2161 10-base DNA training templates.

	Sequence	Dark?	Peak 1 [nm]	Peak 1 area	Peak 2 [nm]	Peak 2 area	Peak 3 [nm]	Peak 3 area
1	GGATCTGTCA	0	633.1	0.51				
2	AAATGACGTC	0	556.0	1.63				
3	ACCCAGTTA	1	546.5	0.25				
4	GGGGTAATGT	0	509.9	0.58				
5	TTAACCAAGAA	0						
6	TACCAATGGG	0	663.4	1.20				
7	GTTAACAAAGA	1						
8	TTGGGCCTGG	1						
9	GCATCGGTCC	0	555.3	0.57				
10	CCATGGTGAC	0	646.8	0.52				
11	AAAGCAAGAG	0						
12	GCGAGTTCTG	0	554.4	0.53				
13	GGACGCGTAT	0	620.1	1.69				
14	GTCCTCTATG	1						
15	CCTCTATGCA	0	639.5	0.40	524.0	0.24		
16	TGACTAAGAG	0						
17	GCGACAGTTG	0						
18	TTGCTTGGCT	1						

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19	GAAGTTCATG	0	634.5	0.43	555.7	0.31		
20	AAAGAGCAAG	0						
21	TGGGCAGACT	0	645.7	0.51				
22	ATTCAGCTTC	1						
23	TTTCCAAACT	0						
24	GAAAGGTGCG	0	589.9	36.21				
25	AGCTTCGGAA	0	560.0	1.16	643.9	0.23		
26	GACGGCGGTA	0	641.5	0.59				
27	ATACCATGCT	0	578.2	0.60				
28	CATGAGGTAA	0						
29	ATAATCCCTG	0	525.4	20.56	553.6	5.39		
30	GCGGTATCTG	0	628.4	0.79				
31	CACTCTCAGC	1						
32	CTCCTTGGCG	0	658.9	1.57	733.1	0.81		
33	TATCCCACTC	0	534.0	0.90				
34	CAAGACTTAT	0	620.2	0.77				
35	GTGGTCCCAT	0	630.2	0.33				
36	ACTGTTTGCA	1	543.6	0.25				
37	GCAATACACA	0						
38	GCCGCTACAA	0	598.8	5.34	536.3	3.24		
39	ACGACATCAG	0	540.8	0.58	639.0	0.27		
40	TGAAGAAGTG	0	593.5	0.88				
41	GTCCAGTGTG	1						
42	ACAATGAAGG	0	680.3	0.51				
43	GCATGGAAAT	0	567.6	0.47				
44	TGCGGCCGTT	0	641.8	0.75				
45	TTCGGAAGCA	0	523.4	0.47				
46	TACTTGAGG	1						
47	CGGGGGGGTC	0	667.0	0.98				
48	GCCACCTCGA	0	633.3	2.98	559.2	0.79	694.2	0.48
49	GCCAGTCCCG	0	702.3	10.13	652.3	3.14	529.2	0.70
50	GCATGTGAGA	1						
51	TGCCTTTATA	1						
52	TATTCGGCG	0	709.5	0.26				
53	TGATTCAAGT	1	638.6	0.21				
54	GGGGGTTAAA	0	677.8	3.22	831.3	0.84		
55	TGCCGCGTCA	0	628.7	0.28				
56	GAAGTGTAAAT	1						
57	ATAAGCTTAG	1						

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58	GCCTCGAGAT	0	622.9	2.18				
59	CCATTTTCGG	1						
60	CTATGCATGA	0	567.8	0.56				
61	ACAACTAAGT	0	787.5	0.30	522.0	0.25		
62	AGCACTGACT	0	492.0	4.89				
63	GCTCGCCGGG	0	627.5	2.69	667.3	1.04		
64	GGGAAACGTT	1						
65	ATTAAGGCCG	0	642.7	0.66				
66	TTGACTAACG	1						
67	TTGATGCACG	1						
68	TACGTAAGGT	1						
69	GGTCCGACAT	0	621.0	0.53	620.8	0.29		
70	GTAGCGATGC	0	544.2	4.57	627.8	0.96		
71	ACCGCGACCG	0	627.6	3.30	697.4	0.27		
72	GGGTCAATATC	0						
73	CTCCCTTACG	0	627.2	0.41	513.6	0.36		
74	GGTGCCTTCG	0	636.9	0.44	716.7	0.22		
75	GTCAAAGTGC	0	718.4	0.37	668.7	0.34		
76	TCGATAACAAT	1						
77	GAAACCTAAA	0	537.3	0.64				
78	CGAATAAGGG	0	620.4	0.50	801.8	0.24		
79	CGGTTAATT	1						
80	TTTCCGTTTC	1						
81	TCGACACCGA	0	542.7	9.50				
82	AGTCACCACT	0						
83	AGTAACACGC	0	514.6	0.57				
84	GATGTGAACA	0	610.4	0.24				
85	TCCTGACTTC	1						
86	CTCTACATAA	0	539.2	0.83				
87	GGTTTAGCCT	1						
88	TCCGGCGTCT	0	652.6	0.68	552.8	0.25		
89	CTCATAGACC	0	650.1	4.47	761.7	0.31		
90	CTCTCATCTC	0						
91	GCTCAGAATG	0	562.2	1.21	638.7	0.35		
92	CATGCACCAAG	0	585.1	0.57				
93	CTTTGCTAC	1						
94	TGAGATAATG	1						
95	TAAGCGAATC	0	582.8	0.53				
96	AAGGGAATAA	0						

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97	GGTACATACT	0						
98	ACACACTTCA	1						
99	CTAGGTCCCTA	0	531.5	1.03				
100	ATCCCACCGAG	0	652.1	1.07	547.6	0.84		
101	GTTGCCATT	0	580.5	0.80				
102	TCCAATTTGT	1	539.3	0.34				
103	ATTACACCAG	0						
104	GCATTTGGGT	1						
105	ACTGTTCGGA	1						
106	AACGCACATT	0	705.9	0.40	615.5	0.20		
107	ACTTCGCTGG	1						
108	GTGACCTACG	0	530.3	0.42				
109	CGAAGCGCGG	0	695.0	2.17	635.3	0.99		
110	GTACGTTGGG	0	647.4	0.37				
111	CAGGTCCCTGG	0						
112	GACGGGCGTG	0	610.1	0.81	673.3	0.42		
113	ACTCGTAGCC	0	703.5	0.27				
114	GTTAATGTCT	1						
115	TAGATCGGGA	0	650.9	1.15				
116	TTTCGTCTCC	0	618.9	0.51				
117	GGGACTCTCA	0	694.9	2.52				
118	CGCCGAGGCT	0	630.1	2.55				
119	TCCGCTCAGT	1						
120	ATAGCTCACC	0	703.4	1.11	644.3	0.62	563.1	0.51
121	AACATCTGTA	1						
122	CCCGCGAAAT	0	569.3	8.07				
123	CTAGGAAAGT	0						
124	GCGGGAGCGG	0	631.4	1.15				
125	CTGACTAAGT	0						
126	GTATCCTCGC	0	730.7	1.59				
127	TGCGAAGTAT	1						
128	CAATCCGTGA	0	542.0	0.81				
129	TGACAAGGTA	0	639.6	0.25				
130	AATAGACTGG	1						
131	GGGCGAACAT	0	678.4	2.26				
132	CCGCAGCTGG	0	638.2	7.80	552.2	0.50		
133	TAAGGTGAAA	1						
134	AAGATGTTCT	1						
135	TGTGAAGGAC	1	534.1	0.28				

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136	GACCCTAAAG	0	633.5	0.60	550.4	0.34		
137	ACCGCAAATA	0	631.0	0.60				
138	TCGCCGGCGC	0	665.4	1.35	562.7	0.29		
139	CCAAGCCCAG	0	621.8	13.33				
140	GCGCCAGTCC	0	631.8	1.15				
141	GCCTAGAAGG	0	556.9	0.47				
142	AAGCACTCAC	1						
143	ACGGGCGAGG	0	552.8	0.35	675.9	0.33		
144	GTCGCGGGAA	0	647.8	0.60				
145	GGTATTGACC	1						
146	AGTGCCGATC	0	664.2	0.38				
147	TAGTGTTCT	0	692.3	0.57				
148	GAGACCTTGT	1						
149	GAATATTC	1						
150	TGGTCTTGAG	1						
151	GAGCGCACGG	0	607.9	0.38				
152	AACCATTGCG	0	555.3	0.86	666.2	0.24		
153	TGCATACTCC	0	576.2	0.44	632.6	0.22		
154	TAGCCACCAA	0	637.7	0.67	528.5	0.31		
155	TAATTCGCAA	0	544.5	1.51				
156	TTGGCTCCCG	0	713.1	0.80	638.1	0.76		
157	GAGCGTTATC	0						
158	GTCCCTGCGA	0	642.4	0.58				
159	CGGGCACTGG	0	647.6	1.88				
160	GGTATAGGTC	0	685.3	0.64				
161	CAGCAGTTAG	1						
162	GGCCCGGACA	0	670.6	2.41	552.4	1.80		
163	CCCATGCCCG	0	619.8	1.60	538.3	0.30		
164	CCCAGGACTT	0	681.5	21.47				
165	TTAACAAAGCC	0	545.5	0.82				
166	TAATAGGATT	1						
167	AGCGACATAT	0	641.4	0.37	538.3	0.24		
168	TGTTTATGTC	1						
169	GACACTGCAG	1						
170	ACCTTGGCGT	0	630.4	0.22				
171	CCGAGCTCGT	0	611.6	4.65	683.1	0.74		
172	GTACGGGTAA	0	542.5	0.69				
173	TCTCCGACCA	0						
174	AACCTTTCTA	0			582.3	0.39		

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175	TCTCTACTCG	0	633.4	4.74					
176	ACGTATTCGA	1							
177	ACGGACTGCA	0	637.8	0.80					
178	AATGGAGGGA	0	653.0	3.44	567.6	1.53	523.0	0.89	
179	GTGTCTGGAA	1							
180	TTGGGATCAA	1	545.9	0.31					
181	TCTCACGTCT	1							
182	GACTGCGACC	0	642.9	3.46	665.8	1.83			
183	TGACTCACGC	0	623.5	2.65	545.7	1.84			
184	CCAGGCAACT	0	648.7	2.16					
185	CGAGCTAGCG	0	620.2	0.32					
186	GGACTATCTC	0	638.6	1.87					
187	CGCAGGCAAT	0	528.1	0.83	629.4	0.25			
188	TGCTATCCGT	0	527.2	1.48					
189	AAGGAATTCTG	0	661.2	0.28	576.7	0.28			
190	TATCTGAGGC	0							
191	TCACAAGAAT	0	556.8	2.43					
192	CGGCACTTAC	0	509.9	3.32	610.5	0.49			
193	CAGATGGGTT	1							
194	CGTTAAATAC	1							
195	CGAGAAAGAG	0	507.1	2.47					
196	ACCGGACACA	0	641.5	5.77					
197	TTTACAATCC	1	544.5	0.21					
198	GGGAGCGTAA	0	510.1	0.49	657.6	0.48			
199	TCTGGGGTCA	0	707.9	0.46					
200	AGTTTCCCCA	0	559.7	1.01					
201	AACTAACCTA	0	555.9	1.57					
202	AGCGAAAAAT	1	607.7	0.23					
203	TCCCCTCCTG	0	573.2	0.26					
204	CCAAGACCGT	1							
205	GACATACGTG	0	636.8	0.39					
206	TTAGGTCCCTC	0	547.1	0.74					
207	CCTTCACGCT	1							
208	TTCGGCGTCT	0	550.0	0.24					
209	GTACCTGGAG	0							
210	CAGATTGGTA	0	578.5	0.24					
211	CCTAGTCCTC	1	518.2	0.33					
212	TAGGTGAAAG	1							
213	AGGACAACTG	1							

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214	GTGACCAACG	0	610.9	0.55				
215	CGGCCTCTAG	0	627.7	1.71	545.1	0.32	691.7	0.32
216	CGTCAGCGTT	0	665.6	0.30				
217	CGTACTTGGC	0	637.6	0.74				
218	GATCAAAGGC	0	564.7	0.34				
219	CCCACGCAAA	0	629.8	3.27	715.7	0.26		
220	CCCCGATATC	0	697.3	1.34	637.9	0.75	544.8	0.49
221	ATCATGCCT	0	590.3	0.99				
222	TCGTTCAAGG	1						
223	GCGGTGAAGC	0	665.9	0.45				
224	TCTCGGGTTA	0	566.6	0.69	657.2	0.45		
225	CGGATCAAGC	0	546.8	0.39				
226	CTAACTGCTG	1						
227	CTCTAAAGAG	0	553.4	0.58				
228	AATACATGGC	1						
229	AACATGGCTC	0	530.3	1.74	622.2	0.29		
230	TCCAGGCTAG	0	632.6	1.60	692.5	0.56		
231	TCCGTTGTAT	1						
232	TCGTACAGCT	1						
233	CGAACGGGTC	0	606.1	3.33	678.7	0.41		
234	GGGCGCTACA	0	642.5	0.53	543.4	0.28		
235	TAAAGCGGGG	0	642.8	0.84	532.8	0.58		
236	GCCGCTCTAC	0	613.2	1.16				
237	GCTTGCTCTA	1						
238	CATACAGATA	0	541.3	0.32	640.8	0.27		
239	GTCAGAGTGT	0	536.9	0.59	409.1	0.39		
240	CGCACTGTTT	0	587.2	0.34	631.5	0.26		
241	CGGCAGTAAG	0	633.0	0.24				
242	ACAGAAAAAG	1						
243	TCCAATTTC	0	641.8	0.39				
244	AAAGCTCCTT	0	507.5	0.34				
245	CACGGGCAGA	0	639.8	3.11				
246	GGGTTCTTAG	0	668.3	17.53				
247	AGAACATTGCG	1	523.0	0.42				
248	TGAGTATGCA	1						
249	TGAAGGGTCG	0	549.9	0.27				
250	ACGAGCGCTC	0						
251	CCTACGGCGT	0	682.8	0.68				
252	TGCATGGCCT	1						

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253	GTGGTACATG	1						
254	GGGTCCGTCT	0	719.0	1.04	603.4	0.55		
255	AGGCGTGCTG	0	651.8	3.22				
256	GACGACTAGA	0	631.0	0.23				
257	GAGAGGTGCG	0	657.6	0.34				
258	GTAGCCTATA	1						
259	GCAAGCGGGA	0	651.3	3.41	543.0	0.68		
260	ATCTCCTACT	0	549.5	0.76				
261	GCTACACAGT	1	529.7	0.22				
262	TATCCGGCAC	0	577.7	0.44	650.7	0.35		
263	TTTGATCCTC	1	428.8	0.42				
264	TTCTCCCCTG	0	518.2	2.66	699.6	0.64		
265	TCACTAGTTT	1						
266	GGGAAATACA	0	676.8	1.96	772.7	1.50	584.5	1.25
267	TTAGCATTGG	1						
268	GCGGAGTAAG	0	647.1	0.38				
269	TTTACCATCG	1						
270	AAAGATACGG	0	616.8	0.24				
271	CTCTCCGAAC	0	667.7	2.60	606.6	0.45		
272	GGGCGGTACT	0	639.3	1.68				
273	ACACCGTTAA	0	546.8	0.86				
274	TTTAGGAGCC	0						
275	CCACCTTTTC	0	547.2	71.22				
276	AAGTGGCGTC	0	631.1	1.28				
277	ACAAGACCTT	0	536.0	0.22				
278	TATGAGCCTC	0	508.3	1.10	638.6	0.23		
279	AGTTAGCAAT	1						
280	GAAGGACCT	0	550.0	0.40				
281	GTACTACACA	0	527.7	2.58	655.6	0.79		
282	ACAACCTAGA	0	516.1	0.71				
283	GGCAGCGTCG	0	612.1	2.18	555.4	0.52		
284	ATCGTTCATT	1						
285	ACGTGCACTA	0	532.5	9.89	629.1	2.57		
286	CCCCAGTTAC	0	661.0	0.38	541.0	0.21		
287	CGCTGCAATC	0	605.8	0.31				
288	CGGATAAACGC	0	571.8	0.72				
289	GCCC GTTTCG	0	633.8	0.32				
290	AGGGAAAGAG	0	487.6	56.95	529.2	27.39		
291	GTAACCTGCA	1						

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292	TTGCAGGAAT	1	549.7	0.21				
293	AGTACTCGGC	0			492.4	0.23		
294	CGGGCGGCTA	0	629.7	1.26	532.8	0.28		
295	CGACTGGCGA	0	655.1	7.37				
296	ATTGGACCAC	0	652.3	0.51				
297	ATGTCGATAC	1						
298	GATCGCTGTA	1						
299	GAGCCTCAGC	0	638.9	1.21				
300	GAACATAATG	1						
301	CAATTGGGG	0						
302	CACTCCACGG	0	594.0	1.98				
303	CTTCTGGATT	1						
304	CGCCCTATCC	0	618.4	9.78	685.7	0.78		
305	TTGGCAGCAA	0	531.8	1.13				
306	CGCGCGACCA	0	543.9	3.71	648.1	0.69		
307	CTTACATCTA	0	506.4	0.68				
308	ATTAACGAGT	1						
309	GGTGTTTCGC	1						
310	ATGACAGAAAG	1						
311	CTGCGTGTCT	0	553.0	1.04				
312	TGCAGCGAAT	1						
313	TGGCGGCCACT	0	619.8	10.27	746.4	2.58		
314	AGGCGAACAG	0	518.7	3.86				
315	ACGTCAACGT	0	697.0	32.68				
316	CATGATCGCT	0	549.8	0.79				
317	GGAATCCGCC	0	660.2	2.61	532.8	0.83	766.2	0.25
318	CCTCGTTTT	1						
319	GTATGGTTGG	1						
320	CTGATGACCT	0	528.2	0.68				
321	GGCGTCTCAG	0	687.6	1.18				
322	TCCAGCCCCG	0	682.2	9.80	619.1	1.75	558.2	0.85
323	TTACTGGGTC	1						
324	CTTGGCTTTG	1						
325	TGCCCTGTCG	0	636.0	3.80				
326	CTAATATCGG	0	551.5	0.94				
327	TTGGAACCTA	0	536.9	0.60	623.2	0.27		
328	GGGATTACCC	0	685.2	1.10	809.4	0.79		
329	CACCCCCAGT	0	611.0	8.07				
330	GCACTTCTTT	0	595.7	1.57				

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331	TTCAAAAGCA	1	553.2	0.21				
332	GTCCATTAT	1						
333	GTACGTCCTT	0	642.5	0.23				
334	TATCTATCCA	0	541.7	2.17				
335	CGTCCGTGTT	0	643.1	3.16				
336	AACTCGCAA	0	645.2	3.78	522.7	0.68	768.6	0.38
337	AGGATAGGAA	0	536.1	1.76				
338	ATGGGGAAC	0	695.7	6.51	638.4	4.70		
339	TAAAGCGGTA	0	649.9	1.66				
340	AACAACCGAA	0	646.1	33.04	569.8	12.21		
341	AGAAGATCCA	0	584.1	1.24				
342	CGTCGGATC	0	545.5	0.60	638.0	0.21		
343	GCTCGTCTAT	0	662.1	3.15				
344	TGAGATATCG	0						
345	GGCGATTGCT	0	616.2	0.96				
346	AGTGGCTAGT	0						
347	GGAATCGACA	0	552.9	0.53	708.0	0.41		
348	CACGGCATGG	0	683.8	3.76				
349	TTGATCTAAG	1						
350	GCTGTATTAA	0	564.7	0.41				
351	AATCGTGGCG	0	646.4	0.69				
352	GCCTACGCAA	0	533.6	3.10	634.5	1.81		
353	ACCTTTATGA	0						
354	ATCGCTGTCA	0	559.1	13.50				
355	TCCACGAGAA	0	532.8	47.06	558.2	15.05		
356	GCCGACCTAT	0	640.7	39.35	510.7	0.70		
357	TGTTTGCCTG	1						
358	GTCAACCGCT	0	601.0	9.59				
359	CACTTCCGTG	0	602.4	0.94				
360	GGACAGAACG	0	667.4	4.20	536.1	2.38		
361	CAAGATCGCG	0	650.7	2.14	734.1	0.28		
362	TTGATTGTCA	1						
363	TCTCATCTT	1	538.9	0.26				
364	TTCCCGCCGA	0	558.2	0.46				
365	TGAGGCCGAAG	0	534.2	2.28	642.3	0.23		
366	CAACTAGTTA	1						
367	CCGTCCATT	1						
368	TAACCGCGAG	0	629.1	1.93	690.0	0.60		
369	TACAGACGTC	0	615.0	2.32	535.6	0.64		

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370	ACTGCCCGA	0	645.0	7.29					
371	CGCGGAGGAT	0	635.8	1.77					
372	CCTAGATACT	1							
373	GCTGGATATT	1							
374	TACAGAGCCG	0	546.9	1.13	640.6	0.74			
375	ATCACAGGGC	0	642.1	7.41	544.0	0.42			
376	ATCCCCAAC	0	562.4	85.20	684.3	26.52			
377	TACTGTAGGG	1							
378	GCTACAAATA	0	548.7	0.77					
379	ACACCCGTCT	0	632.5	0.39					
380	TAAACTGAAC	1							
381	AGAGTCAAAC	0	482.5	19.20					
382	GACAAGTGCA	0	541.5	0.86					
383	ACCTCGGAAA	0	686.0	6.42	590.1	2.74			
384	GGGGCCAGGC	0	641.0	0.64					
385	GCAGACCAGT	0	550.4	0.36					
386	CCTACACTGT	0	541.5	1.98					
387	ATCCTTAATG	1							
388	GAGTTAACAGT	1							
389	TTGCCGTGCC	0	660.5	0.34					
390	AGCCAACCTGG	0	673.7	2.26	588.9	0.30			
391	GTTTAGCGAT	1							
392	TTACGACCCA	0	629.8	37.13	684.6	8.87			
393	GGTTAACACT	1							
394	CATAGATGTC	0	553.8	0.45					
395	GCTCTTGAGA	0	633.6	1.38	549.3	0.32			
396	ACGTATTC	1							
397	TCTACTCTCA	0							
398	CAACCTGCAG	0	530.4	0.49					
399	TGGGTCAGGA	1	557.2	0.37					
400	GGACAGCTCT	0	662.9	3.01	538.0	0.82	748.3	0.80	
401	CTATACGAAG	0	549.4	0.36					
402	TAAGCAAGAG	0	535.0	4.78					
403	AAAGAACAC	0							
404	ATCATGTACC	1							
405	TCGTGCCGGT	0	566.4	0.23					
406	TTTGGGAGGG	1							
407	AGCAGCCGGT	0	589.3	2.12	507.1	0.33			
408	AGTACCACAG	0	497.6	0.60					

