

Additional file 7: (a) Genomic densities in different genomic regions of *Daphnia pulex* (Dappu), *Drosophila melanogaster* (DroMel) and *Apis mellifera* (ApiMel). A=normal B=reverse complement of repeat motif A; "-" denotes palindromic motifs; a and b are used of only only the normal form (a) OR its reverse complement (b) were found.

unit size [bp]	motif form	unit	Dappu v1.1 3UTR bp/Mbp	Dappu v1.1 5UTR bp/Mbp	Dappu v1.1 CDS bp/Mbp	Dappu v1.1 introns bp/Mbp	Dappu v1.1 intergenic bp/Mbp	DroMel-5.5 3UTR bp/Mbp	DroMel-5.5 5UTR bp/Mbp	DroMel-5.5 CDS bp/Mbp	DroMel-5.5 introns bp/Mbp	DroMel-5.5 intergenic bp/Mbp	ApiMel-2.0 CDS bp/Mbp	ApiMel-2.0 introns bp/Mbp	ApiMel-2.0 intergenic bp/Mbp	min bp/Mbp	max bp/Mbp
1	A	A	866.73	333.07	11.46	799.57	635.80	993.48	834.60	4.92	1119.99	800.70	106.21	1966.65	2069.87	4.92	2069.87
1	B	T	1163.64	266.46	7.33	1284.48	647.18	565.78	308.60	3.91	2994.52	806.02	18.74	2058.86	2058.86	3.91	2792.61
1	A	C	392.30	22.75	4.83	498.42	295.83	76.52	16.65	0.00	110.57	85.22	5.08	27.13	38.34	0.00	498.42
2	B	G	144.03	3.47	0.00	464.79	299.47	12.02	0.00	0.00	107.63	5.08	5.08	0.00	40.47	0.00	464.79
2	A	AC	503.48	180.34	7.36	576.42	446.85	1076.86	678.25	0.70	703.07	107.67	5.47	160.77	167.79	0.70	1076.86
2	B	GT	425.79	437.05	1.99	768.48	440.71	180.74	775.61	5.05	767.16	644.75	0.00	167.83	158.27	0.00	775.61
2	A	AG	182.57	84.48	6.31	776.33	506.09	154.26	450.60	1.93	155.01	132.12	20.30	1353.26	1606.35	1.93	1606.35
2	B	CT	500.33	432.18	8.77	940.65	518.59	70.63	141.51	0.61	251.81	155.40	435.76	1401.68	1542.87	0.61	1542.87
2	A	AT	1.17	45.50	3.47	208.75	299.17	12.02	7.38	0.00	718.69	718.69	718.69	4069.04	4069.04	1.17	4069.04
3	A	AAC	157.93	63.36	328.02	548.89	188.97	285.46	265.87	135.52	80.28	281.92	19.63	45.66	54.66	19.63	542.89
3	B	GTT	70.75	105.61	13.68	389.97	198.37	13.24	91.93	1.05	115.83	101.73	59.74	33.69	48.59	1.05	389.97
3	A	AAG	160.45	118.61	259.00	641.87	473.49	5.40	54.29	30.30	14.52	11.81	807.09	285.16	360.74	5.40	807.09
3	B	CTT	120.03	0.00	29.19	814.34	496.04	3.68	20.63	1.84	21.67	12.00	56.62	345.60	367.32	0.00	814.34
3	A	AAT	128.24	26.00	6.12	139.18	109.37	150.09	62.25	33.41	140.47	213.85	365.08	1014.35	596.03	6.12	1014.35
3	B	ATT	216.05	24.37	2.88	217.96	122.18	239.36	0.92	165.63	192.06	644.38	89.42	561.82	0.92	644.38	
3	A	ACC	34.75	55.25	94.19	92.61	67.39	90.49	77.09	122.73	35.38	18.65	351.81	27.61	44.48	18.65	351.81
3	B	GGT	0.00	30.87	41.78	96.54	60.35	5.40	24.61	50.45	24.43	24.99	466.22	35.96	44.41	0.00	466.22
3	A	ACG	11.38	0.00	93.92	93.01	76.17	12.75	39.09	45.97	14.15	11.40	158.53	59.46	86.18	0.00	158.53
3	B	CGT	0.00	24.37	37.02	106.15	69.56	22.08	8.47	24.91	16.88	13.89	71.46	57.25	86.92	0.00	106.15
3	A	ACT	52.43	48.75	7.05	74.25	42.31	29.92	5.43	1.84	26.88	12.90	747.74	41.60	377.77	1.84	747.74
3	B	AGT	0.00	0.00	2.26	64.02	37.95	6.38	0.00	2.99	17.63	12.18	733.29	107.39	37.36	0.00	733.29
3	A	AGC	21.48	191.72	340.68	324.05	233.16	442.17	993.13	1658.93	262.27	217.25	219.05	7.36	27.05	7.36	1658.93
3	B	CTG	70.75	126.73	74.74	335.09	249.51	40.96	46.69	26.87	174.35	157.82	173.76	7.67	19.23	7.67	335.09
3	A	AGG	15.03	0.00	0.00	111.47	34.68	61.97	50.07	111.47	166.77	192.89	223.30	310.11	310.11	0.00	310.11
3	B	CCT	22.11	37.37	21.59	96.57	33.17	23.30	14.48	21.56	29.24	213.19	213.19	315.61	315.61	14.48	315.61
3	A	ATC	50.54	87.73	24.55	70.49	45.75	45.62	66.96	46.68	73.95	65.51	102.30	29.89	41.02	24.55	102.30
3	B	ATG	23.37	0.00	19.52	72.59	43.04	106.19	27.51	29.46	94.49	62.51	986.71	59.89	40.81	0.00	986.71
3	A	CCG	12.01	0.00	59.39	36.15	40.52	3.68	30.76	27.53	7.45	13.34	53.10	19.09	24.06	0.00	59.39
3	B	CGG	0.00	0.00	73.14	46.51	38.54	17.73	54.43	10.11	10.11	13.40	20.69	16.51	27.54	0.00	73.14
4	A	AAAC	40.43	53.62	1.60	92.42	39.29	12.62	0.00	0.00	14.75	31.12	0.00	6.04	9.00	0.00	92.42
4	B	GTTT	20.22	0.00	2.42	79.66	34.70	11.53	32.94	0.00	35.56	22.28	0.00	3.32	8.39	0.00	79.66
