SUPPLEMENTAL MATERIAL

Supplemental Figure S1. Nucleosome profiling in A. thaliana

(A) Electrophoresis on 2% agarose of the MNase-digested nucleosome genomic DNA (gDNA) sample. Mono- and di-nucleosomes are marked by * (~150 nt) and ** (~330 nt), respectively. Rep: biological replicate. COR+: 5 μM coronatine treatment for 1 hr. COR-: water treatment for 1 hr. (B) Electrophoresis of MNase-digested naked gDNA sample for 1.75 min (middle lane) and 3 min (right lane). The gel image is chopped since there are samples between ladder and naked gDNA. (C) Nucleosome occupancy around the transcription start site (TSS) and transcription termination site (TTS) for nucleosome gDNA (black line) and naked gDNA (gray line), respectively. The x-axis indicates the position relative to TSS or TTS. The y-axis shows the median nucleosome occupancy score (NOC) of all protein coding genes per base (see **Methods**). NDR: nucleosome-depleted region. +1: the first major nucleosome position after TSS. (D) Same as (C) except that NOCs were calculated by considering only the midpoints of regions covered by paired-end reads (see **Methods**).

Supplemental Figure S2. Nucleosome occupancy of example motif sites and background

(A) Nucleosome occupancy profiles around motif sites and background locations. Upper panel: the NOC (per base) profiles on G-box (CACGTG) and the shuffled motif (CTGCAG, with the same G/C content). Lower panel: the background NOC profiles of sites at the same positions relative to TSS as the G-box and the shuffled motifs but from randomly chosen genes (see **Methods**). Proximal: 500 bp upstream to TSS. Distal: 1.0 kb to 500 bp upstream of TSS. Blue lines indicate the median and gray areas indicate the 25th and 75th percentile NOC scores. (B) An illustration of how the normalized NOC scores on 6-mer motifs is determined.

Supplemental Figure S3. The anti-correlation between normalized NOC and DHSs for 6-mer motifs.

(A) The normalized NOC and DHS profiles for GGGCCG and TCTATA motifs. The x-axis represents the distance to motif sites located in proximal (proximal, 500 bp upstream to TSS) or distal promoters (1.0 kb to 500 bp upstream of TSS). NOC: nucleosome occupancy score. DHS: DNase I hypersensitivity score. (B) The relationship between median normalized NOC scores of all sites (y-axes) and NOC scores of sites passing different DHS thresholds (0.03, 0.02, and, 0.01, respectively, from left to right, x-axes) (n=4,096).

Supplemental Figure S4. Nucleosome occupancy profiles of 6-mer sites located in 5'UTR

The *A. thaliana* nucleosome occupancy around 6-mer motif sites located within 5' untranslated region (5'UTR) as described in **Fig. 4A** except 1 kb region centered on motif sites are shown here. The nucleosome depletion occurs immediately upstream of the motif sites, likely due to NFR, but not within the motif sites. Arrowhead: 6-mer motif position.

Supplemental Figure S5. Relationships between transcript abundance, nucleosome occupancy and DHS on two Type I motifs.

Supplemental Figure S6. PCC distances between motifs in the Type I, II, III sets.

PCC distances are used to generate dendrograms with the Unweighted Pair Group Method with Arithmetic Mean for (A) type I, (B) type II, and (C) type III motifs.

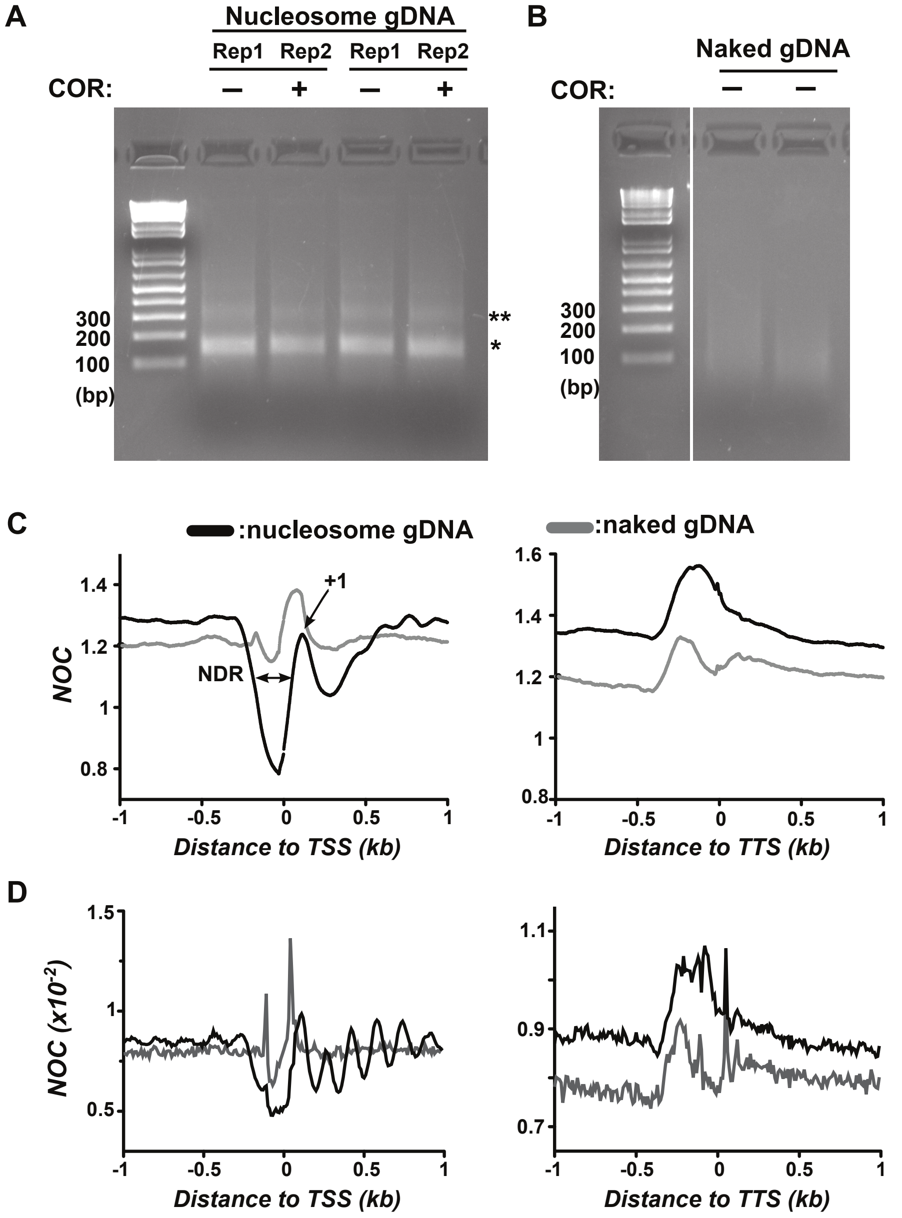
Supplemental Figure S7. Enrichment of in vivo TF binding sites overlapping with sites of Type I, II, and III motifs.

Pink: 6-mer motif where its sites tend to overlap significantly with ChIP peaks of a TF (Heyndrickx et al. 2014) (adjusted *p-value*<1E-04; see **Methods**).

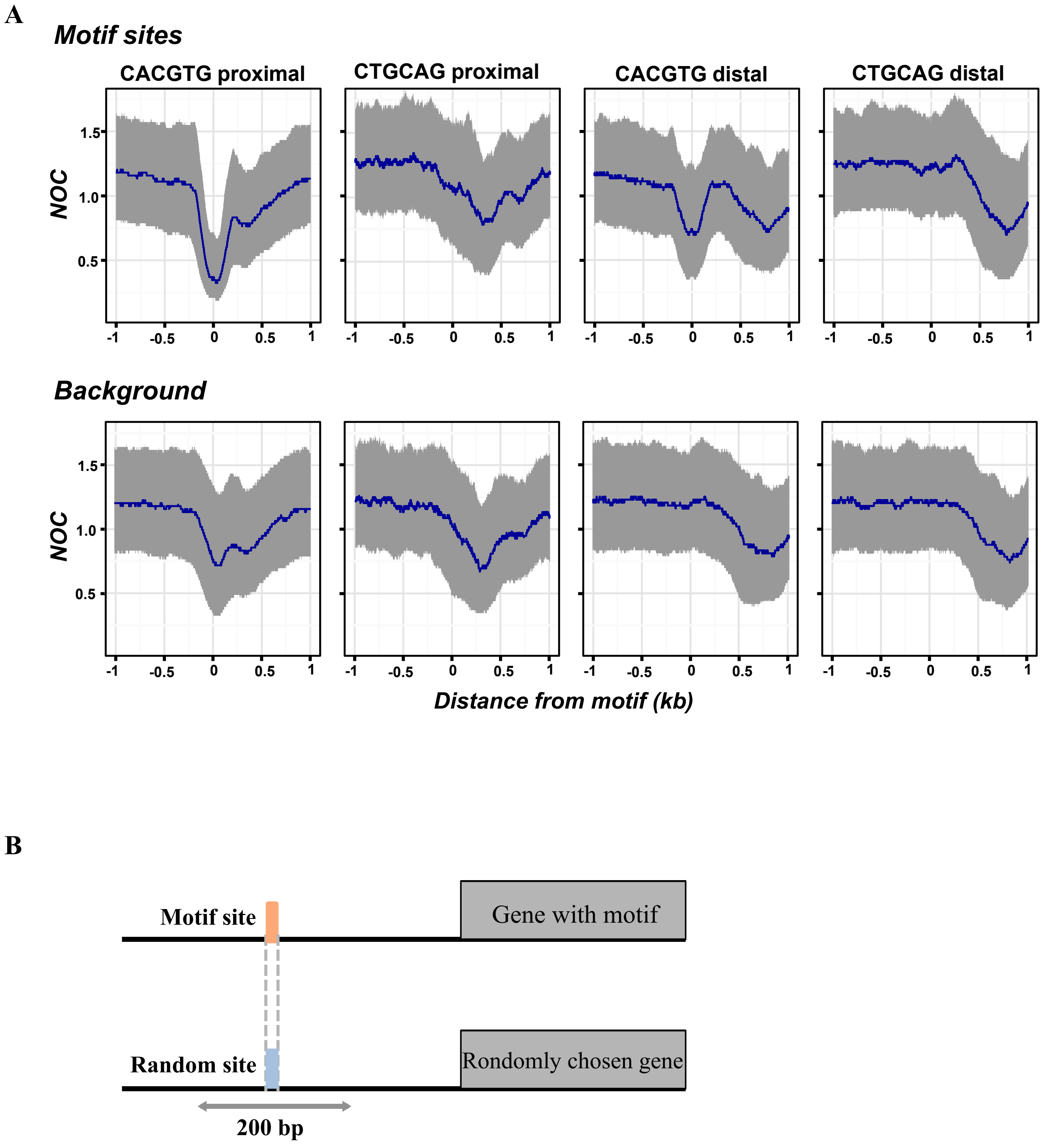
Supplemental Figure S8. Nucleosome occupancy and RNA expression for COR-induced genes

(A) The RNA expression changes of two known COR-induced genes *MYC2* and *JAZ10.1* (Lorenzo et al. 2004; Yan et al. 2007; Chung and Howe 2009). The 1-hr COR-treatment was chosen because *MYC2* and *JAZ10.1* were highly induced at 1-hr but not 30-min. The qRT-PCR results confirmed the RNA level induction detected by RNA-seq. (B) Comparison of transcript levels (Fragments Per Kilobase per Million fragments mapped, FPKM) between control and COR-treated samples for protein coding genes. Red: COR-induced genes (see **Methods**). (C) Differences in nucleosome occupancy between COR-treated and control samples. Y-axis: log ratio (base 2) of the average NOCs in the indicated regions between COR treatment and control. COR: coronatine. TSS and TTS: transcription start and transcription termination site.

Supplemental Figure S1

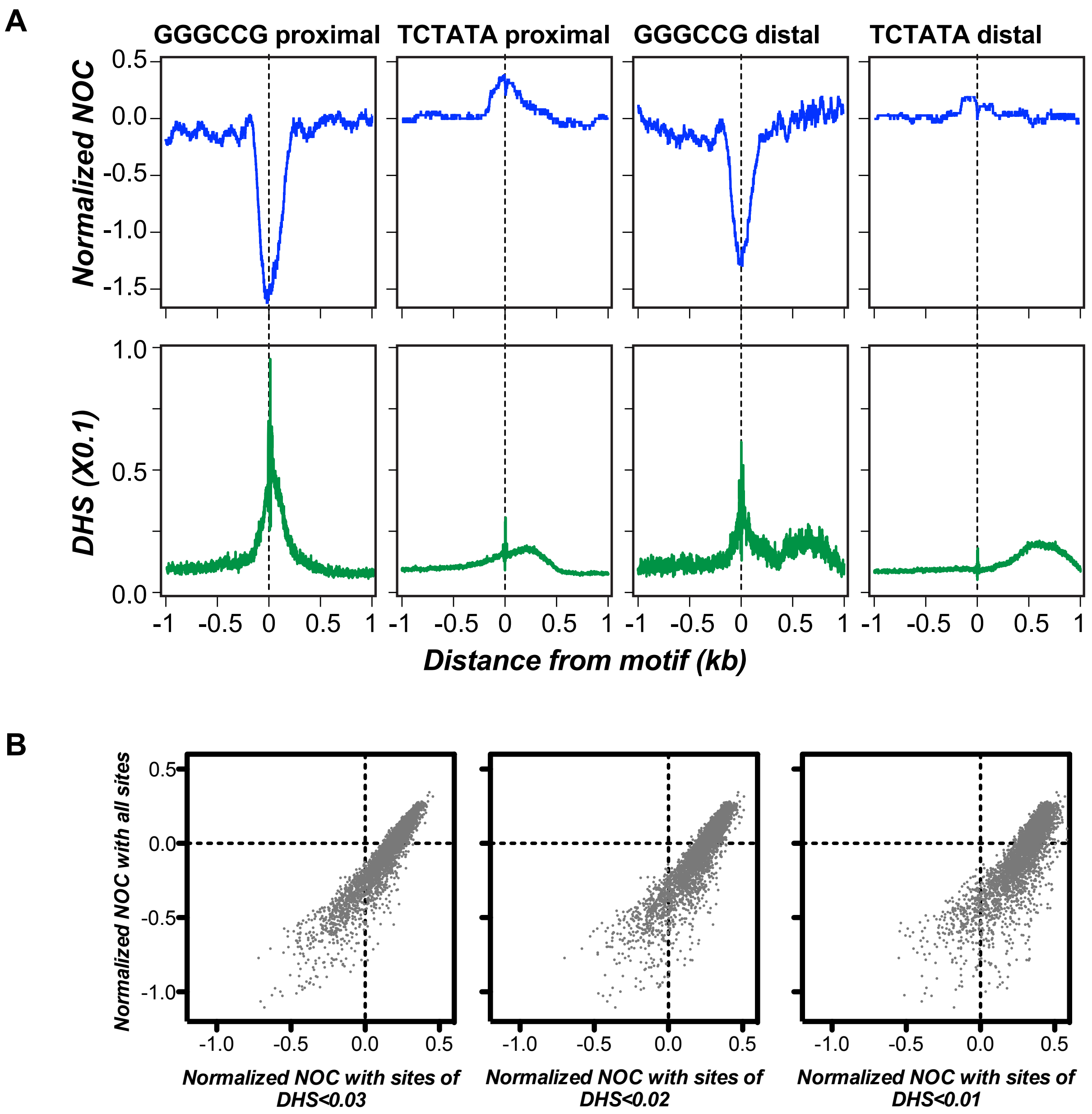


Supplemental Figure S2

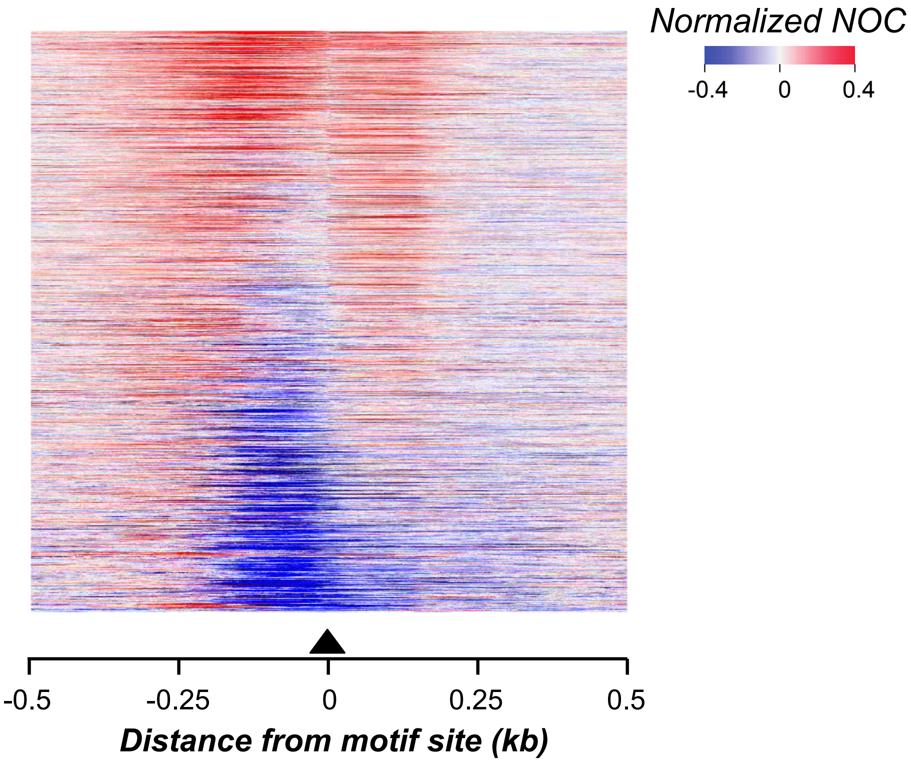


Regional nucleosome occupancy for each 6-mer site:
Log2 (nucleosome occupancy with a 200-bp region centered on motif site/
nucleosome occupancy with a 200-bp region on the same coordinates of a randomly chosen gene)

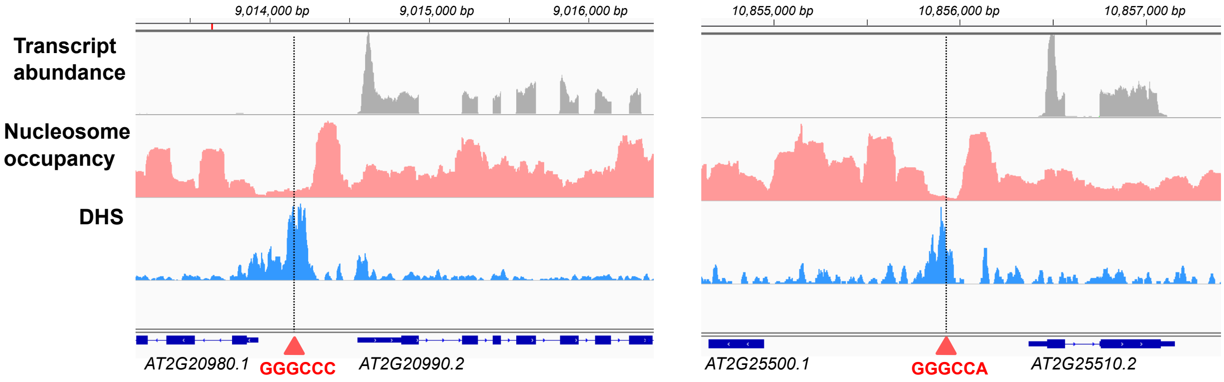
Supplemental Figure S3



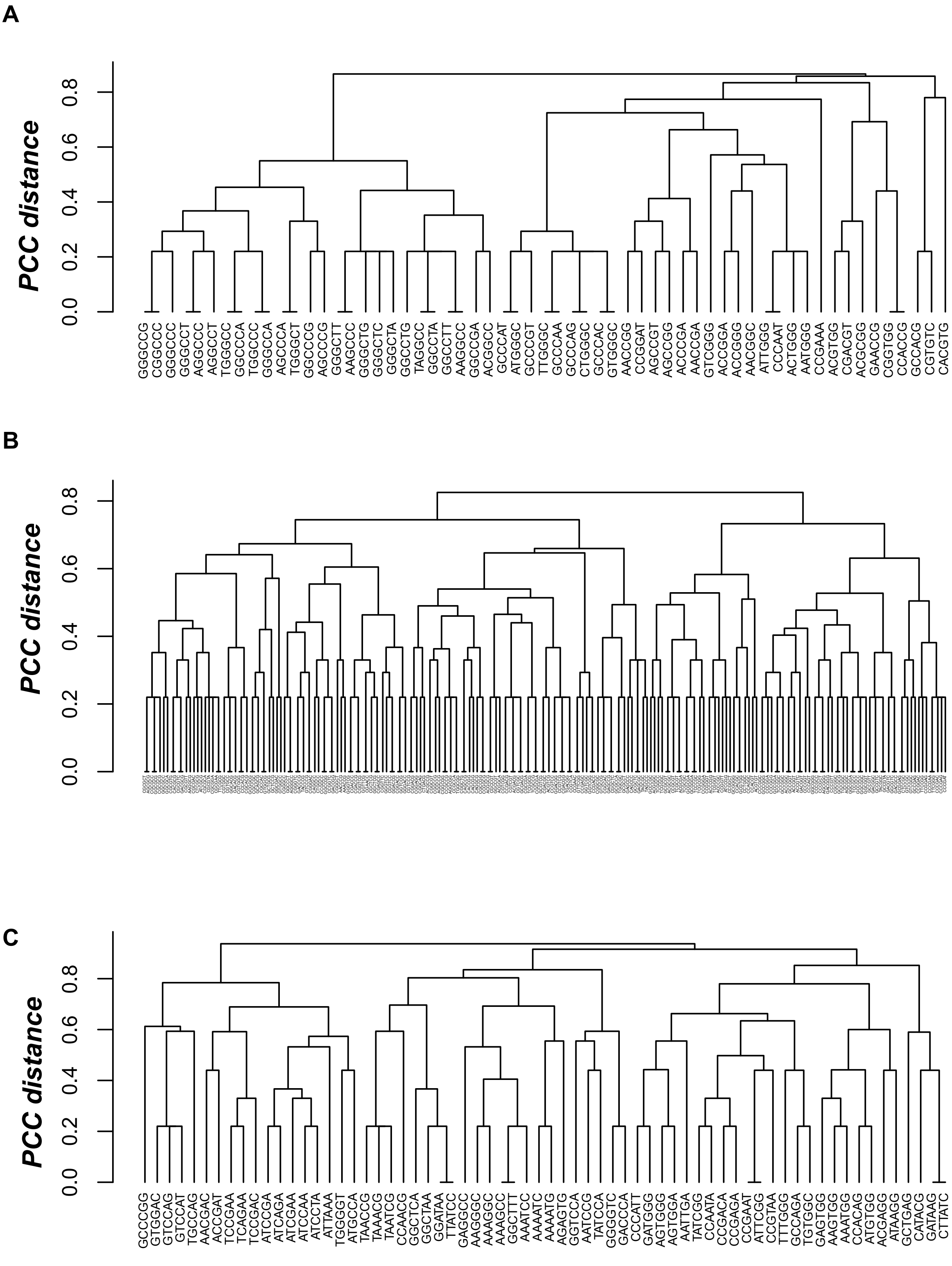
Supplemental Figure S4



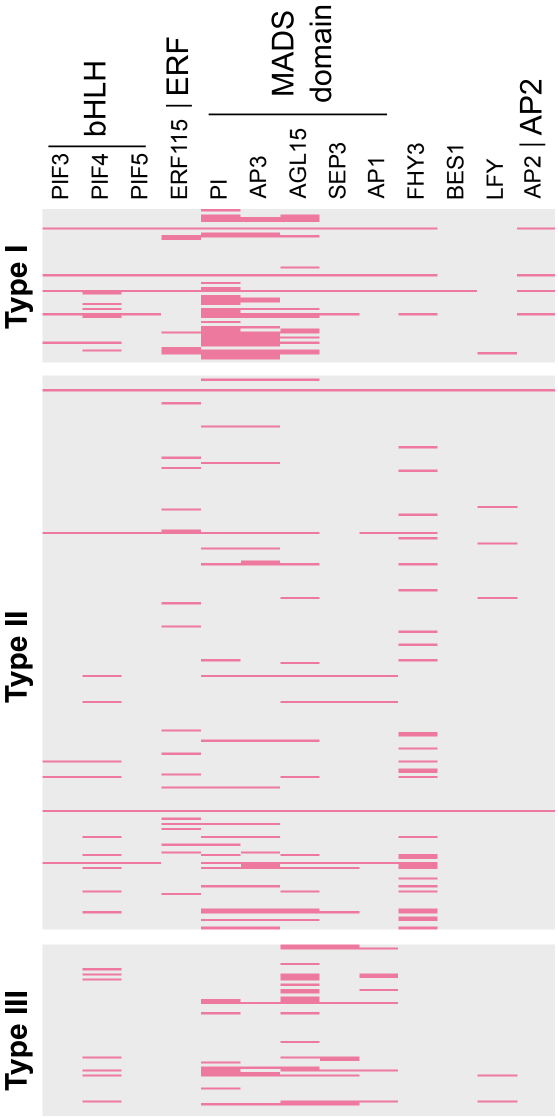
Supplemental Figure S5



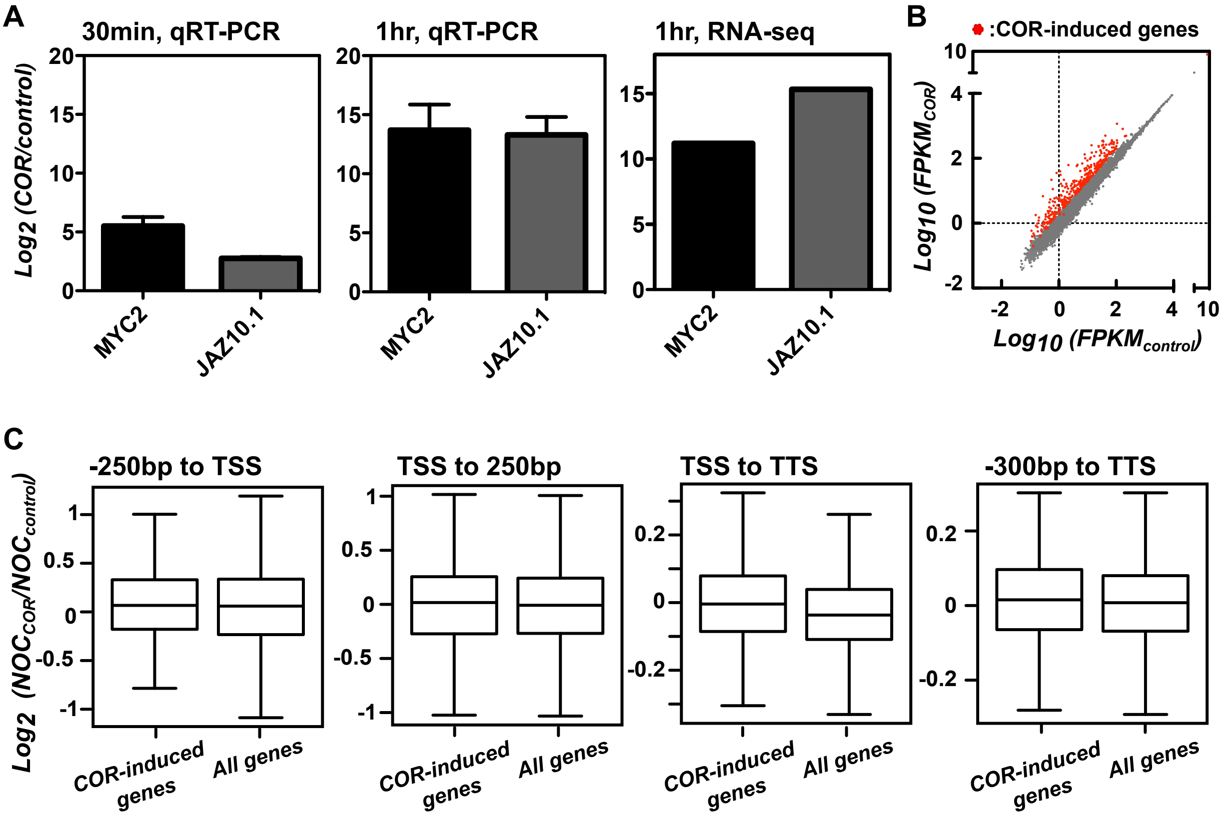
Supplemental Figure S6



Supplemental Figure S7



Supplemental Figure S8



Supplemental Table S1. Comparison of sequence-specific nucleosome occupancy amongst A. thaliana, rice and yeast

Region	***A. thaliana***		***A. thaliana* vs. rice**		***A. thaliana* vs. yeast**	
	ρ	***P-value***	**ρ**	***P-value***	**ρ**	***P-value***
Distal promoter	0.78	<2.2e-16	0.21	<2.2e-16	--	--
Proximal promoter	NA	NA	0.61	<2.2e-16	0.12	1.1E-13
5'UTR	0.77	<2.2e-16	0.64	<2.2e-16	--	--
CDS	0.88	<2.2e-16	0.71	<2.2e-16	-0.08	4.8E-07
Intron	0.76	<2.2e-16	0.43	<2.2e-16	--	--
3'UTR	0.76	<2.2e-16	0.43	<2.2e-16	--	--
TTS to +0.5kb	0.67	<2.2e-16	0.37	<2.2e-16	--	--

ρ: Spearman's rank correlation coefficient determined by comparing of the median normalized NOC values of 6-mer sites located within proximal promoter regions and the values of sites located in other genomic regions in *A. thaliana* or between species. Only proximal promoter and CDS regions in yeast are included for comparison (See **Methods**). NA: Not applicable.