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409	CTCGTCCGCT	0	603.1	0.67					
410	GTCTCGAGTT	0	538.1	0.42					
411	CGGGTGTGGC	1							
412	GGACTTCAGG	1							
413	GGACGGCTCA	0	632.1	1.47					
414	TTCAAATAGC	0	577.7	0.93					
415	AACAGAAAACC	0	547.6	0.55					
416	TCCTATCGGG	1							
417	CTCAGATTAA	0	516.6	0.81					
418	AGACCACTCT	0	543.1	0.45					
419	ACCTGGACCG	0	681.8	5.63	571.8	0.24			
420	GCAAGATTGA	0	537.0	2.31					
421	TCTATACAAC	1							
422	AACACGATTG	0	556.8	0.55					
423	CCTATTAAAC	1							
424	CATACTAAGT	1							
425	TTCTTGAACT	1							
426	TAAGGCCCCA	0	628.5	2.59	562.0	1.15			
427	CTGGACTACG	0	647.0	2.72	539.5	0.31			
428	ATGTAGTGTC	1							
429	GTCCTTCATC	1	554.1	0.24					
430	CGAACGGGTT	0	544.5	1.74	609.9	0.49			
431	GC GGAGCCAA	0							
432	CTAGGGCCCT	0	619.6	64.15					
433	CAGTGCCTCT	1							
434	CGGGGGGAGC	0	675.1	2.38					
435	GTCGACGCC	0	619.5	3.47					
436	GCCAACTCGT	0	501.1	9.00	671.8	5.79			
437	GGAAGGCAGC	0	645.4	0.49					
438	TTTAGCGATA	1							
439	CCTGGCTAGC	0	699.2	32.78					
440	CACCCCTAGA	0			612.6	0.89			
441	CGTTGGTACA	1							
442	AGATTGGTAT	0	539.8	0.84					
443	ACCAGGATCG	0	565.6	0.40					
444	GGCTCTACAA	0	544.5	2.32	715.3	1.70			
445	AAGAATCGGT	0	580.9	1.48	667.6	0.26			
446	GAGCTAGTGG	0	539.1	2.07					
447	ACTGCCTGTA	1							

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448	GATTTCAAGG	1						
449	CGTCAATAAT	1	553.0	0.22				
450	G TGATTGTGT	1						
451	ATCTATCGGT	0	556.2	0.89				
452	GGTCATAACT	0	569.2	1.58	518.6	1.45		
453	GTCCACCACA	1						
454	CTTTATCACC	0						
455	ACGAATTGGA	0	550.5	0.78				
456	ACAAGCCCCA	0	510.6	23.30	621.7	11.69		
457	GGTGGACGGC	0	578.5	0.60	634.7	0.27		
458	CGGTCGTAGT	1						
459	GAAATCGCAC	0	556.3	8.08				
460	CTCCGACGAG	0	636.5	0.47				
461	TTCCCTGGTT	0	524.0	1.10				
462	TGCATGTGGT	1						
463	CTGTCTGGAC	1						
464	GGCGTGCAGG	0	519.3	1.09				
465	TTCTAACGT	1						
466	GCCTACCGTA	0	544.7	1.43	642.3	0.51		
467	CTGGTAGCAG	1						
468	ACAGAGCGGA	0	562.9	0.57	661.6	0.52		
469	AAAAATCCCA	0	550.9	4.64				
470	ATGGTCCCGC	0	533.0	6.70	695.4	2.68		
471	GCAAAGCAAA	0						
472	TGACGCTGTG	0	540.6	20.60				
473	TTCGTCCAGT	1						
474	TGGCATGGAA	1						
475	GGCACGAGTT	0	602.8	1.50	536.3	0.60		
476	AGGACGATCG	0	543.5	5.24	651.6	1.18		
477	TTTAGAGTGC	0	583.3	0.43				
478	GGGCCGCAAG	0	648.2	1.55				
479	GGGTGGGGTA	0	695.0	4.32				
480	ACTGCGTTGG	0						
481	TAATTTGTGG	1						
482	AGAATACGCC	0	518.6	0.33	551.7	0.33		
483	CTCGGCGGCA	0	658.1	5.88				
484	GTGCTTATGG	1						
485	GTCTGCGGCT	0	636.5	0.25				
486	GACGAGGAAC	0						

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487	GGCACAGGCT	0	659.3	1.70	594.7	0.80		
488	TTTGTACAG	1						
489	TGAGTTGCCG	0	521.2	1.17				
490	GATTATAACCC	0						
491	GGCTAGCGCG	0	672.2	15.26				
492	GCATCCAGAT	0	627.7	1.41	577.4	0.63		
493	GAGACTAGCC	0	668.2	1.52	575.5	0.31		
494	GCATAGCGGT	1						
495	GAATAGGGTC	1						
496	CTTTATAGAC	1						
497	CTTTACCTCT	0						
498	TGTAGTCCTT	1						
499	TGTCTTGTGT	1						
500	TTGATTTCCC	1						
501	AGCGAATAAA	0	546.3	0.71				
502	TTAGTGCTTC	0	660.3	0.24				
503	TGTGAACGTG	0	559.4	4.41				
504	TACTGTCTCC	0	551.2	0.60				
505	AGACAAAGTAC	0	763.1	0.34				
506	AACGTTCTGT	0	571.2	0.55				
507	CTTGGTAATA	1						
508	TAGAACCATC	0						
509	AATGCACGAG	0						
510	GCCGTAGCGA	0	539.6	1.55	654.5	1.20		
511	CTACGAGATG	0						
512	CGGAGCTACT	0	631.5	0.52				
513	AGGGGAACAA	0	702.9	10.27	631.3	7.33	533.5	1.36
514	AGCCGCGATA	0	523.3	0.60				
515	GTGGAGAATG	0	573.7	7.41	710.2	5.96		
516	ATACGGGTTA	0	535.0	23.92				
517	AAGTCAAAGT	1						
518	GAAAAGCCCC	0	535.8	1.57				
519	TTCGGCTTCA	0	588.1	1.60	689.1	0.56		
520	CGACTGCCGC	0	642.7	0.60				
521	CGGTTTGGCC	0	657.9	2.91	777.7	0.93		
522	CCTAATACAT	1						
523	TGGCACAATT	1						
524	TAACTATGGT	0	633.7	1.96				
525	AACCACCCCA	0	619.0	7.56	540.1	1.42		

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526	CGTCTAACTT	1						
527	CGGACCATCG	0	635.3	2.46				
528	GGGAGGGAGT	0						
529	TTAGCGAAGA	1	552.1	0.21				
530	ACGCTGGTGA	0						
531	CGTCTGCGCA	0	582.9	0.35	636.3	0.21		
532	TTTTACTCAC	1						
533	CAGCTGCGCG	0	633.5	0.77				
534	GGGGTGCAGT	1						
535	TAGGGTGTAC	1						
536	AGGTTTGTG	1						
537	TTCAATTG	1						
538	CAGTCAGCAC	1						
539	CCGCAAAGTA	0	591.4	0.87				
540	AGCTTGGTAA	0	554.4	0.54	620.0	0.41		
541	CGAAGGGATC	0	630.8	0.38				
542	ATATCCCCGT	0	565.6	0.86				
543	TCTGATTGG	1						
544	TGTCGACGGG	0						
545	TGGATTAAGA	1						
546	CAACCATGTA	0	583.9	1.21				
547	ACCGTTCTAT	1						
548	TCCTCCGGCC	0	632.6	3.82				
549	CACAGCGGAG	0	615.6	0.73				
550	CCAACAGCCT	0						
551	GCTAACCTAC	0	540.6	0.33				
552	GCAGGGGTGTG	0	674.1	1.11	793.8	0.93		
553	ACCATAACGT	0	561.0	0.53				
554	GCGTTGGCCC	0	670.9	24.57	551.4	0.46		
555	TAGCGAGCGG	0	630.8	1.49	539.8	0.32		
556	TTGTCGCGAT	0	703.4	0.20				
557	GCTGATCACA	0	618.7	0.37				
558	TCAGAGACTT	0	559.6	0.52				
559	CACCGCGGAG	0	677.6	1.07				
560	CAGGGTCGAA	0	559.9	0.50				
561	TCTCAAGTAG	0	560.5	0.43				
562	ATGCGCTCAT	0	613.0	0.34				
563	CTGTAGGTCC	1						
564	TTCGTTGCGC	0	659.2	0.63	710.9	0.29		

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565	ACATGATACC	1							
566	ATGAACAGAA	1							
567	CTACCGAAGA	0							
568	ACTCTTGTAC	1							
569	ACTCGGGCAG	0	695.5	2.10	615.0	1.73	562.2	0.46	
570	TGGCGTGTAG	0							
571	TGTCATTCTC	1							
572	ATTCTTCTTG	1							
573	TCTCACATAT	1							
574	CTTGACTCAT	1							
575	GTTGGCTCGC	0	545.2	0.86					
576	CTGCGCTTG	0	633.3	0.33					
577	ACGGTCCGAT	1							
578	TCTACTCATT	0							
579	TCGTATTCAA	0	536.7	2.88					
580	CTGAATAAGC	1							
581	AGGACTGGCC	0	643.1	0.51	553.8	0.24			
582	ATGGGCACTT	1							
583	CGAAAGGGAA	0	646.3	2.32					
584	CCAAACATTC	0	539.1	4.09					
585	GGACTCGATC	0	576.7	0.35					
586	CGTTTCGACT	1							
587	CGACTCATAG	0	560.7	1.39					
588	GAAGTAGTACA	0	541.7	1.04					
589	GCCGATACCC	0	628.7	6.79					
590	CGTGAAGCGG	0	616.8	0.43					
591	AGATTAACCT	0	602.5	0.25					
592	GCATAGAACG	0	614.1	4.00					
593	ATCCTGCTTG	0	525.0	0.95					
594	GAAGTGATAT	0	531.8	1.27					
595	TTTCGTCCGT	1							
596	CATAGAGGCG	1							
597	AGCTGAGGTC	1							
598	CGGGACAGAC	0	669.9	3.94					
599	TGGAACTCGT	0							
600	ATTTTGTGTT	1							
601	GTATCAAAGC	0	677.1	1.89	546.3	0.78			
602	AGGCGATCAT	0	549.4	1.40					
603	GTGGACGGTC	0							

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604	GTGCGGGCGG	0	643.0	0.50	542.4	0.22		
605	GTTTAGCATT	1						
606	AGACCATTTC	0	570.8	0.43				
607	ACCGTCGGCC	0	621.4	2.81	529.7	0.42		
608	CTCATGTCCC	0						
609	CGAGCTGAAC	0	694.9	1.55				
610	TCGCCGGGAA	0	560.0	0.78	655.5	0.26		
611	AGTCCATTAA	1						
612	TGAGTCACGC	0	646.9	0.70	532.3	0.20		
613	AAAACCATTG	1						
614	ACCGATGCAA	0	536.0	22.59	584.9	5.52		
615	GGAACTAAAG	0	543.7	2.21	631.0	0.68		
616	GGGCTTGCTG	0	614.0	0.21				
617	TAGTTGCCGT	0	636.9	0.90				
618	GACCCCGAAG	0	618.3	7.56	704.3	0.58		
619	AAGCTCACTG	1						
620	GACGGGTCCC	0	705.8	19.46				
621	GCTTAACGCC	0	633.2	5.11	697.2	2.69		
622	GACTGTGGTA	1						
623	GTCTAAAAAC	0						
624	TCCGGACAAT	0						
625	TGTTGGTAAC	1						
626	TTGCCAAGTG	0	673.6	0.97				
627	AGCCTCCAGG	0	612.9	0.92				
628	TCTTGATTC	1						
629	CGTTTGGCA	1						
630	TGTCAACAAA	0	639.5	25.92				
631	TGTTCAAGGA	1						
632	CCTCTAGCAC	0	542.9	0.44				
633	AAACTTCCGT	0	562.8	0.64				
634	ATTATAGGAC	0	510.0	0.54				
635	CTCTGCCCG	0	588.6	2.98				
636	ATGTCTACCA	0	529.1	0.84				
637	GTGATCCCGC	0	711.2	8.01	657.4	3.89		
638	TGTTCCACGT	0	561.2	0.30				
639	AATACAGCTG	1						
640	GCCAGCCGTT	0	583.0	0.22				
641	ATCTCACCGC	0	600.5	1.13				
642	TCATTGGCAC	0						

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643	CAAAGCGCAT	0						
644	CTTGTAAAG	1						
645	AACCCCTACG	0	606.8	15.31	686.4	14.42	522.4	1.44
646	GTTAACGCA	1						
647	TCAGATATGC	0	720.4	0.48				
648	CGAGTTCTCG	0	646.4	0.34				
649	TCTAAAACGT	0						
650	CATGTGGTGC	1						
651	GAAAAGGTCT	0	557.6	0.78				
652	CGAGATAAGT	0	553.4	0.49				
653	CCTCCTTAA	1						
654	TTCTTGTGCGT	1						
655	TTACGCCGGG	0						
656	GGTTCCGGGC	0	667.0	18.82				
657	CGCGCCTGAG	0	647.7	2.47	704.7	0.91		
658	CGCTCGTGAA	0	590.6	8.71	671.2	1.43		
659	ACTAAGAACCC	1						
660	TGTTCGTGAC	1						
661	CAGATGTCCA	0	549.1	8.45				
662	GTAGAACGTT	0	811.1	0.35				
663	AGTTTTGTG	1						
664	CAGGGATAGA	0						
665	GGCTAGTCG	0	572.3	0.25				
666	CTAGCGTCGC	0	652.4	4.75				
667	TATCCTTATC	0	520.5	0.53	435.9	0.34		
668	CTAATTCAAGG	0						
669	AAACCCCTGT	0	564.1	3.97	606.6	1.66		
670	TTTCGGAAA	1						
671	ATAGCAACGC	0	541.8	0.66	652.1	0.52		
672	GACTAGGTAG	1						
673	GGATACACTG	0	563.9	0.27				
674	GCGTCACGAG	0	641.8	0.51				
675	AGTTGCCAG	0	655.5	1.03				
676	GGTATTGCAA	1						
677	GAAATTAGCG	0	550.6	0.26				
678	ATTGCATACA	1						
679	GACATATCTT	1						
680	CCCCGTTGTT	0	683.5	3.02				
681	ACGAACATGC	0	622.0	2.66				

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682	AATACAGACG	0	664.8	0.93	561.2	0.54		
683	CTAGCCTTAA	0	544.4	0.43				
684	TAAAGCAGGT	1						
685	ACCCGAGCCG	0	606.0	3.80	665.6	3.63	546.5	2.19
686	AGGGCGCCGC	0	646.8	1.32	690.3	1.17		
687	CACCCGGCGG	0	643.6	1.07				
688	CACCGACCCG	0	673.2	1.39	607.3	1.35		
689	CCACGCCCGC	0	621.3	0.74	673.7	0.33		
690	CCACGCCCGC	0	634.7	2.08				
691	CCCACCGCGC	0	653.9	5.92				
692	CCCACCGGCC	0	649.0	3.68				
693	CCCCCGGACG	0	678.4	7.77	682.8	6.39	625.5	5.75
694	CCCGGACCCC	0	660.2	4.68	676.4	2.40	556.5	0.75
695	CCCGGCCGAA	0	669.4	8.43	719.1	8.37	706.6	6.35
696	CCGAACCCGC	0	664.6	4.84	779.6	1.33		
697	CCGCCCCGAG	0	688.2	7.60	593.5	1.98		
698	CCGCCCGCCC	0	633.8	3.23	686.5	3.00	670.0	1.54
699	CGACGCCCG	0	626.7	0.24				
700	GACGCGGCC	0	655.7	6.17	700.4	0.50	768.7	0.45
701	GCCCCCGACA	0	657.0	5.82	595.4	1.48	530.4	0.97
702	GCCGAGCCCG	0	649.3	2.67				
703	GCCGCCGCC	0	562.8	19.15	600.4	10.51		
704	GCCGCGCCGA	0	662.7	2.72	429.7	0.44		
705	GCCGGCCCCG	0	663.7	2.73	534.6	1.24		
706	GGCCGACCCA	0	620.5	12.57	677.6	0.90	719.7	0.80
707	TCCCGGCC	0	663.9	2.12				
708	ACCCGGCGCG	0	673.5	6.80				
709	ACCGCCGGGA	0	664.9	16.23	784.0	7.10		
710	AGCCCGAACCA	0	535.6	0.82				
711	ATCCCGAGCG	0	680.4	7.94	721.2	3.28		
712	ATCCCGCCCA	0	606.7	6.02				
713	CACCCCGAGC	0	634.1	1.73				
714	CCACGCCCG	0	636.5	31.93				
715	CCACGCCGG	0	644.4	1.74	718.6	0.55		
716	CCAGCCCGA	0	666.5	61.22				
717	CCCAACCCGA	0	634.5	19.91	821.4	9.95		
718	CCCAAGCCGC	0	626.5	3.60				
719	CCCAGCGCGG	0	668.9	1.67	557.2	0.52	612.3	0.36
720	CCCCCGGGCG	0	735.4	7.42	773.4	5.66	625.3	1.56

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721	CCCGGACGAC	0	668.5	13.91				
722	CCGACCCGA	0	623.6	6.38	540.0	1.30		
723	CCGCCACGCG	0	632.1	1.68	698.4	0.41		
724	CCGCCCAGAA	0	663.6	3.40	638.9	1.38		
725	CCGCCCAGAT	0	676.1	3.50	623.1	1.21		
726	CCTCGCGGCG	0	641.0	26.77	681.7	10.38		
727	GACGGAACCC	0	671.5	1.13	601.1	0.40		
728	GCAAGCCCGC	0	670.3	3.16				
729	GCACGCCCA	0	624.3	1.10				
730	GCCGACCGCG	0	621.6	8.20	651.6	6.62		
731	GCCGCCCGAA	0	619.0	4.20	572.4	3.41		
732	GCCGGCTCCC	0	633.5	20.45	655.1	7.25	538.7	0.92
733	GCCGGGCCGG	0	707.0	2.98	718.6	0.88		
734	GCCTCGCCCC	0	633.0	1.32	680.7	1.13	682.0	0.22
735	GCGACCCAG	0	630.9	23.53				
736	GCGATCGCCC	0	655.9	1.69				
737	GGCAACCGCG	0	603.7	3.82	667.6	2.17		
738	GGCGACGCCA	0	585.2	3.13	641.7	2.28		
739	GGGCTCCCGA	0	673.8	1.51				
740	TCCCGACGCG	0	627.4	0.94	568.0	0.33		
741	ACCACGCCGA	0	628.1	1.33	529.8	0.29		
742	ACCCCACCCG	0	617.2	9.22			697.0	3.46
743	ACCCCGGAGA	0	622.9	14.19	553.3	9.62		
744	ACCGGCCCTC	0	532.8	2.76	679.5	1.76		
745	ACGCACCCAG	0	609.5	14.71				
746	ACGGGCCTCG	0	549.5	1.82	661.7	1.24		
747	AGCGACGCC	0	645.5	0.83				
748	AGCGAGCCA	0	691.9	3.85	579.3	2.45		
749	ATCCCACCGA	0	632.2	2.99	660.5	2.08	556.3	1.39
750	CCAGCCGCGC	0	614.1	3.04	643.7	1.57	512.2	0.68
751	CCCCAGCCCT	0	682.3	1.87	546.7	1.73		
752	CCGAAGCGCG	0	678.1	2.36	596.3	0.31		
753	CCGACGCCCT	0	683.4	3.48	604.8	1.12	666.0	0.37
754	CCGCAACCGA	0	603.5	0.73	512.4	0.30		
755	CCGCGACCAAG	0	638.7	0.51	544.8	0.30		
756	CCGCGCTCCA	0	628.0	0.26				
757	CGCAAGCCCG	0	643.6	0.82	604.0	0.40		
758	CGCCAGCGCT	0	643.9	0.84				
759	CGGGAACGCG	0	639.0	1.04				

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760	GCCGCGAGGG	0	640.1	1.24					
761	GCCGTCCCCA	0	632.1	8.01					
762	GCTACGCGCC	0	648.6	5.86					
763	GCTCGCGGCG	0	681.0	1.50	594.8	0.64			
764	GGCAGCGCAC	0	634.4	4.21	434.9	0.63			
765	GGCGAACCGA	0	632.3	1.17	549.5	1.02			
766	GGGCTCGCGA	0	655.1	0.42					
767	GGGCTGCCCG	0	670.3	1.23					
768	TCGACGCCGC	0	640.0	12.04					
769	AACCCGCCAC	0	481.5	0.77	641.1	0.69			
770	ACGGCAACCG	0	622.1	38.14					
771	AGGGCAACGC	0	688.1	2.13					
772	AGGGCCCCAAC	0	666.2	1.58	628.5	0.66			
773	ATCCCCCGCG	0	622.9	10.71	676.6	10.56	761.9	1.21	
774	ATCCGAGCGG	0	630.7	1.09					
775	CCAGCTCCCG	0	649.4	35.62					
776	CCCACACGCC	0	655.4	18.46					
777	CCCCAGCTCG	0	655.6	5.24	675.7	1.16			
778	CCCGCCCCAT	0	665.7	4.07	679.1	3.40	620.1	3.11	
779	CCGACAACGC	0	617.1	4.75	517.1	0.71			
780	CCGAGCCGGG	0	643.5	1.76	748.3	0.67			
781	CCGCGACTCG	0	605.3	0.39	646.7	0.29			
782	CCGGAACCGA	0	652.0	0.54					
783	CCGTCCCCGC	0	725.4	3.76					
784	CGAACCGGGC	0	662.6	1.45	808.6	1.25	519.9	0.20	
785	CGACCCACCC	0	613.9	6.44	652.1	5.86			
786	GAAGCGCCCC	0	571.6	2.23	675.7	0.23			
787	GCCGATCCCG	0	671.7	6.33					
788	GCCGCCAGG	0	579.0	7.43	626.0	3.28			
789	GGAACCCCGC	0	655.8	4.49	575.2	2.58			
790	GGACCCCCGC	0	617.0	9.53	675.1	3.55			
791	GGCGAACCGG	0	647.4	9.92	756.6	4.26			
792	AACAGCGCCC	0	595.0	4.89	497.1	4.19			
793	ACCAACCCGC	0	656.0	25.47	553.9	1.19			
794	ACCCATCCCG	0	714.8	7.09	618.9	5.51			
795	ACCGATCCCG	0	649.6	2.70	681.0	1.29			
796	ACGCCCCCCA	0	659.9	2.78	525.8	1.56			
797	ATCGGCCCTC	0	639.0	0.32					
798	CACCCGACGT	0	615.8	1.99					