4	A	AAAG	13.90	0.00	0.62	108.69	69.75	33.35	15.20	0.00	6.49	4.66	48.03	222.51	257.91	0.00	257.91
4	B	CTTT	48.01	35.75	3.43	140.33	67.64	0.00	3.43	0.00	3.89	8.59	276.38	266.20	0.00	276.38	
4	A	AAT	95.39	0.00	0.00	36.91	31.62	51.75	83.97	0.00	45.84	67.47	0.00	172.49	194.13	0.00	194.13
4	B	ATTT	94.73	0.00	0.62	144.22	38.93	14.73	38.93	7.03	18.94	234.66	194.61	234.66	194.61	0.00	234.66
4	A	AACC	10.10	0.00	0.00	6.94	6.91	107.91	77.45	0.88	33.09	11.87	0.00	2.34	4.21	0.00	107.91
4	A	AAGG	0.00	0.00	4.40	10.29	12.03	3.92	0.00	0.00	3.60	19.52	82.90	0.00	84.94	0.00	84.94
4	B	CTTT	0.00	0.00	0.00	24.49	8.36	0.00	0.00	0.00	5.83	2.12	0.00	54.49	98.48	0.00	98.48
4	A	AATT	0.00	0.00	0.00	17.51	5.19	18.15	15.20	0.00	17.83	14.38	0.00	54.31	55.13	0.00	55.13
4	B	ACAT	0.00	0.00	0.62	13.01	44.89	185.70	40.56	0.00	40.56	31.61	118.70	118.70	118.70	0.00	118.70
4	B	ATGT	0.00	0.00	0.00	15.64	39.39	66.22	12.67	0.00	68.79	60.63	0.00	26.94	31.02	0.00	68.79
4	A	AGCC	0.00	26.00	4.17	22.62	20.87	33.35	57.91	0.83	32.02	16.20	0.00	9.38	0.00	57.91	33.35
4	A	AGGG	0.00	0.00	0.00	6.50	4.89	0.00	0.00	0.00	1.01	0.40	0.00	49.34	56.43	0.00	56.43
4	B	CCCT	0.00	0.00	0.00	5.22	3.23	0.00	0.00	0.00	1.21	0.81	6.25	40.87	55.36	0.00	55.36
4	A	ATCC	0.00	0.00	2.96	68.15	26.01	9.56	26.01	0.00	26.01	12.03	15.95	68.15	68.15	0.00	68.15
5	A	AAAAC	108.02	0.00	0.74	41.94	31.78	134.88	27.87	0.00	15.32	10.44	0.00	3.92	5.18	0.00	134.88
5	B	GTTTT	34.75	27.62	1.32	57.35	31.77	7.96	17.96	0.00	17.96	6.94	0.00	5.34	4.70	0.00	57.35
5	A	AAAAG	22.74	67.91	1.71	60.56	40.56	29.18	6.51	0.00	11.59	10.38	16.40	115.18	118.58	0.00	118.58
5	B	CTTTT	27.17	40.62	0.00	85.42	37.86	5.89	0.00	0.00	7.03	5.76	19.91	135.49	119.54	0.00	135.49
5	A	AAAT	32.85	69.86	0.00	32.85	66.61	38.00	33.11	0.00	23.00	35.41	85.14	85.14	85.14	0.00	85.14
5	B	ATTTT	25.90	27.62	0.00	132.33	50.53	16.43	0.00	0.00	20.31	19.90	0.00	92.46	92.46	0.00	132.33
5	A	AACCT	0.00	0.00	0.00	10.03	59.76	0.00	0.00	0.00	0.00	18.00	0.00	15.89	18.00	0.00	59.76
5	B	AGGTT	0.00	0.00	0.00	12.16	52.52	0.00	0.00	0.00	0.00	0.00	0.00	35.22	23.91	0.00	52.52
5	A	AAGAT	0.00	0.00	0.00	4.94	4.78	0.00	0.00	0.00	0.35	178.52	0.00	1.66	3.59	0.00	178.52
5	B	ATCTT	0.00	0.00	0.00	4.07	6.04	0.00	1.87	0.00	1.87	59.34	0.00	2.34	2.72	0.00	59.34
5	A	AATAG	0.00	0.00	0.00	3.79	4.10	0.00	6.51	0.00	2.72	8.98	5.03	4.02	4.02	0.00	4.10
5	B	ATTCT	0.00	0.00	0.00	3.50	0.00	0.00	6.51	0.00	3.76	143.05	0.00	6.50	3.53	0.00	143.05
5	A	AATAT	0.00	0.00	0.00	2.50	3.32	6.38	0.00	0.00	17.92	125.16	0.00	172.19	177.61	0.00	177.61
5	B	ATATT	11.38	0.00	0.00	10.94	18.39	18.39	0.00	0.00	25.15	68.09	13.28	163.29	163.29	0.00	163.29
5	A	AATCG	0.00	0.00	0.00	1.22	0.00	24.77	1.22	0.00	22.56	15.35	0.00	11.78	8.57	0.00	59.72
5	B	ATTCG	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	16.43	7.91	0.00	9.44	77.09	0.00	77.09
5	A	ATCCG	0.00	0.00	0.66	0.00	0.62	10.79	61.53	0.79	10.47	13.70	0.00	2.27	1.35	0.00	61.53
5	B	ATCCG	0.00	0.00	0.00	0.00	0.19	10.30	63.34	0.75	14.69	9.81	0.00	0.00	1.49	0.00	63.34
6	A	AAAAAC	46.75	29.25	0.90	9.38	12.84	75.53	0.00	0.00	11.13	10.95	0.00	0.00	2.00	0.00	75.53
6	A	AAAAAG	27.17	0.00	4.01	43.16	37.87	5.40	0.00	1.58	4.06	3.08	20.69	81.61	89.08	0.00	89.08
6	B	CTTTTT	25.90	0.00	0.00	69.27	34.57	5.15	0.00	0.00	2.58	1.96	0.00	81.00	81.00	0.00	81.00
6	b	ATTTTT	11.38	0.00	0.00	60.15	21.19	5.64	0.00	0.00	17.11	11.87	49.82	42.94	0.00	60.15	49.82
6	A	AAAAGC	0.00	0.00	1.13	0.00	1.91	22.32	50.67	0.00	9.96	6.30	0.00	0.00	0.19	0.00	50.67
6	a	AAATAC	0.00	0.00	0.00	0.00	0.70	6.62	6.51	0.00	4.91	4.36	82.78	0.00	1.04	0.00	82.78
6	A	AAATAT	0.00	0.00	0.00	1.53	1.18	20.11	6.51	0.00	8.74	7.69	0.00	48.18	51.47	0.00	51.47
6	B	ATATT	0.00	0.00	0.85	3.93	0.85	4.41	7.96	0.00	2						

10	b	AAGGTTCGCC	0.00	0.00	105.65	0.00	4.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	105.65
10	b	ACTTGGATGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	354.93	14.67	0.73	354.93