Supplemental Table S2. Normalized NOC scores of Type I-III motifs as mentioned in Fig. 5. _*: 6-mer motifs with PCC distance <0.38 are clustered together._

Type I				Type II				Type III			
6-mer motif	**Normalized NOC score**	**-Log$_{10}$ (p-value)**	**Cluster***	**6-mer motif**	**Normalized NOC score**	**-Log$_{10}$ (p-value)**	**Cluster***	**6-mer motif**	**Normalized NOC score**	**-Log$_{10}$ (p-value)**	**Cluster***
GGGCCG	-1.21	66.97	1	CGCGCT	-1.07	31.71	1	GCCCGG	-0.71	6.54	1
GGGCCC	-1.18	70.76	1	GCCCGC	-1.02	10.80	2	TAACCG	-0.46	46.22	2
GGGCCT	-1.17	197.18	2	ACGGGC	-1.02	27.74	3	GAGGCC	-0.46	12.72	3
TGGGCC	-1.15	278.08	3	GCGCGT	-1.01	49.94	4	AAGGGC	-0.45	17.55	4
GGCCCA	-1.15	278.08	3	AGCGCG	-0.98	24.49	1	CCCATT	-0.45	64.65	5
CGGCCC	-1.14	72.33	1	CGGGCC	-0.96	27.52	5	GGTCCA	-0.45	28.80	6
AGGCCC	-1.09	217.38	2	ACGCGC	-0.93	40.19	4	AGTGGG	-0.45	22.81	7
GCCCAT	-1.02	278.08	4	CGCGTG	-0.93	40.26	6	AACGAC	-0.43	48.01	8
GGGCTT	-1.02	179.51	5	CAGGCC	-0.91	34.17	7	TATCGG	-0.42	16.75	9
AGCCCA	-1.00	248.92	3	CCGGCC	-0.90	26.32	5	CCGAAT	-0.42	39.06	10
TTGGGC	-1.00	228.95	6	CGGGCT	-0.90	18.61	1	AAAGCC	-0.41	55.74	11
GCCCAA	-0.98	259.07	6	CGTCCG	-0.86	23.60	8	TCCGAA	-0.41	29.25	12
TGGCCC	-0.98	87.05	1	TCGGCC	-0.86	34.74	9	GGGGTC	-0.40	8.76	13
TGGGCT	-0.98	237.06	3	GCGGCG	-0.85	33.42	10	TCCGAC	-0.38	16.92	14
GCCCAG	-0.97	44.49	6	CGCGTC	-0.85	29.17	6	ATTCGG	-0.37	25.53	10
AAGCCC	-0.96	185.21	5	GGCCGG	-0.84	27.54	5	CCAACG	-0.36	18.76	15
GGCCCG	-0.93	23.18	7	CGCGCC	-0.84	19.57	11	GGCTTT	-0.34	43.82	11
ATGGGC	-0.93	220.32	4	GCGGGG	-0.81	10.64	12	GACCCA	-0.34	18.54	13
GCCACG	-0.90	72.22	8	CCGGGT	-0.81	29.89	13	TTTGGG	-0.34	46.91	16
CTGGGC	-0.88	40.93	6	GGCGCG	-0.80	15.18	11	AATCCG	-0.32	22.14	17
GCCCAC	-0.84	56.67	6	GGCGCC	-0.80	16.40	11	AAAGGC	-0.32	28.04	4
GGCCTG	-0.84	29.02	9	CCCGGC	-0.79	11.27	14	CCGACA	-0.32	10.93	18
GTGGGC	-0.84	53.41	6	CGGGTC	-0.79	38.55	15	GTGGAC	-0.32	15.75	19
TAGGCC	-0.84	70.37	9	CACGCG	-0.78	48.21	6	GTCCAG	-0.31	9.37	19
GGCCTT	-0.82	79.76	9	CGCGCG	-0.78	15.74	16	GATGGG	-0.31	13.13	5
AAGGCC	-0.82	104.82	9	CGTGGC	-0.78	63.10	17	ATCCGA	-0.31	21.25	20
GGGCCA	-0.82	70.79	1	GACCCG	-0.77	44.17	15	CCGAGA	-0.30	13.52	18
CACGTG	-0.81	170.82	10	CGGCGC	-0.76	17.72	18	CCGTAA	-0.28	12.47	21
GGGCTG	-0.80	19.97	5	CGCCAC	-0.76	40.70	19	CCAATA	-0.26	29.37	9
AGCCCG	-0.76	17.80	7	ACGGCG	-0.76	49.33	20	GAGTGG	-0.26	8.80	22
GGCCTA	-0.74	65.72	9	TCGGGC	-0.75	15.14	9	ACGAGG	-0.25	8.79	23
AACCGG	-0.74	125.74	11	CCCGGT	-0.75	31.38	21	GGCTCA	-0.25	11.62	24
GCCCGT	-0.73	21.28	4	ACGCCG	-0.75	36.32	22	GCTGAG	-0.24	7.04	25
ACGTGG	-0.72	85.56	12	TCGCGC	-0.75	15.38	23	GGCTAA	-0.22	6.94	24
GGGCTC	-0.71	29.80	5	GGCCGT	-0.74	23.19	24	ACCGAT	-0.22	11.84	26
GGCCGA	-0.70	27.19	13	CCACGC	-0.74	28.39	25	TGCCAG	-0.22	2.58	27
ACGCGG	-0.68	18.90	14	GCGTCG	-0.73	23.24	26	GCCAGA	-0.21	5.73	28
GGGCTA	-0.67	37.84	5	CGGCTG	-0.73	21.08	27	TGGGGT	-0.18	7.83	29
GTCGGG	-0.67	18.39	15	CGCCGC	-0.72	28.19	10	TGTGGC	-0.18	3.01	28
ACGGCC	-0.66	24.77	13	CCTGGC	-0.72	11.84	28	AAGTGG	-0.18	9.10	30
CGACGT	-0.65	41.87	12	GCCGTT	-0.71	55.62	29	TAAACG	-0.17	14.16	2
GAACCG	-0.65	62.14	16	GGCGGG	-0.71	22.10	30	TAATCG	-0.16	8.74	2
ACCCGA	-0.61	43.91	17	CGGCGG	-0.71	40.21	31	ATCGAA	-0.16	11.81	31
ACCGGA	-0.61	62.53	18	CGTCGG	-0.71	31.78	32	AAATGG	-0.15	17.28	30
ACCGGG	-0.59	20.53	18	CGCGAC	-0.71	12.63	33	GGATAA	-0.14	6.07	32
CCGGAT	-0.58	30.48	11	CCACGT	-0.70	95.06	34	ATAAGG	-0.13	5.19	33
AGGCCT	-0.58	29.34	2	CGACGC	-0.70	20.83	26	CCACAG	-0.12	2.24	34
AGCCGT	-0.58	27.74	19	CCGGTT	-0.70	114.12	35	AAATCC	-0.10	7.92	11
AACGGC	-0.58	49.97	20	GGGTCG	-0.69	25.49	36	ATCCAA	-0.10	7.69	35
ATTGGG	-0.57	83.52	21	GTCCCG	-0.69	12.57	37	AGTGGA	-0.09	3.68	7
ACTGGG	-0.57	17.73	21	CGCGGC	-0.69	12.46	10	ATGCCA	-0.08	1.59	36
CGTGTC	-0.56	45.60	8	GAGCCC	-0.69	29.26	38	CATACG	-0.07	1.15	37
AACCGA	-0.56	103.65	17	CGCCGA	-0.69	27.37	39	TTATCC	-0.06	2.67	32
AGCCGG	-0.56	14.69	19	CGGCCG	-0.68	14.94	8	GTCCAT	-0.06	1.58	19
AATGGG	-0.54	90.11	21	CGCCGT	-0.68	41.83	20	TATCCA	-0.06	2.55	38
CCCAAT	-0.53	83.95	21	CGTGCC	-0.68	15.77	17	GATAAG	-0.03	0.68	39
CCGAAA	-0.52	61.02	22	CCGAAC	-0.68	56.85	40	ATGTGG	-0.03	0.87	34
CGGTGG	-0.51	25.63	23	CGGTTC	-0.68	63.72	41	ATCCTA	-0.02	0.47	35
CCACCG	-0.50	29.72	23	CGTGGG	-0.67	21.55	42	AAAATC	-0.02	2.69	40
				CCGCCG	-0.67	29.33	31	AATTGA	-0.01	0.56	41
				GCGCCA	-0.67	21.02	18	AGAGTG	0.02	0.32	42

TGGCGC	-0.67	21.87	18
CGACCC	-0.67	27.45	36
ACCGGC	-0.67	25.64	3
CCCACG	-0.66	31.78	42
CTGGCC	-0.66	14.28	5
GCCGGA	-0.66	32.67	43
ACGTCG	-0.66	46.56	26
CGGACC	-0.65	16.21	44
GCGCTC	-0.65	12.07	45
CAGCCC	-0.65	21.41	38
GCGCGA	-0.64	12.58	23
CCGTCC	-0.64	21.81	46
CCCGGA	-0.64	11.69	14
CGCGCA	-0.64	12.81	47
GACGCG	-0.64	15.35	6
TCGCCG	-0.64	39.80	22
GCGGGA	-0.64	24.40	23
TAGCGC	-0.63	10.50	48
CGCACG	-0.63	19.69	16
GTGCCG	-0.63	12.23	37
GAGCGC	-0.63	10.90	45
CCCGCT	-0.62	13.47	30
GGTTCG	-0.62	52.97	36
GGCCCT	-0.62	17.27	49
GGTCCG	-0.62	17.07	44
CCGAGC	-0.62	11.21	40
GGGACC	-0.62	21.33	50
GCCGGT	-0.62	26.91	3
CGACCG	-0.62	12.99	8
TCGCGG	-0.61	11.05	51
CAGGCG	-0.61	10.10	7
CGTCGT	-0.61	57.66	32
CGCTCG	-0.61	11.80	16
CCCGGG	-0.61	10.38	14
CCGACG	-0.61	28.35	32
GCCGGG	-0.61	13.21	14
GGGTCC	-0.61	23.69	52
GCCGCG	-0.61	12.04	10
CGGCGA	-0.60	43.43	22
TCCCGC	-0.60	21.35	23
CCGTCG	-0.60	31.59	26
CCGCGT	-0.60	14.56	4
CGCGTT	-0.60	19.72	53
CGCCGG	-0.60	27.71	39
GCGGAG	-0.60	18.54	12
AGCGGG	-0.60	11.61	30
CGGCGT	-0.59	25.71	22
GACGGC	-0.59	26.46	54
GCGCCT	-0.59	10.08	18
CCGGCG	-0.59	27.82	39
GGCGGA	-0.59	19.30	43
CCGGAC	-0.59	15.88	55
ACGACG	-0.59	54.12	32
TCGCGT	-0.59	15.38	4
GCCGGC	-0.59	19.41	56
CAGCCG	-0.59	17.46	27
TCCGGC	-0.59	23.19	43
CCCAGT	-0.58	19.14	57
GTTCGG	-0.58	40.82	40
GAGCCG	-0.58	17.73	41
GACGTC	-0.58	34.29	54
CGGCAG	-0.58	11.64	58
ACCCGG	-0.58	26.92	13
CCCGAA	-0.58	28.38	59
GCCGTC	-0.58	25.29	54
TCGGGT	-0.58	30.64	13
CGGTCC	-0.58	20.55	52
TCCGCC	-0.58	20.76	43
GTCCGC	-0.58	10.05	2

ATCAGA	0.02	0.72	20
TCAGAA	0.03	0.79	12
ATTAAA	0.03	3.10	43
AAAATG	0.03	1.50	40
CTTATC	0.04	0.47	39

CTCGCG	-0.58	10.87	33
CGTCGC	-0.57	22.91	32
CGAACC	-0.57	50.63	36
GGCGTC	-0.57	12.80	54
CCGGTC	-0.57	21.73	60
CGACGG	-0.57	34.87	26
TACCCG	-0.57	14.59	15
CCAGGC	-0.57	11.70	28
GACCGG	-0.57	21.11	60
TGACGG	-0.57	23.99	61
ACCGTC	-0.57	29.44	62
TAGCCC	-0.57	28.18	48
GGCGCA	-0.57	13.68	11
CACCGG	-0.56	25.10	63
CGGCAC	-0.56	13.25	37
AACCCG	-0.56	35.17	64
ACGGCA	-0.56	20.58	20
CGGAGG	-0.56	22.28	31
GGACCG	-0.56	22.79	52
TCGGCG	-0.56	22.70	39
CGCGTA	-0.56	15.35	47
CTCCGC	-0.56	17.75	12
GACACG	-0.56	42.21	17
GCCGCC	-0.56	18.42	56
CGGACG	-0.56	11.76	8
CGGCTC	-0.56	20.20	41
GGCACG	-0.55	12.07	17
GCTGCG	-0.55	10.42	65
GACGCC	-0.55	17.85	54
ATCGCG	-0.55	14.04	33
CCGGGA	-0.55	15.74	51
TACGGC	-0.55	12.03	29
ACCGGT	-0.55	62.80	21
GGCTCG	-0.55	14.27	36
AGGCGG	-0.55	16.39	66
CCCGAC	-0.55	15.12	59
CCCGCC	-0.55	15.49	30
CGGTCG	-0.54	15.83	8
GGTCGC	-0.54	10.79	50
CCCGAG	-0.54	14.72	59
AGGGCC	-0.54	12.56	49
GGCGAC	-0.54	16.17	67
CGCGGA	-0.54	12.20	47
TTCCGG	-0.54	35.16	55
GCAGCG	-0.54	12.67	10
ATCCGG	-0.54	27.47	35
ACGCGA	-0.54	15.43	4
GGCGGC	-0.54	17.46	56
GTCGGC	-0.53	18.89	68
GACGGT	-0.53	33.25	62
GGACGG	-0.53	13.76	46
TGCGGC	-0.53	10.27	69
GCTCCG	-0.53	15.28	65
CGCGAA	-0.53	15.17	47
CCCGAT	-0.53	12.89	59
GCGTGG	-0.53	17.27	25
AGGCCG	-0.52	12.52	66
ACCCGC	-0.52	12.47	13
GCCGTA	-0.52	13.87	29
TTCGCG	-0.52	15.34	47
CTGACG	-0.52	19.55	58
GCGACG	-0.52	22.65	32
GACGGG	-0.52	10.96	70
GTGGCG	-0.52	21.54	19
AAGGCG	-0.52	18.10	53
CGAGCC	-0.52	16.09	36
GGTCGG	-0.52	20.40	40
GTGGCC	-0.51	19.81	67
AGCGGC	-0.51	10.54	69

AAACCG	-0.51	113.03	64
TTCGGG	-0.51	20.71	59
GGCGGT	-0.51	14.54	24
CCGCCA	-0.51	24.61	61
TGGCGG	-0.51	22.30	61
CCGGAG	-0.51	26.39	55
CCGACC	-0.51	28.48	40
CCGGCT	-0.51	13.93	35
ACGTGT	-0.50	59.44	34
CAGCGG	-0.50	11.38	63
GCCGAG	-0.50	13.62	68
CGGGAC	-0.50	10.78	37
CCGTCA	-0.50	20.02	61
CCCGTT	-0.50	20.78	70

Supplemental Table S3. Nucleosome occupancy for 31 6-mer motifs enriched in COR-induced genes

Motif	Motif occurrence (%)[1]			Control[2]		COR[2]		COR vs. control
	COR-induced genes	All genes	*P-value*[3]	Normalized NOC	*P-value*[4]	Normalized NOC	*P-value*[4]	*P-value*[5]
GCACGT	8.2	3.3	1.5E-03	-0.23	1.0E-01	-0.58	1.0E-01	5.0E-01
ATACAT	32.8	23.7	7.5E-03	0.30	3.2E-05	0.28	1.2E-06	5.0E-01
GTACAC	12.6	5.7	2.4E-04	0.02	3.9E-01	0.00	4.1E-01	5.0E-01
ACGTGT	25.7	11.2	3.1E-11	-0.24	1.9E-01	-0.25	1.7E-01	5.0E-01
ACACGT	24.6	11.4	1.6E-09	-0.30	1.2E-02	-0.31	4.5E-02	5.0E-01
CACGTG	27.9	12.2	3.3E-12	-0.49	1.2E-05	-0.46	1.4E-04	5.0E-01
ACGTTT	22.7	13.4	3.0E-04	-0.08	4.9E-01	-0.02	4.4E-01	5.0E-01
CTATAT	37.7	22.4	2.5E-08	0.27	9.0E-03	0.32	3.6E-05	5.0E-01
TCTATA	33.6	21.9	8.2E-05	0.26	1.0E-02	0.32	1.4E-04	5.0E-01
ACATAA	38.8	27.3	3.3E-04	0.22	1.9E-02	0.30	2.2E-04	5.0E-01
CATATA	39.1	27.0	1.5E-04	0.20	5.3E-04	0.28	1.6E-06	5.0E-01
AAACGT	23.2	14.9	2.7E-03	-0.14	3.6E-01	-0.06	4.3E-01	5.0E-01
CGTGTG	12.0	5.1	7.0E-05	-0.05	4.9E-01	0.04	4.7E-01	5.0E-01
CACGTT	18.3	6.9	5.5E-10	-0.29	2.4E-01	-0.19	3.2E-01	5.0E-01
TATATA	65.0	46.5	9.9E-10	0.21	2.3E-07	0.31	2.8E-15	5.0E-01
AACGTG	22.1	7.4	6.6E-15	-0.14	4.3E-01	-0.04	5.0E-01	5.0E-01
CTCGTG	10.7	4.6	4.4E-04	-0.09	4.9E-01	0.02	4.9E-01	5.0E-01
TATAAA	65.3	50.0	1.6E-06	0.12	2.3E-02	0.22	1.4E-05	5.0E-01
ATATAA	57.4	45.4	6.6E-04	0.11	1.4E-02	0.22	8.6E-07	5.0E-01
ATAAAT	60.9	49.9	2.4E-03	0.06	1.8E-01	0.18	1.8E-03	5.0E-01
AACACG	16.4	8.5	2.7E-04	-0.35	1.5E-01	-0.23	3.0E-01	5.0E-01
TAAATA	58.2	45.6	3.0E-04	0.09	2.4E-01	0.21	2.2E-04	5.0E-01
CGTGTT	14.5	7.2	3.2E-04	-0.23	2.8E-01	-0.09	3.5E-01	5.0E-01
CTATAA	29.5	20.8	8.0E-03	0.19	4.8E-02	0.32	7.1E-03	5.0E-01
ATATAT	64.5	46.2	1.6E-09	0.14	4.0E-05	0.28	8.2E-13	5.0E-01
TATAGT	28.1	18.9	2.2E-03	0.21	2.7E-03	0.35	9.6E-04	5.0E-01
TAATAT	49.7	38.3	1.2E-03	0.08	1.0E-02	0.22	1.6E-06	5.0E-01
CCACGT	18.3	9.2	2.8E-05	-0.44	3.7E-02	-0.29	8.8E-02	5.0E-01
ACGTGG	15.8	8.6	1.2E-03	-0.54	1.8E-02	-0.36	5.8E-03	5.0E-01
ACACAT	28.7	19.1	1.2E-03	0.08	1.3E-01	0.29	1.0E-02	5.0E-01
ACGTGC	8.7	3.5	5.9E-04	-0.34	1.8E-01	-0.03	4.4E-01	5.0E-01

1. Motif occurrence is defined as the percentage of genes in the specified category (COR or all) with a particular motif.
2. COR: coronatine. Control: water-treated.
3. Multiple testing corrected *p*-value of one-tailed Fisher's exact test testing motif enrichment.
4. Multiple testing corrected *p*-value of Mann-Whitney test comparing the NOC scores between motif sites.
5. Multiple testing corrected *p*-values of Mann-Whitney tests comparing the NOC score distributions of motif sites between COR and control samples.

Supplemental Table S4. Summary of sequence mapping steps of nucleosome gDNA, naked gDNA and total RNA samples

Read processing and coverage	Biological replicates	Nucleosome gDNA		Naked gDNA	Total RNA	
		Control	COR	Control	Control	COR
Raw	Rep1	65,695,220	59,383,778	36,896,109	42,376,288	37,967,991
	Rep2	66,553,178	68,659,109		37,172,743	31,708,672
Quality-filtered	Rep1	64,559,815	58,114,258	36,243,664	42,258,986	37,877,552
	Rep2	65,759,890	67,432,786		37,076,671	31,647,268
Mapped	Rep1	45,141,036	40,323,706	25,929,703	37,132,426	33,490,924
	Rep2	44,824,610	46,075,949		32,5418,87	28,171,953
140-170 bp	Rep1	20,743,892	18,043,667	3,973,487	--	--
	Rep2	22,326,177	22,967,677		--	--
Sequencing coverage[1]	Rep1	56.83	50.40	32.41	--	--
	Rep2	56.03	57.59		--	--

[1] Sequencing coverage of nucleosome and naked gDNA of the *A. thaliana* genome (119,146,348 bp). The length of mapped paired-end fragments was assumed to be 150 bp.

Supplemental Table S5. Pearson's correlation coefficients of genome-wide nucleosome occupancy among nucleosome gDNA samples.

Sample	Control#rep1	Control#rep2	COR#rep1	COR#rep2	Naked gDNA
Control#rep1	--	--	--	--	--
Control#rep2	0.976	--	--	--	--
COR#rep1	0.965	0.971	--	--	--
COR#rep2	0.965	0.973	0.965	--	--
Naked gDNA	0.652	0.649	0.634	0.632	--

Supplemental Table S6. Variance inflation factors (VIFs) and regression coefficients of nucleosome and naked gDNA samples for linear regression model with 50 bp, 100 bp and 250 bp bin size.

Nucleosome gDNA, bin size= 50 bp			
Central position of bin	Gene end[1]	VIF	Regression coefficient
-975	5'	5.3	0.2
-925	5'	14.3	0.0
-875	5'	14.5	-0.1
-825	5'	15.9	0.1
-775	5'	21.3	-0.1
-725	5'	21.9	0.0
-675	5'	22.0	0.1
-625	5'	26.1	0.0
-575	5'	27.0	-0.1
-525	5'	27.0	0.1
-475	5'	32.0	0.1
-425	5'	33.7	-0.3
-375	5'	32.7	0.1
-325	5'	36.4	0.1
-275	5'	41.6	-0.3
-225	5'	41.0	0.3
-175	5'	39.1	0.1
-125	5'	35.0	-0.5
-75	5'	31.4	0.0
-25	5'	30.6	-0.1
25	5'	33.4	-0.9
75	5'	38.8	0.2
125	5'	43.9	0.3
175	5'	35.9	-0.3
225	5'	29.8	0.2
275	5'	33.0	0.0
325	5'	29.0	-0.2
375	5'	27.4	0.1
425	5'	33.8	-0.2
475	5'	30.5	0.1
525	5'	25.2	0.0
575	5'	30.2	-0.2
625	5'	28.1	0.2
675	5'	21.5	-0.1
725	5'	23.9	-0.1
775	5'	23.0	0.1
825	5'	15.4	-0.2
875	5'	14.3	0.0
925	5'	14.4	0.1
975	5'	5.3	-0.3
-975	3'	4.7	-0.2
-925	3'	12.3	0.1
-875	3'	13.6	0.0
-825	3'	15.1	-0.2
-775	3'	19.3	0.1
-725	3'	20.3	0.0
-675	3'	20.9	-0.1
-625	3'	24.0	0.1
-575	3'	24.5	0.0
-525	3'	25.1	-0.1
-475	3'	27.6	0.1
-425	3'	27.6	0.0
-375	3'	27.2	-0.2
-325	3'	30.1	0.1
-275	3'	33.7	0.1
-225	3'	36.1	-0.1
-175	3'	37.2	0.1
-125	3'	35.5	0.0
-75	3'	33.9	-0.1
-25	3'	34.6	0.0
25	3'	35.2	0.0
75	3'	35.7	0.0

125	3'	37.7	-0.2
175	3'	38.0	0.0
225	3'	35.8	0.0
275	3'	35.9	-0.1
325	3'	34.0	0.0
375	3'	32.1	0.0
425	3'	33.2	-0.1
475	3'	31.1	0.1
525	3'	28.5	0.0
575	3'	29.5	-0.1
625	3'	27.7	0.1
675	3'	23.0	0.0
725	3'	22.0	0.0
775	3'	21.1	0.0
825	3'	16.5	0.0
875	3'	15.2	0.0
925	3'	13.9	0.0
975	3'	5.0	0.0
Nucleosome gDNA, bin size=100 bp			
Central position of bin	Gene end[1]	VIF	Regression coefficient
-950	5'	1.7	0.0
-850	5'	2.6	0.0
-750	5'	2.7	0.0
-650	5'	2.7	0.0
-550	5'	2.6	-0.1
-450	5'	2.5	0.0
-350	5'	2.4	-0.1
-250	5'	2.4	0.1
-150	5'	2.8	-0.1
-50	5'	2.8	-0.6
50	5'	2.7	-0.5
150	5'	2.6	0.3
250	5'	2.6	-0.1
350	5'	3.1	-0.1
450	5'	2.8	0.0
550	5'	2.8	-0.1
650	5'	3.0	0.0
750	5'	2.7	-0.1
850	5'	2.7	-0.1
950	5'	1.9	-0.2
-950	3'	1.8	-0.1
-850	3'	2.6	-0.1
-750	3'	2.7	0.0
-650	3'	2.7	0.0
-550	3'	2.7	0.0
-450	3'	2.6	-0.1
-350	3'	2.5	-0.1
-250	3'	2.5	0.1
-150	3'	2.4	0.0
-50	3'	2.3	-0.1
50	3'	2.6	0.0
150	3'	2.8	-0.2
250	3'	2.8	0.0
350	3'	2.8	0.0
450	3'	2.7	0.0
550	3'	2.8	-0.1
650	3'	2.9	0.1
750	3'	2.8	0.0
850	3'	2.7	0.0
950	3'	1.8	0.0
Nucleosome gDNA, bin size=250 bp			
Central position of bin	Gene end[1]	VIF	Regression coefficient
-875	5'	1.2	0.0
-625	5'	1.3	0.0
-375	5'	1.3	0.1
-125	5'	1.2	-0.8
125	5'	1.3	-0.2

375	5'	1.5	-0.2
625	5'	1.6	-0.1
875	5'	1.4	-0.4
-875	3'	1.4	-0.3
-625	3'	1.5	0.0
-375	3'	1.4	0.0
-125	3'	1.3	0.0
125	3'	1.3	-0.3
375	3'	1.4	0.0
625	3'	1.4	0.0
875	3'	1.2	0.1
Naked gDNA, bin size=100 bp			
Central position of bin	Gene end[1]	VIF	Regression coefficient
-950	5'	1.2	0.0
-850	5'	1.5	0.0
-750	5'	1.6	0.0
-650	5'	1.6	0.0
-550	5'	1.6	0.0
-450	5'	1.6	0.0
-350	5'	1.6	0.0
-250	5'	1.5	0.0
-150	5'	1.6	0.0
-50	5'	1.6	-0.1
50	5'	1.6	0.0
150	5'	1.7	0.0
250	5'	1.7	0.0
350	5'	1.7	0.0
450	5'	1.7	0.0
550	5'	1.7	0.0
650	5'	1.7	0.1
750	5'	1.6	0.0
850	5'	1.6	0.0
950	5'	1.3	0.0
-950	3'	1.3	0.0
-850	3'	1.6	0.0
-750	3'	1.6	0.0
-650	3'	1.6	0.0
-550	3'	1.6	0.0
-450	3'	1.6	0.0
-350	3'	1.6	0.0
-250	3'	1.6	0.1
-150	3'	1.6	0.0
-50	3'	1.5	-0.1
50	3'	1.5	0.1
150	3'	1.6	0.0
250	3'	1.6	0.0
350	3'	1.6	0.0
450	3'	1.6	0.0
550	3'	1.6	0.0
650	3'	1.6	0.0
750	3'	1.6	0.0
850	3'	1.5	0.0
950	3'	1.2	0.0

1. The positions of the 5' and 3’ bins are relative to the transcription start sites and the transcription termination site.

Supplemental Table S7. Parameter combinations of the support vector machine method for predicting gene expression.