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799	CACCCGGCTA	0	520.1	2.04	657.6	1.28		
800	CCACGGGCAA	0	696.7	4.94	732.9	1.44		
801	CCAGGCCCCC	0	666.1	0.36				
802	CCAGGCCGAC	0	660.0	3.86				
803	CCAGGGCGCC	0	665.6	0.63	770.9	0.49	721.0	0.29
804	CCCGGCCACGT	0	603.5	1.28				
805	CCGCCCCCAT	0	712.5	1.70	633.3	1.44	532.1	0.49
806	CCGCCCCTGG	0	716.5	4.65	633.0	1.98	660.5	0.25
807	CGCCCCCACC	0	682.6	12.96				
808	CTCCGCCGCC	0	633.2	0.28				
809	GAACAGCCGA	0	538.0	5.20	626.8	3.59		
810	GCCACCCCCG	0	630.4	0.33	690.5	0.24	756.5	0.23
811	GCCAGAACGC	0	557.3	7.54				
812	GCGATGCCCA	0	688.1	3.32				
813	GCTCCCGGCT	0	619.7	5.89	654.7	3.88		
814	GGAGCGCCCT	0	617.0	1.63	684.4	0.59	642.7	0.49
815	GGCAACGAAC	0	638.7	4.17	527.6	0.45		
816	GGCGCCGCCT	0	677.8	0.61				
817	GGCGCGAGGG	0	678.7	1.34	632.7	0.97		
818	GGCGGGCAAA	0	650.6	2.74				
819	GGGGCCAACG	0	578.5	0.32	727.3	0.30		
820	TACGCCAAA	0	696.4	0.47	565.6	0.22		
821	TCCGCGCCAA	0	671.2	1.03	631.0	0.71		
822	TCGGACCGCT	0						
823	TGCGCCCCGC	0	628.2	6.30				
824	ACAGCCCGCA	0	659.2	1.69	509.3	0.30		
825	ACCCGAAACG	0	661.0	3.45	607.4	2.36		
826	ACCGACCCCC	0			653.7	2.30	693.0	0.74
827	ACGCCCATGC	0	675.0	7.38	607.8	3.73		
828	ACTCCGGCCG	0	644.0	9.83				
829	AGCCCTCCCC	0	633.6	1.62	538.9	1.45		
830	AGGGGCCAG	0	685.7	1.10	661.3	0.38		
831	ATCGCAGCGG	0	722.7	4.82	630.4	3.13		
832	CCACTCCCGC	0	629.2	1.11	639.1	0.46		
833	CCAGCACCGA	0	623.2	10.38	526.4	2.70		
834	CCCAAGCTCG	0	669.3	0.97	597.7	0.80		
835	CCCCCGAAAA	0	679.8	23.86	618.4	4.09		
836	CCCGAAGGCC	0	639.3	1.38	538.1	0.84		
837	CCGGAATCCG	0	710.6	11.97				

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838	CGACGGCAAA	0	612.3	1.93				
839	CGGCCCACCT	0	663.4	28.08	549.3	1.55		
840	CTACGCGAAG	0	617.6	1.11				
841	CTGCCCCCGC	0	686.5	6.70	542.6	1.29		
842	GACAGACCAGG	0	655.3	1.15	700.0	0.51	780.9	0.27
843	GACGGAAGGCC	0	652.0	0.22				
844	GAGGCACCAGG	0	771.2	0.70	644.8	0.54	709.4	0.24
845	GAGGGCGGCA	0	669.5	1.47				
846	GCCCATGCC	0	612.2	2.09				
847	GCGAATCCCC	0	597.0	3.77	645.7	2.76		
848	GCGCCCAAAC	0	638.4	1.21				
849	GCGCCCATCG	0	605.9	1.32	532.0	0.69		
850	GCGGCGCCTA	0	639.4	2.54				
851	GCTCCCCGAC	0	637.8	3.68	519.9	0.58		
852	GGACCCCCGT	0	615.1	17.62	662.5	7.35	543.3	0.80
853	GGGCCACGAA	0	624.9	1.48	669.9	0.57		
854	TCGGGCAGAC	0	675.0	0.79				
855	AACGAACCCA	0	536.5	1.07	629.8	1.03		
856	ACCCGGAAAG	0	670.7	4.50	610.0	2.66		
857	ACCGCGCAA	0	657.2	1.67	543.0	1.49		
858	AGGCTACCCC	0	633.6	1.14	745.4	0.60	694.2	0.42
859	AGGGGCCGAA	0	646.9	1.53				
860	ATCCACCGAC	0	660.0	2.58	549.1	0.99		
861	ATCCGCGAAT	0						
862	CACCTCCCCG	0	593.0	1.84	705.5	0.88		
863	CCGGGGCCCA	0	730.8	2.36	654.5	2.07	710.0	0.41
864	CGCCGATCCG	0	641.2	1.08	524.9	0.27		
865	GCCCCCTAG	0	650.4	15.49	614.0	2.89	518.2	1.26
866	GCGACGAGAC	0	658.6	1.28				
867	GGCGACTCCA	0	644.4	1.30	526.9	0.40		
868	GGGAGACCCCT	0	653.7	6.34	565.6	0.78		
869	AACGACCCGG	0	685.3	2.08	663.2	1.47		
870	ACGGCAACCA	0	645.5	180.65				
871	ATCCCACCTC	0	638.7	15.75	551.3	5.30		
872	ATCCCTCCCA	0	596.8	7.92				
873	ATCCGGGCAC	0	659.1	11.02				
874	CCTAGCCCCG	0	664.1	3.45	541.9	0.61		
875	CGAGAAGCCG	0	629.8	0.97				
876	CGCCGGGAGT	0	681.9	0.55	629.2	0.20		

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877	GAGAGCCCGA	0	558.7	2.69	665.0	0.57		
878	GCCATCCCGC	0	650.3	3.70	702.5	2.50	650.0	1.90
879	GCCCACACAA	0	628.1	10.27				
880	GCGTGCCCAG	0	673.3	0.38				
881	GCTCCGGACT	0	669.7	5.21				
882	GGAGAGCCCC	0	662.8	8.38	532.0	1.64		
883	GGCTCGCCAA	0	650.7	2.43				
884	TCGAACGCGC	0	688.2	1.86				
885	ACGAACCGGG	0	719.4	0.50				
886	AGCCGAAAC	0	624.7	2.62				
887	CCACCCCTGC	0	652.3	13.41	708.3	3.30	742.2	2.27
888	GCCAACCAAA	0	652.7	5.23	703.3	1.68	529.6	0.34
889	GCCGCAGCAA	0	653.6	0.50				
890	GGCAACCTCG	0	605.4	4.99	690.1	2.68		
891	TCCGACCCCC	0	807.6	4.34	665.8	3.04		
892	AACCCCCGGT	0	636.1	27.11	601.6	18.43		
893	AGGACACCGA	0	632.1	1.03	589.9	0.71		
894	AGGACCCGAA	0	692.5	4.50	694.9	0.86		
895	ATCGCGCAAA	0	673.6	17.64	699.5	7.93	545.0	3.51
896	CACCCCCCGA	0	651.7	3.40	544.1	2.92		
897	CACGATCCGA	0	645.5	0.84				
898	CCCAGGAAAA	0	687.9	0.99	562.4	0.34		
899	GAAAGCGCGA	0	693.1	4.03	686.7	1.21	507.4	0.57
900	GAACCTGCC	0	548.5	4.34	644.4	3.72		
901	GCCAAAGCGC	0	684.4	1.97	591.9	0.20		
902	GCCTCTCGCG	0	648.8	10.34				
903	GCTACTCCCC	0	645.2	1.50				
904	GGACACCCCT	0	652.3	4.20	780.3	1.70		
905	GTCACGCC	0	654.7	1.29				
906	TCACTCCCCG	0	638.6	0.65				
907	TCGCCAAC	0	632.3	2.15	624.3	1.16		
908	AACCCCCAGC	0	608.6	17.96	675.9	10.56	535.1	2.65
909	ACACAGCGA	0	642.0	24.36	623.6	23.83	534.9	4.29
910	ATCCGAAGGG	0						
911	CCACCGTGAA	0						
912	CCCACCAACA	0	626.0	2.22	667.2	1.37	530.0	0.62
913	CTCCGATCGC	0	645.4	1.85	545.0	0.36		
914	GACCCCCCG	0			635.3	0.80	695.6	0.67
915	GACGAGGCAA	0	519.8	0.68	661.5	0.32		

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916	GGCCCTGCGA	0	677.7	23.23				
917	TACCGAACCA	0	740.0	0.60	569.8	0.42		
918	AAGCCCGCAT	0	676.7	0.39				
919	ACCTACGCC	0	615.9	1.34	589.8	0.33		
920	CACAAGCCCC	0	501.0	5.27	537.3	4.68	672.9	3.79
921	GATCCGGGG	0	659.8	2.40				
922	GGACGACGGG	0	673.8	0.32				
923	TGACCGACCC	0	651.4	0.24				
924	AGAGCCCTAC	0	655.3	1.93	685.2	0.93		
925	CACAGACCCG	0						
926	CCGGGTCCGC	0	644.6	1.25	547.2	0.21		
927	GACCCGGTGG	0	672.2	0.92				
928	GACGAAACCC	0	654.8	1.38	613.3	0.86		
929	GCCGACCCTT	0	596.8	0.32				
930	GCGTCCCCCT	0	630.0	2.25	517.8	0.29		
931	GCTCCGCTAG	0	624.0	0.71				
932	GGGACGCGTA	0	656.3	0.96				
933	TCGATCCCGC	0	550.3	11.53	752.2	10.22		
934	TTCCCCACCC	0	560.4	1.31				
935	AACCCGCGGT	0	646.9	0.32				
936	AATCCCCCAA	0	607.4	40.36	678.6	7.99	631.1	1.61
937	ACCTCCCCAA	0	598.2	26.69				
938	ACGAGGGCCC	0	680.8	3.76	580.8	2.74		
939	ATCCCCCAA	0	620.2	15.21	682.0	4.79		
940	CACCAACAAA	0	534.9	1.99				
941	CCAGCGGGTT	0	585.0	9.27	628.8	4.45		
942	CCGCCGAATA	0	571.4	25.98	608.9	15.51		
943	CCTCCCCAAA	0	663.3	4.18	537.0	1.08		
944	GAGATCCGGC	0	634.5	0.97	686.2	0.61	726.3	0.57
945	GGAAGGACCG	0	508.1	2.49	639.3	0.36		
946	GGCCGCCTGT	0	685.7	0.43				
947	TACGAGGCC	0	671.7	0.90				
948	TCCCTCGGGA	0	695.6	1.88	685.7	0.39		
949	AACAGACCCC	0	633.5	2.89	524.0	1.42		
950	AATCCGACCG	0	628.0	0.72	688.1	0.66	678.1	0.51
951	ACCGACCTAC	0	639.5	2.88				
952	CCACTCCCCG	0	640.2	3.43	513.6	0.59		
953	CGCGAGAGAA	0	675.5	1.30				
954	CGGCTGGGCG	0	615.8	3.49				

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955	GAACGGCGGT	0	569.9	1.72				
956	GACGTGCGAG	0	641.4	0.51				
957	GGGCCCAAAAC	0	709.6	2.43	542.0	0.23		
958	TCCCACGGAT	0	601.5	3.35	548.9	2.34		
959	ACCGGGGCTC	0	689.3	0.46				
960	AGGGTGCCCC	0	677.1	2.79	688.7	0.43		
961	ATCCCAAGCT	0	548.4	0.99	663.8	0.94		
962	CCCTCCCCCT	0	526.0	2.71			605.5	0.63
963	CGCGCGCCTA	0	685.5	1.73	584.3	0.43		
964	GACGACGGAT	0	737.8	2.19	730.7	0.69		
965	GTCCCCAACG	0	643.6	4.61				
966	CCAAGACCCA	0	634.5	2.32	609.7	1.39	526.4	0.57
967	CCGAGAGAAG	0	604.3	15.86				
968	GAACAGGGAC	0						
969	GCACCCACCT	0	542.7	0.84	620.5	0.73		
970	GC GGAGAACAA	0	539.1	1.23	637.7	1.22		
971	GGCGCTAGT	0	614.4	0.60				
972	ACCCCACCTA	0	582.0	41.14	691.6	5.22		
973	ACGGGGCAAA	0	666.5	34.77				
974	ACGTCCCGGG	0	694.8	1.71				
975	AGGCCCGCTT	0						
976	CAAGGCGGGG	0	645.7	1.07				
977	CAAGGGACCC	0	716.6	3.74				
978	CCACCGCTGT	0	625.4	2.28				
979	CCCCCCCAT	0	718.0	5.26	712.2	3.80	534.5	1.91
980	CCCCCCCA	0	710.3	6.30	538.2	1.47		
981	CCGAGCGTCC	0	655.2	5.49	781.5	0.58		
982	CCGCCCTAGT	0	662.3	2.27	697.3	0.66		
983	CCTCGCAAAC	0	632.8	1.43	534.4	0.58		
984	CCTGGCCCCC	0	673.8	1.74	662.1	1.21		
985	TCCGCAACGT	0	680.4	0.78				
986	AACACCCCCG	0	653.5	8.95	602.0	1.07	525.0	0.50
987	ATCCCCCCCCG	0	692.9	20.25				
988	CGGGAAGAAT	0	582.4	0.83	760.3	0.42		
989	TAACGAGCGC	0						
990	TCAACCCCCG	0	638.2	14.86	719.9	1.18		
991	TCGGCTCAA	0						
992	TGCCCTCCG	0	672.0	26.25	547.1	2.72		
993	CCACGTCCCCG	0	618.1	0.63	637.1	0.26		

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994	CCCAGAGAGT	0	673.4	0.23				
995	GGGCAGGAGA	0						
996	CCAGCCTCCT	0						
997	CCCCCGCATA	0	736.4	2.88	639.1	1.71	708.9	1.09
998	GATCCGGGAG	0	617.8	2.91				
999	GCTCGTCGCC	0	612.9	0.44	665.4	0.30	846.7	0.26
1000	GGGGAACAAA	0	781.4	6.27	526.4	0.94		
1001	TCCAACCCGG	0	641.6	58.16				
1002	AGCCGACAGT	0	683.4	0.35	627.4	0.26		
1003	ATCCCGTCGT	0	642.3	0.78				
1004	ATCCGGGGGA	0	694.8	0.69				
1005	CAAGACCCCG	0	627.2	1.82	680.8	1.70		
1006	CCTGCGCAGA	0	641.8	0.89				
1007	GACAGGGGCG	0	647.5	1.90				
1008	TCCC GG TCCC	0	659.6	2.15	702.1	0.42		
1009	TGCTCGCCCT	0						
1010	TTCGCCGCAC	0	625.0	0.61				
1011	CCGAAACAAAC	0	652.6	0.50				
1012	CCGACGGGGT	0	679.4	3.13	755.8	1.60	563.6	0.26
1013	CCGATCCCTT	0	594.5	0.30	417.0	0.21		
1014	CCGGTCACGC	0	615.3	0.74	728.2	0.30		
1015	CGGTCCGGCA	0	673.4	2.07				
1016	CTCGCAGAAC	0	576.9	0.61				
1017	AGGC GGGATA	0	650.1	0.72				
1018	TAGGGCTCCG	0	715.9	3.14				
1019	TCCGCCGTCT	0	665.0	0.36				
1020	AGCCGAAACT	0	636.4	4.25	723.3	0.66		
1021	CACAAACCCA	0	649.9	47.28	495.0	2.90		
1022	CCGCGAGCAT	0	639.8	1.42	581.6	0.79		
1023	CGTGGCCCTG	0	635.0	0.77				
1024	CTCCGCAAGT	0	637.1	0.38				
1025	GACACGGACC	0			676.5	1.62		
1026	GTATCGCCCG	0	560.5	4.93	664.2	2.23		
1027	TACGACTCCC	0	637.9	0.97				
1028	AATCCCCCA	0	688.9	30.65	558.1	2.94	612.3	1.20
1029	ATCCCTGGCA	0	701.1	0.69				
1030	CGTCTCCGCG	0	651.6	0.68	526.7	0.40		
1031	GCAAGGGGCC	0	642.5	3.31				
1032	GCACGTCCCA	0	643.9	1.04				

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1033	GGACGACACT	0	526.3	11.73				
1034	GTCCACGAAC	0	540.8	1.50	634.5	0.87		
1035	ATGCGGAATG	0	696.0	0.56	663.4	0.35		
1036	CCAGGCCGTCA	0	684.6	1.17	555.4	0.38		
1037	CCGCCCCCTTC	0	667.2	4.47	691.7	1.91	531.1	1.91
1038	CGGGGCCAAC	0	642.4	1.58				
1039	GAGGCCGTCA	0	693.0	1.85	676.0	0.58		
1040	ACAACAGGCC	0	581.4	1.42	631.9	0.76		
1041	CCACCCCAAT	0	534.1	2.63	677.2	0.59		
1042	ACAACCGCCT	0	649.0	2.03	548.4	1.34	708.2	1.02
1043	ACCGACACTA	0						
1044	AGAAACCCAC	0	538.1	2.60	608.9	0.95	651.4	0.62
1045	CCGACCAATC	0	575.3	0.56				
1046	TCAAGGCCCA	0	651.2	1.42				
1047	GATCCCCAAA	0	674.3	6.71	598.1	2.90		
1048	GATCCCCAAC	0	560.3	23.92	622.0	21.80		
1049	TGGGACCGAA	0	558.5	1.15	673.0	0.99		
1050	AACAGATCCC	0						
1051	TTATCCCAACC	0	580.8	6.43				
1052	TCCAAGATGC	1						
1053	CGACGATGCA	0	561.4	0.41	642.8	0.25		
1054	CGAGAATGTC	0	563.5	1.20				
1055	AGAGAACGTT	1						
1056	TGATCCCTGT	0	525.9	0.59				
1057	GCAAGAGAGA	0	566.2	0.76				
1058	TGGACGAGAA	0	634.0	0.61	534.3	0.45		
1059	GAACGGGTCT	0	659.1	0.49				
1060	GGAGAACAG	0						
1061	AACAGAAATG	1						
1062	CAAAGAGCGG	0	657.7	2.79				
1063	ATACGGAGAT	1						
1064	AACAGAACGC	1	558.5	0.24				
1065	TCGAGAAATG	1						
1066	AACAGAGCTT	1						
1067	CACCGATGCT	0	556.7	0.68				
1068	TACCGGGTTA	1						
1069	AATGACGTAC	1						
1070	GGAGGAGAAG	0			667.0	0.27		
1071	GAGAACTAAT	1						

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1072	GGAAGAGAAT	1						
1073	CGACACGATG	0	631.1	0.60				
1074	ACGATCCCTC	0	564.0	1.01	663.5	0.78		
1075	TTTCCACGAC	0	548.5	1.45				
1076	AATCCCTGTC	1						
1077	GGAAGAAATT	0	639.3	0.42				
1078	TGTGCAAGAT	0	694.0	0.94	573.9	0.31		
1079	GCGCAAGATG	0	730.0	55.23				
1080	CGGAGAACAG	1						
1081	GGAAGAACAG	1						
1082	ACCGAACGTC	0	629.8	6.81				
1083	AACCAGAAC	1						
1084	AATGGAGAAC	0	521.3	1.22				
1085	CAACGAGAAT	1						
1086	GCGTGCAC TG	0	589.2	0.60				
1087	ATGCGAGAAC	0	542.6	0.50	606.4	0.23		
1088	GAGAACGAGA	0	533.6	1.00	645.4	0.29		
1089	TGGAGAATTG	1						
1090	GAAGAATTGC	1						
1091	CTGCAAGATT	0	656.7	0.95				
1092	AGAGCGAGAA	0	542.9	0.51				
1093	TCCAAGAATG	0	588.4	0.46				
1094	CGCGAGAATA	0	648.3	1.43	566.5	0.72		
1095	ACGGGTTCAC	0	655.7	1.46				
1096	TGGAGAACCC	0	677.7	2.85				
1097	TCACAAGCCC	0	599.8	3.80				
1098	AGAGCACTGT	1						
1099	AACTAACACC	0	636.8	1.07				
1100	GAAGAATTAA	1						
1101	ACAAAGAATT	1						
1102	ATCCCAACAG	0	543.8	1.62	696.2	0.60		
1103	CACCGAATGA	0	636.0	0.91	522.1	0.65		
1104	GCACGATGCC	0	686.7	4.67				
1105	GACGGGTTTT	1						
1106	CCGCAAGAAG	0	659.2	0.49	498.5	0.29		
1107	TAGGGAGAAT	1						
1108	CCAACAGAAT	1						
1109	GAAGCAAGAT	0	614.4	1.50				
1110	AGAGAACCGAG	0						

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1111	ATAGGAGAAT	0	640.7	0.66				
1112	GAGGAGAAGA	1						
1113	AAACGGGGTT	0	585.1	4.49				
1114	TAGCCCCTGT	0	561.6	9.27				
1115	GCAAGAACCC	0	647.5	1.03	628.0	0.63		
1116	TGCAAGATGT	1						
1117	CCTCCCCCTCA	0	680.4	4.48	539.5	3.65		
1118	TGC GGAGATT	0	667.5	0.39				
1119	CGAGAAGAAA	1						
1120	TGCACAAGAA	0	556.5	6.89				
1121	AGCAAGATTA	1						
1122	CGAAGAATCA	0	542.8	4.36				
1123	GAGATCCCAA	0	656.2	3.26	559.4	1.65		
1124	TAGCAAGATA	1						
1125	AGCACGATGC	0						
1126	TGGATCCCAA	0	649.4	1.28				
1127	TACCGAGAAT	0						
1128	AACCGGGTTG	0						
1129	TGCGAAGAGA	0	659.2	0.49	498.5	0.29		
1130	CCTCCACGAA	0	538.8	1.42	639.6	0.95		
1131	CCCGCGATGCG	0	648.8	1.24				
1132	GCGTGCAATA	0	532.5	0.28	651.6	0.26		
1133	GAGCGAGAAT	0	551.9	0.24				
1134	AACTAACAAAT	1						
1135	ATTCCCCTGT	0						
1136	TCGTAGCGTA	0	673.9	2.21				
1137	CAACGGGTTT	1						
1138	TTCACGGGTT	1						
1139	ACCCGGAGAT	0	565.7	12.07	654.5	7.67		
1140	CGACAAACCGT	0	639.5	0.54				
1141	GGAAGCCCCG	0	663.9	1.99	678.4	0.60		
1142	TGAGGCGATA	0	653.8	0.30				
1143	AGGAGAAATT	1						
1144	CCGCAGAACATC	0	614.0	0.70	644.3	0.62		
1145	GAGAAGATGT	1						
1146	CCAAACTAAT	0						
1147	CGAGAAATGA	0						
1148	CGCGCAAATT	0	635.4	3.27				
1149	AAACGAACAG	0						

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1150	TCCCCACAGAA	0	525.3	6.06					
1151	TTCCAGAACG	1	470.8	0.29					
1152	GCGCGAGAAG	0	652.5	4.21	525.9	1.84			
1153	ATGGCGAGAA	0	587.5	0.24					
1154	CGCGAGAAAT	0	662.8	0.33	584.2	0.31			
1155	AACGAATGCG	0	679.2	0.38					
1156	TTCCCCAACATC	0	560.3	3.65					
1157	CGACCAGAAAT	0							
1158	ACCAACGATG	0							
1159	ATCCCAGAAG	0	585.8	5.32	531.5	4.20			
1160	GAGAAATGAA	0							
1161	CCCCACGAAT	0	567.2	18.53	673.5	16.62			
1162	TGCAAGATTTC	0	616.1	1.04					
1163	ATGCAAGAAG	1							
1164	GGAGAACATCAC	0	502.3	0.78					
1165	GGAGAACATTCT	1	408.7	0.34					
1166	CCCCAACAAAT	0	579.1	2.17	703.3	0.57			
1167	ATCCCCCTGC	0	678.9	11.58	540.8	0.41			
1168	AACGGGAGATT	0	538.1	0.42					
1169	CCGCAAGATA	0	608.7	2.32	516.4	0.23			
1170	GAAGAACATCAG	1							
1171	AGGGAACTCG	0	659.2	0.70					
1172	TAGTCCCCAA	0	628.4	0.83	546.7	0.32			
1173	GTGAGAACATGT	0	595.5	0.47	413.0	0.30			
1174	ATCCCCCTGCA	0	688.0	2.94	555.3	0.38			
1175	TGCCAGAATT	0	562.1	4.09					
1176	ACGGGTTGTC	1							
1177	GTAGCGAGTT	1	662.8	0.33	584.2	0.31			
1178	GAAGAACGTC	0							
1179	TCACGGGTCT	0	532.5	1.85	599.7	0.87			
1180	GCCAAGAGAT	1							
1181	ATGGAGAACATC	0	596.4	0.33					
1182	CGACCACTGT	1							
1183	AACAGCCCCA	0	650.9	10.89	625.3	7.60	532.7	0.50	
1184	CAAAGATGCA	1							
1185	GAAGAAAGAA	1							
1186	CGACGGGTTA	0	669.3	0.21					
1187	ACGTAGCGTC	0	635.3	3.50					
1188	ACACGAAGAA	1							