10	b	ATCGTGGTCC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	303.00	0.00	0.00	303.00
10	a	ACCATGGACT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	140.96	0.00	0.00	140.96
10	b	ACGGTSGACT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	192.11	0.00	0.69	192.11
10	a	ACGATGGACT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	78.09	37.43	5.18	78.09
10	b	CGTGCTCTGG	0.00	0.00	40.26	0.00	81.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	81.72
10	A	ACGCCAGTGC	0.00	0.00	74.82	0.00	14.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	74.82
10	B	ACTGCGGTGC	0.00	0.00	0.00	0.00	62.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	62.40
11	a	AAACAGACTC	0.00	71.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	71.48
11	A	ACCAGTACGGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.43	2471.11	0.00	0.00	0.00	0.00	0.00	2471.11
11	B	ACTGGTCCCGT	0.00	0.00	0.00	0.00	0.00	0.00	114.87	29.55	2518.69	0.00	0.00	0.00	0.00	0.00	0.00	2518.69
12	a	AACAGCAGCAGC	0.00	0.00	3.58	3.66	0.58	8.09	0.00	0.00	5.59	3.08	12.49	0.00	0.68	0.00	0.00	61.82
12	b	ATGCGTGGTTC	63.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	63.17
12	a	AATGATGATGAT	0.00	0.00	0.00	0.00	6.87	0.00	0.00	1.08	54.27	0.00	0.00	0.00	0.21	54.27	0.00	54.27
12	A	ACCGAGTACGGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	11.84	678.35	0.00	0.00	0.00	0.00	0.00	0.00	678.35
12	B	ACTCGGTCCCGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	22.06	1006.27	0.00	0.00	0.00	0.00	0.00	0.00	1006.27
12	a	AGCAGCCTATCC	0.00	94.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	94.23
15	a	AAAAATAGTGGACCG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	194.84	0.00	0.00	194.84
15	a	AAAAGTCTACTGATT	0.00	56.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	56.87
15	b	AACCTAGTTTATTTG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	569.69	7.67	0.00	569.69
15	b	AACCTAGTTCATTTG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	57.01	0.00	0.00	57.01
15	b	ACATTTGCTCCGCCG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	55.06	0.00	0.00	55.06
15	a	AAUCCAGCGTGACCC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	160.09	0.00	0.00	160.09
15	a	AAGTCAGCGGAGCGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	137.05	0.00	0.00	137.05
15	b	ACGATGCGTCTGATG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	83.95	0.00	0.00	83.95
16	a	AAAAATCTCAAGAGCC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	228.81	0.00	0.00	228.81
16	a	AAATTGGAAGGCATCC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	284.26	0.00	0.00	284.26
17	A	AAAAAGTAGAATTTTCT	0.00	0.00	0.00	0.00	223.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	223.16
17	B	AAAAGTCTACTTTTAG	0.00	0.00	0.00	0.00	122.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	122.27
17	A	AAAAGTTCACATTTATG	0.00	0.00	0.00	0.00	173.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	173.70
17	B	AAAGTTGAACTTTTCAT	0.00	0.00	0.00	0.00	269.49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	269.49
17	b	AAAGTAGAATTTTGTG	0.00	0.00	0.00	0.00	106.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	106.10
18	a	AAAGAAAGAGAGAGAGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	57.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	57.56
18	a	AAATTCGAAGGACGTGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	438.88	0.00	0.00	438.88
18	b	ACGGTCTGGACTCGGTT	0.00	63.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	63.36
18	a	AACGTGAACGTGATCGTG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	79.65	0.00	0.00	79.65
19	a	AAGAAGTAAGAATAAGAGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	168.68	0.00	0.00	168.68
20	b	ACGTCCATCTGGTCCATCT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	66.38	0.00	0.00	66.38
21	a	AAAATGATGGAATCAGAGACG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	117.14	0.00	0.00	117.14