Parameter	Description	Values
C	Soft margin of the SVM	$(2^{-5},2\text{-}3, \ldots,1,2^{1},2^{3, \ldots}2^{15)}$
Gamma	The parameter of the RBF kernel	$(2^{-15},2^{-13}, \ldots,1,2^{1},2^{3)}$
M	Maximum class distribution spread as implemented in weka.filters.supervised.instance.SpreadSubsample	(0.2, 0.4, 0.8, 1, 2, 4, 8, 10)

Supplemental Table S8. The adjusted p-values from bootstrap analyses that tested whether the in vitro binding affinity of a given 6-mer to TFs (Weirauch et al., 2014)

Type	Motif	AT hook	B3	C2H2 ZF	CG-1	CSD	CxC	Dof	E2F	EIN3	ERF	GATA	GRAS	Homeodomain	LOB	MADF	Myb /SANT	NAC /NAM	RAV	SBP	Sox	Storekeeper	TCP	WRC	WRKY	bHLH	bZIP
I	GGGCCG	0.925	0.946	0.874	0.499	0.935	0.568	0.958	0.978	0.788	0.008	0.246	0.974	0.781	0.121	0.972	0.279	0.807	0.946	0.154	0.960	0.007	0.016	0.902	0.584	0.254	0.691
I	GGGCCC	0.973	0.825	0.649	0.145	0.966	0.941	0.760	0.967	0.755	0.037	0.446	0.957	0.855	0.128	0.887	0.050	0.954	0.968	0.775	0.947	0.001	0.000	0.952	0.522	0.280	0.729
I	GGGCCT	0.936	0.966	0.785	0.549	0.959	0.691	0.520	0.976	0.956	0.141	0.811	0.962	0.816	0.826	0.964	0.119	0.961	0.951	0.867	0.862	0.026	0.030	0.815	0.690	0.218	0.856
I	TGGGCC	0.873	0.833	0.490	0.604	0.848	0.828	0.774	0.938	0.852	0.024	0.609	0.964	0.663	0.218	0.720	0.240	0.864	0.442	0.289	0.820	0.015	0.000	0.611	0.449	0.116	0.282
I	GGCCCA	0.942	0.935	0.360	0.141	0.935	0.743	0.662	0.949	0.937	0.015	0.500	0.940	0.828	0.236	0.840	0.615	0.903	0.620	0.606	0.789	0.010	0.002	0.910	0.572	0.151	0.394
I	CGGCCC	0.959	0.961	0.823	0.238	0.978	0.574	0.893	0.966	0.846	0.007	0.280	0.903	0.481	0.051	0.946	0.287	0.887	0.913	0.102	0.953	0.009	0.008	0.941	0.085	0.233	0.379
I	AGGCCC	0.955	0.978	0.766	0.455	0.958	0.859	0.873	0.986	0.956	0.069	0.884	0.971	0.813	0.892	0.985	0.532	0.978	0.976	0.957	0.878	0.023	0.017	0.823	0.737	0.555	0.916
I	GCCCAT	0.527	0.736	0.710	0.358	0.834	0.564	0.373	0.812	0.740	0.028	0.229	0.804	0.194	0.178	0.573	0.235	0.684	0.565	0.614	0.565	0.055	0.021	0.884	0.508	0.024	0.485
I	GGGCTT	0.828	0.755	0.332	0.628	0.819	0.369	0.628	0.963	0.875	0.305	0.476	0.869	0.744	0.285	0.371	0.018	0.711	0.881	0.577	0.707	0.179	0.505	0.953	0.592	0.214	0.342
I	AGCCCA	0.773	0.664	0.181	0.587	0.856	0.636	0.600	0.891	0.866	0.037	0.614	0.740	0.286	0.688	0.677	0.413	0.792	0.760	0.753	0.763	0.071	0.089	0.639	0.622	0.208	0.336
I	TTGGGC	0.645	0.606	0.571	0.651	0.668	0.168	0.411	0.487	0.422	0.042	0.254	0.335	0.225	0.505	0.315	0.114	0.597	0.579	0.434	0.785	0.022	0.047	0.835	0.346	0.159	0.391
I	GCCCAA	0.612	0.548	0.428	0.684	0.730	0.241	0.149	0.653	0.589	0.019	0.457	0.349	0.139	0.323	0.665	0.115	0.479	0.623	0.434	0.671	0.042	0.053	0.897	0.426	0.236	0.314
I	TGGCCC	0.901	0.812	0.558	0.521	0.896	0.699	0.743	0.925	0.825	0.036	0.426	0.838	0.605	0.648	0.752	0.321	0.641	0.444	0.362	0.747	0.017	0.001	0.731	0.605	0.049	0.176
I	TGGGCT	0.544	0.553	0.122	0.733	0.856	0.462	0.202	0.762	0.446	0.033	0.083	0.838	0.014	0.938	0.315	0.246	0.259	0.485	0.749	0.434	0.086	0.050	0.682	0.361	0.114	0.047
I	GCCCAG	0.917	0.877	0.272	0.673	0.896	0.635	0.597	0.801	0.863	0.009	0.229	0.909	0.587	0.729	0.677	0.236	0.662	0.508	0.269	0.864	0.045	0.023	0.172	0.591	0.230	0.297
I	AAGCCC	0.924	0.923	0.410	0.677	0.923	0.282	0.449	0.940	0.967	0.224	0.893	0.957	0.793	0.620	0.861	0.152	0.911	0.927	0.875	0.830	0.165	0.388	0.872	0.302	0.204	0.726
I	GGCCCG	0.960	0.931	0.622	0.210	0.895	0.647	0.881	0.972	0.767	0.020	0.130	0.840	0.778	0.065	0.973	0.395	0.894	0.894	0.370	0.851	0.005	0.008	0.868	0.273	0.063	0.419
I	ATGGGC	0.578	0.807	0.638	0.651	0.865	0.574	0.696	0.765	0.563	0.020	0.414	0.750	0.527	0.381	0.657	0.402	0.621	0.403	0.626	0.688	0.033	0.044	0.938	0.510	0.122	0.328
I	GCCACG	0.877	0.778	0.679	0.031	0.916	0.766	0.482	0.851	0.717	0.016	0.594	0.820	0.718	0.228	0.785	0.098	0.202	0.681	0.383	0.888	0.051	0.061	0.951	0.336	0.010	0.002
I	CTGGGC	0.897	0.857	0.131	0.670	0.893	0.573	0.730	0.826	0.598	0.034	0.511	0.876	0.465	0.683	0.742	0.359	0.796	0.503	0.417	0.901	0.049	0.048	0.168	0.590	0.173	0.408
I	GCCCAC	0.836	0.659	0.115	0.139	0.939	0.598	0.357	0.827	0.612	0.005	0.151	0.437	0.042	0.625	0.532	0.162	0.492	0.300	0.302	0.786	0.050	0.003	0.721	0.387	0.041	0.093
I	GGCCTG	0.921	0.924	0.682	0.650	0.962	0.218	0.688	0.943	0.746	0.047	0.102	0.872	0.190	0.992	0.911	0.369	0.769	0.847	0.593	0.816	0.003	0.242	0.021	0.201	0.255	0.768
I	GTGGGC	0.782	0.741	0.075	0.228	0.929	0.598	0.578	0.667	0.649	0.007	0.122	0.483	0.042	0.554	0.600	0.088	0.446	0.289	0.219	0.809	0.050	0.003	0.707	0.287	0.028	0.052
I	TAGGCC	0.605	0.804	0.380	0.540	0.772	0.713	0.740	0.826	0.623	0.085	0.574	0.775	0.666	0.853	0.419	0.150	0.706	0.681	0.493	0.617	0.010	0.145	0.799	0.684	0.285	0.310
I	GGCCTT	0.489	0.777	0.513	0.912	0.632	0.534	0.543	0.892	0.879	0.124	0.609	0.771	0.317	0.895	0.864	0.182	0.702	0.837	0.546	0.448	0.017	0.335	0.405	0.127	0.152	0.567
I	AAGGCC	0.840	0.892	0.735	0.636	0.805	0.550	0.308	0.945	0.938	0.131	0.481	0.878	0.691	0.788	0.961	0.343	0.895	0.922	0.708	0.665	0.017	0.325	0.578	0.729	0.168	0.745
I	GGGCCA	0.716	0.936	0.386	0.561	0.915	0.642	0.761	0.931	0.895	0.045	0.349	0.743	0.435	0.549	0.714	0.136	0.663	0.649	0.595	0.763	0.015	0.003	0.627	0.731	0.041	0.118
I	CACGTG	0.482	0.371	0.465	0.013	0.761	0.363	0.343	0.627	0.073	0.118	0.281	0.226	0.097	0.290	0.350	0.054	0.152	0.528	0.207	0.118	0.107	0.052	0.727	0.173	0.000	0.000
I	GGGCTG	0.828	0.867	0.429	0.665	0.862	0.489	0.426	0.936	0.665	0.038	0.406	0.816	0.526	0.758	0.731	0.059	0.784	0.821	0.470	0.734	0.094	0.082	0.590	0.166	0.152	0.194
I	AGCCCG	0.841	0.839	0.335	0.426	0.859	0.697	0.643	0.656	0.467	0.048	0.360	0.688	0.597	0.031	0.769	0.384	0.777	0.856	0.492	0.799	0.058	0.218	0.813	0.585	0.111	0.519
I	GGCCTA	0.787	0.771	0.564	0.492	0.810	0.745	0.505	0.841	0.896	0.063	0.564	0.627	0.745	0.543	0.714	0.020	0.810	0.812	0.545	0.660	0.008	0.360	0.707	0.495	0.330	0.562
I	AACCGG	0.447	0.407	0.438	0.187	0.818	0.214	0.469	0.750	0.303	0.040	0.147	0.690	0.040	0.017	0.016	0.014	0.389	0.619	0.323	0.591	0.012	0.085	0.896	0.176	0.146	0.246
I	GCCCGT	0.559	0.294	0.797	0.235	0.652	0.251	0.149	0.543	0.241	0.018	0.099	0.230	0.060	0.063	0.149	0.111	0.302	0.561	0.023	0.691	0.029	0.018	0.257	0.184	0.034	0.116
I	ACGTGG	0.605	0.564	0.750	0.038	0.733	0.534	0.127	0.662	0.389	0.083	0.354	0.428	0.156	0.302	0.363	0.144	0.136	0.366	0.337	0.445	0.141	0.021	0.831	0.107	0.000	0.000
I	GGGCTC	0.975	0.976	0.584	0.444	0.931	0.766	0.645	0.977	0.955	0.186	0.721	0.956	0.619	0.177	0.721	0.020	0.928	0.926	0.449	0.949	0.087	0.147	0.977	0.826	0.638	0.782
I	GGCCGA	0.733	0.153	0.606	0.331	0.802	0.299	0.579	0.890	0.304	0.004	0.207	0.483	0.414	0.153	0.742	0.074	0.733	0.669	0.376	0.763	0.002	0.218	0.752	0.491	0.351	0.284
I	ACGCGG	0.717	0.635	0.687	0.000	0.920	0.220	0.195	0.027	0.223	0.046	0.319	0.529	0.416	0.006	0.484	0.248	0.420	0.688	0.320	0.725	0.063	0.475	0.874	0.065	0.031	0.046
I	GGGCTA	0.520	0.848	0.292	0.676	0.753	0.498	0.433	0.769	0.505	0.120	0.121	0.654	0.086	0.583	0.199	0.087	0.533	0.659	0.526	0.616	0.137	0.049	0.876	0.724	0.257	0.152
I	GTCGGG	0.715	0.465	0.407	0.203	0.787	0.443	0.497	0.873	0.355	0.020	0.240	0.919	0.129	0.213	0.337	0.205	0.236	0.658	0.177	0.715	0.063	0.095	0.904	0.093	0.227	0.218
I	ACGGCC	0.846	0.850	0.818	0.277	0.816	0.652	0.265	0.865	0.763	0.010	0.542	0.508	0.499	0.274	0.721	0.070	0.669	0.871	0.023	0.672	0.001	0.074	0.781	0.275	0.114	0.390
I	CGACGT	0.490	0.436	0.702	0.021	0.554	0.420	0.246	0.384	0.269	0.005	0.171	0.352	0.008	0.544	0.384	0.120	0.052	0.419	0.033	0.323	0.008	0.528	0.515	0.071	0.045	0.012

I	GAACCG	0.767	0.569	0.309	0.180	0.813	0.229	0.612	0.565	0.060	0.014	0.181	0.793	0.030	0.026	0.098	0.028	0.381	0.506	0.088	0.661	0.075	0.216	0.145	0.149	0.152	0.293
I	ACCCGA	0.674	0.203	0.395	0.144	0.731	0.342	0.308	0.591	0.202	0.214	0.148	0.289	0.119	0.122	0.017	0.017	0.221	0.602	0.288	0.699	0.074	0.068	0.809	0.134	0.333	0.210
I	ACCGGA	0.510	0.442	0.477	0.051	0.795	0.615	0.591	0.756	0.382	0.068	0.140	0.719	0.103	0.006	0.064	0.019	0.096	0.484	0.070	0.619	0.001	0.134	0.890	0.052	0.405	0.340
I	ACCGGG	0.740	0.460	0.649	0.107	0.983	0.501	0.755	0.795	0.251	0.151	0.531	0.828	0.238	0.010	0.053	0.086	0.131	0.759	0.382	0.810	0.029	0.032	0.956	0.104	0.121	0.305
I	CCGGAT	0.332	0.597	0.368	0.045	0.785	0.377	0.428	0.695	0.222	0.141	0.022	0.592	0.282	0.012	0.415	0.004	0.326	0.416	0.089	0.401	0.019	0.056	0.845	0.131	0.091	0.162
I	AGGCCT	0.897	0.851	0.531	0.656	0.770	0.517	0.638	0.917	0.819	0.117	0.416	0.753	0.669	0.988	0.850	0.301	0.901	0.834	0.681	0.505	0.020	0.304	0.090	0.774	0.428	0.757
I	AGCCGT	0.689	0.735	0.484	0.336	0.745	0.567	0.525	0.841	0.733	0.008	0.609	0.602	0.130	0.092	0.682	0.160	0.042	0.629	0.026	0.495	0.036	0.250	0.550	0.198	0.207	0.422
I	AACGGC	0.597	0.370	0.552	0.422	0.587	0.290	0.035	0.347	0.563	0.009	0.514	0.276	0.339	0.057	0.200	0.003	0.221	0.383	0.110	0.435	0.032	0.145	0.690	0.146	0.085	0.219
I	ATTGGG	0.199	0.365	0.679	0.611	0.545	0.121	0.275	0.584	0.093	0.122	0.125	0.074	0.060	0.170	0.312	0.090	0.288	0.402	0.342	0.456	0.086	0.036	0.732	0.174	0.135	0.048
I	ACTGGG	0.669	0.569	0.036	0.524	0.875	0.411	0.394	0.862	0.327	0.243	0.254	0.894	0.268	0.928	0.119	0.412	0.437	0.375	0.549	0.702	0.182	0.034	0.344	0.218	0.280	0.179
I	CGTGTC	0.572	0.023	0.373	0.004	0.457	0.263	0.221	0.398	0.196	0.087	0.190	0.450	0.028	0.171	0.293	0.118	0.010	0.414	0.134	0.311	0.061	0.200	0.511	0.130	0.002	0.001
I	AACCGA	0.324	0.068	0.178	0.054	0.418	0.129	0.261	0.213	0.322	0.007	0.212	0.224	0.038	0.100	0.044	0.005	0.197	0.224	0.387	0.490	0.047	0.103	0.244	0.203	0.144	0.195
I	AGCCGG	0.824	0.732	0.572	0.516	0.924	0.696	0.561	0.914	0.739	0.008	0.616	0.823	0.534	0.062	0.807	0.298	0.716	0.902	0.446	0.819	0.016	0.290	0.890	0.205	0.154	0.546
I	AATGGG	0.178	0.395	0.693	0.732	0.707	0.228	0.556	0.703	0.086	0.072	0.333	0.528	0.241	0.378	0.695	0.263	0.326	0.385	0.492	0.541	0.147	0.030	0.754	0.190	0.089	0.169
I	CCCAAT	0.281	0.413	0.387	0.514	0.552	0.298	0.357	0.390	0.118	0.026	0.099	0.198	0.023	0.259	0.251	0.064	0.296	0.398	0.331	0.398	0.095	0.040	0.670	0.214	0.032	0.050
I	CCGAAA	0.121	0.250	0.369	0.211	0.321	0.100	0.051	0.483	0.168	0.023	0.301	0.028	0.366	0.099	0.583	0.039	0.448	0.445	0.415	0.534	0.134	0.378	0.730	0.347	0.104	0.213
I	CGGTGG	0.405	0.367	0.383	0.164	0.867	0.505	0.233	0.717	0.250	0.002	0.208	0.672	0.159	0.059	0.136	0.052	0.139	0.412	0.052	0.757	0.034	0.016	0.899	0.095	0.020	0.020
I	CCACCG	0.717	0.233	0.304	0.212	0.919	0.728	0.544	0.766	0.228	0.001	0.241	0.369	0.148	0.068	0.155	0.028	0.253	0.728	0.083	0.523	0.041	0.031	0.605	0.106	0.028	0.031
II	CGCGCT	0.356	0.266	0.187	0.008	0.698	0.604	0.192	0.003	0.347	0.027	0.188	0.311	0.199	0.012	0.139	0.008	0.343	0.594	0.196	0.491	0.080	0.319	0.701	0.063	0.039	0.057
II	GCCCGC	0.889	0.871	0.400	0.212	0.977	0.772	0.546	0.369	0.381	0.002	0.551	0.689	0.461	0.028	0.947	0.250	0.913	0.741	0.386	0.873	0.007	0.047	0.816	0.458	0.064	0.404
II	ACGGGC	0.598	0.665	0.678	0.321	0.843	0.629	0.417	0.853	0.498	0.032	0.479	0.670	0.296	0.072	0.456	0.146	0.566	0.694	0.039	0.652	0.032	0.108	0.272	0.163	0.029	0.099
II	GCGCGT	0.439	0.119	0.413	0.002	0.454	0.264	0.055	0.002	0.122	0.018	0.228	0.478	0.164	0.017	0.117	0.035	0.245	0.424	0.041	0.505	0.049	0.063	0.658	0.067	0.005	0.011
II	AGCGCG	0.397	0.376	0.222	0.012	0.503	0.575	0.286	0.004	0.414	0.028	0.129	0.391	0.163	0.011	0.184	0.015	0.338	0.629	0.160	0.673	0.108	0.329	0.218	0.046	0.037	0.063
II	CGGGCC	0.952	0.962	0.504	0.292	0.984	0.900	0.853	0.975	0.273	0.018	0.228	0.957	0.789	0.037	0.812	0.430	0.777	0.928	0.322	0.956	0.006	0.005	0.850	0.601	0.015	0.344
II	ACGCGC	0.559	0.269	0.537	0.002	0.712	0.650	0.196	0.004	0.102	0.018	0.136	0.437	0.166	0.020	0.330	0.030	0.236	0.502	0.097	0.587	0.043	0.128	0.551	0.128	0.007	0.010
II	CGCGTG	0.522	0.569	0.481	0.000	0.659	0.324	0.292	0.115	0.069	0.028	0.204	0.441	0.146	0.044	0.384	0.054	0.056	0.591	0.284	0.383	0.057	0.407	0.774	0.123	0.000	0.015
II	CAGGCC	0.926	0.863	0.562	0.547	0.964	0.432	0.247	0.967	0.783	0.049	0.370	0.943	0.799	0.924	0.879	0.178	0.922	0.740	0.577	0.808	0.004	0.165	0.165	0.666	0.535	0.731
II	CCGGCC	0.837	0.792	0.718	0.812	0.845	0.726	0.757	0.945	0.489	0.000	0.312	0.893	0.357	0.053	0.728	0.051	0.689	0.434	0.137	0.885	0.001	0.033	0.882	0.322	0.029	0.142
II	CGGGCT	0.778	0.754	0.300	0.148	0.778	0.518	0.390	0.696	0.614	0.053	0.375	0.780	0.239	0.071	0.213	0.297	0.585	0.730	0.113	0.748	0.053	0.111	0.842	0.299	0.155	0.357
II	CGTCCG	0.655	0.706	0.819	0.052	0.777	0.550	0.248	0.797	0.395	0.020	0.242	0.774	0.065	0.070	0.127	0.166	0.164	0.711	0.022	0.734	0.008	0.272	0.782	0.158	0.220	0.193
II	TCGGCC	0.800	0.863	0.601	0.219	0.821	0.490	0.673	0.881	0.441	0.011	0.147	0.870	0.312	0.142	0.894	0.084	0.605	0.667	0.352	0.807	0.002	0.053	0.902	0.380	0.216	0.352
II	GCGGCG	0.698	0.652	0.391	0.084	0.899	0.734	0.566	0.134	0.260	0.000	0.277	0.514	0.253	0.005	0.503	0.097	0.706	0.524	0.434	0.672	0.003	0.302	0.723	0.045	0.031	0.309
II	CGCGTC	0.480	0.198	0.849	0.001	0.742	0.607	0.286	0.153	0.430	0.028	0.145	0.449	0.032	0.055	0.189	0.182	0.116	0.477	0.104	0.367	0.018	0.359	0.824	0.063	0.048	0.012
II	GGCCGG	0.811	0.492	0.774	0.622	0.881	0.428	0.463	0.957	0.183	0.002	0.166	0.878	0.433	0.023	0.859	0.050	0.575	0.618	0.051	0.835	0.000	0.080	0.670	0.380	0.039	0.317
II	CGCGCC	0.774	0.656	0.806	0.014	0.958	0.854	0.625	0.001	0.073	0.008	0.195	0.630	0.494	0.015	0.489	0.226	0.534	0.660	0.363	0.839	0.027	0.165	0.869	0.419	0.008	0.096
II	GCGGGG	0.287	0.773	0.515	0.072	0.989	0.764	0.340	0.765	0.084	0.079	0.048	0.865	0.094	0.012	0.462	0.090	0.342	0.787	0.178	0.802	0.090	0.007	0.967	0.389	0.003	0.143
II	CCGGGT	0.884	0.800	0.728	0.062	0.939	0.384	0.433	0.753	0.217	0.247	0.326	0.629	0.072	0.025	0.025	0.046	0.215	0.739	0.107	0.698	0.010	0.039	0.891	0.028	0.068	0.091
II	GGCGCG	0.693	0.809	0.683	0.021	0.954	0.404	0.548	0.001	0.151	0.010	0.136	0.430	0.290	0.007	0.864	0.274	0.673	0.741	0.264	0.822	0.020	0.299	0.116	0.119	0.003	0.136
II	GGCGCC	0.872	0.880	0.550	0.259	0.949	0.541	0.701	0.071	0.395	0.000	0.163	0.526	0.400	0.020	0.458	0.225	0.783	0.688	0.217	0.873	0.009	0.115	0.314	0.060	0.004	0.156
II	CCCGGC	0.859	0.620	0.690	0.427	0.961	0.715	0.878	0.938	0.355	0.045	0.620	0.947	0.422	0.009	0.807	0.141	0.686	0.891	0.314	0.960	0.004	0.128	0.875	0.364	0.255	0.619
II	CGGGTC	0.852	0.711	0.643	0.090	0.923	0.394	0.784	0.771	0.808	0.082	0.226	0.733	0.035	0.051	0.121	0.392	0.019	0.702	0.353	0.948	0.042	0.027	0.949	0.012	0.052	0.494
II	CACGCG	0.611	0.415	0.543	0.001	0.776	0.306	0.405	0.064	0.026	0.018	0.151	0.256	0.181	0.047	0.217	0.036	0.024	0.377	0.280	0.583	0.036	0.120	0.742	0.187	0.000	0.017
II	CGCGCG	0.239	0.180	0.622	0.009	0.820	0.284	0.118	0.000	0.011	0.007	0.037	0.272	0.078	0.001	0.060	0.008	0.054	0.375	0.081	0.313	0.011	0.036	0.153	0.031	0.001	0.009
II	CGTGGC	0.846	0.853	0.551	0.045	0.867	0.391	0.451	0.775	0.576	0.032	0.496	0.801	0.533	0.273	0.575	0.206	0.419	0.349	0.295	0.842	0.048	0.090	0.761	0.334	0.005	0.000
II	GACCCG	0.879	0.487	0.604	0.147	0.886	0.342	0.570	0.610	0.728	0.079	0.236	0.933	0.045	0.019	0.199	0.339	0.028	0.752	0.301	0.812	0.038	0.092	0.806	0.014	0.197	0.612
II	CGGCGC	0.821	0.722	0.433	0.081	0.922	0.878	0.541	0.138	0.051	0.000	0.143	0.445	0.162	0.002	0.628	0.420	0.688	0.816	0.084	0.732	0.010	0.386	0.296	0.040	0.044	0.371

II	CGCCAC	0.783	0.399	0.160	0.062	0.890	0.574	0.320	0.029	0.235	0.004	0.424	0.620	0.152	0.097	0.432	0.081	0.220	0.188	0.311	0.778	0.075	0.071	0.875	0.297	0.029	0.006
II	ACGGCG	0.659	0.786	0.684	0.046	0.875	0.309	0.269	0.387	0.274	0.002	0.332	0.321	0.223	0.023	0.649	0.217	0.315	0.693	0.039	0.592	0.014	0.547	0.785	0.083	0.101	0.145
II	TCGGGC	0.578	0.726	0.412	0.204	0.888	0.431	0.766	0.869	0.440	0.035	0.097	0.922	0.159	0.337	0.892	0.072	0.409	0.720	0.427	0.466	0.020	0.077	0.925	0.141	0.118	0.376
II	CCCGGT	0.806	0.876	0.436	0.076	0.981	0.741	0.815	0.881	0.303	0.106	0.303	0.922	0.128	0.026	0.024	0.099	0.094	0.700	0.073	0.875	0.048	0.033	0.934	0.044	0.053	0.243
II	ACGCCG	0.622	0.204	0.624	0.027	0.924	0.264	0.176	0.530	0.204	0.003	0.336	0.161	0.180	0.044	0.571	0.186	0.402	0.675	0.053	0.523	0.017	0.497	0.812	0.078	0.051	0.188
II	TCGCGC	0.401	0.468	0.387	0.085	0.727	0.243	0.229	0.006	0.262	0.027	0.046	0.570	0.270	0.010	0.573	0.027	0.179	0.375	0.174	0.346	0.116	0.143	0.304	0.097	0.018	0.086
II	GGCCGT	0.506	0.784	0.792	0.397	0.806	0.618	0.264	0.902	0.556	0.007	0.202	0.613	0.212	0.060	0.733	0.078	0.514	0.774	0.019	0.641	0.000	0.576	0.732	0.194	0.056	0.452
II	CCACGC	0.887	0.760	0.455	0.013	0.905	0.438	0.388	0.779	0.295	0.044	0.405	0.889	0.307	0.085	0.182	0.054	0.061	0.664	0.129	0.878	0.177	0.017	0.740	0.141	0.005	0.011
II	GCGTCG	0.655	0.577	0.641	0.024	0.643	0.648	0.606	0.431	0.279	0.020	0.115	0.492	0.095	0.131	0.384	0.300	0.390	0.411	0.123	0.409	0.046	0.240	0.737	0.096	0.150	0.129
II	CGGCTG	0.751	0.608	0.335	0.262	0.893	0.672	0.399	0.700	0.517	0.002	0.584	0.421	0.266	0.126	0.691	0.195	0.698	0.484	0.296	0.732	0.023	0.474	0.242	0.040	0.035	0.127
II	CGCCGC	0.845	0.857	0.390	0.071	0.941	0.444	0.634	0.578	0.176	0.000	0.279	0.454	0.119	0.008	0.455	0.358	0.666	0.765	0.206	0.903	0.003	0.179	0.784	0.079	0.026	0.330
II	CCTGGC	0.922	0.805	0.569	0.515	0.930	0.294	0.674	0.901	0.799	0.055	0.316	0.959	0.681	0.942	0.408	0.207	0.565	0.300	0.460	0.903	0.041	0.389	0.065	0.398	0.057	0.012
II	GCCGTT	0.482	0.390	0.456	0.263	0.598	0.247	0.022	0.418	0.495	0.005	0.357	0.464	0.275	0.095	0.369	0.002	0.373	0.458	0.188	0.199	0.025	0.139	0.802	0.171	0.110	0.292
II	GGCGGG	0.394	0.484	0.575	0.499	0.946	0.724	0.195	0.004	0.213	0.007	0.504	0.633	0.111	0.033	0.547	0.217	0.323	0.852	0.137	0.879	0.007	0.032	0.887	0.352	0.139	0.315
II	CGGCGG	0.610	0.613	0.475	0.188	0.966	0.812	0.149	0.850	0.054	0.001	0.310	0.515	0.058	0.002	0.710	0.191	0.546	0.920	0.069	0.814	0.000	0.230	0.957	0.029	0.099	0.217
II	CGTCGG	0.648	0.813	0.716	0.043	0.843	0.182	0.595	0.820	0.116	0.002	0.249	0.723	0.072	0.142	0.170	0.169	0.406	0.261	0.130	0.698	0.006	0.438	0.956	0.113	0.119	0.065
II	CGCGAC	0.552	0.016	0.508	0.026	0.811	0.479	0.632	0.241	0.266	0.050	0.141	0.332	0.040	0.059	0.608	0.172	0.039	0.122	0.245	0.631	0.028	0.483	0.507	0.034	0.021	0.077
II	CCACGT	0.518	0.522	0.684	0.037	0.648	0.605	0.210	0.529	0.266	0.041	0.339	0.612	0.154	0.282	0.109	0.076	0.133	0.350	0.178	0.490	0.099	0.005	0.853	0.144	0.001	0.000
II	CGACGC	0.875	0.707	0.616	0.027	0.774	0.590	0.635	0.533	0.454	0.019	0.237	0.476	0.143	0.104	0.524	0.338	0.287	0.575	0.073	0.747	0.058	0.401	0.416	0.085	0.094	0.111
II	CCGGTT	0.703	0.671	0.288	0.132	0.863	0.191	0.596	0.795	0.274	0.022	0.552	0.654	0.017	0.017	0.013	0.009	0.411	0.708	0.471	0.404	0.008	0.074	0.633	0.121	0.089	0.176
II	GGGTCG	0.683	0.843	0.843	0.314	0.936	0.644	0.784	0.923	0.458	0.177	0.213	0.902	0.092	0.827	0.338	0.105	0.095	0.826	0.263	0.907	0.090	0.208	0.973	0.041	0.242	0.390
II	GTCCCG	0.791	0.845	0.414	0.063	0.934	0.560	0.786	0.792	0.412	0.285	0.259	0.811	0.077	0.063	0.597	0.209	0.070	0.561	0.117	0.831	0.037	0.040	0.982	0.079	0.275	0.318
II	CGCGGC	0.805	0.339	0.611	0.007	0.911	0.863	0.600	0.028	0.093	0.002	0.440	0.511	0.477	0.007	0.462	0.237	0.583	0.395	0.412	0.717	0.007	0.151	0.796	0.087	0.034	0.205
II	GAGCCC	0.911	0.964	0.392	0.488	0.859	0.801	0.727	0.944	0.664	0.171	0.847	0.932	0.836	0.367	0.830	0.403	0.935	0.871	0.659	0.954	0.216	0.080	0.971	0.539	0.597	0.702
II	CGCCGA	0.569	0.191	0.733	0.065	0.882	0.539	0.531	0.389	0.253	0.004	0.277	0.298	0.266	0.056	0.622	0.060	0.571	0.738	0.405	0.692	0.016	0.705	0.812	0.037	0.087	0.273
II	CGGCCG	0.686	0.157	0.780	0.253	0.751	0.744	0.361	0.715	0.023	0.000	0.121	0.181	0.087	0.011	0.199	0.045	0.326	0.235	0.019	0.554	0.000	0.051	0.766	0.069	0.023	0.102
II	CGCCGT	0.529	0.613	0.579	0.048	0.969	0.601	0.216	0.258	0.185	0.001	0.599	0.433	0.308	0.010	0.525	0.362	0.239	0.752	0.017	0.490	0.014	0.517	0.734	0.130	0.016	0.119
II	CGTGCC	0.422	0.741	0.798	0.099	0.775	0.680	0.558	0.893	0.367	0.027	0.601	0.434	0.520	0.191	0.454	0.282	0.095	0.714	0.114	0.776	0.046	0.204	0.806	0.188	0.002	0.018
II	CCGAAC	0.468	0.438	0.131	0.129	0.832	0.174	0.176	0.507	0.187	0.023	0.220	0.278	0.138	0.294	0.402	0.002	0.467	0.485	0.355	0.638	0.082	0.236	0.778	0.296	0.268	0.337
II	CGGTTC	0.716	0.621	0.249	0.078	0.734	0.151	0.334	0.638	0.023	0.018	0.289	0.668	0.019	0.086	0.091	0.028	0.286	0.676	0.133	0.655	0.096	0.161	0.631	0.121	0.223	0.369
II	CGTGGG	0.779	0.575	0.643	0.029	0.852	0.584	0.415	0.793	0.218	0.090	0.060	0.558	0.109	0.139	0.089	0.168	0.212	0.617	0.091	0.810	0.059	0.004	0.870	0.187	0.002	0.014
II	CCGCCG	0.640	0.519	0.671	0.134	0.969	0.602	0.642	0.736	0.059	0.000	0.218	0.408	0.121	0.003	0.719	0.113	0.647	0.887	0.150	0.841	0.002	0.118	0.895	0.031	0.020	0.169
II	GCGCCA	0.867	0.772	0.307	0.069	0.895	0.462	0.576	0.002	0.306	0.003	0.294	0.709	0.523	0.060	0.841	0.142	0.758	0.214	0.497	0.825	0.073	0.181	0.497	0.361	0.084	0.047
II	TGGCGC	0.919	0.532	0.573	0.069	0.888	0.558	0.118	0.003	0.247	0.006	0.247	0.787	0.437	0.027	0.747	0.045	0.665	0.084	0.275	0.652	0.039	0.497	0.365	0.088	0.058	0.085
II	CGACCC	0.921	0.770	0.801	0.436	0.946	0.549	0.682	0.942	0.754	0.119	0.190	0.956	0.127	0.491	0.243	0.309	0.056	0.896	0.198	0.914	0.057	0.155	0.907	0.024	0.031	0.638
II	ACCGGC	0.772	0.525	0.463	0.680	0.891	0.534	0.699	0.804	0.216	0.002	0.640	0.716	0.288	0.013	0.261	0.037	0.161	0.628	0.093	0.640	0.002	0.254	0.453	0.074	0.008	0.201
II	CCCACG	0.831	0.792	0.670	0.056	0.859	0.573	0.519	0.860	0.455	0.051	0.144	0.548	0.181	0.153	0.291	0.209	0.216	0.383	0.256	0.779	0.071	0.006	0.867	0.224	0.006	0.075
II	CTGGCC	0.851	0.901	0.196	0.683	0.926	0.677	0.700	0.887	0.772	0.062	0.621	0.845	0.616	0.842	0.943	0.306	0.772	0.698	0.579	0.851	0.005	0.113	0.065	0.283	0.141	0.025
II	GCCGGA	0.751	0.390	0.623	0.233	0.904	0.239	0.621	0.858	0.630	0.019	0.227	0.799	0.682	0.029	0.893	0.104	0.529	0.623	0.080	0.777	0.001	0.323	0.773	0.333	0.199	0.483
II	ACGTCG	0.521	0.417	0.700	0.028	0.668	0.383	0.098	0.403	0.192	0.008	0.156	0.436	0.007	0.368	0.354	0.051	0.130	0.384	0.083	0.175	0.013	0.603	0.752	0.090	0.044	0.005
II	CGGACC	0.951	0.840	0.563	0.126	0.876	0.590	0.550	0.951	0.576	0.056	0.268	0.936	0.302	0.054	0.336	0.124	0.026	0.799	0.047	0.823	0.042	0.017	0.936	0.021	0.141	0.580
II	GCGCTC	0.901	0.627	0.097	0.186	0.819	0.793	0.293	0.265	0.573	0.036	0.406	0.738	0.147	0.074	0.702	0.228	0.789	0.843	0.535	0.843	0.213	0.554	0.606	0.303	0.007	0.353
II	CAGCCC	0.937	0.933	0.274	0.752	0.963	0.694	0.848	0.948	0.805	0.016	0.383	0.866	0.621	0.482	0.798	0.346	0.875	0.746	0.409	0.919	0.068	0.045	0.373	0.171	0.031	0.174
II	GCGCGA	0.265	0.473	0.542	0.170	0.671	0.285	0.245	0.003	0.273	0.036	0.050	0.413	0.227	0.019	0.637	0.012	0.195	0.599	0.145	0.427	0.090	0.093	0.092	0.033	0.012	0.096
II	CCGTCC	0.756	0.860	0.640	0.192	0.766	0.536	0.211	0.837	0.642	0.001	0.414	0.860	0.117	0.145	0.640	0.196	0.212	0.802	0.025	0.845	0.008	0.040	0.930	0.214	0.173	0.267
II	CCCGGA	0.690	0.818	0.658	0.090	0.947	0.617	0.424	0.825	0.219	0.229	0.202	0.844	0.609	0.002	0.500	0.031	0.269	0.830	0.250	0.913	0.021	0.115	0.801	0.218	0.420	0.589