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1189	TACTACACCG	1						
1190	GGAGAACACC	1						
1191	ACACCAGAAT	0	518.1	0.69				
1192	GCGAGAATTG	0	819.8	1.05				
1193	ACCAAAGAAT	1						
1194	GCGACAGAAT	0	676.7	0.43				
1195	TGAACGGAGA	0	612.3	1.06				
1196	GAACGGGTGA	1						
1197	CGCGCAATCA	0	583.4	1.67				
1198	CGAGAAAGATG	0	517.3	1.24				
1199	ACCAAGAGAA	0	726.3	0.83	529.1	0.76	580.1	0.46
1200	GTAGCGAGAA	0	544.6	0.34				
1201	GAGCGATGCC	0	659.4	1.86				
1202	TCCCAACTGT	0						
1203	AACAGAGAAC	1						
1204	CGCGCAAGAA	0	640.4	1.66				
1205	GAGACACTGT	1						
1206	TCAGAACTCG	0						
1207	TGCGAGAAGG	0	731.2	1.66				
1208	TAACGGGAAG	0	606.7	5.39	672.9	2.28		
1209	CCCAACTCGG	0	566.9	0.68				
1210	GCACGGGTTA	0	633.8	0.72				
1211	GAGCCCCCAA	0	647.0	22.56	520.6	1.28		
1212	CCAAAGAATA	0	507.5	0.46				
1213	AGAAGAATTG	1	424.6	0.48				
1214	ATACAACCGA	0	566.7	0.54				
1215	GAGGAGAATT	1						
1216	GAAGAACCGAG	0	597.5	0.41	736.6	0.20		
1217	ATACGATGCG	0						
1218	GAAGAGAATG	0						
1219	GTAGCGATCA	0	641.4	0.62				
1220	CGAGAACATCA	0	567.0	0.78				
1221	CGAGAATTG	0						
1222	ACGGGAAGAA	0	642.8	1.35	548.6	0.35		
1223	ACGCGAGAAT	0	566.1	0.93				
1224	CGAGAACTCA	0	587.0	2.44				
1225	GCCAAGAATT	1						
1226	GCACTACCGT	0	773.4	0.35	569.9	0.27		
1227	CAAAGAACAG	1						

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1228	GAGAACGTCA	0						
1229	CGGAGAGCTT	0	550.2	2.41	639.1	0.90		
1230	GGCACAGAAAT	0						
1231	CAAAGAGATG	0	679.6	0.38	642.9	0.37		
1232	CGACACGAGA	0	636.7	2.23				
1233	TCCAAAGAAG	0	616.8	0.60	567.9	0.43		
1234	GAACTAACCC	0	685.8	1.33				
1235	ACGGAGAATT	0						
1236	GCGAGAAGAA	0	606.0	0.24				
1237	CCCCGGAGAG	0	660.3	5.20	567.9	2.51		
1238	GTAGCGAACG	0	688.0	1.11	669.8	0.99		
1239	TGCAAGAGAT	0	712.5	0.44	600.1	0.26		
1240	AGAAGAGATG	1						
1241	CGACAAGAAG	0						
1242	GGAGAACTGT	0	599.5	0.47				
1243	CCGACGAACG	0	620.2	3.11	694.3	0.62		
1244	ACGGAGAGAA	0	590.4	2.78				
1245	TGTGGAGAAG	1						
1246	CCGACACAAA	0	636.0	1.19	532.0	0.22		
1247	GAGAACAAATT	1						
1248	ATGCGATGCA	0	652.4	0.66				
1249	AACTAACTCG	0						
1250	CCAAGAACGC	0	638.5	1.13				
1251	GCGTGCATGG	0	676.4	1.18				
1252	CGCGTGCAAT	0	680.8	0.33				
1253	GCAAGATGTT	0	778.9	0.48				
1254	TCAGAACTGA	1						
1255	GCCAAGAACG	0						
1256	ATCCCCCTGTC	0	713.9	1.51	567.1	0.35		
1257	CGGGAAAGTGT	1						
1258	GCACGGAGAA	0	636.9	0.34				
1259	GCCACGATGC	0	641.7	2.23				
1260	GAACCGATGC	0	652.5	0.49				
1261	GGAGAAATGG	0						
1262	AACGAACCGT	1						
1263	ATCCCAAGAA	0	552.2	3.57	690.0	1.14		
1264	CGAGAACTAG	0						
1265	TGACGGGTTC	1						
1266	CCGACAGAAC	0	642.3	0.20				

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1267	TCGAGAACAG	1						
1268	CCGAGAAATT	1						
1269	GCAAGAGAAG	0	591.4	1.77				
1270	CCTCAAGAAT	1						
1271	CCACGACACC	0	626.6	0.21				
1272	CGCGGAGAAA	0	675.0	3.16	715.7	0.38		
1273	CGGGGAAGAA	0	690.3	1.46				
1274	ATCCCCACTT	0	583.6	1.29				
1275	ATCCCCACCA	0	552.8	9.27	682.1	2.09		
1276	CCCTCCCTG	0	692.2	5.28	549.8	0.88		
1277	AACGCCCCA	0	659.5	2.30	530.8	1.85		
1278	CGGGAGAAC	0	580.5	7.87	620.8	6.16		
1279	TAGCAAGAAT	1						
1280	ATACGAGAAC	0	602.8	31.33				
1281	TGAGCGATGT	0	608.8	0.45				
1282	GTAGCGACCC	0	638.7	0.73				
1283	CTTCCCAC TG	1						
1284	TCCCGAGAAC	0	636.5	14.65	584.5	4.27	676.3	1.95
1285	GCCAAGAAGA	0						
1286	GATGGAGAAC	0						
1287	GAAGAACATCCT	1						
1288	GCGCGATGCA	0	633.8	1.08	693.5	0.36		
1289	TAGGAGAATA	0						
1290	TCACCGATGA	0	612.9	0.66	527.2	0.35		
1291	GCGCAAGAAC	0	745.3	0.30				
1292	AACCGAGAAC	0	591.4	10.86	639.3	7.80		
1293	CCAAC TAA CG	0	679.6	0.76				
1294	GAAGCCCCGA	0	631.1	3.47	681.1	2.25	540.7	0.38
1295	ATGGAAGAGA	0						
1296	AGCACGAAACG	0	523.9	0.94				
1297	CAAAGAGCTT	1						
1298	TTCCCCCTCGT	0	686.4	0.32				
1299	AGAGCCCCCA	0	644.3	18.59	521.1	1.70		
1300	GAAGCCCCAC	0	643.3	9.68	527.8	0.62		
1301	CCACGAGAGA	0	525.6	0.86	615.4	0.22		
1302	CCGCGAATGA	0	639.4	7.78	523.9	1.46		
1303	CGAGAACATCAG	0	551.6	5.22				
1304	CGACCAAGAA	0	641.7	0.54				
1305	ATGGGAGAAC	0						

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1306	CGGAGAAAAT	0	596.2	0.49				
1307	GCAAGATCCT	0	663.9	0.24				
1308	GAGCGAATGC	0	626.9	0.73				
1309	GAGGGAGAAG	0						
1310	TTCCCCAAAG	0						
1311	ACACCGATGC	0						
1312	CGCCAAGAAT	0	646.3	0.45				
1313	CAAAGCCCCA	0	637.7	7.19	524.8	1.61		
1314	GACCGAAGAA	1						
1315	TCCCACGATA	0	641.9	17.45				
1316	CCCGGAGAAG	0	720.3	119.58				
1317	CCCGCGCAATA	0	683.0	1.71				
1318	GAGAAGCCCC	0	686.9	12.47	593.5	1.09		
1319	CCGCGAGAAC	0	611.8	1.07	563.2	0.86		
1320	TAGGCAAGAA	1						
1321	TTCCCCACTGA	0	666.3	1.24	550.4	0.27		
1322	GAAGCCCCCG	0	656.8	16.28	587.0	2.01	516.8	1.61
1323	GCAAGATGCA	0	578.8	0.36				
1324	AACGGGAGAGA	0	590.9	15.52	564.1	10.25		
1325	GGCAAGATGC	0	641.2	1.30				
1326	ACCGAAGAGA	0	667.7	0.56	584.0	0.44		
1327	AACGGGTGCA	0	619.9	0.27				
1328	GAGCGAACAG	0						
1329	GCACGAACAG	0	543.2	0.64				
1330	GTAGCGGAGA	0	621.1	0.85	506.6	0.51		
1331	AGAAGAGAGA	0						
1332	GAAGAAATGT	0	599.8	0.70				
1333	GGAGAACCGC	0	640.4	1.02				
1334	TGGAGAAATA	1						
1335	GAGAGCACTG	0						
1336	GAAGAGATGC	0						
1337	AACGGGTCTT	1						
1338	TGCGGAGAAC	0	698.4	0.34				
1339	TAACGGAGAA	0						
1340	CGCACACTGT	0	594.8	0.42				
1341	GCAAGAGTCT	1						
1342	CCGAGAATCA	0	532.3	1.43	574.3	1.32		
1343	GGAGAAGATA	0	503.3	0.21				
1344	GCCAGAATAG	0	489.6	0.39				

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1345	CGAGAACGTA	0	596.4	0.29				
1346	CGCCAGAATG	0						
1347	ACGACCAATG	0						
1348	TGGACGGGTT	1						
1349	ACGGAGAAGA	0						
1350	CGTATCCCAA	0	675.7	5.84	617.7	1.83	539.3	0.58
1351	TTCCCACGAT	0	542.6	0.68				
1352	TGGAAGAACG	0						
1353	GGAGAAGAAT	0						
1354	CCAAGAACATT	0	550.9	0.33				
1355	CGCGCAGAAG	0	647.9	1.54				
1356	TCGACAGAACG	0	559.1	1.65				
1357	GCCAACATAAT	0	661.4	41.58				
1358	ACCGGAGATG	0	696.6	0.32				
1359	GCGCGCAATT	0	703.6	2.72				
1360	CCAAGAACATAG	1						
1361	TCACGAGAAC	0	580.2	0.29				
1362	GAGAAAGAAT	1	422.3	0.47				
1363	TATCCCAATT	0						
1364	GGAGAACCTTA	0						
1365	TATCCCCATG	0	580.2	1.21	668.9	0.40		
1366	AATACGGGTT	0	577.0	2.26	697.4	0.71		
1367	GGAGAACGTT	1	596.4	0.29				
1368	CAACGAATGC	0	593.7	0.33				
1369	TCGACACTGC	0						
1370	GCACAAGCCA	0						
1371	CGGGAGAACG	0	653.9	0.86				
1372	CGAGAACATG	0	526.1	0.43				
1373	AATCCCAATA	0	543.0	1.05				
1374	TTCCCCACCAA	0	717.8	8.21	560.2	2.02		
1375	AATGCAAGAA	0						
1376	GAATGACGTA	1						
1377	AACAGGAGAA	1						
1378	GCAAGAGCTT	0	735.7	7.06				
1379	AACTAACGAG	0	727.6	2.02				
1380	TGCAAGATAG	1						
1381	GAGAACACCG	0	626.8	0.37	542.7	0.33		
1382	CCGAGAACATG	0	649.1	1.47				
1383	ATCCCCAAATC	0	584.1	4.91	686.7	3.82		

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1384	GAACGTGCGG	0	711.3	1.02				
1385	ACACGAACCG	0						
1386	GCGTGACGTC	0	664.0	0.31				
1387	CCGACACTGG	0						
1388	AATTCCCCAC	0	612.3	1.46	676.1	0.25		
1389	CATCCCTGTT	0	636.7	1.46	527.5	1.10		
1390	TCCCGAACAG	0	681.5	3.65				
1391	GTAGCGACTG	0	634.6	0.34				
1392	CCAAGAGAAC	0						
1393	GCAAGAAATG	1						
1394	TGGGAACGAG	1						
1395	AATTCCCACG	0	687.8	0.28				
1396	GGCAAGATT	1						
1397	CCCAGAACGA	0	636.5	2.54	532.0	1.65		
1398	ACCCGATGCA	0	628.6	5.14				
1399	CGCGCAATGT	0	677.3	2.52				
1400	ACCCAGAATA	0	561.6	1.42				
1401	CCAACGAGAA	0	612.3	0.53				
1402	ATCACGAGAA	0						
1403	CGTAGCGTCA	0	600.7	1.12	676.8	0.53		
1404	CGAGCGATGC	0	593.3	2.40	657.1	1.42		
1405	ATCCCAATCA	0	561.3	2.05				
1406	GGGAGAAAGTT	1						
1407	GGGAGAAATG	0	531.0	1.40	716.0	0.23		
1408	TCCCGGAGAA	0	668.0	3.06	618.4	2.14		
1409	TGCGACACCA	0	634.4	0.87	667.2	0.81		
1410	AAATCCCCAA	0	580.6	2.45	704.3	0.69		
1411	AACAGAATCA	1						
1412	TCAGCAAGAC	0	579.9	0.91	518.7	0.40		
1413	TCGACGATCA	0						
1414	ACGGGTTTCG	0						
1415	ACCGAGAAAT	0	698.6	0.51				
1416	TCGCGCAATG	0	701.5	20.60	627.3	7.17		
1417	CCGACACCGT	0	572.1	0.26				
1418	GGAGAAATAGA	0	628.4	0.68				
1419	ATCCCAACGC	0	628.4	4.87				
1420	TTCAATCCCA	0	553.2	0.51	664.9	0.23		
1421	CTGAATCCCA	1	530.6	0.36				
1422	GTAATCCCAC	0	534.3	1.20	643.0	0.78		

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1423	CTAAATCCAC	1							
1424	TTCAATCCAC	1	526.8	0.82					
1425	TGAATCCACC	0	570.0	1.11					
1426	TGTCCAATCC	1	573.7	0.32					
1427	GGTAATCCCA	0	662.2	1.11	538.8	0.78			
1428	AATCCACGTT	0	561.2	2.03					
1429	GTACAATCCC	0	557.2	0.44	652.3	0.31			
1430	CAATCCAATC	1	538.4	0.36					
1431	TAAATCCCAT	0	608.7	0.34	577.2	1.31			
1432	GTAATCCCAG	1	541.5	0.57					
1433	CCAATCAATC	1	621.3	0.83					
1434	CCAGTCAATC	0	561.9	1.13					
1435	CAATCAATCC	1							
1436	CTGTCCAATC	1	606.5	0.42					
1437	CAGTCCAATC	1							
1438	TCCACAATCT	1							
1439	AGTCCAATCC	0	570.8	1.00					
1440	CTTCCCAATC	0	557.3	0.69	671.1	0.39			
1441	CAGTCAATCC	1	580.8	0.34					
1442	TGTCAATCCC	1							
1443	AATCCAATCC	0	530.7	0.81	633.8	0.26			
1444	ACCACAATCA	1	554.9	0.31					
1445	TCCACTCAAT	1	551.9	0.51					
1446	AAATCCAATC	1	562.2	0.29					
1447	AAAATCCCTA	0	569.9	2.85					
1448	AAAATCCCAA	0	562.5	2.56	644.1	0.37			
1449	CAATCCAGAA	0	547.0	5.63					
1450	AATCCAATCG	0	569.3	0.78					
1451	CGACAAATCA	0	546.5	1.61					
1452	TCGACAATCT	1							
1453	CCAGTCAATG	1							
1454	AATGTCCCAC	0	560.9	1.64	636.4	0.24			
1455	CGACACAATA	1							
1456	TCCCCAAATCT	1	588.9	0.48					
1457	GTTCAATCCC	1	562.1	0.53					
1458	CTGTCAATCC	1							
1459	CCAGTCCAAT	1							
1460	AAATCACCGAC	1			567.8	0.76			
1461	CCCTAAATCA	0	593.4	8.18					

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1462	CCGTACAATC	1	573.2	0.29					
1463	CCACAAATCA	0	555.7	1.12					
1464	CCTGTCAATC	1	570.1	0.63					
1465	TTCCAATCCC	1							
1466	AGTGTCCACG	1							
1467	AGTAATCCCA	0	565.8	4.50					
1468	CAGTCAATGC	0	613.3	8.46					
1469	CCTGTCCAAT	1							
1470	TAAATCCACT	1							
1471	AATCAATGGG	1	590.7	0.28					
1472	CCCACAATGT	0	516.2	4.06	639.2	0.68			
1473	TCCACTAAC	0							
1474	TTCCAATCG	1			543.7	0.26			
1475	CGTTCCCAAT	1							
1476	CCCACAATAA	0	653.6	5.78	504.5	2.71	610.9	1.44	
1477	TCCCATAATC	0	573.1	1.48					
1478	CCACAATCCC	0	559.6	1.21					
1479	CCACAGTGGG	1							
1480	CTTCCAATCC	0	699.5	0.29					
1481	GTGAGTCCAC	1							
1482	CCCAATCTGA	0	563.0	3.53					
1483	CGTTCCAATC	1							
1484	GGTTCCCAAT	0	652.8	1.03					
1485	GGAATCAATC	1							
1486	CCTTCCAATC	1	565.4	0.41					
1487	TCCACCCCTT	0	678.3	24.04					
1488	CCACAATCGG	0	555.2	0.75	608.2	0.44			
1489	AATCACAATA	1							
1490	GTTCACCCCTA	0	632.7	1.04	682.0	0.42			
1491	GTACCAATCC	1	564.7	0.22					
1492	ACGACAAATC	0	555.1	8.82					
1493	CCACAAAATC	1	541.7	0.62					
1494	CTTCAATCCC	0	548.6	0.81	641.3	0.47			
1495	CAATGCCTGT	1	512.9	0.35					
1496	ACCACAAATC	1							
1497	ACGACAATGA	1	607.4	0.32					
1498	AATGTCCCTA	1	526.1	0.39					
1499	CCACTTCCAC	1							
1500	AATGCAATCC	1							

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1501	CCGAGTCAAT	1	542.2	0.57					
1502	CCACACAATA	1	555.8	0.67					
1503	ACCACAATGA	1							
1504	GGCAATCCAC	0	581.3	2.28	654.9	0.66			
1505	AATGTCCACA	1							
1506	TGACCACGTA	1							
1507	AATCAGAACCC	1							
1508	TCCCAAGTGA	0	584.0	2.48	720.2	0.25			
1509	ACCCACATTTC	0	547.6	0.52					
1510	AATCTCCCAC	1	547.4	0.45					
1511	TAATCTCCAC	1							
1512	CCCCACATTTC	0	546.9	0.67	697.1	0.32			
1513	ACCCTAATCT	0	612.3	1.76	549.9	1.10			
1514	AATCGAATCG	1	400.7	0.20					
1515	CCACAGAACCC	1							
1516	GGCAATCAAT	0	570.3	0.71					
1517	TTCACCACAA	0	536.1	1.55					
1518	CCATTCCACC	0	793.9	0.85	557.6	0.40			
1519	TCCACAGTGA	1							
1520	CTGACAATCC	1							
1521	TAACCAATCC	1	522.6	0.73					
1522	AGTAATCCAC	1	513.4	0.30					
1523	AGTCCCAATC	0	716.1	2.11	578.0	0.78			
1524	GGGTGTCCAC	1	656.3	0.33					
1525	AGTCAATGGG	1	494.6	0.24					
1526	GTGAGTCCCT	0	708.5	2.57					
1527	CCTGACAATC	0	655.4	0.26					
1528	TGTACCCACT	1							
1529	TTCAATCCGA	1	576.0	0.33					
1530	GTAATCCCTA	0	730.5	21.38					
1531	TTCAATCGAC	1	552.3	0.53					
1532	CAATCCTGTC	0	659.7	13.75	725.9	4.19			
1533	TCCACCACTT	1							
1534	AATGACGACA	1	552.7	0.23					
1535	TCGACTAAC	1							
1536	AGTACCCCTGA	0	526.8	0.37	631.0	0.28			
1537	CCATTCCAC	0	520.3	0.37	609.2	0.30			
1538	AATGCAATCG	1							
1539	TCCACTAATG	1							

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1540	ATGACCCCTAA	0	612.0	1.62	499.8	1.12		
1541	CAATGAGTCC	1						
1542	AATGAGTCCC	1						
1543	CTAACCAATC	0	530.4	5.19	451.8	0.64		
1544	CGACAAAATG	1						
1545	CCCACAATGC	0	531.0	0.52	645.5	0.50		
1546	AACAATCCGA	0	632.9	0.71				
1547	CAATGAATCC	1	543.0	0.49				
1548	CCCACATTCC	0	543.0	3.17	688.3	0.43		
1549	CCACGGTGT	0	576.1	0.80				
1550	GTGAATCGAC	1	542.8	0.59				
1551	AATCAATCAA	0	594.2	0.68				
1552	CAATGCCTGA	1	405.8	0.28				
1553	CGACATTCCC	0	689.8	3.40	627.1	2.09	620.3	0.55
1554	TACCCTAATC	0	603.9	1.61				
1555	AAATGCGACA	0	670.8	0.41				
1556	AGTACCCAAT	1	566.6	0.32				
1557	CAATGCTGAC	1						
1558	CTTTCCCACC	0	627.8	12.71				
1559	CCCAAAATCA	0	622.8	2.05	573.1	2.73		
1560	TCAGAACGAC	1						
1561	CCCCCACATT	0	557.2	10.22	706.4	2.15		
1562	CCACAAAATG	0	667.1	0.22	560.0	0.20		
1563	AGTTCCACGG	1	558.1	0.28				
1564	CCCACAATCC	0	552.5	1.28				
1565	GGAATCAATG	1						
1566	CTGAAATCCC	1	411.3	0.24				
1567	GTACCCTGTG	0	502.8	0.25	657.7	0.28	563.6	0.35
1568	CCCTAAAATG	1	539.6	0.23				
1569	GAATCAATGG	0	541.3	0.85				
1570	GAATCCAGAA	0	530.4	1.11				
1571	CGACAGAAGG	1	417.0	0.29				
1572	TGACCCTAAA	0	625.9	1.45	550.2	0.42		
1573	TCCACAATGT	1						
1574	ACCACAAATG	0	670.1	2.41	685.4	0.73		
1575	CCCCAATCTT	0	531.9	1.12	622.6	0.37		
1576	TCCCAATCTT	0	587.0	0.52				
1577	CCACGTAATC	1	569.3	0.26				
1578	AATCCAGTCC	1	532.4	0.32				