21	a	AATATAATAATGATATGAT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	66.38	0.00	0.00	66.38
21	a	AATAGTAGTAGTAGTAGTAGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	136.66	0.00	0.00	136.66
21	b	ACTGGTCCCGTACTGGTCCGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	84.82	0.00	0.00	0.00	0.00	0.00	0.00	84.82
22	b	AACTACTACATTTATTACTTTT	63.81	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	63.81
22	a	AAAGAATCGTGAAGAAATCGTC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	71.46	0.00	0.00	71.46
22	a	ACCAGTACGGGACGAGTACGGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	174.04	0.00	0.00	0.00	0.00	0.00	0.00	174.04
23	a	ACCAGTACGGGACCCAGTACGGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	93.21	0.00	0.00	0.00	0.00	0.00	0.00	93.21
23	A	ACCAGTACGGGACCGAGTACGGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	175.42	0.00	0.00	0.00	0.00	0.00	0.00	175.42
23	B	ACTCGGTCCCGTACTGGTCCCGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	41.90	158.93	0.00	0.00	0.00	0.00	0.00	0.00	158.93
24	b	AAATTTTAGTTATATTTGAAGTTC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	151.89	6.69	0.53	151.89
24	b	CGGTGTTGTTCTTGCTGTGGCTT	0.00	451.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	451.68
24	a	AAGGCAGCGGAGTAGTACACCACC	0.00	0.00	79.43	6.75	22.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	79.43
24	a	ACCCTCTGCTCCGCCGCCACGCC	0.00	0.00	65.55	2.75	8.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	65.55
26	b	AAATTTCCGTGTGAAGGAATTGAT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	53.63	6.32	53.63
28	a	AAAAATAAATATTTCGTTTGCACCCTTT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	56.94
30	b	AAATACGTGCGTTTGAATAATCCAGAAATC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	179.22	0.00	0.00	0.00	0.00	0.00	0.00	179.22
30	b	ATGATGATGATGATGATGATGATGATT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	73.41	0.00	0.00	73.41
30	b	AGTCCATCGTAGTCCATCTATGTCATCGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	99.18	0.00	0.00	99.18
30	a	ACATAGATGGACTACGATGGGTACGATGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	105.04	0.00	0.00	105.04
31	a	AAAAATAAATATTTCGTTTGCACCCTTT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	157.22	36.33	0.00	0.00	0.00	0.00	0.00	0.00	157.22
31	b	AAACGAATAAATTTAATTTTAAAGGGTGGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	53.34	48.49	0.00	0.00	0.00	0.00	0.00	0.00	53.34
31	a	AAGTAGTAGTAGTAGTAGTAGTAGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	106.21	0.00	0.00	0.00	0.00	0.00	106.21
33	b	ACTCGGTCCCGTACTGGTCCCGTACTGGTCCGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	476.83	0.00	0.00	0.00	0.00	0.00	0.00	476.83
34	b	ATCGTTCCTGTGGCTTATCGCGGCTCGTGCCC	0.00	0.00	53.12	0.00	2.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	53.12
34	b	ACTCGGTCCCGTACTGGTCCCGTACTGGTCCCGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	71.24	0.00	0.00	0.00	0.00	0.00	0.00	71.24
35	b	ACTCGTCCCGTACTCGGTCCCGTACTGGTCCCGT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	38.95	141.75	0.00	0.00	0.00	0.00	0.00	0.00	141.75
36	a	AAATTTGAAGTTACAAATTTGTTATATTTGAAGTTC	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	98.01	0.00	0.00	0.79	98.01	0.00	98.01
36	b	AAAAATTTTGTATATTTTGAAGTTCAAAGTTGAAGTT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	69.11	0.00	0.00	0.00	0.00	0.00	69.11
36	b	AAAAATTTTGTATATCTGAAGTTCAAATTTGAAGTT	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	251.07	59.83	0.00	5.15	0.00	0.00	251.07
36	b	AAAAATTTTGTATATCTGAAGTTCAAATTTGAAGTT	0.00	0.00														

Additional file 7: (b) Mean lengths of repeat types in different genomic regions of *Daphnia pulex* (Dappu), *Drosophila melanogaster* (DroMel) and *Apis mellifera* (ApiMel). A=normal B=reverse complement of repeat motif A; "*" denotes palindromic motifs; a and b are used if only the normal form (a) OR its reverse complement (b) were found.