II	CGCGCA	0.242	0.377	0.497	0.010	0.711	0.376	0.442	0.005	0.092	0.017	0.141	0.474	0.086	0.013	0.730	0.057	0.296	0.335	0.170	0.708	0.240	0.091	0.186	0.372	0.011	0.031
II	GACGCG	0.824	0.541	0.890	0.002	0.773	0.689	0.732	0.091	0.180	0.046	0.109	0.514	0.061	0.054	0.412	0.202	0.125	0.391	0.068	0.605	0.013	0.397	0.687	0.085	0.096	0.101
II	TCGCCG	0.583	0.701	0.591	0.066	0.779	0.567	0.330	0.531	0.495	0.004	0.101	0.360	0.313	0.033	0.509	0.118	0.441	0.643	0.267	0.646	0.004	0.587	0.884	0.036	0.130	0.312
II	GCGGGA	0.387	0.461	0.413	0.060	0.923	0.405	0.586	0.001	0.372	0.039	0.308	0.884	0.392	0.011	0.702	0.164	0.531	0.501	0.246	0.857	0.062	0.086	0.950	0.523	0.422	0.387
II	TAGCGC	0.607	0.495	0.134	0.133	0.508	0.335	0.283	0.177	0.643	0.028	0.072	0.557	0.377	0.033	0.658	0.009	0.356	0.590	0.421	0.389	0.257	0.521	0.757	0.255	0.030	0.104
II	CGCACG	0.653	0.404	0.453	0.060	0.874	0.467	0.438	0.449	0.031	0.031	0.513	0.408	0.347	0.052	0.502	0.081	0.020	0.473	0.059	0.567	0.074	0.044	0.740	0.145	0.003	0.090
II	GTGCCG	0.735	0.296	0.265	0.116	0.673	0.567	0.296	0.862	0.325	0.006	0.426	0.716	0.488	0.062	0.598	0.190	0.126	0.448	0.102	0.805	0.014	0.197	0.379	0.451	0.007	0.191
II	GAGCGC	0.804	0.645	0.126	0.190	0.864	0.689	0.638	0.413	0.473	0.074	0.433	0.665	0.281	0.073	0.855	0.496	0.706	0.745	0.307	0.771	0.173	0.449	0.322	0.487	0.044	0.469
II	CCCGCT	0.514	0.832	0.210	0.145	0.907	0.241	0.582	0.359	0.275	0.104	0.359	0.912	0.192	0.060	0.253	0.331	0.640	0.798	0.280	0.878	0.198	0.085	0.751	0.326	0.050	0.530
II	GGTTCG	0.708	0.728	0.118	0.327	0.784	0.082	0.609	0.706	0.118	0.064	0.191	0.610	0.022	0.174	0.039	0.033	0.589	0.653	0.155	0.669	0.209	0.497	0.733	0.359	0.026	0.412
II	GGCCCT	0.887	0.903	0.825	0.606	0.904	0.510	0.346	0.948	0.917	0.049	0.714	0.736	0.745	0.931	0.951	0.001	0.917	0.885	0.793	0.726	0.012	0.017	0.791	0.657	0.598	0.679
II	GGTCCG	0.788	0.752	0.676	0.120	0.779	0.624	0.659	0.792	0.561	0.063	0.174	0.698	0.192	0.079	0.551	0.072	0.027	0.777	0.044	0.772	0.023	0.101	0.822	0.014	0.305	0.320
II	CCGAGC	0.782	0.751	0.225	0.301	0.893	0.679	0.755	0.792	0.571	0.054	0.324	0.712	0.680	0.368	0.308	0.354	0.704	0.860	0.338	0.911	0.124	0.304	0.606	0.430	0.101	0.348
II	GGGACC	0.945	0.858	0.667	0.262	0.954	0.623	0.677	0.968	0.753	0.458	0.408	0.988	0.614	0.422	0.662	0.174	0.060	0.948	0.499	0.922	0.080	0.000	0.928	0.063	0.626	0.799
II	GCCGGT	0.867	0.546	0.295	0.686	0.794	0.712	0.313	0.855	0.358	0.004	0.564	0.559	0.142	0.012	0.244	0.036	0.530	0.786	0.156	0.632	0.002	0.172	0.823	0.070	0.146	0.141
II	CGACCG	0.485	0.011	0.600	0.162	0.895	0.669	0.347	0.800	0.544	0.007	0.088	0.508	0.034	0.108	0.253	0.033	0.019	0.573	0.177	0.679	0.008	0.211	0.941	0.012	0.099	0.254
II	TCGCGG	0.329	0.626	0.579	0.132	0.658	0.349	0.501	0.132	0.159	0.043	0.080	0.744	0.301	0.011	0.297	0.059	0.078	0.525	0.405	0.649	0.067	0.178	0.577	0.067	0.049	0.139
II	CAGGCG	0.648	0.683	0.684	0.294	0.802	0.343	0.712	0.624	0.457	0.023	0.120	0.813	0.406	0.166	0.515	0.234	0.365	0.369	0.102	0.813	0.027	0.521	0.020	0.225	0.151	0.282
II	CGTCGT	0.531	0.343	0.607	0.016	0.577	0.362	0.145	0.412	0.303	0.024	0.150	0.150	0.027	0.294	0.283	0.133	0.093	0.409	0.034	0.389	0.031	0.439	0.803	0.032	0.061	0.021
II	CGCTCG	0.565	0.625	0.287	0.268	0.716	0.708	0.328	0.531	0.237	0.080	0.217	0.765	0.382	0.154	0.453	0.262	0.567	0.703	0.458	0.808	0.062	0.288	0.679	0.654	0.191	0.337
II	CCCGGG	0.917	0.961	0.829	0.196	0.993	0.929	0.835	0.841	0.392	0.241	0.203	0.644	0.657	0.001	0.606	0.023	0.583	0.941	0.526	0.957	0.003	0.015	0.986	0.236	0.069	0.539
II	CCGACG	0.701	0.453	0.687	0.043	0.786	0.467	0.537	0.721	0.150	0.001	0.273	0.491	0.107	0.159	0.543	0.161	0.256	0.717	0.224	0.770	0.007	0.486	0.880	0.050	0.063	0.160
II	GCCGGG	0.746	0.676	0.525	0.315	0.920	0.718	0.453	0.933	0.494	0.017	0.243	0.899	0.484	0.018	0.675	0.124	0.438	0.881	0.218	0.916	0.006	0.036	0.817	0.360	0.076	0.523
II	GGGTCC	0.916	0.972	0.677	0.361	0.906	0.688	0.763	0.962	0.722	0.364	0.491	0.985	0.142	0.465	0.348	0.408	0.060	0.837	0.438	0.913	0.081	0.002	0.985	0.034	0.415	0.679
II	GCCGCG	0.875	0.743	0.611	0.008	0.908	0.718	0.526	0.015	0.110	0.002	0.292	0.840	0.328	0.011	0.348	0.236	0.420	0.343	0.268	0.780	0.007	0.231	0.769	0.236	0.028	0.062
II	CGGCGA	0.601	0.487	0.630	0.155	0.745	0.409	0.323	0.674	0.261	0.005	0.250	0.461	0.337	0.048	0.829	0.101	0.295	0.652	0.242	0.719	0.003	0.449	0.833	0.040	0.120	0.469
II	TCCCGC	0.413	0.472	0.631	0.048	0.911	0.337	0.784	0.006	0.191	0.054	0.168	0.366	0.247	0.007	0.830	0.075	0.385	0.285	0.284	0.885	0.079	0.074	0.937	0.244	0.427	0.330
II	CCGTCG	0.720	0.628	0.833	0.168	0.912	0.484	0.569	0.805	0.496	0.011	0.345	0.717	0.059	0.127	0.261	0.177	0.312	0.628	0.240	0.661	0.009	0.260	0.876	0.079	0.263	0.331
II	CCGCGT	0.627	0.402	0.751	0.000	0.907	0.401	0.334	0.006	0.136	0.027	0.382	0.564	0.215	0.007	0.229	0.125	0.267	0.500	0.049	0.485	0.102	0.348	0.867	0.138	0.070	0.069
II	CGCGTT	0.282	0.400	0.607	0.000	0.630	0.259	0.012	0.035	0.072	0.032	0.170	0.293	0.159	0.020	0.181	0.050	0.208	0.443	0.225	0.263	0.044	0.384	0.781	0.084	0.046	0.026
II	CGCCGG	0.701	0.477	0.513	0.169	0.907	0.814	0.511	0.589	0.125	0.002	0.107	0.313	0.099	0.007	0.482	0.115	0.403	0.860	0.122	0.696	0.000	0.093	0.628	0.122	0.089	0.283
II	GCGGAG	0.918	0.755	0.337	0.134	0.772	0.615	0.242	0.807	0.266	0.060	0.511	0.770	0.509	0.009	0.616	0.249	0.662	0.636	0.411	0.932	0.203	0.323	0.746	0.141	0.434	0.425
II	AGCGGG	0.624	0.864	0.244	0.307	0.865	0.416	0.490	0.552	0.231	0.101	0.115	0.891	0.393	0.028	0.637	0.250	0.683	0.805	0.336	0.836	0.215	0.080	0.922	0.736	0.582	0.502
II	CGGCGT	0.581	0.561	0.497	0.039	0.804	0.331	0.428	0.834	0.671	0.003	0.192	0.303	0.280	0.025	0.375	0.176	0.294	0.687	0.043	0.461	0.004	0.706	0.571	0.094	0.006	0.116
II	GACGGC	0.768	0.832	0.795	0.203	0.825	0.691	0.623	0.846	0.680	0.001	0.305	0.701	0.053	0.174	0.828	0.203	0.114	0.602	0.214	0.652	0.006	0.281	0.864	0.029	0.163	0.238
II	GCGCCT	0.565	0.653	0.547	0.098	0.786	0.311	0.226	0.007	0.602	0.012	0.546	0.879	0.330	0.058	0.826	0.366	0.533	0.639	0.294	0.678	0.033	0.237	0.582	0.075	0.165	0.321
II	CCGGCG	0.916	0.739	0.514	0.256	0.968	0.727	0.534	0.883	0.084	0.001	0.132	0.519	0.289	0.001	0.465	0.162	0.282	0.904	0.268	0.801	0.000	0.208	0.817	0.032	0.038	0.404
II	GGCGGA	0.696	0.481	0.447	0.180	0.908	0.601	0.544	0.912	0.509	0.010	0.309	0.572	0.353	0.015	0.411	0.082	0.437	0.618	0.316	0.886	0.011	0.128	0.797	0.156	0.291	0.489
II	CCGGAC	0.801	0.482	0.604	0.091	0.891	0.604	0.672	0.801	0.257	0.032	0.251	0.792	0.098	0.006	0.285	0.087	0.081	0.678	0.016	0.722	0.006	0.102	0.817	0.068	0.295	0.160
II	ACGACG	0.447	0.400	0.656	0.020	0.579	0.385	0.125	0.428	0.355	0.016	0.130	0.328	0.050	0.274	0.451	0.081	0.070	0.407	0.048	0.363	0.025	0.319	0.243	0.039	0.038	0.020
II	TCGCGT	0.251	0.399	0.474	0.007	0.402	0.366	0.194	0.293	0.177	0.076	0.012	0.378	0.050	0.082	0.069	0.050	0.006	0.190	0.048	0.297	0.127	0.088	0.716	0.034	0.017	0.005
II	GCCGGC	0.732	0.050	0.614	0.380	0.785	0.874	0.092	0.740	0.249	0.000	0.390	0.351	0.048	0.026	0.699	0.044	0.550	0.515	0.220	0.710	0.000	0.049	0.181	0.012	0.018	0.147
II	CAGCCG	0.708	0.724	0.324	0.242	0.879	0.680	0.650	0.716	0.234	0.001	0.432	0.676	0.263	0.102	0.661	0.228	0.571	0.428	0.194	0.777	0.046	0.191	0.488	0.101	0.040	0.241
II	TCCGGC	0.673	0.205	0.563	0.171	0.933	0.506	0.526	0.866	0.586	0.023	0.107	0.560	0.389	0.036	0.798	0.028	0.657	0.608	0.106	0.810	0.001	0.308	0.928	0.119	0.116	0.220
II	CCCAGT	0.760	0.760	0.033	0.377	0.901	0.401	0.234	0.858	0.126	0.159	0.333	0.761	0.187	0.787	0.055	0.313	0.358	0.409	0.134	0.673	0.139	0.020	0.182	0.149	0.114	0.080
II	GTTCGG	0.462	0.311	0.039	0.192	0.699	0.099	0.193	0.307	0.065	0.053	0.448	0.250	0.114	0.387	0.166	0.004	0.351	0.311	0.186	0.697	0.047	0.338	0.564	0.347	0.177	0.367

II	GAGCCG	0.806	0.721	0.621	0.243	0.879	0.614	0.713	0.875	0.913	0.009	0.534	0.856	0.788	0.200	0.858	0.405	0.677	0.663	0.626	0.936	0.047	0.729	0.869	0.471	0.564	0.326
II	GACGTC	0.482	0.571	0.668	0.067	0.651	0.557	0.253	0.457	0.317	0.008	0.066	0.502	0.000	0.533	0.607	0.084	0.012	0.443	0.222	0.193	0.008	0.814	0.325	0.025	0.093	0.002
II	CGGCAG	0.838	0.050	0.364	0.301	0.768	0.449	0.461	0.759	0.371	0.003	0.133	0.612	0.180	0.060	0.394	0.092	0.465	0.151	0.051	0.831	0.011	0.343	0.071	0.178	0.171	0.288
II	ACCCGG	0.714	0.880	0.617	0.067	0.943	0.602	0.296	0.730	0.381	0.117	0.294	0.523	0.199	0.004	0.052	0.037	0.253	0.851	0.301	0.701	0.014	0.060	0.666	0.152	0.065	0.115
II	CCCGAA	0.345	0.583	0.395	0.333	0.669	0.120	0.352	0.837	0.359	0.294	0.346	0.622	0.534	0.098	0.557	0.068	0.530	0.776	0.468	0.618	0.110	0.152	0.806	0.480	0.182	0.448
II	GCCGTC	0.799	0.841	0.514	0.268	0.861	0.610	0.165	0.855	0.609	0.000	0.586	0.762	0.038	0.138	0.707	0.408	0.266	0.716	0.045	0.654	0.010	0.217	0.732	0.010	0.219	0.240
II	TCGGGT	0.481	0.399	0.403	0.210	0.688	0.215	0.108	0.232	0.122	0.029	0.068	0.248	0.079	0.201	0.014	0.028	0.096	0.447	0.132	0.593	0.059	0.019	0.687	0.036	0.156	0.035
II	CGGTCC	0.898	0.453	0.377	0.173	0.913	0.790	0.742	0.909	0.534	0.027	0.203	0.934	0.055	0.095	0.478	0.211	0.007	0.653	0.078	0.860	0.019	0.004	0.891	0.007	0.104	0.207
II	TCCGCC	0.751	0.809	0.702	0.250	0.925	0.445	0.505	0.897	0.385	0.012	0.089	0.765	0.399	0.018	0.421	0.102	0.470	0.820	0.484	0.823	0.008	0.181	0.833	0.106	0.094	0.388
II	GTCCGC	0.617	0.690	0.273	0.070	0.824	0.397	0.583	0.700	0.445	0.021	0.449	0.883	0.124	0.031	0.326	0.414	0.064	0.480	0.065	0.640	0.030	0.149	0.839	0.059	0.140	0.198
II	CTCGCG	0.793	0.614	0.303	0.032	0.852	0.621	0.542	0.185	0.512	0.068	0.125	0.685	0.306	0.046	0.131	0.208	0.175	0.771	0.149	0.853	0.119	0.342	0.360	0.106	0.084	0.286
II	CGTCGC	0.567	0.426	0.800	0.054	0.754	0.648	0.288	0.432	0.113	0.026	0.304	0.650	0.048	0.135	0.407	0.221	0.240	0.323	0.107	0.637	0.025	0.454	0.617	0.169	0.041	0.080
II	CGAACC	0.786	0.724	0.220	0.235	0.816	0.177	0.430	0.706	0.120	0.076	0.289	0.442	0.015	0.145	0.032	0.044	0.611	0.631	0.113	0.694	0.114	0.200	0.586	0.431	0.227	0.389
II	GGCGTC	0.928	0.875	0.680	0.098	0.934	0.609	0.725	0.886	0.633	0.005	0.322	0.902	0.093	0.291	0.408	0.502	0.303	0.730	0.095	0.762	0.015	0.579	0.719	0.100	0.198	0.225
II	CCGGTC	0.814	0.302	0.518	0.477	0.852	0.687	0.527	0.851	0.507	0.042	0.146	0.590	0.018	0.035	0.045	0.053	0.004	0.771	0.156	0.678	0.005	0.064	0.808	0.004	0.081	0.162
II	CGACGG	0.675	0.583	0.838	0.141	0.692	0.639	0.416	0.843	0.310	0.016	0.415	0.628	0.064	0.139	0.393	0.161	0.131	0.643	0.184	0.577	0.011	0.211	0.807	0.070	0.098	0.327
II	TACCCG	0.401	0.145	0.454	0.137	0.524	0.422	0.271	0.022	0.158	0.107	0.260	0.119	0.131	0.072	0.038	0.013	0.168	0.451	0.065	0.514	0.035	0.065	0.774	0.158	0.198	0.225
II	CCAGGC	0.872	0.841	0.711	0.635	0.959	0.516	0.781	0.881	0.478	0.066	0.350	0.944	0.757	0.663	0.154	0.178	0.725	0.762	0.366	0.905	0.024	0.152	0.208	0.380	0.478	0.417
II	GACCGG	0.639	0.036	0.540	0.392	0.869	0.418	0.507	0.861	0.479	0.023	0.153	0.656	0.032	0.005	0.106	0.027	0.004	0.771	0.054	0.539	0.004	0.062	0.694	0.003	0.026	0.066
II	TGACGG	0.587	0.439	0.289	0.277	0.700	0.584	0.256	0.378	0.294	0.007	0.169	0.545	0.012	0.058	0.384	0.135	0.013	0.461	0.108	0.293	0.062	0.308	0.084	0.023	0.104	0.004
II	ACCGTC	0.618	0.601	0.450	0.469	0.704	0.366	0.354	0.652	0.365	0.003	0.268	0.462	0.056	0.112	0.106	0.036	0.048	0.578	0.081	0.495	0.030	0.179	0.357	0.038	0.012	0.144
II	TAGCCC	0.667	0.821	0.231	0.597	0.759	0.681	0.765	0.835	0.799	0.144	0.551	0.895	0.245	0.156	0.765	0.142	0.745	0.709	0.706	0.638	0.113	0.102	0.939	0.673	0.340	0.150
II	GGCGCA	0.374	0.367	0.459	0.346	0.651	0.488	0.180	0.224	0.398	0.006	0.121	0.300	0.147	0.033	0.160	0.182	0.292	0.116	0.154	0.711	0.052	0.080	0.303	0.143	0.059	0.050
II	CACCGG	0.733	0.745	0.329	0.219	0.962	0.789	0.847	0.902	0.099	0.018	0.253	0.706	0.095	0.024	0.413	0.063	0.646	0.648	0.136	0.653	0.004	0.121	0.942	0.153	0.055	0.079
II	CGGCAC	0.786	0.295	0.323	0.087	0.763	0.647	0.590	0.854	0.459	0.006	0.512	0.807	0.271	0.082	0.662	0.196	0.239	0.428	0.122	0.666	0.017	0.059	0.644	0.539	0.010	0.147
II	AACCCG	0.369	0.698	0.303	0.072	0.626	0.121	0.312	0.437	0.322	0.149	0.462	0.458	0.039	0.010	0.015	0.078	0.181	0.700	0.168	0.648	0.117	0.177	0.671	0.256	0.046	0.086
II	ACGGCA	0.479	0.165	0.415	0.195	0.592	0.358	0.196	0.455	0.388	0.012	0.255	0.236	0.132	0.094	0.183	0.057	0.003	0.211	0.020	0.449	0.028	0.243	0.492	0.258	0.060	0.073
II	CGGAGG	0.824	0.942	0.879	0.110	0.990	0.250	0.942	0.974	0.762	0.139	0.190	0.906	0.590	0.098	0.262	0.244	0.815	0.958	0.081	0.902	0.133	0.299	0.975	0.121	0.505	0.615
II	GGACCG	0.943	0.825	0.762	0.201	0.838	0.707	0.778	0.945	0.592	0.024	0.236	0.942	0.079	0.211	0.657	0.159	0.010	0.830	0.080	0.821	0.056	0.007	0.758	0.011	0.107	0.472
II	TCGGCG	0.624	0.301	0.544	0.052	0.844	0.731	0.387	0.624	0.128	0.005	0.069	0.646	0.391	0.062	0.619	0.071	0.371	0.652	0.392	0.508	0.011	0.544	0.803	0.115	0.084	0.366
II	CGCGTA	0.270	0.235	0.551	0.001	0.586	0.366	0.311	0.007	0.104	0.016	0.147	0.226	0.145	0.028	0.229	0.022	0.020	0.373	0.029	0.348	0.117	0.154	0.666	0.099	0.023	0.005
II	CTCCGC	0.894	0.873	0.178	0.162	0.926	0.422	0.641	0.888	0.115	0.062	0.118	0.868	0.511	0.014	0.725	0.234	0.734	0.700	0.411	0.967	0.312	0.213	0.664	0.217	0.185	0.638
II	GACACG	0.402	0.021	0.411	0.005	0.518	0.502	0.238	0.467	0.126	0.064	0.104	0.403	0.054	0.143	0.531	0.196	0.005	0.293	0.078	0.351	0.025	0.185	0.236	0.141	0.008	0.003
II	GCCGCC	0.868	0.780	0.581	0.362	0.951	0.595	0.702	0.788	0.317	0.000	0.467	0.321	0.176	0.020	0.771	0.377	0.746	0.829	0.150	0.633	0.005	0.087	0.838	0.003	0.023	0.315
II	CGGACG	0.686	0.743	0.725	0.062	0.839	0.552	0.444	0.806	0.254	0.019	0.152	0.440	0.096	0.066	0.245	0.312	0.123	0.634	0.018	0.704	0.004	0.286	0.787	0.141	0.195	0.311
II	CGGCTC	0.883	0.773	0.514	0.407	0.824	0.489	0.667	0.854	0.944	0.016	0.398	0.903	0.749	0.104	0.741	0.428	0.746	0.793	0.266	0.822	0.072	0.412	0.954	0.196	0.313	0.698
II	GGCACG	0.817	0.767	0.851	0.098	0.756	0.774	0.720	0.860	0.662	0.040	0.324	0.818	0.458	0.249	0.903	0.062	0.036	0.710	0.089	0.768	0.055	0.051	0.743	0.362	0.005	0.071
II	GCTGCG	0.543	0.465	0.222	0.144	0.860	0.740	0.505	0.773	0.494	0.015	0.366	0.775	0.423	0.175	0.769	0.314	0.642	0.221	0.172	0.828	0.158	0.365	0.274	0.305	0.166	0.355
II	GACGCC	0.941	0.914	0.549	0.204	0.914	0.570	0.692	0.790	0.746	0.004	0.622	0.919	0.296	0.199	0.775	0.466	0.262	0.713	0.241	0.836	0.019	0.439	0.913	0.224	0.272	0.244
II	ATCGCG	0.265	0.334	0.604	0.049	0.694	0.216	0.237	0.119	0.142	0.037	0.009	0.467	0.107	0.021	0.214	0.013	0.049	0.390	0.136	0.236	0.128	0.293	0.602	0.061	0.014	0.023
II	CCGGGA	0.651	0.287	0.533	0.275	0.932	0.456	0.559	0.465	0.401	0.191	0.275	0.660	0.305	0.016	0.438	0.058	0.259	0.788	0.352	0.868	0.017	0.143	0.953	0.219	0.586	0.518
II	TACGGC	0.483	0.556	0.493	0.210	0.717	0.513	0.500	0.520	0.316	0.007	0.185	0.153	0.306	0.061	0.586	0.129	0.014	0.473	0.004	0.404	0.022	0.361	0.551	0.453	0.054	0.226
II	ACCGGT	0.673	0.366	0.402	0.385	0.790	0.476	0.532	0.788	0.112	0.008	0.096	0.297	0.011	0.038	0.061	0.000	0.068	0.696	0.194	0.302	0.002	0.112	0.565	0.049	0.067	0.078
II	GGCTCG	0.892	0.820	0.409	0.397	0.844	0.533	0.755	0.856	0.570	0.107	0.418	0.800	0.590	0.775	0.859	0.474	0.781	0.829	0.535	0.793	0.100	0.518	0.817	0.618	0.109	0.722
II	AGGCGG	0.581	0.761	0.768	0.751	0.856	0.362	0.505	0.693	0.745	0.008	0.284	0.752	0.184	0.057	0.714	0.216	0.544	0.605	0.423	0.827	0.027	0.127	0.598	0.291	0.658	0.650
II	CCCGAC	0.905	0.004	0.489	0.117	0.952	0.459	0.579	0.851	0.257	0.022	0.210	0.676	0.108	0.139	0.242	0.093	0.407	0.751	0.371	0.834	0.051	0.046	0.875	0.197	0.035	0.119