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1579	CCAGTCAGAA	1						
1580	AATCGTGAGG	1	400.6	0.24				
1581	GTATCCCTGT	1						
1582	GGGAATCCAC	0	700.1	0.41				
1583	GCAGAACATCGG	0	551.9	0.22				
1584	CCTGACCAAT	1						
1585	CCACAAATGA	0	682.5	10.87				
1586	AAATCCAATA	0	573.1	0.66				
1587	TCCGATAATC	1						
1588	TGACAATCGG	0	540.6	0.45				
1589	GGGAGTCCAC	1						
1590	CCACCATTC	0	532.6	1.06				
1591	CCCTTTCCAC	0	685.9	0.52	578.7	0.48		
1592	AATCCAATAA	1						
1593	AATGTCCCCT	1						
1594	AAAGTCCCTA	1	557.8	0.31				
1595	CAATCTGTCC	1	558.1	0.23				
1596	AATCGAATGG	1	745.3	0.27				
1597	GTTAATCCCA	1						
1598	AATCTGTCCC	0	718.8	3.54	552.0	0.32		
1599	CCACATGAAA	1						
1600	CCCTAATGAA	1						
1601	AAAGTCCACA	1						
1602	TCCACAATCC	1						
1603	CGAATCCACA	1						
1604	TCCAATCCAC	0	565.7	2.28				
1605	CCCACAATCT	0	655.5	1.07	560.2	0.57		
1606	GTCCACTCAA	1						
1607	CCACACTCAG	1	570.8	0.48				
1608	GAATCACCTA	1	533.0	0.33				
1609	GATCCACAGA	0	556.6	0.64				
1610	TCACTCCACA	0	563.1	1.98				
1611	CCATCACATG	0	591.0	0.84				
1612	CCCACAGTCA	0	627.2	0.69				
1613	GACCACATCACA	0	562.3	0.57				
1614	CGTCAATCAG	0	558.5	0.49				
1615	CCACTACACT	0	502.0	0.83				
1616	AGATCCACTG	1	507.4	0.51	593.5	0.24		
1617	CTACATCACA	1	559.6	0.40				

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1618	AGACATCCAC	1						
1619	ATCTCCACAG	0	793.0	2.14				
1620	AGTCACGACA	0	808.6	4.09				
1621	TCCACAGTCG	0	560.5	0.97				
1622	ACAATCCTCT	1	404.7	0.97	585.8	0.25		
1623	AATCCCACAG	0	647.5	3.72	688.3	0.97	711.6	0.87
1624	ATCCCCAAGA	0	548.7	4.65				
1625	GTCACGATCT	0	581.7	13.88				
1626	CAGGTCCACA	1	506.8	0.25	424.5	0.33		
1627	CGTCAATCAA	1	595.6	0.26				
1628	CCACTCACAG	1	454.6	0.26				
1629	ATCGACACAT	0	606.9	1.92				
1630	CGACACTAAG	0	582.6	0.56				
1631	TCCCAATACT	0	820.8	0.53	536.4	0.38		
1632	ATCATCCAAA	0	625.6	0.70				
1633	ATCAATGCGA	0	550.8	1.54				
1634	ATCCACAAAG	0						
1635	TGCTATCCAC	1						
1636	GACATCCATA	1						
1637	TATCGATCAC	0	556.6	1.59				
1638	CAATCGACAA	0	553.1	11.40	602.7	3.16		
1639	GACTGCACAT	1						
1640	AGAATCCACA	1	531.4	0.31				
1641	ATCATCACGA	0	533.5	2.13	628.5	0.77		
1642	GAAATCCACA	0	637.1	3.89	555.4	0.70		
1643	GAGTCACGAA	1	538.0	0.23				
1644	TGTCCACGGAT	0	533.6	1.80	564.3	0.69		
1645	ACAATCGCAG	0	563.3	0.46				
1646	AGATCCAATG	1	596.6	0.24				
1647	CCCACAAACAT	0	544.5	2.65				
1648	ATCACAAGGA	1						
1649	AGTCGACACT	1						
1650	TGGAGTCCAC	1						
1651	ATCACAAAGAC	1						
1652	TCATATCACC	0	558.2	0.71	501.8	1.10		
1653	CCACATCTAC	0	614.9	2.67				
1654	CAATCAGGGAA	0	521.6	7.58				
1655	CCAAATCACT	1	543.5	0.24				
1656	CTGATCCCAT	1	578.5	0.35				

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1657	CATCACACAG	1	677.2	0.23				
1658	CTGTCCACAT	0	565.4	0.70				
1659	GACACATCTC	0	609.3	0.22	670.7	0.21		
1660	CATCCATGAG	1						
1661	CTCTCACAAA	0	564.7	0.73				
1662	TATCCTACAC	0	528.9	1.06	619.8	0.23		
1663	ACTACGTCAC	1						
1664	GAATCCATGC	0	586.3	0.69	511.2	0.25		
1665	AGGAGATCAC	1						
1666	CTCCACTAAA	0	528.7	1.13				
1667	TCACCTCAAT	1	529.3	0.61				
1668	AACATCCATC	1						
1669	AATCTGCACA	1						
1670	CTAGATGCAC	1						
1671	CCACATTCCC	0						
1672	ATATCCACCA	0	536.2	0.45				
1673	CTCCCAATAA	1	526.4	0.27				
1674	CATCAATGCT	1						
1675	AAACCCAATC	1	551.2	0.28				
1676	CATCACAGAA	1						
1677	AGTCACCAAG	1						
1678	CCATCGAACATG	0	651.6	0.26				
1679	GACTGTCCAC	0	669.1	5.09				
1680	AGATCACAAG	1						
1681	TGATCCACCA	1	541.5	0.36				
1682	AACATCACGA	0	572.3	3.69				
1683	ATACACAAACC	0	518.1	0.49				
1684	TCCATCGAGT	1						
1685	GCAATCACCA	0	599.5	0.76	546.9	0.46		
1686	ATTCCCCACA	0	579.9	0.41	665.3	0.26		
1687	CCCATCACAG	0	657.0	0.48				
1688	GATTCACCAC	1						
1689	GAATCCACGA	0	537.6	21.39	648.4	3.61		
1690	AGATCACGGAG	0	645.2	1.35	553.2	0.83		
1691	GACTCACTAG	1						
1692	CGACACTCAC	0	646.4	6.48				
1693	GCTTCACCCAC	1						
1694	GTCCACGGTA	0	553.2	14.18	668.6	4.79		
1695	CTGTATCCAC	0	541.5	1.30	595.3	0.39		

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1696	CCAACTCACA	0	652.5	1.08	478.0	0.64		
1697	AAGTCCATCG	1						
1698	GTAAATCACCA	1						
1699	AGTCCACACA	0	587.0	0.55	748.9	0.27		
1700	TATCTCAACC	0	522.7	0.92				
1701	CTGTCCTCAC	1						
1702	GCCTAATCAG	0	638.4	0.37				
1703	ATCACTGACG	1	543.1	0.52				
1704	ATAGACTCAC	1						
1705	AGAAAATCCC	1						
1706	AGTGGTCCAC	1						
1707	AGTCCCACAA	1						
1708	AGGACGACAT	1	412.2	0.24				
1709	CCGTCACITC	1						
1710	CGTCTCATCA	1						
1711	CCCCAGTCAT	0	534.1	0.67				
1712	CCACAAAGATC	0	538.4	1.88				
1713	GACCCAATAA	1						
1714	TCAGATGCAC	1	412.2	0.23				
1715	TAGGTCCACT	1						
1716	ACGGTCATCA	1						
1717	AATAACCCAC	0	531.3	0.72	451.6	0.54	618.7	0.22
1718	AACCAATCAG	0	583.9	0.90				
1719	ATCGGTCATC	1						
1720	GATCACTGAC	0	538.1	1.67				
1721	TCACATCAAG	1						
1722	TCGACAGAGA	0	522.9	2.64	582.2	1.92		
1723	CCACAAAGACT	1	571.6	0.27				
1724	TCACAAGGAG	0	640.2	0.37				
1725	TCAATCAAGG	1						
1726	TCTCACAGAG	0	648.1	0.32	565.0	0.27		
1727	ATTCCATCCA	1	580.1	0.44				
1728	GAATCCTCAA	1	588.2	0.35				
1729	GACATCGACA	1						
1730	CCACAAACCT	0	639.5	1.43	558.2	0.28		
1731	TGGTCAACCA	1						
1732	GGGAACATCA	1						
1733	CACCAAGTCAC	1						
1734	AATCGCATGA	1	575.9	0.25				

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1735	AACCACCTTC	0	584.1	1.01				
1736	ATCTAATCCC	0	532.8	3.77				
1737	GGCATACACA	1						
1738	CGAATCCACG	0	574.5	2.08	654.0	1.38		
1739	ATCTCAGATC	1	520.1	0.30				
1740	ATCACAAACAA	1	500.1	0.37				
1741	TCGACTACAA	1						
1742	TCTATCACAG	1						
1743	ATCCTACAGA	1						
1744	TATCATCGAC	1	584.5	0.34				
1745	ATCATCACTA	1						
1746	ACCAATGACC	0	657.8	44.07				
1747	TAGGACACTC	0	530.3	1.89				
1748	ACACTCAGAC	1	565.7	0.34				
1749	CAAGACTCAC	1	515.6	0.48				
1750	GTCAAATCGG	1	540.4	0.22				
1751	CATCTCACGA	0	544.5	1.85	655.4	0.51		
1752	GACCACTCAC	1	550.7	0.23				
1753	TCGGTCACTC	1						
1754	TATCACGAAG	1	433.8	0.22				
1755	GTCCAAGTCG	1						
1756	AAGGACACTC	0	535.6	1.48				
1757	AAGCCAATGG	1	756.4	0.25				
1758	TACCATCAGG	1						
1759	CCTACAACTA	0	510.0	0.88	585.2	0.60		
1760	CTGAATCCTC	1						
1761	TGGCCAGAAA	1						
1762	AATCAGTCCA	1	560.2	0.23				
1763	CGACAATCGG	0	650.2	0.76	675.9	0.56		
1764	GAAGATGCAC	1						
1765	CCAATACTAG	1	532.0	0.20				
1766	CGATCCACTA	0	513.9	0.49				
1767	CAAAATCACA	1						
1768	GAATCCAGAG	1						
1769	GACATCCATC	0	628.3	2.66				
1770	AAAATCCATC	1						
1771	AATCATCGGA	1						
1772	ATATCCTCAG	1	564.3	0.26				
1773	TACCCATGAC	0	539.3	0.58				

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1774	GACTAGATCA	0	647.0	0.45				
1775	CAGAAACCTC	1						
1776	CTCACAGGTC	0	528.0	0.55				
1777	ACCAATGCTC	0	571.5	1.13				
1778	CAATGTGAC	0	757.0	1.24				
1779	AGCTGACTCA	0	684.6	1.51				
1780	AAGGGATCACT	1						
1781	CATAGTCTCC	0	665.5	0.83				
1782	CTCACCCCTTA	1						
1783	TCAATTCCACC	1	530.3	0.53				
1784	TGATCCTCAA	1						
1785	TCCGAATGAG	1						
1786	CCCTACAGAA	1						
1787	AGGTCCCCGGA	0	637.9	4.58				
1788	CCGGGGTCCC	0	708.0	6.10	734.7	5.16		
1789	CCCGGGGAAC	0	715.2	17.55				
1790	GGTCCCCGGA	0	653.7	9.33	571.6	0.32		
1791	GGGTCCGGAG	0						
1792	CCGGGGTAGC	0	704.5	10.74	579.4	3.61		
1793	GCCGGGACCC	0	665.6	8.77	756.4	0.35		
1794	GTCCCCGGCG	0	642.8	2.63				
1795	CCTGGCCCGA	0	568.8	2.45	678.6	1.43		
1796	CTGGTCCCGG	0	687.4	1.06	710.2	1.03	611.7	0.81
1797	CCGGGGCCGG	0	724.4	0.82	640.9	0.48		
1798	CCCGGGCGCG	0	684.7	3.88	684.3	2.62		
1799	GGGCCGGGAA	0	646.0	1.64	684.2	0.25		
1800	GGGCCCCGGA	0	685.0	1.37	629.4	1.29		
1801	GCCGGGGCGA	0	649.0	0.64	677.7	0.29		
1802	GGGCCCGGAA	0	694.8	0.84	607.0	0.32		
1803	GTCCCCGGAG	0	655.7	1.28	593.0	0.70		
1804	ATCCCCGGGG	0	696.2	28.11	764.0	5.98		
1805	GGTCCCCGGCG	0	678.7	1.74	614.8	0.74		
1806	CCGGAGCCGG	0	633.5	1.60	537.3	0.24		
1807	TCGGTCCCGG	0	695.6	5.75				
1808	CCCCGGGCCG	0	698.9	5.75	789.0	0.22		
1809	CGGGCCCGGA	0	673.4	0.92				
1810	GATCCC GGCG	0	682.8	3.11				
1811	GGGGTAACCC	0	698.1	12.02	666.5	7.69		
1812	CCGGTCCCGA	0	692.4	1.24	614.1	1.10	541.4	0.56

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1813	CCGGTCCGGC	0	721.3	1.22	669.8	1.17	772.9	0.99
1814	CCGGGCTGCG	0	649.4	0.92	622.8	0.83	690.7	0.35
1815	GCCCGGGGCG	0	645.1	1.44	707.8	0.62		
1816	CCCCTGGGGT	0	726.2	8.11				
1817	CCGGAGGGGA	0	704.5	16.96	653.9	3.89		
1818	AGGGCGCGGA	0	638.7	1.99	721.4	0.30		
1819	GCCCGGGGGA	0	735.5	1.02	685.0	0.84	634.4	0.77
1820	ATGCCGGGAA	1	563.5	0.23	683.2	0.21		
1821	GGGGGCCCGG	0	678.1	5.65	735.6	2.71		
1822	TGCCGGGGCG	0	637.6	1.48	600.0	1.34		
1823	GCGCGGGCGA	0	664.4	3.38				
1824	GCCCGGGGAG	0	623.3	1.34	676.8	0.76		
1825	GTGGGGTCCG	0	505.7	6.80	697.6	2.63		
1826	CCCGGGGGCC	0	711.8	1.92	718.7	1.67	635.9	0.31
1827	TGACCCCCGA	0	630.9	15.71	685.0	8.09	721.8	7.48
1828	GGGGGGACCC	0	698.9	4.54	563.2	0.76		
1829	CCCCGGGGGG	0	710.3	5.36	566.8	1.37		
1830	TCCGGGGGCG	0	664.5	1.53				
1831	GCCGGAGGGG	0	647.3	4.18				
1832	CGGGGCCCGG	0	678.4	7.18				
1833	CGGCGCGGGA	0	651.5	7.14	588.4	3.45	710.7	1.69
1834	GCCGGGGGAC	0	682.7	1.46	597.4	0.32		
1835	GCCCCGGGGC	0	696.4	3.35	658.9	1.19		
1836	C GGACCCGGG	0	668.5	2.51	538.5	0.29		
1837	CCGGGGCTCC	0	730.0	9.00	675.3	1.27	718.7	0.64
1838	CCGGGGCAGG	0	727.8	2.07	735.6	0.76		
1839	GGTCCCCGG	0	679.2	0.79	558.3	0.40		
1840	CCGGGGGCAA	0	833.3	2.86	665.4	2.55	714.8	2.14
1841	GGCCCCGGAG	0	669.4	5.15				
1842	CGCCGGAGCG	0	677.5	0.52	631.2	0.40	596.1	0.26
1843	ACCCCGGGGG	0	701.0	9.42	558.5	2.54		
1844	CCGGGCCCGT	0	665.6	1.64				
1845	GCTTGCCGGA	0	670.5	1.98	529.9	1.35		
1846	TCCGGGAAAG	0	640.2	0.44				
1847	GCCCGGGCCG	0	668.1	0.62	634.0	0.45	682.0	0.27
1848	GAGTCCCCGG	0	716.3	1.00	637.1	0.82	692.1	0.74
1849	TCCCCCGGGG	0	704.3	10.62	603.1	0.40		
1850	GAACCCCCGG	0	697.3	16.72	597.9	1.86		
1851	GGGCCGGAAA	1						

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1852	GGGGGAAGCC	0	684.7	0.42				
1853	GGTCCCGGCA	0	619.1	0.48	692.1	0.29		
1854	AGGCCGGGCG	0	663.5	1.23				
1855	GACCCCCGGG	0	721.9	10.54	681.9	6.69	700.0	4.24
1856	GCCGGCCGGG	0	640.1	3.16				
1857	CCCGGGGACA	0	715.6	9.97	727.1	9.76	637.4	1.51
1858	AGGCGCGGGA	0	635.2	8.76	590.4	0.20		
1859	CGGGGGTCCC	0	724.5	3.01	681.8	2.66	598.7	2.01
1860	GCCGGTGCAC	0	619.4	0.84	750.1	0.71		
1861	GGGGCTGCCG	0	644.8	1.58	613.5	0.27		
1862	CCGGAGGGCT	0	638.6	2.63	649.6	1.57	695.5	0.44
1863	TCCCCGGGCC	0	678.3	4.48	699.7	1.80	705.5	1.73
1864	CGGGTCCCGC	0	692.4	4.22				
1865	GCCCCGGGTT	0	702.6	0.48	614.6	0.23		
1866	GCGCGGGCGT	0	627.5	2.39	673.7	1.36		
1867	GGCCCAGGAG	1						
1868	GGGGTCCGAC	0	541.2	3.87	680.8	2.89		
1869	AGTTCCGGGG	0	610.6	0.60				
1870	AGCCCCGGGCC	0	683.6	2.83				
1871	CCCCGGCCGG	0	674.1	5.72	658.8	0.69		
1872	AGGGGCCGGG	1						
1873	GATCCC GGAC	0	679.8	2.91	571.6	1.03		
1874	AGCCCCGGGA	0	693.3	8.38	598.6	4.11		
1875	CGGGGATCCG	0	682.6	2.08	605.3	0.33		
1876	GGGGAATCCG	0	785.3	1.65	682.3	1.39	609.3	0.86
1877	TCCGGGGGCC	0	620.5	2.75	663.0	1.37		
1878	CCGGCCCCGG	0	655.3	3.88	709.8	2.29		
1879	CCGGAACCCC	0	664.8	4.34	537.0	0.58		
1880	GCCGGGAGCA	0	648.5	1.16				
1881	GGCGCGGGCG	0	635.7	1.80	689.9	1.46		
1882	GAACCCCCGGT	0	637.3	44.91	681.5	8.09		
1883	GGGCCGGACG	0	655.3	0.93				
1884	CGTTCCGGAC	0	665.6	1.62				
1885	GAACCCGGGC	0	670.0	5.89	659.5	5.84	784.7	1.26
1886	GGGCGCGGGC	0	641.7	1.75				
1887	GAAGCCGGGG	1	665.3	0.35				
1888	CAGTCCGGGG	0	627.0	0.26				
1889	CCGGGGGGAGG	0	700.7	3.06	726.0	0.82	758.0	0.67
1890	CGCCGGGGTT	0	678.6	1.13	599.8	0.28		

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1891	CGGGGGTAAC	0	641.9	7.47	680.2	3.54		
1892	TGCCGGGGCC	0	667.4	1.09	625.8	0.39		
1893	GCCGGGTGGA	0	699.1	1.22				
1894	GGAGTCCGGA	1						
1895	GCGCGGATCC	0	663.9	1.84				
1896	AGGTTCCCGG	0	678.3	0.36				
1897	GCGCCGGGGC	0	728.1	0.74	604.7	0.31		
1898	GAGCCGGGCC	0	656.4	0.69				
1899	CCCCGGGCAG	0	689.5	4.16			762.1	1.24
1900	CCGGGGCATA	0	729.2	3.72	714.5	0.60		
1901	GGCCCAGGAAG	0	688.8	1.39				
1902	CCCCCGGGC	0	689.0	5.54	685.4	4.34		
1903	GGGGTAGGCC	0	683.1	1.95				
1904	GTCCGGGTTC	1						
1905	GGATGTCCGG	0	638.1	0.63				
1906	GTCCGGGCCA	0	642.4	60.29				
1907	CGGATCCGGA	0	608.5	1.84	693.1	0.58		
1908	CCGGGATCGA	0	692.1	9.85	660.0	3.29		
1909	CAGGGCCCGGA	0	639.9	1.91	546.4	0.22		
1910	CCCGGCCGGC	0	665.8	4.18	705.7	3.51		
1911	CGCTGCCGGA	0	650.9	0.32	574.0	0.24		
1912	CGTCCGGGTG	1						
1913	CGGAGTCCGG	0	634.2	0.30	674.0	0.26		
1914	GTGGGGAACC	0	681.9	2.31				
1915	GCCC GG GTCC	0	650.5	0.57				
1916	CCGCCGGGGGA	0	747.5	7.46	702.6	7.36		
1917	CCGGGCTGTG	0	612.6	0.41	679.4	0.33		
1918	CCGGGCTCCC	0	683.6	8.80	774.9	2.01		
1919	CGCGGGGGCG	0	652.0	0.63	787.1	0.35	704.5	0.21
1920	GATCCGGGGC	1	677.0	0.24				
1921	AAGGCCGGGC	0	646.1	0.37	509.2	0.36		
1922	GGCGCGGACC	0	635.0	1.96				
1923	CCGGATGCGC	0	681.2	4.69	684.3	1.96		
1924	CCGCGGGGTA	0	736.0	6.31	716.7	5.49	692.6	4.81
1925	GAGGCCGGGG	0	608.4	3.05	692.8	1.38		
1926	GGGCGCGCGG	0	755.7	1.62	683.7	1.42	613.4	1.15
1927	GGCCCGGGAC	0	698.8	1.28	632.6	0.66		
1928	CGCCGGGCC	0	642.1	1.08	827.5	0.65	689.6	0.51
1929	GCCGGGCGCC	0	653.3	0.89				