unit size	motif		Dappu v1.1 3UTR	Dappu v1.1 5UTR	Dappu v1.1 CDS	Dappu v1.1 introns	Dappu v1.1 intergenic	DroMel-5.5 3UTR	DroMel-5.5 5UTR	DroMel-5.5 CDS	DroMel-5.5 introns	DroMel-5.5 intergenic	ApiMel-2.0 CDS	ApiMel-2.0 introns	ApiMel-2.0 intergenic	min	max
[bp]	form	unit	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]	[bp]
1	A	A	16.5	15.8	19.6	16.3	16.8	15.6	15.9	16.0	16.8	16.9	16.0	18.1	17.8	15.6	19.6
1	B	T	15.9	14.9	17.1	16.6	16.8	15.6	15.2	17.8	16.7	16.9	16.0	18.0	17.8	14.9	18.0
1	A	C	14.4	14.0	13.8	15.4	15.1	14.2	15.3		14.7	14.8	13.0	14.7	14.7	15.3	15.3
1	B	G	15.2	17.0	14.8	15.1	15.1	16.3			14.7	15.0	13.0	15.0	15.3	13.0	17.0
2	A	AC	19.0	18.5	17.2	18.0	18.5	21.0	19.1	16.0	20.6	20.6	14.0	26.2	24.4	14.0	26.2
2	B	GT	17.3	22.4	17.0	18.2	18.2	21.7	17.4	23.0	20.4	20.6		23.8	24.4	17.0	24.4
2	A	AG	17.0	17.3	16.2	19.8	19.8	22.5	22.2	22.0	21.4	21.4	17.3	23.7	23.7	16.2	23.9
2	B	CT	18.4	17.7	18.8	19.1	18.9	19.2	18.6	14.0	21.6	21.3	27.9	23.5	23.3	14.0	27.9
3	-	AT	17.5	14.0	15.0	18.0	18.1	24.1	23.1	24.0	24.2	24.5	22.0	27.2	26.8	14.0	27.2
3	A	AAC	17.9	19.5	20.7	20.0	19.6	23.3	20.0	22.2	22.1	21.8	31.4	21.3	23.1	17.9	31.4
3	B	ATT	18.7	21.7	19.5	18.7	18.0	18.1	24.0	21.3	21.5	22.9	25.5	23.9	18.9	25.5	23.9
3	A	AAG	18.1	18.3	22.6	19.8	20.6	22.0	16.7	19.2	18.7	18.3	38.3	24.1	24.4	16.7	38.3
3	B	CTT	19.0		20.2	20.5	20.6	15.0	28.5	21.0	18.9	18.7	29.0	23.9	24.7	15.0	29.0
3	A	AAT	16.9	16.0	19.6	19.7	19.2	21.9	19.1	20.6	29.3	38.9	33.4	40.4	27.4	16.0	40.4
3	B	ATT	19.0	15.0	18.5	19.7	19.7	25.0	21.0	21.0	25.0	25.4	26.0	27.0	25.0	32.2	27.0
3	A	ACC	18.3	17.0	19.0	18.4	18.7	21.7	19.4	21.0	20.5	20.7	26.0	28.1	27.4	17.0	36.0
3	B	GGT		19.0	18.5	18.6	18.5	22.0	22.7	20.9	20.3	20.7	34.1	21.7	25.2	18.5	34.1
3	A	ACG	18.0		19.1	18.3	19.0	17.3	18.0	18.7	19.2	21.4	29.0	23.6	29.3	17.3	29.3
3	B	AGT		15.0	19.4	18.8	18.7	14.3	20.3	21.4	19.2	49.2	29.2	27.5	45.8	15.0	49.2
3	A	ACT	27.7	30.0	22.6	21.7	21.1	20.3	15.0	21.0	25.2	22.8	136.8	48.4	44.8	15.0	136.8
3	B	AGT			19.3	20.8	20.8	26.0		22.7	23.9	24.3	93.9	53.0	42.2	19.3	93.9
3	A	AGC	17.0		19.6	18.6	19.0	24.4	23.9	25.6	26.3	28.0	29.5	24.0	27.1	17.0	29.5
3	B	CTG	18.7	15.6	19.8	19.2	19.1	20.5	18.4	20.4	20.4	20.3	26.2	25.3	26.2	17.0	26.2
3	A	AGG			18.3	17.8	18.2	21.4	20.5	21.7	22.5	21.8	22.9	22.9	22.4	17.8	22.9