II	CCCGCC	0.599	0.660	0.491	0.292	0.978	0.847	0.358	0.008	0.087	0.007	0.228	0.394	0.159	0.031	0.416	0.081	0.474	0.810	0.141	0.889	0.008	0.022	0.940	0.459	0.028	0.354
II	CGGTCG	0.827	0.016	0.611	0.147	0.865	0.779	0.628	0.816	0.645	0.009	0.186	0.602	0.037	0.160	0.251	0.127	0.024	0.809	0.072	0.770	0.007	0.129	0.897	0.018	0.007	0.363
II	GGTCGC	0.914	0.062	0.574	0.138	0.803	0.803	0.567	0.788	0.786	0.071	0.417	0.748	0.090	0.188	0.606	0.253	0.023	0.583	0.419	0.910	0.011	0.480	0.893	0.021	0.116	0.350
II	CCCGAG	0.480	0.946	0.482	0.080	0.933	0.467	0.854	0.910	0.344	0.211	0.471	0.952	0.475	0.255	0.308	0.182	0.587	0.910	0.337	0.947	0.156	0.179	0.950	0.098	0.051	0.373
II	AGGGCC	0.971	0.908	0.863	0.480	0.862	0.730	0.722	0.969	0.936	0.057	0.683	0.934	0.863	0.923	0.981	0.002	0.959	0.969	0.906	0.951	0.024	0.026	0.729	0.559	0.378	0.716
II	GGCGAC	0.777	0.065	0.497	0.197	0.836	0.164	0.598	0.667	0.545	0.011	0.610	0.630	0.102	0.148	0.754	0.376	0.074	0.358	0.430	0.737	0.033	0.295	0.903	0.021	0.144	0.216
II	CGCGGA	0.699	0.496	0.570	0.007	0.715	0.486	0.309	0.025	0.104	0.041	0.198	0.476	0.408	0.001	0.427	0.117	0.145	0.612	0.136	0.787	0.045	0.411	0.723	0.052	0.017	0.129
II	TTCCGG	0.277	0.692	0.185	0.087	0.889	0.191	0.242	0.841	0.080	0.185	0.111	0.734	0.320	0.000	0.705	0.029	0.095	0.623	0.059	0.820	0.007	0.348	0.736	0.091	0.298	0.192
II	GCAGCG	0.472	0.586	0.162	0.056	0.847	0.714	0.431	0.781	0.203	0.017	0.372	0.602	0.612	0.068	0.791	0.060	0.609	0.157	0.297	0.754	0.090	0.275	0.071	0.082	0.190	0.348
II	ATCCGG	0.299	0.652	0.565	0.099	0.743	0.263	0.578	0.582	0.126	0.103	0.027	0.547	0.416	0.004	0.516	0.011	0.510	0.514	0.075	0.503	0.012	0.146	0.846	0.100	0.085	0.273
II	ACGCGA	0.337	0.270	0.453	0.008	0.611	0.367	0.203	0.323	0.117	0.105	0.130	0.226	0.125	0.095	0.116	0.102	0.018	0.341	0.103	0.537	0.127	0.144	0.426	0.093	0.018	0.036
II	GGCGGC	0.769	0.619	0.769	0.358	0.957	0.673	0.571	0.333	0.666	0.000	0.289	0.688	0.305	0.015	0.705	0.217	0.732	0.711	0.320	0.708	0.003	0.144	0.760	0.005	0.019	0.275
II	GTCGGC	0.884	0.057	0.260	0.258	0.755	0.738	0.540	0.790	0.532	0.000	0.454	0.810	0.203	0.229	0.669	0.033	0.691	0.507	0.261	0.892	0.011	0.581	0.584	0.060	0.150	0.090
II	GACGGT	0.572	0.384	0.342	0.398	0.603	0.320	0.182	0.558	0.315	0.003	0.158	0.379	0.045	0.288	0.051	0.089	0.048	0.466	0.043	0.439	0.022	0.261	0.343	0.024	0.048	0.047
II	GGACGG	0.731	0.757	0.804	0.380	0.754	0.615	0.136	0.915	0.618	0.002	0.596	0.773	0.113	0.144	0.700	0.105	0.100	0.880	0.017	0.927	0.005	0.088	0.981	0.114	0.238	0.602
II	TGCGGC	0.555	0.633	0.395	0.263	0.946	0.542	0.634	0.632	0.353	0.003	0.562	0.857	0.238	0.030	0.483	0.161	0.495	0.195	0.085	0.802	0.007	0.204	0.252	0.161	0.100	0.100
II	GCTCCG	0.832	0.785	0.225	0.074	0.891	0.658	0.602	0.879	0.563	0.083	0.144	0.855	0.652	0.035	0.781	0.127	0.684	0.718	0.365	0.883	0.024	0.803	0.947	0.481	0.373	0.454
II	CGCGAA	0.237	0.467	0.266	0.038	0.640	0.173	0.166	0.005	0.056	0.043	0.220	0.242	0.277	0.016	0.348	0.076	0.252	0.475	0.239	0.489	0.160	0.281	0.131	0.173	0.053	0.155
II	CCCGAT	0.239	0.600	0.452	0.352	0.771	0.310	0.555	0.757	0.227	0.257	0.019	0.875	0.224	0.091	0.310	0.028	0.566	0.438	0.337	0.592	0.128	0.070	0.918	0.275	0.220	0.224
II	GCGTGG	0.654	0.440	0.619	0.010	0.784	0.573	0.378	0.369	0.266	0.041	0.222	0.440	0.250	0.091	0.302	0.031	0.026	0.469	0.093	0.755	0.157	0.032	0.844	0.046	0.007	0.002
II	AGGCCG	0.910	0.812	0.790	0.401	0.834	0.299	0.654	0.913	0.719	0.020	0.260	0.844	0.603	0.125	0.910	0.484	0.776	0.893	0.194	0.861	0.001	0.614	0.573	0.574	0.331	0.609
II	ACCCGC	0.759	0.758	0.518	0.073	0.910	0.414	0.364	0.008	0.033	0.032	0.370	0.663	0.102	0.015	0.063	0.044	0.265	0.554	0.159	0.780	0.084	0.064	0.777	0.136	0.024	0.184
II	GCCGTA	0.567	0.678	0.451	0.132	0.764	0.480	0.503	0.601	0.341	0.006	0.208	0.012	0.430	0.050	0.581	0.146	0.073	0.709	0.004	0.385	0.019	0.482	0.505	0.167	0.036	0.132
II	TTCGCG	0.281	0.507	0.221	0.058	0.696	0.111	0.311	0.006	0.098	0.035	0.109	0.367	0.083	0.041	0.529	0.035	0.223	0.509	0.293	0.484	0.283	0.344	0.416	0.096	0.074	0.054
II	CTGACG	0.528	0.464	0.197	0.290	0.700	0.600	0.452	0.566	0.487	0.051	0.208	0.398	0.025	0.322	0.277	0.173	0.073	0.371	0.334	0.402	0.184	0.152	0.042	0.036	0.142	0.002
II	GCGACG	0.722	0.399	0.725	0.101	0.611	0.345	0.522	0.430	0.301	0.018	0.121	0.721	0.126	0.129	0.293	0.239	0.128	0.197	0.207	0.598	0.034	0.321	0.561	0.021	0.081	0.099
II	GACGGG	0.587	0.747	0.704	0.113	0.678	0.426	0.528	0.882	0.460	0.095	0.141	0.945	0.056	0.024	0.382	0.128	0.163	0.663	0.182	0.706	0.067	0.031	0.933	0.109	0.077	0.187
II	GTGGCG	0.682	0.727	0.129	0.043	0.882	0.721	0.258	0.121	0.182	0.010	0.366	0.579	0.603	0.069	0.720	0.070	0.243	0.208	0.252	0.758	0.036	0.167	0.743	0.476	0.025	0.004
II	AAGGCG	0.435	0.751	0.837	0.487	0.651	0.349	0.105	0.751	0.758	0.037	0.324	0.808	0.514	0.122	0.744	0.156	0.547	0.754	0.610	0.753	0.123	0.585	0.921	0.120	0.363	0.232
II	CGAGCC	0.800	0.875	0.353	0.384	0.899	0.585	0.646	0.875	0.793	0.071	0.647	0.873	0.788	0.565	0.755	0.551	0.814	0.868	0.428	0.918	0.084	0.453	0.887	0.641	0.058	0.514
II	GGTCGG	0.624	0.008	0.617	0.323	0.941	0.669	0.301	0.954	0.866	0.001	0.156	0.914	0.100	0.241	0.516	0.020	0.101	0.907	0.180	0.966	0.021	0.467	0.976	0.077	0.546	0.761
II	GTGGCC	0.878	0.843	0.142	0.146	0.885	0.284	0.473	0.838	0.592	0.019	0.505	0.796	0.455	0.535	0.614	0.218	0.442	0.283	0.615	0.720	0.006	0.013	0.862	0.516	0.010	0.013
II	AGCGGC	0.742	0.830	0.183	0.637	0.726	0.639	0.602	0.818	0.665	0.006	0.735	0.830	0.375	0.064	0.885	0.423	0.509	0.353	0.402	0.758	0.026	0.658	0.513	0.252	0.237	0.379
II	AAACCG	0.214	0.217	0.261	0.028	0.424	0.039	0.210	0.348	0.372	0.021	0.185	0.197	0.030	0.047	0.053	0.006	0.274	0.381	0.230	0.536	0.026	0.181	0.706	0.164	0.270	0.291
II	TTCGGG	0.219	0.575	0.284	0.410	0.651	0.093	0.529	0.697	0.231	0.162	0.333	0.214	0.159	0.099	0.607	0.069	0.304	0.559	0.407	0.382	0.095	0.104	0.789	0.259	0.368	0.360
II	GGCGGT	0.556	0.511	0.441	0.157	0.847	0.198	0.317	0.082	0.074	0.001	0.128	0.313	0.075	0.048	0.053	0.124	0.287	0.583	0.101	0.509	0.016	0.182	0.786	0.069	0.137	0.230
II	CCGCCA	0.680	0.486	0.314	0.163	0.820	0.225	0.526	0.003	0.258	0.002	0.328	0.545	0.148	0.045	0.445	0.109	0.358	0.435	0.305	0.799	0.014	0.076	0.838	0.029	0.117	0.033
II	TGGCGG	0.639	0.488	0.441	0.078	0.900	0.474	0.652	0.008	0.153	0.002	0.173	0.662	0.109	0.019	0.326	0.074	0.292	0.430	0.327	0.686	0.012	0.042	0.870	0.075	0.056	0.148
II	CCGGAG	0.889	0.924	0.632	0.081	0.934	0.688	0.791	0.930	0.435	0.110	0.258	0.812	0.477	0.005	0.661	0.117	0.366	0.880	0.293	0.929	0.005	0.207	0.971	0.166	0.743	0.473
II	CCGACC	0.863	0.004	0.484	0.276	0.987	0.643	0.747	0.950	0.631	0.000	0.185	0.963	0.158	0.353	0.104	0.011	0.244	0.905	0.426	0.937	0.028	0.186	0.853	0.082	0.048	0.362
II	CCGGCT	0.730	0.608	0.417	0.582	0.848	0.788	0.539	0.919	0.831	0.005	0.664	0.581	0.408	0.050	0.683	0.189	0.445	0.872	0.635	0.814	0.008	0.180	0.907	0.340	0.079	0.546
II	ACGTGT	0.364	0.260	0.317	0.005	0.477	0.370	0.084	0.272	0.228	0.091	0.212	0.158	0.029	0.516	0.323	0.029	0.003	0.327	0.041	0.076	0.043	0.079	0.184	0.036	0.000	0.000
II	CAGCGG	0.749	0.585	0.142	0.078	0.930	0.443	0.695	0.789	0.364	0.038	0.706	0.898	0.174	0.066	0.721	0.254	0.555	0.117	0.334	0.776	0.106	0.127	0.382	0.130	0.152	0.193
II	GCCGAG	0.689	0.736	0.491	0.029	0.838	0.783	0.623	0.836	0.520	0.027	0.278	0.439	0.415	0.261	0.703	0.270	0.661	0.871	0.499	0.847	0.042	0.793	0.887	0.378	0.133	0.080
II	CGGGAC	0.817	0.487	0.586	0.074	0.944	0.613	0.765	0.540	0.507	0.205	0.403	0.783	0.077	0.055	0.736	0.433	0.098	0.567	0.130	0.793	0.036	0.020	0.942	0.091	0.213	0.398
II	CCGTCA	0.739	0.566	0.405	0.279	0.755	0.533	0.367	0.693	0.332	0.006	0.231	0.487	0.015	0.089	0.391	0.103	0.033	0.557	0.114	0.520	0.033	0.246	0.180	0.024	0.109	0.013

II	CCCGTT	0.361	0.515	0.662	0.351	0.619	0.112	0.066	0.818	0.233	0.099	0.215	0.376	0.110	0.097	0.319	0.060	0.328	0.354	0.346	0.409	0.119	0.086	0.871	0.095	0.105	0.525
III	GCCCGG	0.884	0.877	0.587	0.450	0.927	0.790	0.672	0.903	0.340	0.014	0.669	0.920	0.325	0.004	0.433	0.095	0.736	0.844	0.176	0.933	0.002	0.028	0.901	0.272	0.153	0.257
III	TAACCG	0.165	0.222	0.156	0.088	0.389	0.249	0.112	0.146	0.183	0.009	0.201	0.160	0.036	0.126	0.002	0.000	0.093	0.293	0.237	0.175	0.034	0.186	0.702	0.125	0.077	0.046
III	GAGGCC	0.941	0.879	0.725	0.406	0.798	0.560	0.591	0.926	0.788	0.042	0.758	0.942	0.781	0.344	0.928	0.500	0.890	0.897	0.828	0.859	0.022	0.134	0.263	0.578	0.642	0.767
III	AAGGGC	0.755	0.893	0.738	0.918	0.572	0.441	0.097	0.923	0.856	0.139	0.544	0.913	0.432	0.467	0.731	0.004	0.823	0.913	0.579	0.875	0.069	0.191	0.870	0.635	0.583	0.806
III	CCCATT	0.274	0.478	0.579	0.497	0.646	0.181	0.468	0.661	0.312	0.067	0.163	0.649	0.188	0.163	0.251	0.184	0.406	0.272	0.498	0.552	0.133	0.019	0.533	0.062	0.079	0.027
III	GGTCCA	0.745	0.450	0.289	0.426	0.806	0.573	0.413	0.813	0.316	0.161	0.273	0.773	0.082	0.392	0.105	0.267	0.009	0.417	0.582	0.748	0.054	0.003	0.688	0.006	0.058	0.072
III	AGTGGG	0.599	0.784	0.014	0.328	0.788	0.588	0.303	0.861	0.529	0.168	0.235	0.599	0.269	0.526	0.452	0.140	0.630	0.657	0.595	0.655	0.219	0.006	0.706	0.325	0.384	0.289
III	AACGAC	0.280	0.083	0.361	0.083	0.282	0.265	0.011	0.273	0.327	0.049	0.163	0.277	0.036	0.327	0.121	0.010	0.052	0.146	0.177	0.239	0.060	0.214	0.216	0.018	0.012	0.086
III	TATCGG	0.179	0.127	0.282	0.241	0.161	0.050	0.101	0.098	0.137	0.029	0.059	0.529	0.038	0.095	0.034	0.013	0.120	0.146	0.094	0.205	0.010	0.027	0.681	0.142	0.039	0.105
III	CCGAAT	0.132	0.281	0.404	0.071	0.397	0.067	0.284	0.177	0.014	0.027	0.057	0.048	0.049	0.150	0.336	0.007	0.198	0.253	0.157	0.286	0.117	0.120	0.697	0.092	0.016	0.080
III	AAAGCC	0.395	0.548	0.163	0.788	0.239	0.133	0.015	0.753	0.718	0.115	0.434	0.593	0.320	0.739	0.740	0.370	0.483	0.543	0.727	0.329	0.492	0.712	0.616	0.164	0.195	0.271
III	TCCGAA	0.263	0.388	0.068	0.071	0.331	0.092	0.062	0.363	0.106	0.285	0.169	0.275	0.368	0.121	0.455	0.044	0.373	0.413	0.392	0.516	0.100	0.441	0.449	0.217	0.224	0.430
III	GGGGTC	0.621	0.988	0.714	0.513	0.976	0.509	0.860	0.993	0.571	0.212	0.135	0.982	0.100	0.075	0.125	0.497	0.069	0.973	0.494	0.959	0.429	0.017	0.970	0.012	0.189	0.140
III	TCCGAC	0.453	0.009	0.425	0.085	0.761	0.321	0.508	0.606	0.479	0.007	0.135	0.673	0.063	0.303	0.242	0.101	0.179	0.313	0.328	0.686	0.002	0.401	0.574	0.099	0.233	0.127
III	ATTCGG	0.086	0.194	0.571	0.080	0.518	0.046	0.511	0.149	0.022	0.038	0.119	0.046	0.113	0.126	0.420	0.010	0.316	0.371	0.130	0.342	0.093	0.132	0.570	0.165	0.156	0.135
III	CCAACG	0.803	0.533	0.710	0.149	0.762	0.648	0.041	0.371	0.528	0.042	0.293	0.822	0.111	0.490	0.183	0.015	0.288	0.064	0.415	0.760	0.199	0.186	0.909	0.106	0.161	0.181
III	GGCTTT	0.199	0.531	0.035	0.599	0.267	0.083	0.011	0.339	0.409	0.095	0.380	0.411	0.120	0.705	0.631	0.369	0.368	0.474	0.637	0.266	0.489	0.438	0.759	0.054	0.019	0.323
III	GACCCA	0.842	0.577	0.206	0.436	0.809	0.527	0.361	0.760	0.655	0.131	0.106	0.406	0.097	0.669	0.093	0.113	0.036	0.331	0.213	0.610	0.092	0.008	0.647	0.016	0.126	0.229
III	TTTGGG	0.217	0.087	0.410	0.348	0.318	0.041	0.137	0.199	0.058	0.021	0.039	0.007	0.025	0.217	0.428	0.068	0.045	0.158	0.251	0.459	0.051	0.035	0.471	0.122	0.020	0.024
III	AATCCG	0.133	0.308	0.621	0.079	0.501	0.076	0.347	0.258	0.135	0.140	0.039	0.272	0.106	0.023	0.344	0.009	0.270	0.420	0.172	0.364	0.068	0.348	0.716	0.180	0.308	0.191
III	AAAGGC	0.327	0.777	0.812	0.614	0.357	0.194	0.009	0.802	0.745	0.118	0.675	0.648	0.252	0.601	0.818	0.385	0.526	0.758	0.625	0.580	0.272	0.425	0.619	0.404	0.203	0.494
III	CCGACA	0.619	0.000	0.382	0.105	0.632	0.371	0.403	0.429	0.175	0.000	0.208	0.451	0.052	0.127	0.459	0.055	0.334	0.046	0.165	0.598	0.013	0.200	0.487	0.240	0.023	0.038
III	GTGGAC	0.442	0.499	0.049	0.080	0.584	0.489	0.128	0.613	0.314	0.091	0.396	0.456	0.094	0.253	0.215	0.316	0.035	0.401	0.293	0.528	0.142	0.006	0.678	0.007	0.079	0.006
III	GTCCAG	0.682	0.653	0.205	0.389	0.555	0.711	0.253	0.660	0.278	0.049	0.158	0.716	0.072	0.675	0.546	0.345	0.035	0.635	0.452	0.655	0.032	0.084	0.134	0.006	0.103	0.023
III	GATGGG	0.491	0.532	0.320	0.593	0.725	0.131	0.422	0.852	0.412	0.099	0.024	0.874	0.186	0.471	0.339	0.034	0.294	0.375	0.473	0.504	0.206	0.009	0.888	0.460	0.054	0.043
III	ATCCGA	0.327	0.154	0.230	0.092	0.258	0.182	0.180	0.260	0.159	0.176	0.020	0.298	0.147	0.279	0.333	0.007	0.161	0.184	0.233	0.353	0.046	0.289	0.536	0.186	0.014	0.073
III	CCGAGA	0.482	0.723	0.425	0.368	0.631	0.538	0.569	0.722	0.325	0.061	0.133	0.648	0.361	0.203	0.621	0.101	0.155	0.709	0.662	0.630	0.145	0.300	0.888	0.136	0.252	0.458
III	CCGTAA	0.169	0.278	0.334	0.108	0.382	0.200	0.126	0.137	0.115	0.050	0.244	0.117	0.131	0.023	0.093	0.084	0.018	0.267	0.014	0.330	0.105	0.175	0.499	0.213	0.241	0.161
III	CCAATA	0.144	0.105	0.410	0.323	0.241	0.104	0.123	0.065	0.267	0.075	0.076	0.218	0.029	0.252	0.206	0.060	0.034	0.200	0.098	0.214	0.163	0.023	0.427	0.050	0.046	0.103
III	GAGTGG	0.711	0.708	0.010	0.055	0.580	0.586	0.172	0.762	0.490	0.071	0.391	0.771	0.264	0.347	0.174	0.167	0.427	0.469	0.364	0.815	0.394	0.015	0.668	0.268	0.218	0.116
III	ACGAGG	0.648	0.609	0.777	0.119	0.714	0.658	0.310	0.708	0.642	0.243	0.525	0.712	0.542	0.318	0.500	0.157	0.492	0.698	0.161	0.570	0.311	0.256	0.464	0.199	0.023	0.114
III	GGCTCA	0.747	0.841	0.192	0.577	0.785	0.752	0.386	0.761	0.845	0.115	0.674	0.843	0.397	0.639	0.579	0.307	0.782	0.693	0.684	0.830	0.324	0.483	0.838	0.477	0.303	0.662
III	GCTGAG	0.704	0.797	0.140	0.548	0.781	0.740	0.461	0.791	0.742	0.065	0.355	0.583	0.421	0.529	0.686	0.164	0.512	0.433	0.326	0.860	0.397	0.422	0.310	0.069	0.549	0.188
III	GGCTAA	0.283	0.554	0.327	0.678	0.523	0.255	0.144	0.651	0.652	0.071	0.365	0.389	0.431	0.464	0.119	0.073	0.308	0.450	0.535	0.472	0.158	0.355	0.521	0.419	0.354	0.386
III	ACCGAT	0.345	0.305	0.277	0.086	0.379	0.214	0.186	0.202	0.262	0.013	0.010	0.324	0.051	0.134	0.039	0.028	0.063	0.302	0.073	0.276	0.025	0.164	0.607	0.043	0.101	0.097
III	TGCCAG	0.332	0.617	0.202	0.411	0.666	0.423	0.416	0.647	0.444	0.050	0.136	0.652	0.396	0.571	0.530	0.102	0.357	0.430	0.353	0.537	0.122	0.514	0.013	0.107	0.150	0.000
III	GCCAGA	0.451	0.719	0.272	0.658	0.757	0.521	0.407	0.703	0.551	0.056	0.153	0.482	0.370	0.686	0.807	0.069	0.564	0.510	0.221	0.633	0.097	0.376	0.038	0.334	0.118	0.016
III	TGGGGT	0.303	0.425	0.230	0.175	0.629	0.105	0.310	0.736	0.073	0.010	0.010	0.284	0.030	0.229	0.023	0.038	0.004	0.065	0.064	0.392	0.214	0.007	0.449	0.052	0.000	0.035
III	TGTGGC	0.481	0.238	0.115	0.265	0.604	0.285	0.240	0.388	0.208	0.023	0.260	0.659	0.210	0.239	0.295	0.029	0.187	0.003	0.344	0.545	0.068	0.042	0.212	0.382	0.003	0.007
III	AAGTGG	0.458	0.442	0.021	0.577	0.415	0.291	0.042	0.683	0.328	0.256	0.488	0.440	0.286	0.446	0.357	0.287	0.229	0.418	0.504	0.476	0.347	0.021	0.457	0.214	0.204	0.115
III	TAAACG	0.096	0.133	0.305	0.066	0.259	0.068	0.014	0.301	0.092	0.067	0.148	0.086	0.034	0.151	0.106	0.026	0.078	0.059	0.066	0.052	0.190	0.124	0.609	0.089	0.023	0.023
III	TAATCG	0.067	0.020	0.483	0.155	0.122	0.042	0.117	0.020	0.045	0.034	0.014	0.143	0.011	0.301	0.056	0.017	0.052	0.050	0.080	0.018	0.029	0.109	0.291	0.045	0.017	0.006
III	ATCGAA	0.171	0.270	0.106	0.362	0.286	0.074	0.113	0.266	0.142	0.167	0.022	0.274	0.126	0.571	0.355	0.037	0.197	0.259	0.245	0.093	0.368	0.291	0.473	0.221	0.218	0.248
III	AAATGG	0.081	0.272	0.758	0.510	0.394	0.039	0.164	0.446	0.140	0.134	0.297	0.288	0.160	0.337	0.304	0.203	0.324	0.231	0.399	0.420	0.237	0.074	0.437	0.155	0.171	0.146
III	GGATAA	0.072	0.092	0.148	0.295	0.223	0.092	0.038	0.252	0.206	0.078	0.152	0.251	0.093	0.143	0.114	0.000	0.058	0.103	0.072	0.141	0.183	0.066	0.181	0.102	0.143	0.104

III	ATAAGG	0.149	0.215	0.411	0.741	0.103	0.324	0.184	0.485	0.413	0.091	0.180	0.314	0.078	0.280	0.417	0.023	0.112	0.218	0.211	0.092	0.264	0.048	0.498	0.236	0.034	0.018
III	CCACAG	0.785	0.508	0.060	0.651	0.833	0.557	0.455	0.806	0.501	0.044	0.168	0.796	0.450	0.841	0.075	0.134	0.292	0.011	0.419	0.767	0.136	0.013	0.265	0.214	0.083	0.333
III	AAATCC	0.051	0.515	0.588	0.428	0.293	0.030	0.282	0.383	0.296	0.185	0.031	0.141	0.217	0.168	0.401	0.006	0.303	0.326	0.473	0.417	0.467	0.558	0.548	0.200	0.215	0.208
III	ATCCAA	0.207	0.306	0.193	0.484	0.370	0.086	0.209	0.143	0.061	0.119	0.020	0.207	0.057	0.705	0.323	0.009	0.073	0.127	0.165	0.313	0.327	0.150	0.360	0.205	0.112	0.087
III	AGTGGA	0.458	0.424	0.007	0.299	0.553	0.471	0.083	0.429	0.314	0.390	0.235	0.664	0.258	0.699	0.460	0.165	0.309	0.384	0.402	0.521	0.375	0.082	0.337	0.102	0.352	0.131
III	ATGCCA	0.444	0.332	0.355	0.500	0.674	0.390	0.347	0.443	0.370	0.108	0.200	0.647	0.320	0.483	0.563	0.049	0.301	0.139	0.329	0.455	0.126	0.405	0.514	0.505	0.098	0.008
III	CATACG	0.297	0.273	0.517	0.025	0.525	0.263	0.210	0.202	0.081	0.045	0.088	0.293	0.143	0.216	0.240	0.047	0.045	0.089	0.020	0.121	0.184	0.077	0.663	0.091	0.009	0.015
III	TTATCC	0.088	0.063	0.338	0.225	0.145	0.087	0.031	0.065	0.188	0.033	0.073	0.214	0.043	0.107	0.184	0.000	0.021	0.099	0.035	0.086	0.088	0.042	0.277	0.081	0.081	0.044
III	GTCCAT	0.485	0.402	0.295	0.432	0.530	0.428	0.104	0.554	0.264	0.071	0.172	0.645	0.062	0.668	0.407	0.084	0.049	0.381	0.217	0.636	0.096	0.067	0.767	0.046	0.010	0.057
III	TATCCA	0.148	0.339	0.267	0.285	0.351	0.126	0.153	0.236	0.166	0.139	0.115	0.426	0.169	0.434	0.256	0.000	0.157	0.142	0.126	0.296	0.359	0.154	0.158	0.144	0.059	0.121
III	GATAAG	0.242	0.058	0.068	0.178	0.085	0.086	0.110	0.144	0.156	0.030	0.082	0.066	0.067	0.076	0.130	0.000	0.039	0.153	0.120	0.052	0.086	0.088	0.096	0.054	0.088	0.036
III	ATGTGG	0.305	0.102	0.177	0.233	0.441	0.121	0.088	0.065	0.039	0.028	0.058	0.293	0.047	0.228	0.112	0.033	0.126	0.004	0.112	0.490	0.174	0.002	0.429	0.079	0.003	0.006
III	ATCCTA	0.306	0.321	0.364	0.507	0.214	0.156	0.159	0.307	0.253	0.318	0.049	0.410	0.236	0.754	0.391	0.026	0.464	0.345	0.199	0.304	0.380	0.289	0.488	0.113	0.241	0.141
III	AAAATC	0.015	0.163	0.525	0.648	0.022	0.015	0.109	0.384	0.103	0.096	0.060	0.049	0.051	0.356	0.201	0.002	0.109	0.074	0.342	0.128	0.086	0.187	0.274	0.092	0.044	0.090
III	AATTGA	0.051	0.038	0.445	0.380	0.239	0.016	0.193	0.107	0.062	0.052	0.074	0.057	0.006	0.568	0.115	0.091	0.064	0.134	0.189	0.096	0.321	0.128	0.321	0.010	0.048	0.040
III	AGAGTG	0.450	0.413	0.002	0.303	0.194	0.458	0.182	0.364	0.454	0.216	0.225	0.526	0.220	0.400	0.288	0.210	0.184	0.220	0.473	0.523	0.567	0.133	0.358	0.304	0.079	0.181
III	ATCAGA	0.209	0.203	0.161	0.217	0.231	0.173	0.104	0.200	0.188	0.115	0.011	0.289	0.024	0.586	0.281	0.025	0.218	0.028	0.203	0.097	0.050	0.083	0.036	0.080	0.046	0.072
III	TCAGAA	0.177	0.169	0.105	0.238	0.079	0.073	0.099	0.308	0.046	0.085	0.084	0.176	0.092	0.719	0.264	0.075	0.138	0.124	0.295	0.260	0.046	0.161	0.009	0.059	0.133	0.115
III	ATTAAA	0.008	0.041	0.275	0.282	0.027	0.010	0.020	0.193	0.022	0.023	0.079	0.020	0.002	0.803	0.088	0.055	0.029	0.040	0.161	0.011	0.153	0.067	0.217	0.041	0.018	0.025
III	AAAATG	0.020	0.063	0.445	0.667	0.020	0.027	0.052	0.191	0.010	0.061	0.174	0.031	0.036	0.233	0.150	0.103	0.048	0.108	0.073	0.122	0.266	0.065	0.271	0.061	0.027	0.086
III	CTTATC	0.252	0.101	0.072	0.149	0.147	0.154	0.139	0.254	0.346	0.082	0.057	0.238	0.069	0.088	0.249	0.000	0.060	0.111	0.142	0.061	0.090	0.104	0.240	0.095	0.113	0.064

Supplemental Table S9. The sequence similarity distance (1-Pearson's correlation coefficients) of pair-wise comparisons between 6-mer sequences and known TFBMs in Franco-Zorrilla et al., 2014