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1930	CGGGCGCGGC	0	629.1	0.66	678.8	0.56		
1931	CGACCCCGGA	0	691.1	13.28	617.8	12.79		
1932	GTGCGCGGCG	0	683.1	0.59	619.6	0.30		
1933	CCCAGGCGGGG	0	702.8	11.68				
1934	GGCCGGTCCC	0	680.9	3.25				
1935	GGCCCAGGGTC	0	665.4	2.95				
1936	CCGGGAGGCCG	0	668.0	3.19				
1937	GGCCGGAAATG	1						
1938	GCCTTCCCGA	0	678.7	6.72	745.8	2.90	583.6	0.99
1939	CCCGGAAGGC	0	672.4	29.02				
1940	CCAGGGGTCC	0	728.4	4.55				
1941	TGGCCCAGGG	0	712.8	0.61	713.9	0.57	637.0	0.36
1942	GGGGATGCC	0			696.6	1.87		
1943	GGGACCCGGT	0	639.0	0.73	618.7	0.44		
1944	CCGGGAGGCC	0	703.9	1.86	701.1	0.96	722.8	0.81
1945	AGGCCCGCGG	0	687.9	1.96	616.4	1.04		
1946	CGGGCGAAA	0	664.0	1.77				
1947	CCCGGGCCAG	0	683.5	2.53	716.7	1.09	710.5	0.34
1948	GGGGCGGCC	0	631.7	2.79	672.9	1.59	663.3	0.73
1949	CTGCCGGGCT	0	773.1	1.74	727.5	0.94		
1950	TTCCCAGGGCT	0	700.0	0.92				
1951	GGGTCCCTGA	0	671.0	1.27	709.2	0.77	526.8	0.30
1952	CCCGTCCCGA	0	623.8	2.76	692.2	1.92		
1953	GTCCGGAGTG	1						
1954	GGCCGGGTAG	0	645.8	0.75				
1955	GCCCCGAAAT	0	661.3	0.96				
1956	CCCCTGCCGG	0	657.7	1.13	545.4	0.65		
1957	TCCGGCGGCC	0	659.0	6.21				
1958	GGGGGGCCGG	0	650.3	8.77	706.6	2.26		
1959	AGCCCCCGGA	0	613.5	16.48	678.2	5.78	733.4	2.73
1960	CGAACCCCGA	0	640.5	2.94	672.2	2.76		
1961	CGCCCGGGCC	0	650.9	2.78				
1962	GCGCCGGGCG	0	696.8	0.41	602.9	0.25	664.4	0.23
1963	CAGGGCCCGG	0	670.2	12.91				
1964	AGGGGGGGCGC	0	634.9	1.40			691.9	0.42
1965	CCCCGGGAA	0	713.9	6.65	595.5	3.64		
1966	TCCCGGGGTA	0	721.3	1.37	741.7	1.07	679.4	0.59
1967	GGGGTCCCGG	0	693.6	1.15				
1968	CCCCGGGGTC	0	837.7	6.31	703.6	5.21	746.0	2.00

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1969	CCCGGGGTTC	0	731.9	11.48	601.5	0.69		
1970	CCCGGGGCGA	0	710.8	5.54	624.2	0.61	648.9	0.40
1971	CCCGGGGAGC	0	715.4	8.49	713.7	7.26		
1972	CCCGGGCGGA	0	706.2	6.45	691.9	1.59	717.4	0.60
1973	CCCCGGGCGC	0	711.1	13.11				
1974	CTCCCGGGGT	0	697.2	7.83	725.9	5.02	542.9	1.13
1975	CCGGGCCGGA	0	655.5	5.56				
1976	CCGGGCGAAG	0	704.5	6.86				
1977	GCCGGGGCGC	0	726.7	0.45	619.5	0.40		
1978	CCGGGGAGCG	0	701.4	1.53	606.5	0.73		
1979	CCCGGGGGTC	0	708.0	3.06	603.3	0.41		
1980	GTCCGGGAAT	0	657.3	1.06	685.0	0.54	756.1	0.20
1981	GCCGGGAATG	0	648.5	20.72				
1982	CCCGGGTCCC	0	684.6	2.53	733.0	1.67		
1983	GCCGGGAGCG	0	656.1	1.35				
1984	CCGGGCGCGC	0	699.4	1.79	613.8	0.33		
1985	GCCCGGGCGC	0	734.2	0.68	634.0	0.67		
1986	GACCCCAGGG	0	682.4	5.94	717.9	2.78		
1987	GCCTGGGGTA	0	705.8	1.41	626.0	0.71		
1988	GTATCCCGGG	0	708.9	0.51	544.0	0.22		
1989	CCCCGGGGCC	0	703.8	11.44				
1990	AGCCGGGGCG	1	656.5	0.47				
1991	CGTTCCGGGG	0	700.2	0.85	590.7	0.35		
1992	CCCAGGGCGGG	0	695.1	2.81	714.5	2.00		
1993	CCGGGATGCC	0	673.1	3.28	719.7	3.20	774.4	0.32
1994	CGCCCGGGGA	0	697.7	3.01	711.5	2.45		
1995	CCCAGGGGGGA	0	706.2	10.16				
1996	GCCGGGAATC	0	658.2	1.02				
1997	AGCGCGGGCG	0	678.8	3.81	699.3	2.47		
1998	ATCCCGGGCC	0	715.4	18.35				
1999	CCCCCCCAGGA	0	712.6	25.01	740.0	5.72	705.1	5.64
2000	CCCGGGTGGT	0	718.4	26.37				
2001	CCGGTTCCGG	1	662.9	0.34				
2002	CCCGGGCCGT	0	666.6	3.16	840.3	0.45		
2003	GCCGGGAAGC	0	666.4	3.42				
2004	GAGGTCCCGG	0	660.5	8.12	677.5	4.84		
2005	CCGGGTAGCC	0	714.7	4.96	656.8	1.55	721.0	0.62
2006	CCGGCCGGGG	0	566.9	3.13	669.3	2.21		
2007	CGCGCGGGCG	0	630.4	1.57	700.9	1.16		

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2008	CCGGGTAAATC	0	627.5	3.43	722.6	0.76	701.0	0.65
2009	GCCGGGCGAT	1	674.7	0.29				
2010	CCCGGAGGGC	0	684.6	7.28				
2011	GGGTCCGGGG	0	619.5	1.20	705.7	1.00		
2012	CCGGGCGGAC	0	668.8	1.21				
2013	GCCGGCGCGG	0	645.1	0.42				
2014	TCCGGCGCGG	0	578.8	1.28	647.4	0.65		
2015	ATCCGGGGCG	0	690.0	0.29	633.1	0.28		
2016	GCCGGGGCAA	0	636.1	0.53	708.2	0.42		
2017	CTCCCCGGGG	0	757.7	4.68	714.4	1.84		
2018	GCCGGAATTTC	1						
2019	GGCGCGGGAG	0	624.3	1.25				
2020	CCCCCTGGAG	0	681.2	5.08	677.5	4.63		
2021	GCTGCCGGGG	0	642.9	1.13	579.8	0.24		
2022	CCGGGGGGCGT	0	721.0	0.87	605.9	0.48		
2023	CCGGGTGGCG	0	664.7	1.00				
2024	GCCGGGGGCT	1						
2025	GGCCCCGGGA	0	683.7	27.56				
2026	GAGGGGGTAGC	0	677.8	0.57				
2027	AGCCGGCGGG	0	643.2	1.02				
2028	CGCGGGGGAA	0	638.4	4.91	725.9	2.20	682.0	1.66
2029	CGCCGGGGCA	0	705.9	1.40			604.4	0.30
2030	GGGGCGCGGC	0	623.7	3.98	687.3	1.39		
2031	CGGCGCGGGG	0	592.9	2.36	670.7	2.28	680.9	1.10
2032	CCGGGGGCC	0	725.5	1.98	662.3	1.73	781.1	0.68
2033	CCCGGATTAA	0	671.6	3.49				
2034	GAGCCGGGGA	0	696.3	1.92	597.4	0.91		
2035	GGGGGTATGC	0	700.5	0.78				
2036	CGCCCGGGGC	0	704.8	0.97	660.4	0.32	705.1	0.22
2037	CCGGGGCGGC	0	715.2	1.23				
2038	CCCCGGAGCC	0	590.0	11.39	666.3	7.86		
2039	GGGGGAGCGC	0	673.2	2.55				
2040	GGGCCGGGAG	0	631.3	1.51				
2041	AGGCCGGGGC	0	651.9	0.76				
2042	CCCGCGGGGT	0	730.7	2.61	622.1	2.45	695.0	1.79
2043	AAGCCCGGGG	0	692.4	1.59				
2044	CCTGGGGAAA	0	735.0	18.19				
2045	CCGGGAAGC	0	689.7	10.79	734.9	0.29		
2046	CGCCCGGGAA	0	703.1	1.05	595.1	0.39	629.8	0.26

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2047	GTCCGGGAGG	0	632.6	0.96				
2048	CCTCCC GGGA	0	700.1	24.92	602.6	3.52		
2049	TGGGGTTCCG	0	726.4	4.96				
2050	GGGTCCCCGT	0	665.6	4.02	687.6	0.76	540.0	0.36
2051	GCGCGGGGGC	0	659.4	2.22	681.9	0.53		
2052	GGCCGGGGCA	0	669.7	1.23				
2053	GCCCCCGGGA	0	640.8	16.23	725.3	11.00	689.3	6.47
2054	GTTGCCGGAC	0	709.9	0.48				
2055	CGTTCCCCGG	0	653.8	19.30	560.1	1.66		
2056	CCGGGGGTGG	1	744.3	0.46				
2057	TCCGGGATAG	0	650.0	0.43				
2058	ATCCGGGTGC	0	667.5	0.58	603.0	0.24		
2059	AGGGGCGCGC	0	688.2	2.62				
2060	TCCCCCGGGC	0	699.1	4.38	626.4	0.66		
2061	CCCCCCGGG	0	674.6	13.49	552.4	0.60		
2062	GCGCGGGCCG	0	656.5	1.45				
2063	AACCGGGGAA	0	698.6	1.37				
2064	CCCCGGTGAT	0	709.3	0.88	587.5	0.73		
2065	GGCCGGGAAC	0	648.9	0.76				
2066	GGGCGAAGTA	1						
2067	GGGTCTAGCG	1						
2068	GGCCC GGGGG	0	706.7	1.09	623.8	0.37		
2069	GGGCC CGGGC	0	703.6	1.08				
2070	CTCCCGGAGG	0	678.6	1.74	620.4	1.19		
2071	TCCGGGAGGC	0	667.7	0.87				
2072	CCGGTCCCC	0	658.2	1.36				
2073	CCTGGAGGGG	0	682.6	2.52	778.6	0.83	618.0	0.57
2074	CTCCGGGCCG	0	670.0	4.07				
2075	CGGCC CGGGG	0	691.9	5.52	594.1	0.25		
2076	GGGTGGTCCC	0	680.4	0.67	626.6	0.35		
2077	AGGGCCGGGG	0	674.7	0.46	407.1	0.27		
2078	GGGGGCGAAC	0	708.3	0.50				
2079	CCCGGAAGGG	0	673.8	16.67				
2080	CCGGGGAGGG	0	717.9	2.77				
2081	TGCCCGGGGG	0						
2082	GCCCCTGGGG	0	692.0	3.21	738.0	0.74		
2083	CCTTGGGCGC	0	699.4	8.67	770.5	1.66	731.1	0.66
2084	CCCCCTGGAC	0	586.1	2.06	684.9	1.82		
2085	GCAGTCCCCG	0	698.6	1.21	694.8	0.30		

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2086	CCGGCCGGGC	0	673.8	1.22				
2087	CCGGGATGGC	0	681.2	3.11	698.0	1.43		
2088	GCCGGTTAGG	1						
2089	GGGGGCGCGC	0	694.3	5.81				
2090	GTGGGGCGAA	0						
2091	CGGCGGCCGA	0	652.1	4.59				
2092	CGGCGCGGGC	0	633.8	2.39	667.2	1.14		
2093	GGCCGGGCC	0	641.5	1.10	713.8	0.71		
2094	CCGGAGGGGG	0	692.8	2.23				
2095	CCCGGTGTGG	0	711.4	2.30	676.8	1.94	743.5	1.03
2096	ATCTCCGGGG	0	668.0	0.87				
2097	CGGTCCGGGG	0	667.6	1.59				
2098	GGCCGGGAGG	0	656.8	0.60				
2099	GGGATCCCCG	0	596.9	22.34	679.9	3.88		
2100	CGGGGCGCGC	0			659.1	1.29		
2101	TTGGGCGCGG	0	670.6	0.38				
2102	CCGTCCGGGG	0	708.2	1.12	618.2	0.28		
2103	GGCCCCCGGG	0	700.5	5.06	746.9	3.54	623.0	2.93
2104	GCTGTCCCGA	1	792.0	0.55				
2105	GTCCTGGGCG	0	664.5	1.52				
2106	GGGTGCGGAG	0	596.2	0.70	681.3	0.42		
2107	CGGCCGGGAG	0	646.7	1.03				
2108	GGGGCGTAAA	0	621.8	32.09				
2109	ACGCGGGCGC	0	643.3	1.57	733.6	0.80		
2110	GCGGGGATCC	0	698.9	2.38	692.4	0.47		
2111	CCCTGGAGGA	0	697.9	4.62	596.8	0.30		
2112	GGGGGGAACC	0	703.1	4.92				
2113	GCCTGGCGC	0	825.3	2.04	634.1	0.89		
2114	CCGGAGGCCG	0	637.4	1.22	622.1	0.60		
2115	TCCGGGTCGC	0	708.8	3.41	720.8	0.40	787.6	0.30
2116	CGCGGGGCC	0	719.8	1.39	635.1	0.66	657.5	0.32
2117	GTCCCCGGAC	0	664.1	2.61				
2118	GGGCGTTAAC	1	599.5	0.24				
2119	GGCGCCGGGT	0	661.1	0.40				
2120	GGGCGCGGTC	0	651.3	0.86	765.9	0.36		
2121	CCCCGGTTCC	0	713.2	1.46				
2122	CCCGGGGCAC	0	753.2	6.01	711.8	5.23		
2123	TTCCAGGGCG	0	626.8	0.72				
2124	GGCCGGCGCG	0	656.2	0.54				

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2125	GC <del>GGGGGCGC</del>	0	631.6	0.45	716.7	0.39		
2126	TCCAGGGGGC	0	473.2	1.10	696.8	0.23		
2127	CCGGCGGGGC	0	691.1	1.41				
2128	GCGGGCGCGC	0	608.2	9.02	655.1	1.85		
2129	ACC <del>GGGGTCC</del>	0	720.3	0.78				
2130	AGCGCGGAGT	1						
2131	AGCCCTGGGG	0	716.7	1.92	641.9	0.65		
2132	CGCGGGCGCC	0	664.4	2.46	694.1	0.68		
2133	CAGCCGGGGG	0	649.1	0.50	599.5	0.29		
2134	GGGGCGGGGA	0	694.9	2.03	802.9	0.97	687.9	0.42
2135	GTGGGGAACG	0	694.2	0.72	844.5	0.49	536.6	0.27
2136	TCCGCCGGGG	0	653.9	2.16				
2137	GCGCGCGGAA	0	688.5	0.82	606.8	0.55		
2138	GAATCCGGGC	0	652.5	18.76				
2139	CCC <del>GGTTCCC</del>	0	710.6	0.94				
2140	CGGGGGTGCG	0	704.5	0.65				
2141	GGTCCGGAGG	1	663.0	0.33				
2142	CCGGGT <del>CGGA</del>	0	677.7	0.50				
2143	GCCCCCGGGG	0	704.5	18.53	620.8	3.50		
2144	CCCTGGGGCG	0	747.1	4.66	719.7	3.07		
2145	TTCCGGGGTG	1						
2146	TCCGGGGACG	0	698.3	1.05	610.8	0.23		
2147	GGGGCCGGGA	0	704.5	2.10	643.9	1.07	684.4	0.30
2148	GGGGCCC <del>GGT</del>	0	828.2	0.43	714.7	0.21		
2149	ACCCCCGGGG	0	682.1	8.40	689.8	3.38	627.2	3.06
2150	CGTCCGGGCG	0	660.0	2.11				
2151	CCGGGAGGCG	0	659.7	1.55				
2152	GGGCC <del>GGGT</del>	0	658.0	0.48				
2153	CCTGGCCGGG	0	679.9	3.42	591.9	0.45		
2154	CCGGGCGGGC	0	667.5	4.60				
2155	GGCCGGGCCG	1	665.5	0.39				
2156	CCGGGGGACC	0	712.6	11.46				
2157	GGGCC <del>GGGCG</del>	0	666.6	1.21				
2158	CGCCGGGCCG	0	536.9	0.42	648.8	0.42		
2159	GGCCGGGGCC	1	666.6	0.41				
2160	CGGGCCGGGA	0	669.4	1.54	656.2	0.74	708.2	0.27
2161	GCCCCGGGCC	0	659.5	1.37				

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**Table S4:** 8-base sequences designed to be Red (peak wavelength 600-660 nm).

	Sequence	Dark?	Peak 1 [nm]	Peak 1 area	Peak 2 [nm]	Peak 2 area	Peak 3 [nm]	Peak 3 area
1	GCGGCCGC	0	629.5	0.37				
2	TACACGCC	0	634.7	1.96	601.8	1.65		
3	CGCCACCC	0	532.4	10.65				
4	CGCCACGC	0	650.1	0.89				
5	GCCGCTAC	0	630.5	0.69				
6	AGCGGCCG	0	638.4	0.47				
7	ACACGCCG	0	609.8	1.33	647.8	1.08		
8	CACGCCGC	0	639.9	0.28				
9	ACACGCC	0	647.6	4.03				
10	AGCCGCGA	0	517.6	0.40	637.0	0.32		
11	GCGGCCAT	0	667.3	0.56				
12	TACGCCGC	0	619.4	1.26	649.0	0.46		
13	GACACGCC	0	625.8	0.69				
14	CACGCTAC	0	642.0	0.39				
15	TACGCGGC	0	633.9	1.76	530.2	0.28		
16	CGCGGCCG	0	613.6	1.43	644.7	0.46	701.9	0.40
17	TACACCCG	0	633.1	1.16				
18	CCACGCCG	0	607.3	0.60	689.6	0.51	518.9	0.49
19	AGCCGCC	0	668.5	2.45	644.5	1.14	575.2	0.34
20	ACGCGGCC	0	633.0	45.58				
21	ACACGCCA	0	656.4	1.56	579.9	0.75		
22	CCACGCC	0	639.2	0.50				
23	CGCGACCC	0	650.9	1.59				
24	CGCCACAC	0	647.3	0.36				
25	GCCGCGAA	0	663.5	1.94	581.1	1.67		
26	AGCGGCC	0	622.6	2.07				
27	AAGCGGCC	1						
28	GCGGCCAA	0	644.6	0.42				
29	CGCCGCAT	0	683.2	1.68	621.3	0.48		
30	CCCGGGCC	0	689.1	6.74				
31	TACGGCCG	0	643.7	1.18				
32	CGCCGCAA	0	652.1	2.00				
33	GCCGCGGC	0	666.0	1.33	760.2	0.23		
34	CGCCGCC	0	531.7	21.19				
35	AACACGCC	0	546.0	3.21	636.7	0.71		
36	GACACGCG	0	614.9	1.56	665.5	1.04		
37	CTACGCCG	0	522.7	8.41				
38	ATACGCCG	0	521.4	0.64	637.4	0.29		
39	GGCCACCC	0	631.4	0.41				
40	GCGCCGCA	0	675.2	1.57	659.2	0.36		
41	GTACGCC	0	643.0	1.18				
42	GGCCACGC	0	618.3	0.36				
43	CTACGCC	0	647.5	0.76	701.8	0.60	575.4	0.26
44	ACGCCGCA	0	650.8	1.96				
45	ATACGCC	0	600.5	2.12	711.7	1.19		
46	CATCCGCC	0	658.4	1.58				
47	TGCCGCC	0	626.3	0.20				
48	GCCGCCCT	0	619.3	0.77				
49	GCCGCCCA	0	615.9	1.50				

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50	GGACACGC	0	653.3	0.60					
51	CGCGGCC	0	638.3	0.24					
52	CGCGGCCA	0	620.7	1.12	689.2	0.25			
53	TCGCGGCC	1	649.9	0.20					
54	CGGCCGCT	1							
55	ACGGCCGC	1							
56	ACACGCGG	0	643.7	4.78	717.8	0.69			
57	ATACCGCC	0	632.2	3.85					
58	GGCCGCGA	0							
59	CGCCGCCA	0	626.6	0.52	543.5	0.24			
60	CGCGACGC	0	715.2	2.09					
61	AGCCGCCG	0	647.3	0.33					
62	TGCGCCGC	0	692.9	0.48	674.4	0.37			
63	GCGCCGCT	0	667.2	1.11					
64	GCCGCAAA	0	631.7	8.25					
65	GCGCCCAT	1							
66	CGGCCGCC	0	641.8	0.52	683.4	0.25			
67	GCCGCCAA	0	623.5	3.56	525.5	0.37			
68	GGCGGCCG	0	706.2	12.87					
69	AACGCCGC	0	620.1	3.22					
70	GACGCCGC	0	626.0	0.47	720.6	0.46			
71	AACCGCGA	0	634.8	3.34	695.3	2.50	773.3	0.77	
72	GACACCCG	0	655.9	1.34					
73	CGCCCTAC	0	641.6	5.22					
74	GGCGACCC	0	713.3	0.77	638.0	0.72	602.0	0.43	
75	GCCGACAC	0	649.5	0.62	518.8	0.48			
76	CCACGCCG	0	622.8	0.31	701.5	0.23			
77	AGCCGCCG	0	679.4	0.64					
78	GCGCCGCC	0	666.4	0.57	682.1	0.22			
79	CCCACGCC	0	647.1	3.46	536.0	0.35			
80	AACGCGGC	0	675.0	1.23	635.7	0.78			
81	TACAGCCG	0	537.4	0.77	641.0	0.46			
82	CACGCGCC	0	527.4	1.26	665.1	1.17			
83	CGGCCGCG	0	644.9	0.43					
84	ACGCCGCC	0	649.4	0.95					
85	CGCCGCCG	0			673.1	0.44			
86	CCGCCGCA	0	645.0	1.92					
87	GCCGCCGA	0	633.7	1.39	720.6	0.21			
88	TTACGCCG	1							
89	GCCGCAAT	0	623.2	55.75					
90	CGGCACGC	0	550.7	0.25	636.7	0.22			
91	TACGGCCC	0	631.1	1.44					
92	TTACGCC	1	627.9	0.22					
93	GGCCGCC	0	653.1	0.55					
94	GTACGGCC	0	650.8	1.45					
95	CGGCCTAC	1							
96	CACGCC	0	663.1	0.36					
97	ATACGGCC	1							
98	ACACCCGA	0	647.0	7.59					
99	CTACGGCC	0	643.9	1.36					
100	GCCGCATC	0	741.6	1.83	638.5	1.26			
101	GGCGCCGC	0	664.1	0.36					
102	CGGCCGAA	0	634.8	5.39					