3	B	CCT	17.5	23.0	19.8	17.4	18.8	23.8	20.0	18.9	22.8	22.4	27.3	23.1	22.8	17.4	27.3
3	A	ATC	16.0	18.0	18.5	18.6	18.8	20.7	18.5	21.3	21.6	21.0	29.1	28.7	28.4	16.0	29.1
3	B	AGT	18.5		18.6	18.7	18.7	14.3	20.3	20.3	21.1	51.6	34.9	51.6	18.5	51.6	34.9
3	A	CGG	19.0		19.8	18.4	18.8	15.0	21.3	17.9	16.7	17.1	22.7	20.7	20.8	15.0	22.7
3	B	CGG			20.4	19.1	18.8	20.0	16.3	21.5	18.0	17.1	26.5	19.2	21.6	16.3	26.5
4	A	AAAC	21.3	16.5	20.5	19.7	21.2	19.9	22.2	20.6	21.1	21.1	28.7	21.8	16.5	28.7	21.1
4	B	TTTT	16.0		20.7	20.3	20.3	21.3	20.5	20.3	20.3	18.0	20.3	16.5	23.5	16.0	20.3
4	A	AAAG	22.0		16.0	24.0	23.7	19.4	21.0		19.7	19.8	20.5	24.6	24.5	16.0	24.6
4	B	TTTT	19.0	22.0	17.6	21.3	22.2			19.1	22.6	22.0	24.1	24.8	17.6	24.8	22.0
4	A	AAAT	21.6		16.0	20.2	20.0	19.2	21.1	19.2	20.0	20.0	21.8	22.7	19.2	22.7	21.6
4	B	TTTT	18.2		16.0	20.2	20.2	20.1	20.5	19.1	21.3	21.8	18.0	21.5	23.8	16.0	21.3
4	A	AACC	16.0			20.5	19.6	25.9	21.4	20.0	25.8	23.6		19.0	24.0	16.0	25.9
4	A	AAGG			37.7	21.7	27.6	16.0			20.6	19.6	16.7	27.0	26.6	16.0	37.7
4	B	CCTT			18.0	23.3	20.7			21.4	22.5	20.3	23.4	26.2	18.0	26.2	23.3
4	-	AATT			19.9	19.9	17.9	18.5	21.0	19.3	20.3	20.3	20.6	27.9	20.6	17.9	20.3
4	A	ACAT			16.0	27.4	24.0	18.6	20.3	20.3	21.0	21.0	28.7	29.0	16.0	28.0	24.0
4	B	ATGT				22.0	23.1	18.0	17.5		20.4	20.8		20.7	17.5	29.3	23.1
4	A	AGCC			16.0	26.8	20.2	19.4	26.7	19.0	24.3	24.4	33.0	26.8	26.0	33.0	20.2
4	A	AGGG				27.4	24.9	20.5			21.2	20.5	20.5	27.3	27.4	20.5	27.3
4	B	CCCT				19.3	24.0	20.7			20.7	26.0	16.0	20.2	20.0	16.0	26.0
4	A	ATCC	16.0		38.0	33.5	25.1	19.5			25.3	25.5		24.5	24.3	16.0	38.0
5	B	AAAAAC	21.4		19.0	20.0	22.7	22.0	25.7		22.5	21.0	21.3	21.7	17.0	25.7	21.0
5	A	TTTTT	18.3	17.0	17.0	20.2	21.6		22.0		21.0	21.1	21.8	20.6	17.0	22.0	21.0
5	A	AAAAAG	17.0		22.0	20.8	21.7	19.8	18.0		21.3	21.3	21.0	25.0	17.0	41.3	21.0
5	B	CTTTT	21.5	25.0		20.7	20.6	24.0			22.6	20.4	51.0	24.5	24.5	20.4	51.0
5	A	AAAT	17.3	21.5		20.6	22.6	19.3	26.3		23.8	22.3	23.2	22.9	17.3	26.3	23.2
5	B	ATTTT	20.5	17.0		23.5	21.1	22.3			22.7	23.5	23.6	24.9	17.0	24.9	23.6
5	A	AACCT				37.8	74.8				37.0	25.3	74.8	25.3	74.8	37.0	74.8
5	B	AGGTT				35.9	75.5				44.2	26.3	75.5	26.3	75.5	35.9	75.5
5	A	AAGAT				24.3	27.1				18.0	1137.4	17.0	21.7	18.0	1137.4	21.7
5	B	ATCTT				24.0	25.3				19.2	23.3	23.0	23.3	19.0	236.3	23.3
5	A	ATTAG				56.0	23.2		18.0		20.7	21.7	23.0	455.7	455.7	18.0	455.7