Type	Motif	MYB-R2R3	Myb-related	GARP-ARR-B	GARP-G2	Trihelix	ERF	DREB	AP2	HD-WUS-like	HD-ZIP	SBP_SPL	WRKY	C2H2	C2C2-GATA	C2C2-YABBY	C2C2-DOF	TCP	HSF	bZIP	B3-ARF	B3-REM	NAC	ATHook_AHL	bHLH	LOBAS2	SRS
I	GGGCCG	0.710	0.990	0.698	0.838	0.690	0.324	0.410	0.763	1.055	1.037	0.657	0.557	0.716	0.760	1.035	0.883	0.293	0.795	0.552	0.615	0.760	0.675	1.397	0.720	0.810	0.890
I	GGGCCC	0.897	1.058	0.770	0.876	0.900	0.530	0.615	0.877	1.130	1.233	0.873	0.685	0.726	0.800	1.135	0.977	0.070	0.855	0.777	0.830	0.890	0.888	1.411	0.940	0.870	0.965
I	GGGCCT	0.726	0.853	0.668	0.736	0.880	0.508	0.589	0.698	0.935	1.013	0.727	0.655	0.800	0.630	0.925	0.840	0.283	0.845	0.677	0.805	0.875	0.748	1.207	0.890	0.710	0.905
I	TGGGCC	0.722	0.973	0.818	0.784	0.700	0.532	0.482	0.752	0.985	1.010	0.713	0.462	0.758	0.650	0.925	0.897	0.070	0.790	0.790	0.645	0.765	0.772	1.202	0.710	0.850	0.740
I	GGCCCA	0.722	0.973	0.818	0.784	0.700	0.532	0.482	0.752	0.985	1.010	0.713	0.462	0.758	0.650	0.925	0.897	0.070	0.790	0.790	0.645	0.770	0.772	1.202	0.710	0.850	0.740
I	CGGCCC	0.710	0.990	0.698	0.838	0.690	0.324	0.410	0.763	1.055	1.037	0.657	0.557	0.716	0.760	1.035	0.883	0.293	0.795	0.552	0.615	0.760	0.675	1.397	0.720	0.810	0.890
I	AGGCCC	0.726	0.853	0.668	0.736	0.880	0.508	0.589	0.698	0.935	1.013	0.727	0.655	0.800	0.630	0.925	0.840	0.283	0.845	0.677	0.805	0.875	0.748	1.207	0.890	0.710	0.905
I	GCCCAT	0.670	0.800	0.605	0.686	0.710	0.604	0.596	0.698	0.620	0.810	0.670	0.633	0.696	0.690	0.735	0.707	0.290	0.790	0.728	0.670	0.705	0.698	0.987	0.660	0.760	0.635
I	GGGCTT	0.749	0.670	0.628	0.644	0.770	0.627	0.672	0.667	0.845	0.797	0.727	0.682	0.658	0.690	0.715	0.760	0.510	0.728	0.680	0.820	0.855	0.667	1.010	0.890	0.600	0.740
I	AGCCCA	0.673	0.820	0.715	0.752	0.820	0.598	0.540	0.608	0.795	0.973	0.753	0.545	0.538	0.690	0.775	0.833	0.290	0.818	0.682	0.655	0.765	0.693	1.016	0.880	0.750	0.575
I	TTGGGC	0.562	0.940	0.800	0.870	0.700	0.602	0.577	0.672	0.785	0.877	0.563	0.462	0.616	0.650	0.740	0.840	0.297	0.893	0.790	0.665	0.690	0.583	1.049	0.720	0.680	0.630
I	GCCCAA	0.562	0.940	0.800	0.870	0.700	0.602	0.577	0.672	0.785	0.877	0.563	0.462	0.616	0.650	0.740	0.840	0.297	0.893	0.790	0.665	0.690	0.583	1.049	0.720	0.680	0.630
I	TGGCCC	0.800	0.857	0.833	0.744	0.690	0.485	0.542	0.737	0.995	1.023	0.800	0.465	0.776	0.660	0.930	0.863	0.227	0.797	0.675	0.640	0.780	0.745	1.201	0.930	0.690	0.745
I	TGGGCT	0.673	0.820	0.715	0.752	0.820	0.598	0.540	0.608	0.795	0.973	0.753	0.545	0.538	0.690	0.775	0.833	0.290	0.818	0.682	0.655	0.765	0.693	1.016	0.880	0.750	0.575
I	GCCCAG	0.712	0.993	0.830	0.912	0.710	0.528	0.552	0.685	0.845	0.980	0.650	0.613	0.656	0.840	0.940	0.863	0.290	0.743	0.765	0.675	0.745	0.805	1.202	0.500	0.600	0.555
I	AAGCCC	0.749	0.670	0.628	0.644	0.770	0.627	0.672	0.667	0.845	0.797	0.727	0.682	0.658	0.690	0.715	0.760	0.510	0.728	0.680	0.820	0.855	0.667	1.010	0.890	0.600	0.740
I	GGCCCG	0.758	0.995	0.698	0.862	0.690	0.503	0.518	0.765	1.025	1.023	0.663	0.557	0.784	0.760	1.060	0.917	0.273	0.767	0.677	0.595	0.790	0.598	1.396	0.490	0.620	0.740
I	ATGGGC	0.670	0.800	0.605	0.686	0.710	0.604	0.596	0.698	0.620	0.810	0.670	0.633	0.696	0.690	0.735	0.707	0.290	0.790	0.728	0.670	0.705	0.698	0.987	0.660	0.760	0.635
I	GCCACG	0.631	0.807	0.690	0.900	0.560	0.482	0.536	0.585	0.855	0.820	0.670	0.445	0.682	1.000	0.910	0.790	0.493	0.720	0.420	0.680	0.450	0.460	1.210	0.050	0.700	0.640
I	CTGGGC	0.712	0.993	0.830	0.912	0.710	0.528	0.552	0.685	0.845	0.980	0.650	0.613	0.656	0.840	0.940	0.863	0.290	0.743	0.765	0.675	0.745	0.805	1.202	0.500	0.600	0.555
I	GCCCAC	0.531	0.998	0.810	0.910	0.800	0.458	0.386	0.688	0.835	0.993	0.660	0.490	0.534	0.740	0.885	0.797	0.070	0.830	0.650	0.445	0.665	0.730	1.206	0.720	0.810	0.645
I	GGCCTG	0.732	0.812	0.718	0.752	0.710	0.612	0.570	0.707	0.905	0.800	0.660	0.680	0.644	0.590	0.830	0.823	0.487	0.743	0.627	0.675	0.870	0.565	1.190	0.670	0.780	0.625
I	GTGGGC	0.531	0.998	0.810	0.910	0.800	0.458	0.386	0.688	0.835	0.993	0.660	0.490	0.534	0.740	0.885	0.797	0.070	0.830	0.650	0.445	0.665	0.730	1.206	0.720	0.810	0.645
I	TAGGCC	0.610	0.792	0.737	0.630	0.690	0.627	0.543	0.602	0.890	0.853	0.550	0.465	0.688	0.480	0.690	0.813	0.287	0.688	0.625	0.640	0.655	0.620	0.980	0.890	0.770	0.520
I	GGCCTT	0.714	0.673	0.632	0.726	0.730	0.567	0.610	0.687	0.850	0.777	0.560	0.665	0.746	0.690	0.810	0.603	0.520	0.750	0.680	0.850	0.875	0.700	1.010	0.890	0.790	0.735
I	AAGGCC	0.714	0.673	0.632	0.726	0.730	0.567	0.610	0.687	0.850	0.777	0.560	0.665	0.746	0.690	0.810	0.603	0.520	0.750	0.680	0.850	0.875	0.700	1.010	0.890	0.790	0.735
I	GGGCCA	0.800	0.857	0.833	0.744	0.690	0.485	0.542	0.737	0.995	1.023	0.800	0.465	0.776	0.660	0.930	0.863	0.227	0.797	0.675	0.640	0.780	0.745	1.201	0.930	0.690	0.745
I	CACGTG	0.660	0.833	0.835	0.836	0.490	0.862	0.761	0.585	0.880	0.850	0.740	0.825	0.706	0.810	0.910	0.583	0.883	0.790	0.402	0.870	0.690	0.392	1.012	0.000	0.690	0.780
I	GGGCTG	0.659	0.802	0.740	0.698	0.770	0.468	0.514	0.727	0.900	0.817	0.680	0.590	0.534	0.590	0.840	0.860	0.520	0.750	0.710	0.675	0.700	0.778	1.191	0.890	0.800	0.745
I	AGCCCG	0.753	0.897	0.708	0.772	0.570	0.582	0.595	0.602	1.010	0.993	0.673	0.562	0.636	0.690	0.910	0.847	0.493	0.752	0.720	0.595	0.785	0.568	1.226	0.660	0.520	0.575
I	GGCCTA	0.610	0.792	0.737	0.630	0.690	0.627	0.543	0.602	0.890	0.853	0.550	0.465	0.688	0.480	0.690	0.813	0.287	0.688	0.625	0.640	0.655	0.620	0.980	0.890	0.770	0.520
I	AACCGG	0.573	0.838	0.563	0.762	0.470	0.602	0.492	0.518	0.765	0.770	0.667	0.547	0.688	0.740	0.685	0.580	0.800	0.732	0.848	0.785	0.690	0.650	1.016	0.670	0.370	0.670
I	GCCCGT	0.714	0.898	0.718	0.856	0.500	0.612	0.526	0.593	0.835	0.907	0.483	0.722	0.704	0.900	0.925	0.653	0.510	0.755	0.625	0.750	0.765	0.527	1.206	0.440	0.610	0.520
I	ACGTGG	0.529	0.800	0.730	0.844	0.690	0.687	0.555	0.435	0.875	0.820	0.687	0.497	0.638	0.790	0.850	0.460	0.867	0.757	0.338	0.660	0.460	0.395	1.006	0.000	0.680	0.665
I	GGGCTC	0.824	0.847	0.628	0.704	0.800	0.479	0.594	0.765	1.030	1.010	0.873	0.690	0.592	0.690	0.900	0.910	0.293	0.740	0.712	0.815	0.865	0.850	1.179	0.950	0.770	0.745
I	GGCCGA	0.692	0.978	0.808	0.810	0.690	0.441	0.356	0.675	0.885	0.927	0.513	0.417	0.714	0.700	0.910	0.823	0.290	0.788	0.647	0.425	0.760	0.808	1.201	0.890	0.690	0.740
I	ACGCGG	0.682	0.888	0.732	0.936	0.690	0.494	0.553	0.565	1.000	0.973	0.657	0.683	0.692	0.960	0.910	0.587	0.940	0.795	0.560	0.765	0.460	0.522	1.226	0.220	0.460	0.670
I	GGGCTA	0.678	0.638	0.692	0.562	0.560	0.629	0.673	0.597	0.830	0.860	0.770	0.465	0.588	0.490	0.760	0.783	0.447	0.693	0.840	0.640	0.655	0.778	0.981	1.110	0.580	0.525
I	GTCGGG	0.526	0.993	0.713	1.000	0.700	0.463	0.317	0.603	0.860	0.797	0.450	0.615	0.632	0.790	0.890	0.827	0.510	0.748	0.580	0.315	0.680	0.648	1.217	0.670	0.540	0.645
I	ACGGCC	0.648	0.895	0.735	0.784	0.500	0.418	0.400	0.678	0.845	0.993	0.370	0.607	0.712	0.860	0.910	0.760	0.520	0.825	0.453	0.635	0.825	0.635	1.206	0.660	0.770	0.745

I	CGACGT	0.626	0.713	0.733	0.818	0.570	0.478	0.398	0.440	0.920	0.913	0.603	0.488	0.818	0.690	0.865	0.613	0.810	0.715	0.223	0.440	0.565	0.518	1.006	0.220	0.800	0.665
I	GAACCG	0.539	0.775	0.467	0.600	0.440	0.483	0.439	0.535	0.795	0.760	0.450	0.532	0.624	0.540	0.690	0.657	0.573	0.668	0.750	0.625	0.780	0.675	0.980	0.720	0.700	0.890
I	ACCCGA	0.550	0.785	0.645	0.884	0.690	0.626	0.522	0.520	0.785	0.873	0.607	0.725	0.622	0.540	0.725	0.723	0.673	0.748	0.667	0.555	0.575	0.512	1.017	0.670	0.500	0.470
I	ACCGGA	0.568	0.840	0.723	0.940	0.480	0.585	0.551	0.573	0.870	0.887	0.383	0.835	0.610	0.590	0.740	0.653	0.723	0.708	0.680	0.670	0.750	0.665	1.018	0.670	0.280	0.575
I	ACCGGG	0.704	0.993	0.688	1.006	0.270	0.638	0.555	0.578	0.985	0.973	0.607	0.845	0.738	0.790	0.910	0.663	0.740	0.817	0.788	0.760	0.690	0.722	1.226	0.450	0.330	0.670
I	CCGGAT	0.682	0.750	0.348	0.744	0.670	0.582	0.613	0.630	0.800	0.770	0.447	0.748	0.714	0.520	0.715	0.773	0.807	0.730	0.728	0.650	0.580	0.625	1.010	0.660	0.140	0.670
I	AGGCCT	0.831	0.680	0.683	0.766	0.910	0.653	0.647	0.627	1.005	0.810	0.837	0.675	0.788	0.460	0.700	0.873	0.513	0.877	0.677	0.810	0.820	0.675	1.040	0.890	0.930	0.905
I	AGCCGT	0.724	0.700	0.603	0.760	0.470	0.385	0.518	0.622	0.880	0.807	0.500	0.737	0.592	0.690	0.675	0.723	0.740	0.845	0.453	0.680	0.645	0.557	1.040	0.670	0.590	0.685
I	AACGGC	0.587	0.748	0.598	0.810	0.440	0.438	0.457	0.660	0.835	0.683	0.337	0.785	0.610	0.690	0.780	0.527	0.740	0.810	0.467	0.665	0.800	0.643	1.009	0.670	0.740	0.635
I	ATTGGG	0.538	0.775	0.618	0.786	0.710	0.657	0.700	0.642	0.555	0.673	0.680	0.665	0.668	0.760	0.600	0.713	0.520	0.892	0.715	0.730	0.690	0.420	0.830	0.520	0.590	0.565
I	ACTGGG	0.654	0.840	0.818	0.858	0.490	0.664	0.686	0.603	0.770	0.767	0.740	0.808	0.582	0.980	0.710	0.730	0.520	0.737	0.763	0.800	0.665	0.632	1.013	0.450	0.550	0.445
I	CGTGTC	0.703	0.585	0.515	0.754	0.790	0.664	0.644	0.678	0.865	0.803	0.670	0.610	0.664	0.780	0.860	0.677	0.577	0.670	0.465	0.830	0.425	0.278	0.997	0.280	0.730	0.860
I	AACCGA	0.421	0.668	0.663	0.798	0.470	0.623	0.384	0.442	0.555	0.670	0.537	0.542	0.674	0.540	0.590	0.547	0.603	0.745	0.843	0.585	0.715	0.675	0.800	0.890	0.620	0.575
I	AGCCGG	0.624	0.860	0.575	0.866	0.700	0.378	0.409	0.670	0.980	0.973	0.623	0.713	0.662	0.740	0.885	0.720	0.720	0.770	0.677	0.560	0.650	0.720	1.226	0.670	0.370	0.575
I	AATGGG	0.629	0.645	0.732	0.628	0.660	0.747	0.698	0.678	0.645	0.543	0.727	0.802	0.690	0.780	0.600	0.517	0.520	0.812	0.788	0.790	0.680	0.608	0.796	0.520	0.780	0.565
I	CCCAAT	0.538	0.775	0.618	0.786	0.710	0.657	0.700	0.642	0.555	0.673	0.680	0.665	0.668	0.760	0.600	0.713	0.520	0.892	0.715	0.730	0.690	0.420	0.830	0.520	0.590	0.565
I	CCGAAA	0.588	0.690	0.638	0.670	0.450	0.448	0.463	0.590	0.705	0.757	0.457	0.750	0.772	0.840	0.770	0.687	0.590	0.732	0.660	0.340	0.645	0.472	0.894	0.740	0.290	0.755
I	CGGTGG	0.334	0.907	0.807	0.900	0.430	0.422	0.327	0.600	0.875	0.843	0.667	0.453	0.594	0.910	0.830	0.590	0.693	0.777	0.710	0.540	0.570	0.740	1.220	0.450	0.680	0.670
I	CCACCG	0.334	0.907	0.807	0.900	0.430	0.422	0.327	0.600	0.875	0.843	0.667	0.453	0.594	0.910	0.830	0.590	0.693	0.777	0.710	0.540	0.570	0.740	1.220	0.450	0.680	0.670
II	CGCGCT	0.762	0.887	0.772	0.902	0.340	0.507	0.583	0.728	1.000	0.993	0.667	0.773	0.540	0.690	0.910	0.647	0.717	0.767	0.718	0.795	0.800	0.525	1.226	0.660	0.710	0.665
II	GCCCGC	0.727	1.073	0.732	0.988	0.580	0.420	0.517	0.732	0.990	1.040	0.607	0.627	0.592	0.850	1.095	0.873	0.290	0.800	0.655	0.665	0.765	0.583	1.413	0.660	0.590	0.530
II	ACGGGC	0.714	0.898	0.718	0.856	0.500	0.612	0.526	0.593	0.835	0.907	0.483	0.722	0.704	0.900	0.925	0.653	0.510	0.755	0.625	0.750	0.765	0.527	1.206	0.440	0.610	0.520
II	GCGCGT	0.692	0.873	0.612	0.814	0.720	0.510	0.624	0.650	0.930	0.920	0.620	0.740	0.680	0.850	0.920	0.697	0.727	0.740	0.620	0.845	0.640	0.407	1.204	0.440	0.670	0.585
II	AGCGCG	0.762	0.887	0.772	0.902	0.340	0.507	0.583	0.728	1.000	0.993	0.667	0.773	0.540	0.690	0.910	0.647	0.717	0.767	0.718	0.795	0.800	0.525	1.226	0.660	0.710	0.665
II	CGGGCC	0.758	0.995	0.698	0.862	0.690	0.503	0.518	0.765	1.025	1.023	0.663	0.557	0.784	0.760	1.060	0.917	0.273	0.767	0.677	0.595	0.790	0.598	1.396	0.490	0.620	0.740
II	ACGCGC	0.692	0.873	0.612	0.814	0.720	0.510	0.624	0.648	0.930	0.920	0.620	0.740	0.680	0.850	0.920	0.697	0.727	0.740	0.620	0.845	0.640	0.407	1.204	0.440	0.670	0.585
II	CGCGTG	0.714	0.932	0.723	0.798	0.490	0.664	0.683	0.655	0.895	0.867	0.673	0.807	0.748	0.980	0.830	0.727	0.670	0.795	0.622	0.775	0.650	0.398	1.218	0.220	0.650	0.665
II	CAGGCC	0.732	0.812	0.718	0.752	0.710	0.612	0.570	0.707	0.905	0.800	0.660	0.680	0.644	0.590	0.830	0.823	0.487	0.743	0.627	0.675	0.870	0.565	1.190	0.670	0.780	0.625
II	CCGGCC	0.590	1.040	0.780	0.940	0.730	0.408	0.356	0.732	1.010	0.950	0.437	0.625	0.744	0.810	1.045	0.867	0.497	0.762	0.677	0.530	0.780	0.725	1.398	0.720	0.550	0.740
II	CGGGCT	0.753	0.897	0.708	0.772	0.570	0.582	0.595	0.602	1.010	0.993	0.673	0.562	0.638	0.690	0.910	0.847	0.493	0.752	0.720	0.595	0.785	0.568	1.226	0.660	0.520	0.575
II	CGTCCG	0.592	0.873	0.707	0.688	0.690	0.556	0.446	0.573	0.985	0.993	0.220	0.545	0.724	0.760	0.915	0.760	0.587	0.617	0.430	0.425	0.755	0.682	1.236	0.520	0.630	0.775
II	TCGGCC	0.692	0.978	0.808	0.810	0.690	0.441	0.356	0.675	0.885	0.927	0.513	0.417	0.714	0.700	0.910	0.823	0.290	0.788	0.647	0.425	0.760	0.808	1.201	0.890	0.690	0.740
II	GCGGCG	0.747	1.028	0.747	0.960	0.540	0.113	0.264	0.752	1.125	1.010	0.640	0.613	0.644	0.860	1.080	0.827	0.527	0.807	0.528	0.655	0.670	0.615	1.398	0.500	0.630	0.760
II	CGCGTC	0.791	0.815	0.615	0.772	0.570	0.478	0.548	0.725	1.010	0.903	0.713	0.833	0.768	0.760	0.900	0.687	0.577	0.735	0.400	0.650	0.570	0.475	1.174	0.450	0.700	0.775
II	GGCCGG	0.590	1.038	0.780	0.940	0.730	0.408	0.356	0.732	1.010	0.950	0.437	0.625	0.744	0.810	1.045	0.867	0.497	0.762	0.677	0.530	0.780	0.725	1.398	0.720	0.550	0.740
II	CGCGCC	0.747	1.028	0.790	0.898	0.570	0.413	0.534	0.818	1.035	1.023	0.673	0.770	0.704	0.860	1.055	0.847	0.493	0.750	0.620	0.650	0.760	0.522	1.394	0.490	0.730	0.775
II	GCGGGG	0.700	1.065	0.775	1.038	0.550	0.314	0.433	0.670	1.030	0.927	0.680	0.613	0.634	0.850	1.130	0.773	0.500	0.840	0.672	0.755	0.730	0.615	1.401	0.440	0.450	0.540
II	CCGGGT	0.676	0.950	0.570	0.926	0.490	0.605	0.613	0.575	0.995	0.973	0.670	0.715	0.674	0.740	0.910	0.810	0.737	0.840	0.788	0.765	0.565	0.547	1.226	0.450	0.270	0.575
II	GGCGCG	0.747	1.028	0.790	0.898	0.570	0.413	0.534	0.818	1.035	1.023	0.673	0.770	0.704	0.860	1.055	0.847	0.493	0.750	0.620	0.650	0.760	0.522	1.394	0.490	0.730	0.775
II	GGCGCC	0.889	1.067	0.758	0.950	0.780	0.203	0.414	0.952	1.085	1.217	0.767	0.718	0.732	0.810	1.075	0.990	0.310	0.890	0.527	0.555	0.790	0.738	1.410	0.720	0.910	0.960
II	CCCGGC	0.699	1.050	0.842	1.074	0.490	0.433	0.466	0.732	1.005	0.917	0.560	0.762	0.650	0.910	1.110	0.860	0.613	0.827	0.630	0.540	0.795	0.668	1.401	0.500	0.330	0.645
II	CGGGTC	0.672	0.778	0.475	0.726	0.660	0.488	0.513	0.662	1.005	0.900	0.670	0.705	0.722	0.540	0.920	0.850	0.353	0.747	0.617	0.695	0.650	0.493	1.172	0.500	0.510	0.850
II	CACGCG	0.714	0.932	0.723	0.798	0.490	0.664	0.683	0.655	0.895	0.867	0.673	0.807	0.748	0.980	0.830	0.727	0.670	0.795	0.622	0.775	0.650	0.398	1.218	0.220	0.650	0.665
II	CGCGCG	0.827	1.065	0.917	1.016	0.570	0.623	0.628	0.788	1.120	1.087	0.453	0.773	0.770	0.920	1.070	0.860	0.717	0.820	0.807	0.740	0.875	0.620	1.444	0.440	0.640	0.675
II	CGTGGC	0.631	0.807	0.690	0.900	0.560	0.482	0.536	0.585	0.855	0.820	0.670	0.445	0.682	1.000	0.910	0.790	0.493	0.720	0.420	0.680	0.450	0.460	1.210	0.050	0.700	0.640
II	GACCCG	0.672	0.778	0.475	0.726	0.660	0.488	0.513	0.662	1.005	0.900	0.670	0.705	0.722	0.540	0.920	0.850	0.353	0.747	0.617	0.695	0.650	0.493	1.172	0.500	0.510	0.850

II	CGGCGC	0.691	0.995	0.702	0.916	0.650	0.158	0.314	0.768	1.125	1.010	0.657	0.600	0.656	0.770	1.085	0.830	0.510	0.810	0.528	0.615	0.670	0.682	1.398	0.500	0.660	0.835
II	CGCCAC	0.644	0.862	0.783	0.950	0.670	0.273	0.385	0.770	0.910	0.890	0.670	0.670	0.668	0.750	0.895	0.750	0.443	0.800	0.325	0.435	0.535	0.383	1.218	0.720	0.730	0.665
II	ACGGCG	0.771	0.930	0.815	0.902	0.340	0.269	0.346	0.597	1.005	0.997	0.480	0.618	0.692	0.910	0.890	0.603	0.740	0.862	0.445	0.635	0.695	0.557	1.228	0.440	0.640	0.780
II	TCGGGC	0.717	0.993	0.817	0.936	0.720	0.602	0.503	0.600	0.885	0.897	0.533	0.583	0.624	0.710	0.940	0.840	0.450	0.752	0.792	0.530	0.690	0.695	1.209	0.660	0.500	0.530
II	CCCGGT	0.704	0.993	0.688	1.006	0.270	0.638	0.555	0.578	0.985	0.973	0.607	0.845	0.738	0.790	0.910	0.663	0.740	0.817	0.788	0.760	0.690	0.722	1.226	0.450	0.330	0.670
II	ACGCCG	0.710	0.930	0.805	0.810	0.570	0.302	0.391	0.635	1.005	0.997	0.660	0.643	0.700	0.910	0.880	0.737	0.733	0.840	0.443	0.600	0.565	0.525	1.227	0.450	0.560	0.800
II	TCGCGC	0.790	0.890	0.827	0.916	0.560	0.503	0.596	0.655	0.900	0.900	0.630	0.635	0.652	0.710	0.940	0.747	0.667	0.740	0.672	0.625	0.640	0.552	1.207	0.660	0.510	0.640
II	GGCCGT	0.648	0.895	0.735	0.784	0.500	0.418	0.400	0.678	0.845	0.993	0.370	0.607	0.712	0.860	0.910	0.760	0.520	0.825	0.453	0.635	0.825	0.635	1.206	0.660	0.770	0.745
II	CCACGC	0.576	0.970	0.733	0.892	0.770	0.519	0.548	0.603	0.895	0.783	0.653	0.388	0.650	1.000	0.925	0.690	0.653	0.765	0.560	0.665	0.515	0.398	1.194	0.220	0.670	0.645
II	GCGTCG	0.700	0.870	0.707	0.824	0.770	0.310	0.365	0.613	1.010	0.883	0.657	0.448	0.734	0.860	0.865	0.773	0.593	0.685	0.443	0.440	0.530	0.590	1.191	0.450	0.850	0.755
II	CGGCTG	0.620	0.873	0.712	0.716	0.660	0.341	0.444	0.732	0.870	0.867	0.667	0.600	0.586	0.760	0.810	0.803	0.653	0.708	0.652	0.575	0.775	0.748	1.218	0.670	0.710	0.670
II	CGCCGC	0.747	1.028	0.747	0.960	0.540	0.113	0.264	0.752	1.125	1.010	0.640	0.613	0.644	0.860	1.080	0.827	0.527	0.807	0.528	0.655	0.670	0.615	1.398	0.500	0.630	0.760
II	CCTGGC	0.571	0.845	0.843	0.906	0.710	0.639	0.661	0.583	0.840	0.763	0.677	0.615	0.674	1.040	0.910	0.837	0.690	0.670	0.557	0.770	0.675	0.683	1.208	0.280	0.550	0.430
II	GCCGTT	0.587	0.748	0.598	0.810	0.440	0.438	0.457	0.660	0.835	0.683	0.337	0.785	0.610	0.690	0.780	0.527	0.740	0.810	0.467	0.665	0.800	0.643	1.009	0.670	0.740	0.635
II	GGCGGG	0.558	1.042	0.898	0.934	0.560	0.283	0.370	0.740	1.015	0.947	0.657	0.835	0.714	1.020	1.055	0.793	0.390	0.777	0.625	0.540	0.800	0.555	1.397	0.520	0.540	0.670
II	CGGCGG	0.548	1.078	0.893	0.916	0.650	0.202	0.254	0.665	1.095	1.070	0.653	0.583	0.676	0.990	1.025	0.737	0.733	0.818	0.638	0.460	0.775	0.740	1.444	0.520	0.610	0.780
II	CGTCGG	0.496	0.907	0.777	0.872	0.790	0.393	0.272	0.507	0.965	0.870	0.450	0.508	0.812	0.810	0.885	0.783	0.543	0.693	0.425	0.345	0.645	0.723	1.237	0.300	0.660	0.650
II	CGCGAC	0.704	0.885	0.713	0.946	0.570	0.475	0.463	0.735	0.870	0.863	0.643	0.615	0.702	0.810	0.890	0.847	0.637	0.698	0.525	0.425	0.690	0.443	1.216	0.500	0.540	0.675
II	CCACGT	0.529	0.797	0.730	0.844	0.690	0.687	0.555	0.435	0.875	0.820	0.687	0.497	0.638	0.790	0.850	0.460	0.867	0.757	0.338	0.660	0.460	0.395	1.006	0.000	0.680	0.665
II	CGACGC	0.700	0.870	0.707	0.824	0.770	0.310	0.365	0.613	1.010	0.883	0.657	0.448	0.734	0.860	0.865	0.773	0.593	0.685	0.443	0.440	0.530	0.590	1.191	0.450	0.850	0.755
II	CCGGTT	0.573	0.838	0.563	0.762	0.470	0.602	0.492	0.518	0.765	0.770	0.667	0.547	0.688	0.740	0.685	0.580	0.800	0.732	0.848	0.785	0.690	0.650	1.016	0.670	0.370	0.670
II	GGGTCG	0.514	0.855	0.598	0.732	0.690	0.502	0.371	0.648	0.910	0.877	0.663	0.487	0.766	0.630	0.800	0.810	0.370	0.708	0.545	0.400	0.530	0.682	1.190	0.670	0.790	0.775
II	GTCCCG	0.657	0.873	0.628	0.846	0.450	0.492	0.552	0.763	0.865	0.867	0.443	0.620	0.728	0.760	0.910	0.813	0.423	0.713	0.537	0.495	0.755	0.520	1.217	0.500	0.350	0.855
II	CGCGGC	0.801	1.038	0.795	0.990	0.340	0.278	0.446	0.670	1.085	0.997	0.563	0.665	0.646	0.910	1.100	0.833	0.640	0.785	0.573	0.645	0.670	0.617	1.398	0.280	0.520	0.755
II	GAGCCC	0.824	0.847	0.628	0.704	0.800	0.479	0.594	0.765	1.030	1.010	0.873	0.690	0.592	0.690	0.900	0.910	0.293	0.740	0.712	0.815	0.865	0.850	1.179	0.950	0.770	0.745
II	CGCCGA	0.613	0.940	0.870	0.810	0.570	0.290	0.224	0.653	0.960	0.930	0.600	0.452	0.698	0.770	0.885	0.750	0.520	0.785	0.630	0.445	0.695	0.675	1.220	0.670	0.510	0.670
II	CGGCCG	0.656	1.090	0.862	0.914	0.690	0.378	0.407	0.752	1.105	1.087	0.443	0.557	0.732	0.910	1.045	0.890	0.523	0.823	0.652	0.540	0.935	0.857	1.444	0.740	0.820	0.885
II	CGCCGT	0.771	0.930	0.815	0.902	0.340	0.269	0.346	0.597	1.005	0.997	0.480	0.618	0.692	0.910	0.890	0.603	0.740	0.862	0.445	0.635	0.695	0.557	1.228	0.440	0.640	0.780
II	CGTGCC	0.609	0.807	0.675	0.776	0.710	0.581	0.615	0.592	0.865	0.927	0.450	0.613	0.600	0.860	0.910	0.810	0.493	0.705	0.480	0.815	0.560	0.425	1.208	0.270	0.820	0.775
II	CCGAAC	0.404	0.815	0.532	0.784	0.670	0.623	0.459	0.580	0.680	0.740	0.230	0.665	0.638	0.590	0.780	0.790	0.593	0.667	0.732	0.495	0.760	0.568	1.046	0.750	0.550	0.645
II	CGGTTC	0.539	0.775	0.467	0.600	0.440	0.483	0.439	0.535	0.800	0.760	0.450	0.532	0.624	0.540	0.690	0.657	0.573	0.668	0.750	0.625	0.780	0.675	0.980	0.720	0.700	0.890
II	CGTGGG	0.499	0.990	0.850	0.974	0.570	0.605	0.496	0.527	0.985	0.863	0.453	0.503	0.690	1.040	0.955	0.737	0.337	0.780	0.543	0.570	0.550	0.530	1.237	0.070	0.650	0.645
II	CCGCCG	0.548	1.078	0.893	0.916	0.650	0.202	0.254	0.665	1.095	1.070	0.653	0.580	0.676	0.990	1.025	0.737	0.733	0.818	0.638	0.460	0.775	0.740	1.444	0.520	0.610	0.780
II	GCGCCA	0.661	0.868	0.818	0.858	0.560	0.276	0.428	0.803	0.995	0.930	0.667	0.682	0.660	0.660	0.885	0.767	0.443	0.807	0.445	0.445	0.565	0.520	1.208	0.720	0.690	0.635
II	TGGCGC	0.661	0.868	0.818	0.858	0.560	0.276	0.428	0.803	0.995	0.930	0.667	0.682	0.660	0.660	0.885	0.767	0.443	0.807	0.445	0.445	0.565	0.520	1.207	0.720	0.690	0.635
II	CGACCC	0.514	0.855	0.598	0.732	0.690	0.502	0.371	0.648	0.910	0.877	0.663	0.487	0.766	0.630	0.800	0.810	0.370	0.708	0.545	0.400	0.530	0.682	1.190	0.670	0.790	0.775
II	ACCGGC	0.528	0.900	0.672	0.864	0.480	0.429	0.329	0.592	0.840	0.910	0.513	0.810	0.716	0.680	0.895	0.737	0.687	0.738	0.692	0.575	0.765	0.625	1.206	0.660	0.510	0.575
II	CCCACG	0.499	0.990	0.850	0.974	0.570	0.605	0.496	0.527	0.985	0.863	0.453	0.503	0.690	1.040	0.955	0.737	0.337	0.780	0.543	0.570	0.550	0.530	1.237	0.070	0.650	0.645
II	CTGGCC	0.681	0.893	0.850	0.834	0.730	0.576	0.578	0.782	0.860	1.017	0.637	0.462	0.756	0.830	0.900	0.877	0.447	0.760	0.650	0.555	0.765	0.720	1.203	0.720	0.770	0.555
II	GCCGGA	0.679	1.020	0.837	0.974	0.560	0.387	0.463	0.645	0.880	0.893	0.333	0.778	0.690	0.810	0.945	0.860	0.613	0.732	0.625	0.455	0.755	0.680	1.209	0.720	0.280	0.640
II	ACGTCG	0.626	0.713	0.733	0.818	0.570	0.478	0.398	0.440	0.920	0.913	0.603	0.488	0.818	0.690	0.865	0.613	0.810	0.715	0.223	0.440	0.565	0.518	1.006	0.220	0.800	0.665
II	CGGACC	0.562	0.778	0.475	0.690	0.690	0.524	0.407	0.605	0.905	0.963	0.443	0.460	0.740	0.540	0.900	0.927	0.367	0.643	0.657	0.505	0.765	0.547	1.199	0.720	0.610	0.870
II	GCGCTC	0.798	0.870	0.745	0.790	0.580	0.490	0.582	0.797	0.900	0.837	0.660	0.570	0.530	0.740	0.915	0.693	0.513	0.715	0.750	0.855	0.870	0.768	1.184	0.880	0.950	0.640
II	CAGCCC	0.658	0.802	0.740	0.698	0.770	0.468	0.514	0.727	0.900	0.817	0.680	0.590	0.534	0.590	0.840	0.860	0.520	0.750	0.710	0.675	0.700	0.778	1.191	0.890	0.800	0.745
II	GCGCGA	0.790	0.890	0.827	0.916	0.560	0.503	0.596	0.655	0.900	0.900	0.630	0.635	0.652	0.710	0.940	0.747	0.667	0.740	0.672	0.625	0.640	0.552	1.208	0.660	0.510	0.640
II	CCGTCC	0.566	0.860	0.712	0.778	0.690	0.447	0.384	0.605	0.895	0.810	0.227	0.537	0.690	0.810	0.835	0.700	0.523	0.743	0.453	0.450	0.600	0.667	1.189	0.660	0.780	0.755