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103	ACCCACGC	0	648.6	8.15	729.6	1.98	788.1	0.78
104	ACGGCCGA	0	660.8	0.56	623.0	0.54		
105	CGGCGCCC	1						
106	TCGCCGCT	0	672.2	1.41	577.8	0.22		
107	GCGCGGCC	0	643.1	1.54				
108	ACGCGGCG	0	670.6	1.35				
109	CGGCACCC	0	654.5	1.05	733.4	0.31		
110	GCGCCGCG	0	701.8	0.80				
111	AACACGCG	0	652.0	1.58	755.3	1.47	721.7	1.27
112	CACACGCG	0	692.0	1.07	623.8	0.74		
113	TACGCGCC	0	660.6	2.21				
114	CCGCCCAT	0	669.7	0.38				
115	CGCGCCGC	0	702.5	1.84				
116	ACCGGCC	0	645.5	0.47	568.7	0.34		
117	ACGCCGCG	0	649.1	0.89	695.9	0.34		
118	GCCGCGGA	0	716.8	12.93				
119	ACCGCGGC	0	607.3	3.10	717.0	0.96	643.9	0.27
120	CCGCGGCT	0	674.9	2.00	714.4	0.61		
121	TTGCGGCC	0	672.3	0.50				
122	GCCGACCC	0	503.9	0.55				
123	GCGCCGAA	0	653.8	1.20				
124	GCCCACGC	0	616.1	1.83	713.5	0.67		
125	TACGCC	0	632.3	0.69	697.0	0.53		
126	CCGCCGCC	0	663.5	0.36				
127	CCGCGCT	0	674.2	0.70	636.3	0.37		
128	GCCGCCGC	0	642.3	0.38				
129	GCCGCCGT	0	628.1	0.87				
130	CGCCGCCG	0	645.4	0.21				
131	GGCCGCAT	0	650.6	1.26	686.5	0.46		
132	GCCGCC	0	646.4	0.62				
133	TCGCCGCC	0	662.5	0.57	540.2	0.49		
134	ACACCGCC	0	595.3	2.77	640.0	2.21		
135	GCCGCGCC	0	669.4	2.96				
136	GGCCGCCA	0	666.3	0.51	610.4	0.38		
137	AACGCCGA	0	662.0	3.95	530.6	1.22		
138	ACGCCGCG	0	693.9	0.34	638.3	0.21		
139	TGAGCCGC	1						
140	TGCGCCCT	0						
141	AAGCGCG	0	692.9	1.93	718.7	0.33		
142	CGCCCATC	0	643.5	0.50				
143	GCGCGT	0	661.0	3.32				
144	CCCACGCG	0	707.2	0.91	612.5	0.35		
145	CGCCGTAC	0	650.3	0.25				
146	GCGCCCAA	0	663.7	1.00				
147	AAGCGCCC	0	701.5	0.73	638.6	0.72		
148	CATCGCCC	0	642.7	3.55				
149	CCGCGCCC	1						
150	CGGCGGCC	1						
151	CCGCGGCG	0	652.5	1.26	696.4	0.75	766.0	0.35
152	TTCGCCGC	0	652.1	1.26				
153	TTGCGCCG	0	660.5	0.24				
154	CGCGACAC	0	607.6	0.60	666.5	0.34	721.9	0.20
155	ACACGGCC	0	634.7	3.42	683.6	0.38		

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156	GCGGCGCC	0	708.6	1.58	625.9	0.54		
157	CGGCCGTT	1						
158	AACGGCCG	0	643.8	2.65				
159	CCGCCGAA	0	645.3	1.95				
160	TCGGCCGT	0	647.8	0.85	706.1	0.21		
161	CCGCCATG	0	623.7	0.39				
162	CCGCCATC	1						
163	AAGCCGCG	0	657.8	0.23				
164	CGGCGCCG	0	679.9	1.20				
165	GCCGCGGG	0	692.8	0.55				
166	GCCGCGGT	0	718.7	0.77	576.7	0.44		
167	TCGCCGCG	0	667.9	1.57				
168	GGCGCCGA	0	657.1	1.05				
169	GGCGACGC	0	649.0	0.43				
170	CGCCGCGT	0	657.9	0.60	551.0	0.30		
171	ACACACGC	0	639.3	0.33				
172	CCACACGC	0	644.4	1.44				
173	GCCCACCC	0	626.6	7.02	708.9	4.56	737.0	2.64
174	CTACCGCC	0	631.5	2.80	703.9	0.27		
175	CGCCGCTT	0						
176	GGACGCC	0	566.8	0.67	644.0	0.21		
177	CGGCCCAT	0	637.7	1.01				
178	GGCGGCC	0	593.7	3.31	700.4	0.67		
179	TGCGCCGT	0	644.9	0.44				
180	CACACCG	0	645.3	0.42				
181	GGCGGCCA	0	649.3	0.92				
182	AGGCGGCC	1						
183	TGGCGGCC	0	649.1	0.76				
184	CCGCGCCG	0	708.8	0.32	628.6	0.27		
185	CGGCCATA	0	655.9	0.36				
186	CGGCCATC	0	591.4	0.67	673.6	0.49		
187	CGGCCATG	0	643.7	0.51				

**Table S5:** 10-base sequences designed to be Red (peak wavelength 600-660 nm)

	Sequence	Dark?	Peak 1 [nm]	Peak 1 area	Peak 2 [nm]	Peak 2 area	Peak 3 [nm]	Peak 3 area
1	GCCGCGACAC	0	608.3	1.50	660.0	0.33		
2	GCCGCCACGC	0	648.3	0.59	614.9	0.53		
3	CGGCCACGCC	0	641.4	1.12				
4	CACGCCGCC	0	632.3	0.40				
5	GCCGCGACGC	0	641.7	2.07				
6	TTACACGCCG	0	649.9	1.78				
7	TTACACGCC	0	641.5	1.74				
8	TACACGCC	0	641.0	2.33				
9	GGACACGCC	0	622.5	2.21	649.5	0.96		
10	ACGGCCGCGA	0	635.5	4.65				
11	CGCCGCGGCC	0	650.3	3.38	694.0	0.44	727.7	0.40
12	CCACGCGGCC	0	641.3	7.11	712.6	1.52		
13	GTCACGCGGC	0	675.7	6.07	655.3	4.28	699.8	1.25
14	ACGCGGCCGC	0	640.8	2.36	662.8	1.00		
15	GTCACGCCGG	0	628.5	0.39				

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16	TCACGCCGCC	0	649.9	0.38	575.8	0.30		
17	AGCGGCACGC	0	628.2	4.02				
18	CGCCGCTACC	0	568.9	1.84	663.1	1.39		
19	CGGCACGCC	0	657.6	1.96				
20	GGCCACGCC	0	613.4	3.20	689.7	0.49		
21	GCGGCCGCG	0	661.7	0.85	611.6	0.36		
22	CGCCGCACGC	0	650.6	0.83				
23	CGCCACGCGA	0	614.7	3.42	690.5	1.85		
24	GGGCCACGC	0	663.8	1.62	639.3	0.38		
25	CCGGGGCGC	0	599.0	2.33	669.8	1.95		
26	GGCCGCGGCC	0	641.7	1.83	688.5	1.10	582.7	0.27
27	TGCCGCGGCC	0	602.9	3.32	678.8	2.16		
28	GCCGCGGCCG	0	649.3	28.93				
29	TACACGCGCC	0	535.8	1.36	640.1	1.26		
30	GCGGCCTACC	0	669.6	3.74	719.2	0.70		
31	TACGCGGCCA	0	604.8	0.84				
32	TCGCCACGCT	0	622.7	0.37				
33	AAGCGGCCGA	0	556.5	0.29	648.7	0.28		
34	TACGGCCGCG	0	652.0	0.60				
35	CGGCCGCGGC	0	662.8	2.53	677.3	1.14		
36	CGGGAGCCGC	0	635.5	2.08				
37	GCGCCACACA	0	683.5	0.46				
38	CGGCCGCAAA	0	646.1	194.66				
39	AAAGCGGCCG	0	645.5	0.30	648.6	0.26		
40	CGCGGCCGCC	0	646.3	0.31	598.9	0.29		
41	TACACGCGGA	0	619.9	1.40	644.9	1.08		
42	GCGGCGACAC	0	620.5	0.69	687.7	0.59	582.5	0.39
43	CGCGCCACAC	0	619.0	1.54	674.8	1.13		
44	AAGCCGCCCA	0	634.4	6.03	534.4	0.51		
45	ACACGCCGAA	0	623.6	0.56	533.7	0.32		
46	CGGCACGCAA	0	640.9	36.98				
47	AAAGCGCCC	0	673.5	0.56	607.3	0.32		
48	GCGGCCGCGC	0	642.3	1.34	535.9	0.66		
49	TTCGCCACGC	0	592.5	0.52	730.1	0.23		
50	ACACACGCC	0	657.6	3.57	497.7	0.33	591.6	1.50
51	CCACACGCC	0	656.2	8.77	525.4	0.82		
52	CTCACGCGC	0	681.2	4.75	568.8	0.80	610.4	0.48
53	GCCGCACGCG	0	627.1	26.70				
54	TCGCGGCCGT	0	660.2	4.24				
55	ACGCGACCGC	0	635.3	3.11				
56	CGGCACGCCA	0	629.1	0.97	641.8	0.67		
57	AGCCGCGGCCG	0	592.6	4.49	666.0	0.56		
58	AGCCGCGGCA	0	658.0	2.41	675.2	1.07		
59	CATCACGCC	0	615.5	9.02				
60	AAACACGCCG	0	637.2	1.64	534.7	1.16		
61	AAGCCGCGGC	0	636.5	0.37	680.9	0.31		
62	AGCGGCCGGA	0						
63	AAACACGCC	0	659.8	1.85	565.1	0.90		
64	AGCGCCGCGA	0	683.0	1.59				
65	GCCGCACACG	0	567.1	28.56	616.3	13.53	604.3	6.57
66	CCGCCGCGAA	0	639.8	2.60	633.6	0.70		
67	TTACGCGGCC	0	645.8	0.26				
68	CGGCCGCCGC	0	628.5	7.68				

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69	GGCGCGGCCG	0	648.3	2.74	678.2	1.05			
70	GTACGGCCGG	1							
71	CGGCCGCGCC	0	640.7	0.99	715.6	0.46			
72	ACCGCAGCCG	0	619.4	16.79					
73	GGTACGGCCG	0	629.4	3.37	500.6	0.48			
74	CGGCCAACGC	0	659.9	15.34	573.2	1.56			
75	GCCGCGGGAG	0	635.4	6.97	718.2	0.26			
76	CGCCGCGCCC	0	627.1	0.63					
77	CGGCCAACAC	0	630.4	1.72					
78	CGCGGCCGGA	0	621.0	3.79	712.1	0.20			
79	ACGGCACGCC	0	652.8	2.32					
80	TACGGCGCCC	0	668.3	0.49					
81	CGGCCGCGGG	0	676.7	2.21	615.2	1.11			
82	CGGCCGCGGT	0	650.9	0.48					
83	GGACGCGGCC	0	606.7	0.89	743.8	0.38			
84	AGCCGCCCA	0	629.5	4.32	523.8	0.22			
85	TCACGCCGGA	0	658.4	0.30					
86	CGGGAGCGGC	0	628.9	2.34	713.5	0.68			
87	CCGCCGCGGC	0	640.8	4.37	670.8	0.45			
88	CGCCGCGGCA	0	627.6	1.17	691.5	0.80			
89	CGCCGCCTAC	0	653.6	3.43					
90	TACGCCGCGT	0	581.5	1.37	652.2	0.38			
91	CGCGAGCCGA	0	708.4	6.30	618.3	5.58			
92	GCCGCCTACC	0	681.6	1.34	622.7	1.04			
93	AGCCGCCGCA	0	636.1	0.44					
94	CGCCGCGGGCG	0	647.4	0.81	655.6	0.78	588.6	0.38	
95	CGGGCCGTTT	0	629.3	1.57	673.4	0.51			
96	GCCGCCGCC	0	624.8	25.68	667.2	14.11			
97	GCCGCGTCCA	0	613.0	39.18					
98	GGCGGCCGCC	0	691.4	1.10	624.0	0.64			
99	GGCCACGCGG	0	636.5	6.53					
100	CGCCACGCGC	0	631.8	1.84	721.5	0.46			
101	TCCGCGGCC	0	672.2	4.80					
102	AAAGCGGCC	0	615.4	0.25					
103	ACGCGGCCA	0	642.6	1.22	635.1	0.86			
104	CGGCCGCCCT	0	623.8	1.39	661.1	0.36	626.1	0.30	
105	TACGGCCGGA	0	678.6	0.48					
106	TCGGCCGCC	0	641.8	0.40	645.4	0.29			
107	TGGCACGCT	0	698.1	0.92	639.3	0.74			
108	CGGCCGCCGC	0	616.9	0.55					
109	CGGCCGCCGG	0	652.2	2.33					
110	AAGGCCACGC	0	608.9	2.60	667.5	1.38			
111	CGCGACGCAA	0	691.9	1.47	630.6	1.37	832.0	0.72	
112	TCCGCGCC	0	567.7	0.82	641.2	0.73			
113	AGCCGCGGGA	0	648.3	1.61	703.7	0.63	531.8	0.20	
114	AGCCGCGCCA	0	718.3	6.47					
115	ACCGCGGCCA	0	611.1	1.95	669.1	0.55			
116	CGGCGGCCGA	0	645.2	2.11					
117	TACAAGCCGA	0	644.7	1.76	538.3	1.27			
118	AACGCGGCCA	0	583.5	0.39					
119	GCGGCCAGTC	0	694.8	0.76	641.2	0.21			
120	AAACGCGGCC	0	654.0	2.22					
121	TTACGCCGCT	1							

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122	GCGGCGACGC	0	650.1	1.32					
123	TGCGGCCGCT	0	723.1	0.38					
124	TCGGCCGCT	0	639.9	0.33					
125	CGGCGGCCGG	0	654.2	1.19	611.1	0.58			
126	CGGCCGCGTT	0	665.0	1.26					
127	CACGCGGCCG	0	643.0	0.97	699.0	0.88			
128	ACCGCCGCAA	0	633.0	2.81					
129	GGCACGGCC	0	578.0	9.50	648.4	1.82			
130	CGCCGCGTAC	0	604.8	13.99					
131	AGCCGCCGAA	0	619.4	0.41					
132	AAACACGCCA	0	542.7	1.24	644.8	1.12			
133	AGGCGGCCGA	0	641.6	1.40					
134	GTCCACGCCG	0	598.4	0.40	653.5	0.33			
135	CCGCCGTCAC	0	630.9	0.61					
136	ACGCACGCCA	0	557.9	14.31					
137	TGGCGGCCGT	0	663.2	0.33					
138	TTTCGGCCGC	0	642.0	0.92					
139	AAGGCGGCCG	0	638.7	0.65					
140	AAAGCCGCCG	0							
141	CGCGCCGCAA	0	678.8	3.35	580.8	0.55			
142	GCCGCCTCAC	0	636.0	0.55	536.2	0.27			
143	GGCGCGAAA	0	647.6	0.86					
144	CCACACGGCC	0	644.6	1.29	550.8	0.44			
145	AGGCCGCGAA	0	652.2	0.62					
146	AGTGC CGCCC	0	598.8	0.29					
147	GGACACGGCC	0			643.8	0.34			
148	AGGCCACGCG	0	642.9	0.86	607.4	0.39			
149	GCGCGCAAT	0	625.6	2.50	569.5	1.64			
150	GTACGCGCG	0	614.9	1.25	675.4	0.81	756.7	0.27	
151	AGCCGCGCCG	0	655.6	8.07					
152	GCGCGACACG	0	654.9	0.78					
153	AGCGCCGCCA	0	690.5	2.47			536.5	0.27	
154	TCCAGCGGCC	0	650.9	0.63	642.2	0.31			
155	GGCCGCCCAA	0	634.6	0.47					
156	AAACGCCGCA	0	632.1	0.82	516.8	0.67			
157	AGGCCGCCCA	0	600.2	0.62					
158	GGCGACCGCA	0	611.2	0.94	662.7	0.71	728.6	0.49	
159	GCGCCCTACC	0	680.4	0.46					
160	ACGCCACCGC	0	640.8	3.54	574.8	0.53			
161	CGGCAAGCCG	0	634.5	0.95	616.6	0.66	662.3	0.51	
162	ATACGCCGAA	0	533.0	0.55	583.5	0.23			
163	CCGCACGCGA	0	697.6	30.68	614.8	1.41			
164	ACGCCGCCCA	0	681.0	0.51					
165	TCGGCCGCTT	1							
166	CCTACCGCCG	0	667.2	33.59	543.4	8.46			
167	AGCCGACCGC	0	641.7	13.62	616.7	8.35			
168	GCCGCCGCCA	0	646.7	0.45					
169	CCGCCCTACC	0	674.6	1.87					
170	CGCCGCCAAA	0	685.0	3.40	606.8	0.25	549.4	0.57	
171	AGCCCACGCC	0	669.1	1.16	609.6	0.94			
172	GCCGCCAAATC	0	636.8	0.62					
173	TCACCGGCCGC	0	664.6	1.02					
174	TGAGCCGCCG	0	635.8	1.42					

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175	GCCGCCAGTC	0	642.3	1.97					
176	CGGCGCGGGC	0	637.8	0.91					
177	TCCAAGCCGA	0	649.4	2.32	625.3	1.58	655.9	1.25	
178	GCGGCGCCGG	0	661.4	0.42					
179	GCCCGTACG	0	550.0	28.70	584.1	15.23			
180	AATCCGCCGC	0	675.1	1.62	559.4	0.70			
181	CGGGCCGCC	0	659.8	0.39					
182	AGCCGCCGCG	0	667.0	0.77					
183	CGGCGACGCC	0	623.9	0.50	679.6	0.48			
184	CGCCGCTCAC	0	628.5	1.93					
185	AGCCGCGCGA	0							
186	GCGCAGCCGA	0	653.7	1.67	699.6	0.66			
187	GGCCGCGGGCG	0	592.0	2.03	653.7	1.36			

**Table S6:** 12-base sequences designed to be Red (peak wavelength 600-660 nm)

	Sequence	Dark?	Peak 1 [nm]	Peak 1 area	Peak 2 [nm]	Peak 2 area	Peak 3 [nm]	Peak 3 area
1	GCGGCCACACGG	0	626.6	5.45				
2	CCACGCCGCTAC	0	641.9	6.55				
3	GACACGCGGCCG	0	646.7	2.77	613.9	2.29	611.7	1.80
4	GCCGCGACGCAT	0	694.9	1.60	647.9	1.35		
5	GCGGCCGACAC	0	624.3	3.67	670.6	1.41		
6	GCCGCGACGCC	0	634.7	4.01	711.4	2.78	762.4	1.57
7	CCCGGACACCCCC	0	643.4	11.13				
8	CCCACGCGGCCG	0	635.9	5.65				
9	CCCGGGCCACGC	0	646.5	3.57				
10	CGCCCACGCCGC	0	651.0	1.95	537.1	0.38		
11	CGCCGCCATACC	0	636.9	1.98	633.0	1.77	688.4	1.36
12	CGCCCACACGCC	0	616.3	5.82	722.7	0.66		
13	TACGCCACAGCT	0	643.9	26.91				
14	GCCGAGCGGCCA	0	629.2	1.81	652.9	1.47	689.7	1.16
15	AGCCGCCATACA	0	636.1	6.19	659.6	2.53	521.7	0.59
16	CGCCGCCAACGC	0	623.6	9.49				
17	CCCACGCCGCC	0	669.3	3.58	625.3	2.61		
18	GCCGCACACGCC	0	611.5	4.16	628.7	3.43	671.2	0.69
19	ACGCCACGCCG	0	646.9	6.44				
20	GGTACGCGGCCG	0	637.7	6.88				
21	CCGCCGCGACGC	0	679.8	1.50	628.0	1.21	698.7	0.33
22	GCCGCCACACGC	0	625.5	7.55				
23	CCCACGCCGCC	0	640.7	3.78	699.9	0.71	749.6	0.38
24	GCCGAAGCGGCC	1						
25	CGCGACACCGCC	0	621.5	3.60	674.3	0.87		
26	GCCGCAGCGCG	0	638.8	5.96				
27	AGCCGCAGCGGA	0	663.0	2.56	550.3	1.48		
28	GCGCTACACGCC	0	661.7	7.93				
29	GCGCCACGCC	0	633.4	3.37	581.5	0.59		
30	GCCGCCACGCC	0	683.5	3.56	689.8	1.21	647.3	1.20
31	GCCGCGAGCGA	0	629.9	5.19	715.2	2.36		
32	GCCCACACGCC	0	684.9	13.25				
33	GCCGACACACGC	0	648.6	14.93				
34	CGCGGCCACGC	0	647.4	6.03	688.5	0.91		

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35	TCGGCACGCCCT	0	628.8	4.64	675.1	1.57	700.4	0.61
36	CGGCCGCATTCC	0	638.0	3.02			686.4	1.71
37	AGCCGCGGCCAA	0	669.8	4.86	615.1	1.68	568.8	0.69
38	ACCGCAACGCC	0	653.7	3.46	594.9	1.38		
39	CCGCCCACACTT	0	686.6	68.09	586.3	2.36		
40	GGCGCCCACGCC	0	662.6	10.81	716.3	2.06		
41	ACGCAACGCCA	0	631.3	3.95	564.8	0.58		
42	CCCCACGCGGCC	0	660.8	4.50				
43	AGGCCACGCCGA	0	648.2	1.66				
44	TACACGCGCCC	0	668.1	6.39	621.0	5.16		
45	GGCGCCCACCTAC	0	657.0	2.07	698.6	0.35		
46	CCTACGCCGCC	0	692.0	9.07	618.1	5.01		
47	AGGCGCCACGCC	0	671.7	3.50	580.4	0.87	704.9	0.71
48	GCGCCGCCCTAC	0	679.9	2.45	608.2	1.78		
49	CGGCGACGCCGC	0	649.3	1.44				
50	GCCGAACGCCG	0	652.1	2.65				
51	CCCTACGCCGCC	0	655.7	3.26	618.1	3.06	806.4	0.39
52	CCCACGCCAAA	0	628.5	4.84	653.4	4.00		
53	CGCGCCGCTACC	0	663.6	10.96	722.1	0.75		
54	CACGCCAACGCC	0	647.7	5.57	513.8	1.32	591.1	1.23
55	CGCCGCGGCCCTT	0	690.0	5.87	628.3	2.29	721.5	2.13
56	GGCGACGCACGC	0	630.4	2.98				
57	GCGCCGCACGCG	0			658.4	3.45	683.1	2.16
58	CGGCCGATACAA	0	591.8	19.51	676.6	1.76		
59	GGACGCGGCCAT	0	641.0	4.86				
60	GCCGCACGCGCC	0	652.9	2.44				
61	AGCCGACGCC	0	663.5	4.82	678.9	0.94		
62	GGCCGCCCATAC	0	644.8	2.48				
63	GCCAAGCGGCC	0	683.6	10.85	603.9	1.15		
64	GCCGCAGCGGAA	0	663.5	1.50	622.6	0.69		
65	GGCGCCCATA	0	664.4	3.74	595.3	0.35		
66	CGCGACGCTACG	0	634.9	2.77	731.3	1.04		
67	TACTTGCCGCC	0	654.5	3.05	632.1	1.71		
68	CCGCCGCACGCC	0	645.1	2.54	604.5	1.09		
69	ACGCGACACCCG	0	635.0	9.08				
70	TTTACTGCGGCC	0	707.9	4.20				
71	GCCGTTGCCGCC	0	682.6	0.96				
72	CCGCACACGCC	0	625.7	4.49	673.9	3.07		
73	GCCGTGCCGCC	0	642.6	1.80				
74	ACGCGACGCC	0	651.9	2.42				
75	ACGGCAACGCC	0	626.4	9.84				
76	CGGCCGCCGCC	0	649.5	0.86				
77	GCGGCCGCCGCC	0	652.6	4.33				
78	GCCGCGGCCGCG	0	657.0	3.29				
79	GGCCGCCGCCAA	0	650.8	2.61				
80	CCGCCCCACGCC	0	652.0	6.05	589.2	2.41		
81	GGCCGCCGCCGG	0	630.3	5.71	674.5	1.81	624.6	0.28
82	GCCCCACGCCA	0	690.8	24.33	605.7	2.70		
83	CGCCCCACGCC	0	686.7	4.19	634.6	3.05	782.5	0.31
84	GGCGACACGGCG	0	674.7	6.18	556.8	1.29		
85	TACGGCCGCCGC	0	644.1	2.72	595.9	0.28		
86	AGCCGCCGCATA	0	621.0	1.30	676.0	0.81		
87	CGGCAACGCCA	0	645.4	1.34	619.3	0.93	662.1	0.68