5	B	ATTCT				22.2	30.6		18.0		25.6	70.1	21.2	22.7	18.0	70.1	21.2
5	A	AAAT				18.5	25.6	26.0			31.8	122.7	31.2	35.8	18.5	122.7	31.2
5	B	ATATT				23.1	23.7	37.5	36.0		54.9	83.4	17.0	31.3	33.8	17.0	83.4
5	A	ATCGG	18.0			18.0		33.7	27.9		21.7	21.7		33.7	18.0	33.7	21.7
5	B	ATTCG				17.0	20.0		22.0	17.0	24.9	25.5	22.1	22.6	17.0	26.6	22.1
5	A	ATCCG				17.0	18.0		21.0	18.0	22.5	23.0	18.5	21.5	17.0	24.3	21.5
5	B	ATCGG				18.0	21.0		25.0	17.0	24.4	24.0		23.5	17.0	25.0	24.4
6	A	AAAAAC	24.7	18.0	23.0	21.3	22.9	22.0	28.3		22.8	22.8		23.5	18.0	28.0	22.8
6	A	AAAAAG	21.5		25.8	22.4	22.4	22.0		18.0	26.1	24.5	26.5	27.1	26.1	18.0	27.1
6	B	CTTTTT	20.5			23.8	23.3	21.0			22.2	25.0		26.4	25.4	20.5	26.4
6	b	ATTTTT	18.0			23.1	21.7	23.0			22.6	22.9		23.9	23.3	18.0	23.9
6	A	AAAGG			29.0	19.1	25.7	19.1	23.3		23.6	19.5		45.5	19.5	18.0	45.5
6	A	AAATAC				22.7	22.7	27.0	18.0		23.0	27.8	212.0	23.7	18.0	212.0	23.0
6	B	AAATAT				22.5	56.5	27.3	18.0		21.4	24.5		27.1	28.1	18.0	56.5
6	A	ATATTT				29.0	20.5	18.0	22.0		58.8	24.2		66.9	26.8	18.0	66.9
6	B	ACCAT				20.7	24.7	20.7	24.5	22.1	20.5	108.8	41.0	20.2	108.8	20.7	108.8
6	A	AACAGC			25.9	44.3	23.1	28.0	27.4	30.4	26.4	26.3	24.0	30.6	23.1	44.3	24.0
6	A	AAACCC				89.4	93.0				23.5	23.5		23.5	23.5	89.4	93.0
6	B	GGGGTT				18.0	21.3				18.0	23.7		18.0	18.0	93.3	21.3
6	A	AAGAGT							20.7	30.0	19.0	21.4	24.0	62.8	18.0	240.0	21.4
6	A	AAGCAG			19.0	23.0	23.0					23.0	291.7	101.6	19.0	291.7	23.0
6	A	AAGCGG				20.0	20.0				34.0	27.2		22.5	20.0	272.0	27.2
6	A	AATAGT				19.0	24.3	18.0			27.7	57.7		38.8	18.0	57.7	57.7
6	B	ACTATT						29.0			23.0	25.5	99.0	24.0	99.0	23.0	99.0
6	A	AATCGG							29.7		25.9	22.4		21.0	21.0	29.7	25.9
6	A	AATGAC					26.0		21.0		26.0	33.0		75.0	47.0	21.0	75.0
6	A	AATGAT				26.0				37.0	21.8	40.2	52.4	42.5	24.8	18.0	52.4
6	A	ACGAT					21.7	33.8	25.9	34.0	31.8	24.8		20.0	19.0	40.8	31.8
6	B	ATCTGT					27.8	35.5		31.0	30.3						

[illegible]

Additional file 7: (c) Number of satellites found for a certain repeat motif in the different genomic regions of *Daphnia pulex* (Dappu), *Drosophila melanogaster* (DroMel) and *Apis mellifera* (ApiMel). A=normal B=reverse complement of repeat motif A; "-" denotes palindromic motifs; and a and b are used if only the normal form (a) OR its reverse complement (b) were found.