II	CCCGGA	0.709	0.952	0.867	0.978	0.490	0.605	0.570	0.590	1.000	0.917	0.473	0.653	0.728	0.820	0.950	0.847	0.583	0.805	0.790	0.680	0.775	0.510	1.227	0.670	0.090	0.645
II	CGCGCA	0.748	0.932	0.857	0.844	0.570	0.522	0.535	0.722	0.905	0.877	0.647	0.547	0.602	0.940	0.845	0.780	0.517	0.743	0.785	0.665	0.655	0.402	1.222	0.670	0.490	0.665
II	GACGCG	0.791	0.815	0.615	0.772	0.570	0.478	0.548	0.725	1.010	0.903	0.713	0.833	0.768	0.760	0.900	0.687	0.577	0.735	0.400	0.650	0.570	0.475	1.174	0.450	0.700	0.775
II	TCGCCG	0.666	0.868	0.882	0.776	0.430	0.313	0.342	0.585	0.965	0.933	0.777	0.450	0.762	0.930	0.885	0.643	0.673	0.785	0.660	0.460	0.755	0.708	1.221	0.670	0.440	0.675
II	GCGGGA	0.657	0.892	0.760	0.910	0.340	0.468	0.582	0.703	0.875	0.900	0.547	0.707	0.636	0.850	0.955	0.697	0.473	0.750	0.675	0.545	0.645	0.547	1.207	0.670	0.320	0.675
II	TAGCGC	0.633	0.660	0.702	0.720	0.340	0.492	0.599	0.682	0.825	0.713	0.560	0.595	0.490	0.490	0.800	0.620	0.660	0.667	0.675	0.665	0.755	0.575	0.989	0.890	0.690	0.415
II	CGCACG	0.634	0.978	0.802	0.794	0.790	0.654	0.616	0.570	1.000	0.990	0.227	0.673	0.620	0.920	0.945	0.787	0.540	0.720	0.603	0.650	0.655	0.495	1.236	0.290	0.810	0.665
II	GTGCCG	0.644	0.885	0.690	0.852	0.450	0.290	0.376	0.775	0.905	0.893	0.453	0.690	0.570	0.760	0.890	0.850	0.500	0.777	0.330	0.415	0.535	0.497	1.218	0.720	0.540	0.890
II	GAGCGC	0.798	0.870	0.745	0.790	0.580	0.490	0.582	0.797	0.900	0.837	0.660	0.570	0.530	0.740	0.915	0.693	0.513	0.715	0.750	0.855	0.870	0.768	1.184	0.880	0.950	0.640
II	CCCGCT	0.606	0.882	0.683	0.916	0.490	0.474	0.584	0.733	0.980	0.973	0.727	0.873	0.554	0.800	0.910	0.597	0.520	0.780	0.818	0.760	0.765	0.613	1.226	0.520	0.540	0.555
II	GGTTCG	0.400	0.785	0.510	0.586	0.700	0.702	0.543	0.607	0.795	0.790	0.447	0.668	0.700	0.640	0.770	0.760	0.517	0.603	0.722	0.625	0.670	0.555	1.028	0.720	0.800	0.780
II	GGCCCT	0.719	0.855	0.668	0.786	0.720	0.487	0.551	0.682	0.860	1.000	0.590	0.642	0.666	0.640	0.930	0.760	0.297	0.835	0.680	0.785	0.905	0.763	1.206	0.720	0.850	0.850
II	GGTCCG	0.562	0.778	0.475	0.690	0.690	0.524	0.407	0.605	0.905	0.963	0.443	0.460	0.740	0.540	0.900	0.927	0.367	0.643	0.657	0.505	0.765	0.547	1.199	0.720	0.610	0.870
II	CCGAGC	0.534	0.818	0.615	0.874	0.870	0.528	0.430	0.632	0.790	0.820	0.457	0.633	0.594	0.600	0.905	0.853	0.593	0.668	0.812	0.530	0.565	0.667	1.200	0.660	0.620	0.430
II	GGGACC	0.740	0.847	0.610	0.650	0.660	0.607	0.559	0.768	0.895	1.013	0.663	0.465	0.732	0.680	0.895	0.877	0.220	0.627	0.555	0.610	0.770	0.727	1.199	0.720	0.600	0.865
II	GCCGGT	0.528	0.900	0.672	0.864	0.480	0.429	0.329	0.592	0.840	0.910	0.513	0.810	0.716	0.680	0.895	0.737	0.687	0.738	0.692	0.575	0.765	0.625	1.206	0.660	0.510	0.575
II	CGACCG	0.439	0.920	0.725	0.808	0.470	0.559	0.383	0.672	0.880	0.873	0.450	0.338	0.766	0.690	0.815	0.743	0.597	0.718	0.642	0.320	0.705	0.858	1.213	0.670	0.830	0.675
II	TCGCGG	0.656	0.903	0.918	0.962	0.650	0.319	0.490	0.513	0.995	0.917	0.680	0.615	0.686	0.940	0.925	0.713	0.800	0.792	0.620	0.565	0.645	0.562	1.227	0.440	0.300	0.565
II	CAGGCG	0.620	0.855	0.752	0.764	0.710	0.458	0.536	0.668	0.880	0.867	0.663	0.695	0.686	0.810	0.805	0.673	0.707	0.705	0.645	0.570	0.745	0.625	1.214	0.450	0.640	0.555
II	CGTCGT	0.650	0.743	0.738	0.842	0.560	0.464	0.449	0.492	0.860	0.777	0.553	0.503	0.810	0.910	0.660	0.643	0.690	0.730	0.290	0.455	0.650	0.545	1.014	0.440	0.780	0.670
II	CGCTCG	0.607	0.917	0.750	0.836	0.690	0.672	0.543	0.648	0.890	0.873	0.450	0.547	0.648	0.690	0.830	0.643	0.667	0.608	0.818	0.540	0.820	0.725	1.213	0.510	0.860	0.450
II	CCCGGG	0.850	1.140	0.917	1.158	0.490	0.662	0.695	0.707	1.205	1.067	0.727	0.790	0.850	1.020	1.150	0.903	0.777	0.900	0.853	0.765	0.890	0.728	1.450	0.440	0.240	0.655
II	CCGACG	0.496	0.907	0.777	0.872	0.790	0.393	0.272	0.507	0.965	0.870	0.450	0.508	0.812	0.810	0.885	0.783	0.543	0.693	0.425	0.345	0.645	0.723	1.237	0.300	0.660	0.650
II	GCCGGG	0.699	1.050	0.842	1.074	0.490	0.433	0.466	0.732	1.005	0.917	0.560	0.762	0.650	0.910	1.110	0.860	0.613	0.827	0.630	0.540	0.795	0.668	1.401	0.500	0.330	0.645
II	GGGTCC	0.676	0.845	0.547	0.716	0.690	0.598	0.526	0.695	1.000	1.010	0.650	0.487	0.708	0.580	0.915	0.900	0.147	0.743	0.677	0.625	0.755	0.780	1.193	0.890	0.760	0.960
II	GCCGCG	0.801	1.038	0.795	0.990	0.340	0.278	0.446	0.670	1.085	0.997	0.563	0.665	0.646	0.910	1.100	0.833	0.640	0.785	0.573	0.645	0.670	0.617	1.398	0.280	0.520	0.755
II	CGGCGA	0.666	0.868	0.882	0.776	0.430	0.313	0.342	0.585	0.965	0.933	0.777	0.450	0.762	0.930	0.885	0.643	0.677	0.785	0.660	0.460	0.755	0.708	1.221	0.670	0.440	0.675
II	TCCCGC	0.657	0.892	0.760	0.910	0.340	0.468	0.582	0.703	0.875	0.900	0.547	0.707	0.636	0.850	0.955	0.697	0.473	0.750	0.675	0.545	0.645	0.547	1.207	0.670	0.320	0.675
II	CCGTCG	0.623	0.868	0.762	0.854	0.690	0.377	0.401	0.537	0.875	0.853	0.457	0.388	0.778	0.910	0.810	0.717	0.697	0.705	0.448	0.345	0.600	0.708	1.213	0.440	0.640	0.670
II	CCGCGT	0.682	0.888	0.732	0.936	0.690	0.494	0.553	0.565	1.000	0.973	0.657	0.683	0.692	0.960	0.910	0.587	0.940	0.795	0.560	0.765	0.460	0.522	1.226	0.220	0.460	0.670
II	CGCGTT	0.711	0.828	0.702	0.742	0.340	0.604	0.658	0.580	0.905	0.810	0.700	0.888	0.674	0.880	0.795	0.487	0.797	0.740	0.627	0.820	0.645	0.430	1.017	0.440	0.600	0.665
II	CGCCGG	0.669	1.048	0.797	0.974	0.570	0.272	0.336	0.648	1.100	1.070	0.590	0.583	0.762	0.970	1.030	0.830	0.723	0.792	0.642	0.460	0.780	0.765	1.444	0.520	0.420	0.670
II	GCGGAG	0.738	0.963	0.550	0.824	0.540	0.329	0.419	0.645	0.955	0.997	0.603	0.593	0.574	0.630	0.915	0.850	0.577	0.797	0.670	0.555	0.535	0.655	1.202	0.670	0.410	0.760
II	AGCGGG	0.606	0.882	0.683	0.916	0.490	0.474	0.584	0.733	0.980	0.973	0.727	0.873	0.554	0.800	0.910	0.597	0.520	0.780	0.818	0.760	0.765	0.613	1.226	0.520	0.540	0.555
II	CGGCGT	0.710	0.930	0.805	0.812	0.570	0.302	0.391	0.635	1.005	0.997	0.660	0.643	0.700	0.910	0.880	0.737	0.733	0.840	0.443	0.600	0.565	0.525	1.227	0.450	0.560	0.800
II	GACGGC	0.702	0.915	0.745	0.866	0.480	0.223	0.312	0.692	0.880	0.820	0.333	0.630	0.576	0.910	0.870	0.743	0.517	0.838	0.310	0.450	0.690	0.650	1.186	0.670	0.730	0.640
II	GCGCCT	0.623	0.863	0.607	0.798	0.770	0.313	0.490	0.703	0.925	0.923	0.803	0.775	0.680	0.850	0.895	0.687	0.513	0.820	0.667	0.680	0.650	0.638	1.204	0.660	0.770	0.750
II	CCGGCG	0.669	1.048	0.797	0.974	0.570	0.272	0.336	0.648	1.100	1.070	0.590	0.583	0.762	0.970	1.030	0.830	0.723	0.792	0.642	0.460	0.780	0.765	1.444	0.520	0.420	0.670
II	GGCGGA	0.667	1.002	0.903	0.808	0.560	0.282	0.361	0.705	0.880	0.927	0.453	0.628	0.682	0.820	0.930	0.780	0.400	0.810	0.618	0.430	0.650	0.603	1.202	0.730	0.470	0.855
II	CCGGAC	0.617	0.953	0.570	0.912	0.670	0.584	0.499	0.598	0.850	0.800	0.227	0.610	0.644	0.740	0.910	0.907	0.583	0.725	0.670	0.545	0.765	0.693	1.217	0.720	0.320	0.755
II	ACGACG	0.650	0.743	0.738	0.842	0.560	0.464	0.449	0.492	0.860	0.777	0.553	0.503	0.810	0.910	0.660	0.643	0.690	0.730	0.290	0.455	0.650	0.545	1.014	0.440	0.780	0.670
II	TCGCGT	0.747	0.733	0.775	0.922	0.480	0.524	0.629	0.572	0.795	0.877	0.617	0.765	0.698	0.760	0.805	0.523	0.883	0.685	0.450	0.650	0.575	0.347	1.017	0.450	0.530	0.575
II	GCCGGC	0.751	1.115	0.898	1.060	0.700	0.222	0.320	0.808	0.995	1.047	0.553	0.672	0.676	0.900	1.090	0.953	0.510	0.818	0.532	0.445	0.805	0.765	1.413	0.720	0.510	0.640
II	CAGCCG	0.620	0.873	0.712	0.716	0.660	0.341	0.444	0.732	0.870	0.867	0.667	0.600	0.586	0.760	0.810	0.803	0.653	0.708	0.652	0.575	0.775	0.748	1.218	0.670	0.710	0.670
II	TCCGGC	0.679	1.020	0.837	0.974	0.560	0.387	0.463	0.645	0.880	0.893	0.333	0.778	0.690	0.810	0.945	0.860	0.613	0.732	0.625	0.455	0.755	0.680	1.209	0.720	0.280	0.640
II	CCCAGT	0.654	0.840	0.818	0.858	0.490	0.664	0.686	0.603	0.770	0.767	0.740	0.808	0.582	0.970	0.710	0.730	0.520	0.737	0.763	0.800	0.665	0.632	1.013	0.450	0.550	0.445

II	GTTCGG	0.404	0.815	0.532	0.784	0.670	0.623	0.459	0.580	0.680	0.740	0.230	0.665	0.638	0.590	0.780	0.790	0.593	0.667	0.732	0.495	0.760	0.568	1.046	0.750	0.550	0.645
II	GAGCCG	0.712	0.770	0.475	0.724	0.660	0.281	0.425	0.713	1.005	0.913	0.677	0.703	0.620	0.540	0.890	0.800	0.430	0.685	0.552	0.645	0.730	0.642	1.172	0.720	0.690	0.670
II	GACGTC	0.723	0.708	0.790	0.758	0.700	0.443	0.527	0.682	0.940	0.940	0.570	0.690	0.760	0.740	0.865	0.693	0.667	0.812	0.085	0.555	0.590	0.530	0.997	0.450	0.960	0.855
II	CGGCAG	0.482	0.927	0.822	0.844	0.450	0.347	0.429	0.775	0.980	0.940	0.663	0.682	0.590	0.990	0.885	0.797	0.723	0.765	0.430	0.355	0.710	0.672	1.229	0.740	0.550	0.670
II	ACCCGG	0.676	0.950	0.570	0.924	0.490	0.605	0.613	0.575	0.995	0.970	0.670	0.715	0.674	0.740	0.910	0.810	0.737	0.840	0.788	0.765	0.565	0.547	1.226	0.450	0.270	0.575
II	CCCGAA	0.599	0.892	0.668	0.902	0.670	0.593	0.535	0.540	0.895	0.830	0.507	0.833	0.696	0.710	0.810	0.727	0.587	0.722	0.785	0.545	0.700	0.515	1.066	0.670	0.280	0.665
II	GCCGTC	0.702	0.915	0.745	0.866	0.480	0.223	0.312	0.692	0.880	0.820	0.333	0.630	0.576	0.910	0.870	0.743	0.517	0.838	0.310	0.450	0.690	0.650	1.186	0.670	0.730	0.640
II	TCGGGT	0.550	0.785	0.645	0.884	0.690	0.626	0.522	0.520	0.785	0.873	0.607	0.725	0.622	0.540	0.725	0.723	0.673	0.748	0.667	0.555	0.575	0.512	1.017	0.670	0.500	0.470
II	CGGTCC	0.597	0.858	0.615	0.716	0.470	0.507	0.419	0.647	0.905	0.817	0.450	0.335	0.706	0.630	0.830	0.773	0.370	0.743	0.680	0.520	0.795	0.720	1.188	0.710	0.810	0.890
II	TCCGCC	0.667	1.002	0.903	0.808	0.560	0.282	0.361	0.705	0.880	0.927	0.453	0.628	0.682	0.820	0.930	0.780	0.400	0.810	0.618	0.430	0.650	0.603	1.202	0.730	0.470	0.855
II	GTCCGC	0.683	0.965	0.548	0.820	0.580	0.443	0.364	0.660	0.840	0.980	0.370	0.460	0.522	0.630	0.890	0.907	0.367	0.775	0.645	0.445	0.680	0.622	1.203	0.890	0.510	0.755
II	CTCGCG	0.653	0.872	0.818	0.940	0.570	0.602	0.683	0.662	0.995	0.937	0.677	0.833	0.822	0.920	0.915	0.783	0.740	0.768	0.647	0.545	0.820	0.588	1.229	0.440	0.560	0.455
II	CGTCGC	0.659	0.795	0.677	0.796	0.770	0.312	0.369	0.582	0.905	0.840	0.627	0.508	0.786	0.960	0.870	0.783	0.667	0.642	0.310	0.455	0.550	0.557	1.210	0.280	0.820	0.650
II	CGAACC	0.400	0.785	0.510	0.586	0.700	0.702	0.543	0.607	0.795	0.790	0.447	0.668	0.700	0.640	0.770	0.760	0.517	0.603	0.722	0.625	0.670	0.555	1.028	0.720	0.800	0.780
II	GGCGTC	0.809	0.900	0.723	0.744	0.700	0.263	0.440	0.815	1.000	0.997	0.547	0.698	0.716	0.900	0.850	0.833	0.453	0.823	0.305	0.550	0.655	0.530	1.181	0.670	0.810	0.845
II	CCGGTC	0.643	0.818	0.628	0.816	0.510	0.598	0.496	0.665	0.880	0.793	0.450	0.497	0.736	0.590	0.925	0.730	0.573	0.755	0.632	0.735	0.800	0.698	1.176	0.670	0.550	0.760
II	CGACGG	0.623	0.868	0.762	0.854	0.690	0.377	0.401	0.537	0.875	0.853	0.457	0.388	0.778	0.910	0.810	0.717	0.697	0.705	0.448	0.345	0.600	0.708	1.213	0.440	0.640	0.670
II	TACCCG	0.511	0.630	0.642	0.544	0.440	0.634	0.646	0.510	0.810	0.820	0.710	0.548	0.672	0.780	0.755	0.700	0.577	0.748	0.780	0.610	0.430	0.438	0.998	0.670	0.290	0.670
II	CCAGGC	0.666	0.998	0.780	0.850	0.720	0.653	0.678	0.590	0.880	0.783	0.670	0.560	0.720	0.790	0.955	0.843	0.730	0.672	0.753	0.755	0.735	0.627	1.191	0.450	0.560	0.530
II	GACCGG	0.643	0.818	0.628	0.816	0.510	0.598	0.496	0.665	0.880	0.793	0.450	0.497	0.736	0.590	0.925	0.730	0.573	0.755	0.632	0.735	0.800	0.698	1.176	0.670	0.550	0.760
II	TGACGG	0.593	0.848	0.747	0.866	0.470	0.265	0.388	0.610	0.665	0.630	0.453	0.335	0.774	0.940	0.600	0.610	0.577	0.777	0.228	0.335	0.485	0.507	1.017	0.670	0.520	0.770
II	ACCGTC	0.521	0.725	0.588	0.728	0.250	0.437	0.325	0.528	0.790	0.813	0.380	0.728	0.694	0.780	0.670	0.603	0.687	0.733	0.468	0.570	0.775	0.690	1.002	0.670	0.740	0.575
II	TAGCCC	0.678	0.638	0.692	0.562	0.560	0.629	0.673	0.597	0.830	0.860	0.770	0.465	0.588	0.490	0.760	0.783	0.447	0.693	0.840	0.640	0.655	0.778	0.981	1.110	0.580	0.525
II	GGCGCA	0.824	1.000	0.805	0.812	0.660	0.363	0.508	0.827	1.015	1.017	0.550	0.685	0.662	0.870	0.925	0.893	0.290	0.787	0.615	0.560	0.660	0.585	1.202	0.710	0.680	0.850
II	CACCGG	0.551	0.903	0.778	0.898	0.470	0.478	0.390	0.655	0.980	0.857	0.647	0.385	0.606	0.810	0.915	0.683	0.790	0.820	0.792	0.680	0.720	0.715	1.221	0.450	0.420	0.780
II	CGGCAC	0.644	0.885	0.690	0.852	0.450	0.290	0.376	0.775	0.905	0.893	0.453	0.690	0.570	0.760	0.890	0.850	0.500	0.777	0.330	0.415	0.535	0.497	1.218	0.720	0.540	0.890
II	AACCCG	0.630	0.833	0.633	0.628	0.570	0.642	0.656	0.452	0.795	0.817	0.867	0.752	0.706	0.720	0.710	0.697	0.577	0.747	0.708	0.700	0.650	0.420	1.016	0.670	0.410	0.685
II	ACGGCA	0.711	0.728	0.717	0.856	0.260	0.407	0.463	0.700	0.865	0.950	0.293	0.652	0.582	0.910	0.845	0.610	0.687	0.818	0.228	0.445	0.625	0.407	1.018	0.670	0.510	0.795
II	CGGAGG	0.510	0.873	0.712	0.690	0.650	0.417	0.421	0.440	0.995	0.980	0.450	0.673	0.752	0.760	0.935	0.730	0.690	0.593	0.653	0.580	0.650	0.735	1.236	0.520	0.480	0.645
II	GGACCG	0.597	0.858	0.615	0.716	0.470	0.507	0.419	0.647	0.905	0.817	0.450	0.335	0.706	0.630	0.830	0.773	0.370	0.743	0.680	0.520	0.795	0.720	1.188	0.710	0.810	0.890
II	TCGGCG	0.613	0.940	0.870	0.810	0.570	0.290	0.224	0.653	0.960	0.930	0.600	0.452	0.698	0.770	0.885	0.750	0.520	0.785	0.630	0.445	0.695	0.675	1.220	0.670	0.510	0.670
II	CGCGTA	0.633	0.747	0.683	0.630	0.570	0.632	0.604	0.535	0.900	0.820	0.493	0.663	0.700	0.920	0.690	0.660	0.650	0.688	0.562	0.705	0.425	0.335	1.000	0.450	0.470	0.665
II	CTCCGC	0.738	0.963	0.550	0.824	0.540	0.329	0.418	0.645	0.955	0.997	0.603	0.593	0.574	0.630	0.915	0.850	0.577	0.797	0.670	0.555	0.535	0.655	1.202	0.670	0.410	0.760
II	GACACG	0.703	0.585	0.515	0.754	0.790	0.664	0.644	0.678	0.865	0.803	0.670	0.610	0.664	0.780	0.860	0.677	0.577	0.670	0.465	0.830	0.425	0.278	0.997	0.280	0.730	0.860
II	GCCGCC	0.677	1.085	0.853	0.964	0.560	0.060	0.225	0.773	1.005	1.043	0.557	0.690	0.672	0.910	1.075	0.883	0.483	0.853	0.477	0.450	0.690	0.747	1.409	0.500	0.700	0.750
II	CGGACG	0.592	0.873	0.707	0.688	0.690	0.556	0.446	0.573	0.985	0.993	0.220	0.545	0.724	0.760	0.915	0.760	0.587	0.617	0.430	0.425	0.755	0.682	1.236	0.520	0.630	0.775
II	CGGCTC	0.712	0.770	0.475	0.724	0.660	0.281	0.425	0.713	1.005	0.913	0.677	0.703	0.620	0.540	0.890	0.800	0.430	0.685	0.552	0.645	0.730	0.642	1.172	0.720	0.690	0.670
II	GGCACG	0.609	0.807	0.675	0.776	0.710	0.581	0.615	0.592	0.865	0.927	0.450	0.613	0.600	0.860	0.910	0.810	0.493	0.705	0.480	0.815	0.560	0.425	1.208	0.270	0.820	0.775
II	GCTGCG	0.704	0.818	0.652	0.774	0.560	0.329	0.467	0.593	0.915	0.937	0.670	0.672	0.520	0.760	0.900	0.913	0.593	0.675	0.605	0.725	0.565	0.455	1.202	0.500	0.650	0.650
II	GACGCC	0.809	0.900	0.723	0.744	0.700	0.263	0.440	0.815	1.000	0.997	0.547	0.698	0.716	0.900	0.850	0.833	0.453	0.823	0.305	0.550	0.655	0.530	1.181	0.670	0.810	0.845
II	ATCGCG	0.766	0.698	0.635	0.768	0.340	0.491	0.595	0.673	0.785	0.770	0.747	0.833	0.698	0.720	0.695	0.683	0.860	0.740	0.515	0.590	0.680	0.402	1.010	0.670	0.440	0.670
II	CCGGGA	0.668	0.887	0.790	0.932	0.490	0.489	0.579	0.627	1.000	0.917	0.603	0.658	0.792	0.960	0.950	0.697	0.690	0.805	0.675	0.550	0.660	0.650	1.227	0.670	0.110	0.755
II	TACGGC	0.647	0.835	0.717	0.824	0.340	0.387	0.530	0.537	0.925	0.703	0.113	0.768	0.598	0.710	0.750	0.680	0.663	0.805	0.400	0.565	0.605	0.507	0.989	0.670	0.500	0.635
II	ACCGGT	0.681	0.900	0.693	0.876	0.440	0.645	0.551	0.667	0.880	0.813	0.603	0.998	0.746	0.740	0.795	0.623	0.887	0.755	0.838	0.790	0.760	0.657	1.043	0.670	0.520	0.690
II	GGCTCG	0.620	0.858	0.600	0.760	0.790	0.592	0.530	0.735	0.905	0.877	0.670	0.695	0.692	0.640	0.825	0.857	0.443	0.605	0.680	0.620	0.760	0.595	1.190	0.490	0.870	0.560
II	AGGCGG	0.528	0.875	0.727	0.844	0.880	0.268	0.337	0.617	0.990	0.973	0.670	0.710	0.736	0.910	0.890	0.587	0.730	0.827	0.618	0.565	0.580	0.660	1.227	0.450	0.580	0.670