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88	CCCACGCCGGAG	0	649.3	1.76	675.2	0.26		
89	GCCGCATACGCG	0	643.6	4.61	805.7	0.34		
90	GGCGACACCGCG	0	681.1	2.21	633.1	2.17	700.2	0.41
91	CCGCATGCGCCG	0	642.9	1.23				
92	ACCGGGCCGCC	0	632.6	1.00	677.3	0.31		
93	AGGCGACGCCGA	0	667.5	1.71				
94	GCGCCGCCATGA	0	662.9	5.83	663.1	3.92		
95	AGGCGCCCTACA	0	665.4	2.10				
96	GCCGC GGCCCAA	0	678.6	15.33	616.9	3.87	666.1	2.50
97	AACCGCAACGCG	0	648.8	2.25				
98	CGCGCCCCACGC	0	651.8	4.98				
99	GCGGCACGCGCC	0	697.0	2.14	636.3	0.77		
100	GGCGCCCCATAC	0	663.8	4.35			696.1	0.98
101	CCGCGGCCATCC	0	649.9	1.85			695.6	0.64
102	GCGGCCCATCAT	0	656.6	4.48				
103	ACGCACGCGAGT	0	690.3	25.82	605.8	2.37		
104	GCCCACACCGCG	0	644.8	6.23	806.4	0.30		
105	AAGGCGACGCC	0	631.5	2.14	587.9	0.77		
106	CGCCATCCGCC	0	635.6	3.90	693.6	1.27	707.1	1.26
107	ATCATGCGCCCT	0	656.2	3.76	561.5	0.68		
108	AGCCGCCCAT	0	658.7	18.65	540.0	14.60	668.4	9.76
109	AGCCGCCGCCA	0	665.2	2.32	632.9	1.60		
110	TACTCCGCCCTT	0	602.2	4.39	639.2	1.39		
111	AACCCACGCGCC	0	611.3	6.24	685.5	5.85		
112	GCCCCCACGCC	0	675.1	29.03	676.2	5.59	519.3	2.27
113	ACCGGACGCCAA	0	686.3	1.58	681.5	1.44	636.0	1.11
114	CCGCCCCATACAT	0	692.6	7.23	639.3	3.42	701.5	0.85
115	GCCGCATACCG	0	638.0	8.97				
116	AGCGCGCCGCGA	0	684.7	2.15	724.1	1.41		
117	GCCGTTACGCC	0	626.8	2.89	658.6	2.24		
118	ACCGGGCCGGAG	0	634.1	2.64	622.3	0.24		
119	GCGGCTACCGCG	0	625.5	3.72	719.5	1.02		
120	TCGCGTCCGCC	0	664.9	4.64	590.0	0.35		
121	CGCGACC CGC	0	662.6	3.46	586.6	0.72	495.6	0.63
122	CGCGGCCGCCGG	0	650.6	2.28				
123	CCGCCGCGGCC	0	632.2	1.81	657.0	1.17		
124	GCCGCCGCGGCC	0	647.8	1.18				
125	GCCGCATCGCG	0	665.3	3.31	809.3	0.26		
126	CCATGCCGCC	0	662.8	1.62	624.4	1.11		
127	AACCCACGCGA	0	641.3	1.08	659.4	0.71		
128	GTACGGCCGGAG	0	643.3	1.17				
129	GCGGCCCTTACT	0	636.1	1.95			691.8	0.43
130	GCCGAACGGAA	0	646.7	6.32				
131	GCGGCCGGATTG	0	661.9	2.36				
132	CGCCGCGCGGCC	0	646.1	1.63	757.8	0.98		
133	CGCGGCAACGCG	0	654.2	3.09				
134	CGGCGACGCCAA	0	631.0	2.65	583.5	1.03		
135	GCCGCGGACACG	0	628.0	2.87	691.2	1.72		
136	CGCGCCGCGGCC	0	653.5	2.75	762.7	1.76		
137	AGGCCAACGCC	0	635.7	2.38	794.0	0.75		
138	ACGGCAACGCC	0	639.6	2.00	658.1	1.21		
139	TACGCTCCGCC	0	645.1	2.29				
140	ACCGGACGGAA	0	663.5	2.06				

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141	ACGCCAGCCGCA	0	652.4	2.24				
142	CCGCACGGCGCG	0	628.1	1.95	685.2	1.25		
143	AACGGCCGCCCA	0	646.7	2.67	520.8	0.52		
144	GCCCACGGCCGG	0	656.4	3.01	724.9	0.68		
145	CTACGCGGCC	0	642.1	8.88				
146	GGCGCCGACACG	0	695.7	3.02	616.5	1.00		
147	CCCGGGCCGGAG	0	648.8	8.38				
148	TTGGCGACGCC	0	683.3	3.51	753.0	2.27	590.9	0.53
149	CCCACGCGGCC	0	652.7	4.76	609.7	0.93		
150	AACGGGCACGCC	0	667.7	1.63	701.2	0.33		
151	GCGCGGCCGCTT	0	703.3	0.33	634.6	0.33		
152	ACGGCGGCCGCA	0	667.6	4.91				
153	GCCGCGTCCGGA	0	669.5	52.78				
154	GCGGCGCCGCC	0	678.9	7.20				
155	CCGCAAACGCCG	0	634.7	3.46				
156	AGTACGCCGCCT	0	633.9	2.51	681.8	1.64		
157	AGCCGCCAAATT	0	673.2	2.25				
158	CCGCCGCCGTAC	0	625.3	5.80				
159	TCGCCGCCGTAC	0	627.9	1.39	666.6	1.08		
160	CCGGAGCGGCC	0	676.1	1.93	627.8	1.45		
161	GCCGCGGCC	0	653.0	3.78				
162	CGCGCAGGCC	0	657.0	2.10				
163	GCGGTACCGGC	0	668.7	15.77	597.0	3.64		
164	GCCGAGGCC	0	681.6	3.17				
165	AGGCGACGCCA	0	638.4	6.20	527.4	0.36		
166	AGTACGCCACGC	0	655.7	0.79				
167	CGCGCGCACGC	0	633.3	2.10	702.7	1.30		
168	ACCCACGGAA	0	674.3	1.36	537.2	0.23		
169	GCCGCGGCC	0	640.0	1.66				
170	GCGCGGCCGCG	0	659.3	1.72	582.4	0.83		
171	GGGCGACACCC	0	739.0	13.19	698.8	5.30		
172	AGCGGACACCG	0	642.9	3.86	703.8	1.68		
173	GACACGGGGCC	0	636.8	1.77	716.4	1.52		
174	CGGCCGCGCC	0	656.7	1.78				
175	CGCCTACCGCC	0	617.9	7.26	671.1	6.45	691.7	3.28
176	CGCCGCCCAT	0	673.5	8.80	543.6	1.96		
177	CGCCGCCAAC	0	671.3	8.15	531.5	1.22	591.9	0.56
178	CGGCCGCGCC	0			683.1	1.18	623.6	0.65
179	CGCGCCGCC	0	671.2	5.10	538.3	0.31		
180	TCCGCCGCC	0	682.4	9.39	669.3	4.10	693.4	2.28
181	AAACGCCCCAC	0	617.7	4.07				
182	TTGCCGCC	0	621.4	2.83	757.7	1.24	680.2	0.85
183	TTCGCGACCGT	0	686.9	3.76	706.8	0.97		
184	TTTGAGCGGCC	0	643.7	0.63	683.8	0.45		
185	CCGCCGCC	0	658.8	2.21				
186	GGCGCCCACGGG	0	665.9	1.92	696.9	0.77		
187	ACGCGCCGCC	0	684.4	4.19				

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**Table S7:** 16-base sequences designed to be Red (peak wavelength 600-660 nm)

	Sequence	Dark?	Peak 1 [nm]	Peak 1 area	Peak 2 [nm]	Peak 2 area	Peak 3 [nm]	Peak 3 area
1	CGGCCGCTACACCCCC	0	654.6	8.90				
2	TACACCCATCGGCCGA	0	560.0	5.12	627.2	2.13		
3	ATACGCGGCCACCAA	0	642.6	2.78				
4	TTTACACGCCGGGCC	0	644.3	2.20	514.8	0.67		
5	GCCCATACAGCGGCCG	0	640.2	1.61	532.2	0.87		
6	GGCCGCGGCCACCCCT	0	674.4	3.22	546.7	0.87		
7	GCCGCGGCCGACGCA	0	632.0	1.41	604.0	0.60		
8	GCGGCCTACACGGCCA	0	569.8	2.01	663.4	0.65		
9	GCGGCCACGCCGCC	0	674.8	2.71	612.5	1.63		
10	CGCGCCACGCCCGCAA	0	648.1	0.88	561.5	0.48	712.1	0.29
11	TCACGCCGAGGCCA	0	634.5	1.35				
12	CGCCGCGGCCACGCC	0	687.4	3.09	664.3	2.95	630.0	1.75
13	TACCGCCACACGCGCC	0	645.7	1.29	567.2	1.19		
14	CGCCGCATCGGGCCG	0	670.6	5.35				
15	GGCGCTACGCGGCCGC	0	662.9	0.90				
16	GTACCGGCCGCGGCCG	0	640.8	2.17				
17	GGACACGGCCGCGCG	0	631.5	2.43				
18	CCGCCACACGCCCTT	0	541.1	1.39	655.0	0.63		
19	TACCGGGCCAATACC	0	639.3	2.57				
20	CGGCCTCACGCGGCC	0	640.0	1.93	685.3	0.69		
21	ACCCAGCCGAGCGGCC	0	640.6	2.89	574.2	0.88	575.8	0.83
22	ATTGCCGCCGCCACCC	0	629.3	7.53	526.1	0.65		
23	AACATAACGCCCTAC	0	572.8	1.89	657.4	0.35		
24	TTGCCGCACACACCCCT	0	545.0	13.97	604.2	3.53		
25	AATACCCCACGCCGCA	0	648.9	0.85				
26	AGCCGAACCGCGACGC	0	652.2	2.75	526.3	0.63		
27	AACGCCACGCCGCCGA	0	587.8	2.43	526.3	0.54		
28	ACATGACGCCGCCGAA	0	568.0	0.75	658.5	0.73		
29	CCCATCAACGCCCGCG	0	642.9	1.61	541.6	0.57		
30	CGCCGCGGGAGCGGCC	0	654.1	0.79				
31	TACGCCGCGGCCCT	0	530.4	3.85	634.9	3.64		
32	GGACACGCCGCCATTG	0	664.3	1.26	545.4	1.22		
33	CCGCCGACGCCCAA	0	653.0	1.35				
34	GGCCGCCGCGACATAA	0	615.8	1.84	672.3	0.84	619.3	0.21
35	CCACGCCGCCGCCGC	0	653.2	1.59	561.6	0.94		
36	TACGCCATAGCGGCAA	0	639.1	1.40	532.3	0.83		
37	GCCGCACACGCCGAAA	0	623.3	4.73				
38	CCTCACGCCGCCGCC	0	644.4	2.21	527.5	0.77		
39	TACATTAAAGCGGCC	0	530.6	0.79				
40	CGCCGCGGCCACGC	0	639.3	1.93	517.8	0.46		
41	TACGGCAACGCCGC	0	635.3	2.55	671.7	0.84	529.3	0.22
42	GCGCCCCACGCCACCC	0	647.0	1.38	758.5	0.36		
43	CGCCCAAAGGCCCAT	0	543.1	2.56	631.1	1.16		
44	GGACACGGGAGCGCCG	0	628.4	1.07	529.7	0.54		
45	GCCGCGCCGACGCCG	0	657.1	1.72				
46	CGGCCGCCGCCACGC	0	666.5	2.69	620.1	1.08	522.6	0.42
47	AGGCCGCCGATACAT	0	593.5	6.46				
48	CCGGGCAGCGGCCG	0	674.0	0.72	674.0	0.72		
49	CCGCCCATCACACCC	0						

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50	ACCGGCCGCGGCCAA	0			644.2	0.58		
51	CGCGGCCATTACGCC	0	638.7	1.50			622.1	0.21
52	GGGCCGACAGCCGCG	0	651.3	0.84				
53	TGCCGCGGCGTTACAC	0	656.8	1.06	597.6	0.23		
54	CGGGCGCCCCCACACC	0	648.2	2.03				
55	AAGCCGCATGCGCGA	0	658.4	0.89	536.5	0.42		
56	ACACAGCCCACGCGGA	0	629.8	2.93	531.2	0.55		
57	GCCGTTGCGCCGCTAC	0	561.2	2.20	701.3	1.15	640.2	0.72
58	ACCGGGCATCACCCCC	0	638.6	2.64	533.1	0.39		
59	CGCGGCCGCGGCCGAA	0	647.7	2.02				
60	GCCGTTGCGCCCTAC	0	621.9	0.24				
61	GCGGCGCGCCGCTACG	0	628.7	1.08	677.9	0.60		
62	GCCGGTGACGCGGCCG	0	648.8	0.93				
63	TCGCCGCGGACACCAC	0	658.1	2.49				
64	CCCTACGGCGCCGCC	0	694.8	3.63	509.0	0.85	594.0	0.77
65	AGCCGATAACGCCGCG	0	647.9	0.88	525.2	0.21		
66	GCGGCCGCGTTGCCCT	0	675.2	1.00	563.0	0.61		
67	TGAAACCCAGCCGCA	0	662.7	0.51				
68	CGGCCGACACCCCCC	0	663.7	3.16				
69	ACCCACGCGACCCCTT	0			688.8	0.43		
70	GCCGCCAACATACGCC	0	634.7	0.70				
71	GCGAACGGCACGCCA	0	648.8	1.21				
72	CGGCCGCGGGCTACAA	0	637.9	0.84				
73	GGGCCGACACGGCCG	0	658.2	1.92				
74	AAACCCATACGCCCA	0	647.3	2.31	673.1	1.67	633.1	1.08
75	CCGCGCACGCCGCC	0	667.2	1.02				
76	CGCCGCACACGCCGC	0	563.9	16.15	606.4	9.39		
77	AATACGCGCGGCCAA	0	697.2	0.56	555.1	0.32		
78	CGCCGCCTACCGCGAA	0	641.1	1.86				
79	GCCGCCAACACGGCG	0	638.2	1.27	627.7	0.51	678.6	0.26
80	GGGCCGCCCCACGCGG	0	676.7	4.20				
81	TCCGGGCCGCCGCC	0			647.8	1.52	692.5	0.45
82	GGCCGGCACGCCGCC	0	648.1	2.16				
83	CGGGCCGACGCCGCC	0	670.5	1.80				
84	GCGGCCGCGGAAGGCG	0	630.9	0.76				
85	ATACCGCATACGCCG	0	643.8	1.66				
86	ACGCCGCGAGCGATA	0	661.4	0.96	535.3	0.31		
87	AGGCCGCCCCACGCGA	0	658.0	1.20	623.6	0.98		
88	GGGCCGCGACACCCCC	0	660.0	5.04				
89	TTTCGCGACGCCGCG	0	670.0	1.55	521.9	0.40		
90	CCGCCGCACCCCCC	0	664.6	4.06			650.1	1.56
91	CGCGCATACGCC	0	627.7	2.80	744.4	0.44		
92	AGCGGACACCGCGCG	0	680.9	1.90	687.9	0.39		
93	GCGCGAAACACGCGG	0	656.7	3.26	627.8	1.27		
94	CCGCAAGCGGCCGGCG	0	565.0	0.84	642.5	0.37		
95	GGCCTGCGGGCGCC	0	663.6	4.27				
96	ATACGCCGACGCCA	0	543.6	2.34	655.4	0.98		
97	GCGGCCGGACGCCGA	0	651.0	0.75				
98	AGCCGCCGCCACCGA	0	631.6	4.65	528.8	1.31		
99	CGCGGCCGCCCTACTT	0	630.2	3.35	631.8	0.45	712.9	1.20
100	GGCCGGTACACCCCTAC	0	680.9	0.95	553.2	0.67		
101	AGGCCGCGGCCAATAA	0	555.7	1.15	653.8	0.42		
102	GCCGGGTCACGGCCT	0	664.7	1.66	685.0	1.12	645.0	1.02

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103	ATACCGCCGCCGGCCC	0	634.9	2.06	544.3	1.03		
104	GCGCGCGCCGCCCTAC	0	679.3	3.87	638.8	0.68	702.3	0.61
105	GGCATACGCGGAATG	0	635.1	2.61	534.7	0.56		
106	AGCGCCCCCACCGGGCC	0	622.6	2.17	608.6	1.02	669.1	0.94
107	TTGCGCGCCGCCGGCCC	0	690.3	1.53	653.4	0.73		
108	CGCGAACATCCGCCA	0	521.6	6.00	636.4	2.02		
109	CGCGCCCCATCACCC	0	634.9	0.83				
110	GCGCCCATAAAGGCG	0	660.2	1.10	519.3	0.31		
111	ACCGCGCCGCAAGCCG	0	647.3	1.82				
112	GGCCGACACGTACGGC	0	518.7	17.27	600.9	4.89		
113	CGCGCGCAGCGGCCGC	0	697.0	1.59	631.1	0.79	575.1	0.65
114	GCGCCGCATCCGGATT	0	671.6	1.99	530.3	0.26		
115	GCCGCTCGGGATAACGC	0	674.2	0.83				
116	AAGCGCGCGGCCGCCA	0	660.8	1.87				
117	GCGGGCCCCAAAGCCG	0	659.9	1.39	546.8	0.80		
118	ACACCGCCGCCAAAAA	0	655.2	0.79				
119	TGACCGCCGCCATCCC	0	641.8	5.08	547.5	0.88		
120	GGCCCGCGCTACGGCCC	0	648.6	2.33				
121	ACGCCACGCCAAAAAA	0	528.3	0.72	651.8	0.23		
122	CGCCCCCATCGGGCG	0	588.7	7.45	671.0	1.92	720.8	1.03
123	TCACGCGCCGCCGCG	0	640.8	1.94	527.8	0.28		
124	ATTGCGCCGCCGGCCCT	0	697.7	0.61				
125	CGGCCCACCGGGACAC	0	654.6	2.21				
126	TTTCGGGCCGCCGGCCC	0	684.0	0.73				
127	CGCGCCCATCACGCC	0	661.0	1.87				
128	GCGGCCCTGGCTAC	0	649.6	1.73				
129	GCCGCCACCCCCCCC	0	654.2	7.41	664.4	5.70	775.0	0.48
130	CGCCGGGTACGCGGC	0	647.8	1.39				
131	CACCGCCCCCCACCCCC	0	627.5	4.54				
132	TGGCGGCCACCGGGA	0	655.9	2.42	562.4	2.04		
133	ACCGCGCGGGAGTG	0	641.8	2.13				
134	CGCCGCGCCGTACGCG	0	710.1	2.08	673.8	1.54	621.9	0.59
135	GCCGCCACGCCCTAC	0	635.4	1.02				
136	GGGCGGCCACGCGCCG	0	687.7	2.13	691.7	1.26	639.1	0.99
137	ACGCGCGGCCACGCC	0	662.2	2.04	530.3	0.76		
138	CGCGCCAAACGCTAC	0	651.1	1.70	542.4	0.43		
139	AACGGCCGCCGGCCA	0	647.4	1.80	526.0	0.29		
140	CGCCCCCACGCGCGC	0	656.8	3.84	540.3	1.96		
141	AGTGGCCGCCGTACAC	0	653.7	1.11	516.0	0.20		
142	AACGGCGGCCGCCCTAC	0	636.5	0.77				
143	GCGGCACCCGCCGCG	0	628.8	0.69	535.9	0.26		
144	GCGCCACCCAAGGCCA	0			639.2	0.79	684.1	0.22
145	CGCCGCGCGACCCCCC	0	653.2	1.70				
146	TACACTTGCCGCCGCT	0			654.9	0.56	578.0	0.32
147	TCGCGCCGTACCGGT	0	505.1	3.70	659.3	1.57		
148	CGCCGCGCCGCCACCCC	0	630.6	2.23				
149	CGGCGGCACACGCGCC	0	647.6	2.12				
150	CCGCGCGCGCCCGCAA	0	721.8	2.36	579.0	0.49		
151	CGCGCGGCCGCCGCGG	0	709.0	1.98	661.6	1.59		
152	CCGGCCCACGACACC	0	656.9	0.87	515.9	0.44		
153	AAAGCCGTCACGGCCC	0	644.6	0.78				
154	AGCGGCCGCCGGCCCAA	0	629.3	2.37	505.7	0.24		
155	TTGCCGCCGCCGCCGGCC	0	672.6	1.97				

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156	GGCCGCCATGCGCCGG	0	646.4	0.44				
157	CGGCCGCGGCCGCGACC	0	643.1	2.91				
158	GCGCCGCGGCCGCGC	0	653.4	0.98				
159	GCGCGCGACGCCGCGC	0	719.6	3.25	708.3	1.44		
160	CGGCCGCGCCGCCGGGA	0	679.8	2.84	541.6	0.30	595.0	0.27
161	AGTGCGCGCCCGCGAA	0	656.4	3.08				
162	AGGCGCGGCCACCCGA	0	651.2	1.46				
163	CGCGGCGCGCTACGCC	0	673.3	1.59	519.4	0.26		
164	AAACCGCGCCGCCGC	0			637.9	0.88		
165	TTACGCGGGACGCCG	0	657.8	1.25				
166	CATACCCCTGGCGGCG	0	683.7	2.83	604.0	1.52	521.8	0.87
167	TTGCCGCCCATGGCCC	0	554.3	7.05	600.7	2.10		
168	AAGCCGCGCGGCCGCC	0			643.4	0.78		
169	TCGCCGCATGCCGCT	0	652.2	1.25	535.4	0.74		
170	TACCGCGCGGCCAAA	0	648.9	1.39	526.1	0.97		
171	CGGCCGACCCACATAA	0	579.3	6.79	679.4	0.41		
172	TGTACTCCGCCCGGT	0	648.7	1.77				
173	GGCCGGAGCGGCCGCG	0	670.1	1.19				
174	GCCCGGGAGCCGCCGG	0	618.6	2.74	717.3	0.87		
175	TCGCGGCCTTACTAC	0	614.7	1.55	547.3	0.39		
176	GCGCGCCCCATGCCGC	0			681.1	1.67		
177	CACCCCTGACCGCCGCG	0	655.1	4.12	612.1	3.86		
178	GCCCCACCGCATCACGC	0	589.0	7.37	688.6	0.43		
179	CCGCCGCGGCCGGACC	0	649.4	1.95				
180	CGGCCGTCGCGCGTT	0	672.3	0.68				
181	GCCGCCCCAGAACGCG	0	658.5	1.35	530.0	0.55		
182	CGCCGCATGCCGCCG	0	671.1	1.28				
183	TCGGCCGTACGCTGTT	0						
184	TACGGCCGCCGGCCGG	0	641.6	0.66				
185	TGATTTCACACGCCGC	0	577.5	0.51	660.1	0.34		
186	GCGCCCGTACACGCC	0	643.0	2.08				
187	AAAGGCCTACGCCGGCG	0	643.0	1.14				