II	CCCGAC	0.526	0.993	0.713	1.000	0.700	0.463	0.317	0.603	0.860	0.797	0.450	0.615	0.632	0.790	0.890	0.827	0.510	0.748	0.580	0.315	0.680	0.648	1.217	0.670	0.540	0.645
II	CCCGCC	0.558	1.042	0.898	0.934	0.560	0.283	0.370	0.740	1.015	0.947	0.657	0.835	0.714	1.020	1.055	0.793	0.390	0.777	0.625	0.540	0.800	0.555	1.397	0.520	0.540	0.670
II	CGGTCG	0.439	0.920	0.725	0.808	0.470	0.559	0.383	0.672	0.880	0.873	0.450	0.338	0.766	0.690	0.815	0.743	0.597	0.718	0.642	0.320	0.705	0.858	1.213	0.670	0.830	0.675
II	GGTCGC	0.539	0.878	0.678	0.758	0.680	0.473	0.385	0.792	0.790	0.837	0.623	0.465	0.690	0.740	0.910	0.887	0.447	0.705	0.532	0.415	0.560	0.725	1.199	0.500	0.790	0.680
II	CCCGAG	0.709	0.953	0.715	1.030	0.490	0.673	0.538	0.573	1.005	0.930	0.677	0.750	0.790	0.800	0.925	0.873	0.730	0.808	0.805	0.545	0.860	0.720	1.228	0.440	0.440	0.450
II	AGGGCC	0.719	0.852	0.668	0.786	0.720	0.487	0.551	0.682	0.860	1.000	0.590	0.642	0.666	0.640	0.930	0.760	0.297	0.835	0.680	0.785	0.905	0.763	1.206	0.720	0.850	0.850
II	GGCGAC	0.760	0.850	0.703	0.824	0.640	0.280	0.315	0.803	0.850	1.017	0.690	0.495	0.688	0.800	0.870	0.893	0.447	0.835	0.505	0.330	0.670	0.667	1.203	0.720	0.680	0.780
II	CGCGGA	0.744	0.935	0.858	0.808	0.340	0.500	0.425	0.615	0.990	0.930	0.517	0.500	0.648	0.820	0.910	0.723	0.617	0.752	0.682	0.570	0.650	0.490	1.222	0.510	0.280	0.775
II	TTCCGG	0.688	0.848	0.563	0.834	0.450	0.423	0.587	0.617	0.890	0.830	0.413	0.748	0.730	0.740	0.815	0.777	0.720	0.708	0.667	0.460	0.755	0.467	1.066	0.890	0.060	0.770
II	GCAGCG	0.656	0.872	0.723	0.860	0.570	0.333	0.399	0.728	0.995	0.837	0.670	0.500	0.468	0.690	0.885	0.693	0.673	0.693	0.610	0.830	0.610	0.672	1.193	0.500	0.740	0.670
II	ATCCGG	0.682	0.750	0.348	0.744	0.670	0.582	0.613	0.630	0.800	0.770	0.447	0.748	0.714	0.520	0.715	0.773	0.807	0.730	0.728	0.650	0.580	0.625	1.010	0.660	0.140	0.670
II	ACGCGA	0.747	0.733	0.775	0.922	0.480	0.524	0.629	0.572	0.795	0.877	0.617	0.765	0.698	0.760	0.805	0.523	0.883	0.685	0.450	0.650	0.575	0.347	1.017	0.450	0.520	0.575
II	GGCGGC	0.677	1.087	0.853	0.964	0.560	0.060	0.225	0.773	1.005	1.043	0.557	0.690	0.672	0.910	1.075	0.883	0.483	0.853	0.477	0.450	0.690	0.747	1.409	0.500	0.700	0.750
II	GTCGGC	0.577	1.005	0.693	0.886	0.700	0.242	0.165	0.673	0.840	0.977	0.513	0.490	0.578	0.680	0.870	0.897	0.290	0.825	0.473	0.225	0.660	0.825	1.204	0.720	0.730	0.680
II	GACGGT	0.521	0.725	0.588	0.728	0.250	0.437	0.325	0.528	0.790	0.813	0.380	0.728	0.694	0.780	0.670	0.603	0.687	0.733	0.468	0.570	0.775	0.690	1.002	0.670	0.740	0.575
II	GGACGG	0.566	0.860	0.712	0.778	0.690	0.447	0.384	0.605	0.895	0.810	0.227	0.537	0.690	0.810	0.835	0.700	0.523	0.743	0.453	0.450	0.600	0.667	1.189	0.660	0.780	0.755
II	TGCGGC	0.702	1.010	0.813	0.950	0.560	0.223	0.446	0.732	1.005	0.917	0.337	0.835	0.648	0.880	0.915	0.840	0.447	0.815	0.562	0.565	0.570	0.590	1.210	0.490	0.490	0.740
II	GCTCCG	0.671	0.778	0.475	0.692	0.650	0.376	0.421	0.608	0.915	0.937	0.663	0.667	0.604	0.540	0.920	0.837	0.577	0.620	0.665	0.590	0.565	0.568	1.200	0.500	0.470	0.650
II	CGCGAA	0.704	0.792	0.755	0.788	0.450	0.535	0.600	0.662	0.855	0.840	0.683	0.665	0.688	0.720	0.880	0.677	0.690	0.685	0.710	0.475	0.585	0.505	1.063	0.670	0.320	0.670
II	CCCGAT	0.689	0.787	0.502	0.818	0.490	0.608	0.535	0.670	0.775	0.767	0.670	0.840	0.706	0.570	0.690	0.637	0.730	0.733	0.720	0.540	0.690	0.628	1.010	0.660	0.360	0.565
II	GCGTGG	0.576	0.970	0.733	0.892	0.770	0.519	0.548	0.603	0.895	0.783	0.653	0.388	0.650	1.000	0.925	0.690	0.653	0.765	0.560	0.665	0.515	0.398	1.194	0.220	0.670	0.645
II	AGGCCG	0.671	0.897	0.727	0.778	0.690	0.435	0.422	0.650	1.015	0.997	0.657	0.560	0.732	0.690	0.910	0.737	0.513	0.802	0.520	0.595	0.700	0.657	1.227	0.670	0.710	0.780
II	ACCCGC	0.526	0.865	0.548	0.816	0.550	0.428	0.478	0.592	0.925	0.927	0.723	0.762	0.648	0.630	0.925	0.840	0.513	0.750	0.802	0.760	0.645	0.432	1.204	0.660	0.470	0.470
II	GCCGTA	0.647	0.835	0.717	0.824	0.340	0.387	0.530	0.537	0.925	0.703	0.113	0.768	0.600	0.710	0.750	0.680	0.663	0.805	0.400	0.565	0.605	0.507	0.989	0.670	0.500	0.635
II	TTCGCG	0.704	0.792	0.755	0.788	0.450	0.535	0.600	0.662	0.855	0.840	0.683	0.665	0.688	0.720	0.880	0.677	0.690	0.685	0.710	0.475	0.585	0.505	1.063	0.670	0.320	0.670
II	CTGACG	0.503	0.848	0.797	0.862	0.670	0.496	0.474	0.582	0.755	0.777	0.450	0.460	0.720	0.840	0.680	0.643	0.690	0.762	0.207	0.340	0.635	0.552	1.042	0.520	0.770	0.665
II	GCGACG	0.659	0.795	0.677	0.796	0.770	0.312	0.369	0.582	0.905	0.840	0.627	0.508	0.786	0.960	0.870	0.783	0.667	0.642	0.310	0.455	0.550	0.557	1.210	0.280	0.820	0.650
II	GACGGG	0.661	0.830	0.742	0.902	0.480	0.446	0.464	0.617	0.875	0.797	0.503	0.698	0.702	0.810	0.905	0.637	0.577	0.747	0.402	0.540	0.685	0.535	1.177	0.440	0.550	0.645
II	GTGGCG	0.644	0.862	0.783	0.950	0.670	0.273	0.385	0.770	0.910	0.890	0.670	0.670	0.668	0.750	0.890	0.750	0.443	0.800	0.325	0.435	0.535	0.383	1.218	0.720	0.730	0.665
II	AAGGCG	0.663	0.737	0.717	0.758	0.570	0.400	0.505	0.623	0.915	0.807	0.673	0.800	0.684	0.870	0.825	0.460	0.727	0.700	0.512	0.660	0.645	0.500	1.016	0.670	0.780	0.665
II	CGAGCC	0.620	0.858	0.600	0.760	0.790	0.592	0.530	0.735	0.905	0.877	0.670	0.695	0.692	0.640	0.825	0.857	0.443	0.605	0.680	0.620	0.760	0.595	1.190	0.490	0.870	0.560
II	GGTCGG	0.384	0.820	0.615	0.832	0.730	0.463	0.237	0.610	0.800	0.820	0.457	0.462	0.760	0.590	0.885	0.867	0.370	0.740	0.642	0.305	0.645	0.770	1.201	0.520	0.780	0.650
II	GTGGCC	0.712	0.855	0.747	0.820	0.680	0.481	0.486	0.830	0.845	1.027	0.743	0.443	0.610	0.750	0.895	0.890	0.227	0.825	0.555	0.535	0.675	0.610	1.203	0.940	0.830	0.735
II	AGCGGC	0.664	0.870	0.635	0.874	0.520	0.276	0.369	0.742	0.850	0.913	0.560	0.860	0.574	0.690	0.885	0.667	0.670	0.823	0.635	0.665	0.765	0.800	1.204	0.500	0.700	0.740
II	AAACCG	0.571	0.680	0.560	0.628	0.430	0.640	0.560	0.442	0.755	0.747	0.670	0.530	0.704	0.650	0.690	0.537	0.797	0.808	0.745	0.625	0.570	0.610	0.824	0.890	0.600	0.890
II	TTCGGG	0.599	0.892	0.668	0.902	0.670	0.593	0.535	0.540	0.895	0.830	0.507	0.833	0.696	0.710	0.810	0.727	0.587	0.722	0.785	0.545	0.700	0.515	1.066	0.670	0.280	0.665
II	GGCGGT	0.496	0.895	0.763	0.788	0.330	0.273	0.237	0.540	0.850	1.003	0.463	0.810	0.654	0.830	0.890	0.773	0.540	0.843	0.670	0.570	0.825	0.698	1.207	0.670	0.700	0.690
II	CCGCCA	0.528	0.900	0.915	0.924	0.690	0.102	0.301	0.663	0.885	0.850	0.603	0.560	0.710	0.880	0.835	0.663	0.580	0.808	0.450	0.340	0.650	0.507	1.226	0.670	0.480	0.565
II	TGGCGG	0.528	0.900	0.915	0.924	0.690	0.102	0.301	0.663	0.885	0.850	0.603	0.560	0.710	0.880	0.835	0.663	0.580	0.808	0.450	0.340	0.650	0.507	1.226	0.670	0.480	0.565
II	CCGGAG	0.682	0.955	0.575	0.942	0.670	0.478	0.505	0.603	1.005	0.930	0.453	0.610	0.770	0.740	0.945	0.853	0.803	0.792	0.800	0.545	0.705	0.695	1.228	0.670	0.220	0.670
II	CCGACC	0.384	0.820	0.615	0.832	0.730	0.463	0.237	0.610	0.800	0.820	0.457	0.462	0.760	0.590	0.885	0.867	0.370	0.740	0.642	0.305	0.645	0.770	1.201	0.520	0.780	0.650
II	CCGGCT	0.624	0.860	0.575	0.866	0.700	0.378	0.409	0.670	0.980	0.970	0.623	0.713	0.662	0.740	0.885	0.720	0.720	0.770	0.677	0.560	0.650	0.720	1.226	0.670	0.370	0.575
II	ACGTGT	0.656	0.698	0.587	0.754	0.690	0.830	0.735	0.513	0.870	0.707	0.690	0.663	0.618	0.690	0.675	0.563	0.883	0.753	0.388	0.845	0.365	0.213	0.851	0.220	0.710	0.685
II	CAGCGG	0.644	0.910	0.817	0.902	0.690	0.402	0.454	0.712	0.970	0.857	0.683	0.435	0.450	0.820	0.910	0.583	0.867	0.708	0.795	0.685	0.780	0.800	1.221	0.670	0.610	0.565
II	GCCGAG	0.740	0.950	0.695	0.892	0.480	0.460	0.386	0.628	0.850	0.980	0.563	0.613	0.610	0.690	0.900	0.850	0.520	0.777	0.588	0.445	0.695	0.677	1.201	0.500	0.570	0.555
II	CGGGAC	0.656	0.873	0.628	0.846	0.450	0.492	0.552	0.763	0.865	0.867	0.443	0.620	0.728	0.760	0.910	0.813	0.423	0.713	0.537	0.495	0.755	0.520	1.217	0.500	0.350	0.855

II	CCGTCA	0.593	0.848	0.747	0.866	0.470	0.265	0.388	0.610	0.665	0.630	0.453	0.338	0.774	0.940	0.600	0.610	0.577	0.777	0.228	0.335	0.485	0.507	1.017	0.670	0.520	0.770
II	CCCGTT	0.662	0.823	0.688	0.828	0.440	0.658	0.654	0.578	0.860	0.767	0.507	0.777	0.702	0.800	0.800	0.440	0.727	0.772	0.630	0.760	0.755	0.605	1.016	0.440	0.560	0.560
III	GCCCGG	0.714	1.045	0.782	1.018	0.710	0.497	0.533	0.788	1.000	0.913	0.447	0.655	0.654	0.810	1.130	0.880	0.507	0.797	0.755	0.740	0.685	0.680	1.399	0.500	0.380	0.610
III	TAACCG	0.494	0.658	0.638	0.542	0.210	0.613	0.543	0.443	0.655	0.597	0.673	0.325	0.678	0.780	0.525	0.587	0.800	0.690	0.677	0.590	0.650	0.625	0.796	0.890	0.470	0.670
III	GAGGCC	0.748	0.867	0.688	0.716	0.810	0.466	0.576	0.760	1.000	0.993	0.710	0.667	0.688	0.730	0.880	0.817	0.310	0.708	0.517	0.760	0.710	0.760	1.179	0.890	0.950	0.735
III	AAGGGC	0.663	0.673	0.618	0.836	0.660	0.652	0.672	0.630	0.840	0.683	0.533	0.742	0.618	0.690	0.810	0.487	0.520	0.748	0.695	0.880	0.845	0.753	1.009	0.660	0.830	0.525
III	CCCATT	0.629	0.645	0.732	0.628	0.660	0.747	0.698	0.678	0.645	0.543	0.727	0.802	0.690	0.780	0.600	0.517	0.520	0.812	0.788	0.790	0.680	0.608	0.796	0.520	0.780	0.565
III	GGTCCA	0.739	0.762	0.610	0.688	0.470	0.683	0.568	0.740	0.780	0.950	0.637	0.238	0.636	0.430	0.865	0.827	0.147	0.652	0.737	0.500	0.555	0.765	0.999	0.930	0.830	0.850
III	AGTGGG	0.466	0.843	0.825	0.858	0.710	0.635	0.484	0.603	0.780	0.770	0.677	0.705	0.514	0.920	0.720	0.643	0.300	0.805	0.770	0.575	0.650	0.640	1.014	0.300	0.760	0.665
III	AACGAC	0.440	0.705	0.602	0.744	0.660	0.638	0.393	0.523	0.630	0.547	0.470	0.665	0.734	0.580	0.555	0.533	0.667	0.725	0.465	0.455	0.660	0.642	0.798	0.670	0.860	0.745
III	TATCGG	0.603	0.468	0.528	0.510	0.490	0.497	0.462	0.652	0.695	0.600	0.630	0.605	0.710	0.610	0.625	0.653	0.590	0.747	0.675	0.335	0.645	0.660	0.837	0.730	0.490	0.565
III	CCGAAT	0.597	0.718	0.463	0.656	0.670	0.612	0.507	0.638	0.665	0.697	0.450	0.760	0.794	0.700	0.565	0.790	0.743	0.810	0.715	0.545	0.575	0.532	0.828	0.660	0.370	0.670
III	AAAGCC	0.768	0.647	0.597	0.620	0.780	0.677	0.660	0.670	0.780	0.767	0.707	0.790	0.710	0.600	0.710	0.540	0.670	0.760	0.692	0.890	0.750	0.672	0.822	0.890	0.670	0.735
III	TCCGAA	0.611	0.855	0.733	0.934	0.700	0.629	0.535	0.575	0.820	0.707	0.313	0.835	0.744	0.600	0.610	0.863	0.617	0.815	0.793	0.455	0.760	0.590	0.941	0.890	0.310	0.775
III	GGGGTC	0.686	0.847	0.627	0.698	0.580	0.479	0.536	0.735	1.000	1.010	0.713	0.637	0.734	0.680	0.875	0.843	0.230	0.823	0.527	0.715	0.655	0.682	1.181	0.720	0.620	0.850
III	TCCGAC	0.557	0.923	0.777	0.934	0.700	0.462	0.315	0.570	0.770	0.857	0.423	0.613	0.736	0.590	0.750	0.860	0.480	0.762	0.620	0.235	0.645	0.690	1.063	0.890	0.520	0.780
III	ATTCGG	0.597	0.718	0.463	0.656	0.670	0.612	0.507	0.638	0.665	0.697	0.450	0.760	0.794	0.700	0.565	0.790	0.743	0.810	0.715	0.545	0.575	0.532	0.828	0.660	0.370	0.670
III	CCAACG	0.351	0.868	0.835	0.834	0.650	0.614	0.428	0.508	0.760	0.653	0.453	0.307	0.684	0.910	0.805	0.640	0.557	0.728	0.598	0.540	0.645	0.720	1.048	0.300	0.870	0.560
III	GGCTTT	0.768	0.647	0.597	0.620	0.780	0.677	0.660	0.670	0.780	0.767	0.707	0.790	0.710	0.600	0.710	0.540	0.670	0.760	0.692	0.890	0.750	0.672	0.822	0.890	0.670	0.735
III	GACCCA	0.503	0.757	0.610	0.740	0.720	0.640	0.496	0.605	0.805	0.823	0.707	0.590	0.800	0.430	0.720	0.820	0.157	0.713	0.615	0.755	0.655	0.598	0.988	0.720	0.730	0.630
III	TTTGGG	0.544	0.720	0.820	0.786	0.670	0.615	0.654	0.605	0.700	0.757	0.677	0.670	0.704	0.730	0.800	0.653	0.367	0.833	0.843	0.570	0.650	0.595	0.896	0.520	0.510	0.650
III	AATCCG	0.724	0.620	0.470	0.408	0.660	0.630	0.649	0.513	0.575	0.590	0.673	0.718	0.686	0.500	0.485	0.750	0.793	0.802	0.733	0.610	0.745	0.480	0.793	0.890	0.390	0.885
III	AAAGGC	0.667	0.665	0.563	0.674	0.660	0.661	0.678	0.618	0.830	0.680	0.563	0.617	0.708	0.820	0.735	0.450	0.740	0.755	0.698	0.880	0.705	0.635	0.824	0.720	0.860	0.630
III	CCGACA	0.533	0.692	0.725	0.732	0.690	0.284	0.241	0.588	0.775	0.793	0.547	0.550	0.760	0.830	0.795	0.753	0.367	0.767	0.448	0.115	0.425	0.630	1.050	0.520	0.520	0.755
III	GTGGAC	0.721	0.910	0.672	0.842	0.680	0.663	0.567	0.713	0.625	0.987	0.593	0.268	0.486	0.520	0.865	0.800	0.147	0.775	0.653	0.450	0.455	0.772	1.020	0.950	0.720	0.850
III	GTCCAG	0.761	0.920	0.710	0.880	0.670	0.671	0.650	0.690	0.635	0.840	0.430	0.395	0.634	0.630	0.905	0.753	0.367	0.688	0.715	0.495	0.535	0.730	1.021	0.720	0.540	0.660
III	GATGGG	0.501	0.633	0.580	0.758	0.700	0.654	0.622	0.682	0.655	0.600	0.680	0.670	0.670	0.590	0.700	0.717	0.397	0.747	0.557	0.735	0.600	0.627	0.974	0.520	0.780	0.540
III	ATCCGA	0.643	0.662	0.445	0.746	0.690	0.626	0.521	0.493	0.700	0.773	0.557	0.722	0.726	0.320	0.570	0.750	0.673	0.785	0.845	0.465	0.780	0.630	0.862	0.890	0.380	0.685
III	CCGAGA	0.683	0.688	0.725	0.738	0.650	0.503	0.458	0.572	0.835	0.797	0.657	0.662	0.758	0.840	0.865	0.747	0.590	0.645	0.672	0.340	0.545	0.667	1.050	0.670	0.350	0.535
III	CCGTAA	0.556	0.738	0.603	0.788	0.220	0.428	0.604	0.395	0.690	0.610	0.230	0.535	0.728	0.710	0.595	0.603	0.797	0.733	0.440	0.565	0.585	0.347	0.838	0.670	0.280	0.665
III	CCAATA	0.526	0.557	0.707	0.464	0.710	0.723	0.684	0.670	0.535	0.370	0.730	0.670	0.638	0.800	0.575	0.653	0.587	0.705	0.790	0.560	0.645	0.745	0.647	0.670	0.700	0.640
III	GAGTGG	0.544	0.820	0.740	0.704	0.870	0.672	0.605	0.758	0.665	0.593	0.680	0.580	0.502	0.780	0.845	0.603	0.660	0.737	0.703	0.670	0.535	0.623	0.977	0.450	0.890	0.645
III	ACGAGG	0.643	0.743	0.758	0.874	0.690	0.672	0.632	0.430	0.850	0.770	0.743	0.623	0.806	0.920	0.690	0.547	0.873	0.705	0.445	0.680	0.540	0.608	1.013	0.220	0.680	0.450
III	GGCTCA	0.711	0.810	0.632	0.720	0.660	0.559	0.590	0.742	0.795	0.817	0.760	0.487	0.620	0.660	0.725	0.780	0.290	0.795	0.657	0.765	0.700	0.763	1.000	0.710	0.760	0.740
III	GCTGAG	0.678	0.800	0.680	0.868	0.690	0.513	0.562	0.620	0.715	0.803	0.747	0.490	0.520	0.710	0.690	0.773	0.593	0.785	0.682	0.665	0.605	0.675	1.018	0.720	0.630	0.645
III	GGCTAA	0.538	0.627	0.722	0.626	0.440	0.652	0.657	0.740	0.670	0.763	0.773	0.465	0.670	0.490	0.625	0.710	0.517	0.745	0.810	0.665	0.670	0.685	0.833	0.940	0.530	0.560
III	ACCGAT	0.511	0.675	0.495	0.712	0.430	0.669	0.397	0.577	0.665	0.587	0.550	0.867	0.734	0.520	0.565	0.593	0.740	0.767	0.855	0.565	0.850	0.665	0.814	0.890	0.580	0.675
III	TGCCAG	0.646	0.807	0.897	0.904	0.690	0.482	0.591	0.615	0.760	0.857	0.707	0.567	0.730	0.860	0.770	0.907	0.670	0.677	0.628	0.450	0.760	0.632	1.074	0.890	0.520	0.560
III	GCCAGA	0.700	0.838	0.930	0.814	0.670	0.609	0.665	0.710	0.775	0.743	0.557	0.610	0.654	0.840	0.775	0.833	0.527	0.607	0.677	0.565	0.565	0.775	1.010	0.500	0.500	0.535
III	TGGGGT	0.554	0.828	0.773	0.820	0.600	0.517	0.635	0.463	0.815	0.937	0.540	0.740	0.652	0.680	0.805	0.687	0.440	0.855	0.455	0.655	0.565	0.517	1.018	0.660	0.600	0.575
III	TGTGGC	0.637	0.805	0.863	0.814	0.680	0.448	0.498	0.685	0.845	0.757	0.560	0.667	0.656	0.900	0.780	0.837	0.300	0.698	0.557	0.450	0.345	0.677	1.011	0.270	0.710	0.645
III	AAGTGG	0.486	0.677	0.742	0.800	0.870	0.672	0.561	0.595	0.650	0.597	0.900	0.680	0.492	0.800	0.730	0.380	0.873	0.743	0.568	0.665	0.570	0.617	0.803	0.220	0.810	0.555
III	TAAACG	0.617	0.635	0.615	0.598	0.430	0.797	0.712	0.565	0.640	0.597	0.643	0.278	0.672	0.670	0.500	0.417	0.813	0.570	0.700	0.680	0.420	0.443	0.653	0.730	0.690	0.775
III	TAATCG	0.628	0.680	0.627	0.416	0.430	0.801	0.669	0.557	0.440	0.377	0.863	0.448	0.754	0.670	0.295	0.597	0.873	0.680	0.757	0.485	0.590	0.667	0.573	0.890	0.670	0.770
III	ATCGAA	0.560	0.667	0.597	0.850	0.700	0.793	0.597	0.575	0.455	0.783	0.533	0.657	0.730	0.270	0.540	0.713	0.817	0.638	0.833	0.445	0.680	0.695	0.686	0.890	0.730	0.685
III	AAATGG	0.606	0.455	0.632	0.642	0.870	0.854	0.763	0.678	0.630	0.507	0.670	0.640	0.636	0.650	0.500	0.470	0.950	0.785	0.730	0.875	0.510	0.750	0.606	0.440	0.820	0.665

III	GGATAA	0.618	0.442	0.522	0.414	0.440	0.836	0.725	0.693	0.665	0.563	0.820	0.465	0.694	0.680	0.475	0.567	0.663	0.708	0.762	0.470	0.700	0.772	0.643	1.100	0.330	0.780
III	ATAAGG	0.582	0.568	0.548	0.660	0.670	0.764	0.809	0.455	0.660	0.520	0.450	0.653	0.748	0.820	0.490	0.343	0.950	0.703	0.525	0.840	0.540	0.570	0.634	0.660	0.590	0.560
III	CCACAG	0.527	0.800	0.785	0.858	0.650	0.577	0.502	0.647	0.970	0.747	0.653	0.585	0.614	0.800	0.800	0.750	0.730	0.792	0.590	0.355	0.470	0.723	1.040	0.440	0.630	0.675
III	AAATCC	0.682	0.422	0.438	0.392	0.650	0.877	0.791	0.590	0.570	0.560	0.893	0.780	0.728	0.370	0.500	0.763	0.810	0.887	0.658	0.880	0.685	0.765	0.604	0.880	0.480	0.955
III	ATCCAA	0.506	0.610	0.557	0.782	0.670	0.741	0.711	0.565	0.475	0.783	0.727	0.603	0.738	0.210	0.570	0.793	0.597	0.745	0.867	0.560	0.640	0.588	0.686	1.110	0.600	0.575
III	AGTGGA	0.588	0.865	0.827	0.808	0.660	0.707	0.664	0.670	0.650	0.693	0.713	0.477	0.418	0.780	0.810	0.557	0.377	0.740	0.743	0.570	0.530	0.642	0.800	0.510	0.690	0.775
III	ATGCCA	0.713	0.647	0.765	0.682	0.670	0.512	0.618	0.672	0.670	0.813	0.697	0.662	0.782	0.690	0.635	0.753	0.667	0.735	0.427	0.615	0.780	0.522	0.860	0.890	0.660	0.680
III	CATACG	0.539	0.585	0.528	0.584	0.710	0.743	0.694	0.465	0.775	0.687	0.223	0.720	0.730	0.780	0.680	0.623	0.747	0.685	0.638	0.685	0.550	0.437	0.826	0.520	0.730	0.645
III	TTATCC	0.618	0.442	0.522	0.414	0.440	0.836	0.725	0.693	0.665	0.563	0.820	0.465	0.694	0.680	0.475	0.567	0.663	0.708	0.762	0.470	0.700	0.772	0.643	1.100	0.330	0.780
III	GTCCAT	0.676	0.762	0.645	0.688	0.490	0.699	0.576	0.655	0.405	0.747	0.530	0.443	0.714	0.580	0.695	0.737	0.367	0.703	0.745	0.570	0.485	0.672	0.801	0.880	0.760	0.855
III	TATCCA	0.532	0.385	0.482	0.418	0.650	0.732	0.736	0.620	0.490	0.567	0.717	0.578	0.768	0.450	0.535	0.790	0.597	0.662	0.838	0.480	0.505	0.670	0.677	1.110	0.490	0.660
III	GATAAG	0.561	0.400	0.450	0.538	0.480	0.866	0.822	0.530	0.565	0.477	0.667	0.613	0.792	0.640	0.530	0.407	0.797	0.670	0.645	0.855	0.670	0.520	0.613	0.720	0.840	0.650
III	ATGTGG	0.533	0.578	0.563	0.628	0.690	0.569	0.520	0.585	0.840	0.717	0.673	0.710	0.620	0.570	0.685	0.533	0.727	0.705	0.442	0.430	0.350	0.590	0.816	0.220	0.570	0.665
III	ATCCTA	0.561	0.583	0.437	0.652	0.700	0.818	0.731	0.352	0.690	0.597	0.560	0.785	0.686	0.420	0.350	0.667	0.663	0.568	0.840	0.670	0.830	0.700	0.689	0.890	0.610	0.460
III	AAAATC	0.748	0.270	0.427	0.344	0.850	1.035	0.914	0.750	0.555	0.507	0.930	0.753	0.770	0.430	0.465	0.537	0.963	0.740	0.670	1.040	0.660	0.735	0.431	0.890	0.920	0.795
III	AATTGA	0.630	0.625	0.782	0.674	0.650	1.044	0.777	0.752	0.210	0.333	0.767	0.440	0.614	0.560	0.495	0.487	0.817	0.790	0.688	0.790	0.670	0.750	0.401	0.670	0.740	0.775
III	AGAGTG	0.681	0.640	0.705	0.566	0.490	0.788	0.735	0.707	0.655	0.597	0.820	0.703	0.648	0.650	0.590	0.450	0.677	0.763	0.845	0.795	0.725	0.617	0.796	0.670	0.870	0.665
III	ATCAGA	0.687	0.565	0.603	0.700	0.850	0.836	0.729	0.640	0.465	0.597	0.697	0.665	0.652	0.400	0.340	0.693	0.737	0.743	0.685	0.675	0.765	0.750	0.679	0.890	0.600	0.695
III	TCAGAA	0.721	0.683	0.627	0.752	0.700	0.815	0.739	0.677	0.680	0.487	0.547	0.668	0.628	0.370	0.380	0.780	0.840	0.688	0.728	0.460	0.730	0.692	0.722	0.890	0.520	0.885
III	ATTAAA	0.681	0.565	0.807	0.656	0.450	0.975	0.997	0.632	0.230	0.537	0.833	0.603	0.760	0.470	0.545	0.500	0.940	0.848	0.718	0.815	0.680	0.607	0.288	1.110	0.790	0.780
III	AAAATG	0.752	0.335	0.570	0.512	0.710	0.980	0.867	0.642	0.630	0.513	0.890	0.695	0.704	0.650	0.490	0.407	1.090	0.688	0.705	1.000	0.560	0.623	0.448	0.660	0.980	0.885
III	CTTATC	0.561	0.400	0.450	0.538	0.480	0.866	0.822	0.530	0.565	0.477	0.667	0.613	0.792	0.640	0.530	0.407	0.797	0.670	0.645	0.855	0.670	0.520	0.613	0.720	0.840	0.650

Appendix Table 1