unit size (bp)	motif form	unit	Dappu v1.1 3'UTR #sat	Dappu v1.1 5'UTR #sat	Dappu v1.1 CDS #sat	Dappu v1.1 introns #sat	Dappu v1.1 intergenic #sat	DroMel-5.5 3'UTR #sat	DroMel-5.5 5'UTR #sat	DroMel-5.5 CDS #sat	DroMel-5.5 introns #sat	DroMel-5.5 intergenic #sat	ApiMel-2.0 CDS #sat	ApiMel-2.0 introns #sat	ApiMel-2.0 intergenic #sat	min #sat	max #sat
1	A	A	83	13	15	1446	3647	259	145	7	3425	3023	17	1773	23843	7	23843
1	B	T	116	11	11	2289	3711	148	56	5	3067	3040	3	2571	23671	3	23671
1	A	C	43	1	9	971	1888	22	3	0	385	367	1	30	535	0	1888
1	B	G	15	1	6	908	1915	3	0	0	377	417	1	30	542	0	1915
2	A	AC	42	6	11	945	2329	209	98	1	1756	1890	1	100	1393	1	2329
2	B	GT	39	12	3	1246	2338	34	123	5	1935	1995	0	1134	2338	0	2338
2	A	AG	17	3	10	1208	2588	28	56	2	372	393	3	922	13941	2	13941
2	B	CT	43	15	12	1458	2638	15	21	1	600	465	40	972	13582	1	13582
2	A	AT	20	2	2	342	680	451	84	7	1886	1872	1	2441	29688	1	29688
3	A	AAC	14	2	407	385	931	50	75	273	316	235	23	15	406	2	931
3	B	GTT	6	3	18	586	958	3	14	1	280	302	6	25	418	1	958
3	A	AAG	14	4	294	957	2215	1	9	36	40	41	54	193	3042	1	3042
3	B	CTT	10	0	37	1173	2324	1	2	2	59	41	5	236	3061	0	3061
3	A	AAT	12	1	8	209	549	28	9	37	247	351	28	409	4476	1	4476
3	B	ATT	18	1	4	330	599	39	7	1	289	380	9	404	4284	1	4284
3	A	ACC	3	2	127	149	347	17	11	133	89	58	25	16	370	2	370
3	B	GGT	0	1	58	153	315	1	3	55	62	77	35	27	362	0	362
3	A	ACG	1	0	126	150	387	3	6	56	38	34	14	41	605	0	605
3	B	CGT	0	1	49	167	358	3	3	9	69	46	4	32	650	0	650
3	A	ACT	3	1	8	101	193	6	1	2	55	36	14	14	173	1	193
3	B	AGT	0	0	3	91	176	1	0	3	38	32	20	33	182	0	182
3	A	AGC	1474	6	445	514	1184	74	115	1474	514	404	19	5	1474	2	1474
3	B	CTG	6	5	97	515	1262	9	7	30	393	429	17	6	156	5	1262
3	A	AGG	0	0	59	83	184	22	15	175	73	63	22	159	2838	0	2838
3	B	CCT	2	1	28	96	170	4	2	26	66	71	20	169	2842	1	2842
3	A	ATC	5	3	34	112	235	9	10	50	199	17	17	297	297	0	297
3	B	ATG	2	0	27	117	222	19	4	33	228	189	49	28	301	0	301
3	A	CCG	0	0	77	208	1	4	35	23	51	5	6	15	238	0	238
3	B	CGG	0	0	92	198	6	3	58	29	50	2	14	26	262	0	262
4	A	AAAC	3	2	2	49	147	18	12	0	87	94	0	3	147	0	147
4	B	GTTT	2	0	3	115	157	2	4	0	83	70	0	3	84	0	157
4	A	AAAG	1	0	1	134	284	7	2	0	17	15	6	149	2165	0	2165
4	B	CTTT	4	1	5	195	295	0	0	0	20	11	1	188	2212	0	2212
4	A	AAAT	7	0	0	54	152	11	11	10	123	129	0	1759	1759	0	1759
4	B	ATTT	3	0	1	206	189	15	2	0	182	239	1	178	1763	0	1763
4	a	AACC	1	0	0	10	34	17	10	1	66	32	0	2	66	0	66
4	A	AAGG	0	0	3	14	42	1	0	0	9	7	3	50	655	0	655
4	B	CCTT	0	0	1	31	39	0	0	0	14	6	0	38	772	0	772
4	-	AATT	0	0	0	26	28	4	2	0	47	41	0	43	557	0	557
4	A	ACAT	0	0	0	14	180	26	12	0	216	205	0	23	224	0	224
4	B	ATGT	0	0	0	21	164	15	2	0	174	186	0	15	234	0	234
4	A	AGCC	0	1	4	33	97	7	6	1	68	54	0	7	72	0	97
4	A	AGGG	0	0	0	7	25	0	0	0	3	1	0	38	565	0	565
4	B	CCCT	0	0	0	8	13	0	0	0	3	2	1	33	569	0	569
4	a	ATCG	0	0	2	60	100	2	0	0	54	66	0	8	135	0	135
5	A	AAAC	8	0	1	62	135	25	3	0	35	30	0	3	49	0	135
5	B	GTTT	3	1	2	84	142	0	1	0	44	21	0	4	47	0	142
5	A	AAAG	2	1	2	99	181	6	1	0	23	16	2	75	975	0	975
5	B	CTTT	2	1	2	122	177	18	0	0	1008	16	1	1008	1008	0	1008
5	A	AAAT	3	2	0	56	244	7	4	0	51	59	0	53	767	0	767
5	B	ATTT	2	1	0	166	232	3	0	0	47	54	0	79	764	0	764
5	A	AACCT	0	0	0	8	77	0	0	0	0	0	0	7	146	0	146
5	B	AGGTT	0	0	0	10	67	0	0	0	0	0	0	13	187	0	187
5	A	AAGAT	0	0	0	6	17	0	0	0	1	10	0	1	34	0	34
5	B	ATCTT	0	0	0	5	23	0	0	0	5	16	0	2	24	0	24
5	A	AATAG	0	0	0	2	17	0	0	0	6	9	1	4	38	0	38
5	B	ATTC	0	0	0	5	11	0	0	0	5	13	0	5	32	0	32
5	A	AATAT	0	0	0	4	14	1	0	0	29	65	0	90	1022	0	1022
5	B	ATATT	1	0	0	14	11	2	2	0	29	52	2	85	994	0	994
5	A	AATCG	0	0	0	2	0	3	6	0	42	41	0	9	81	0	81
5	B	ATTCG	0	0	0	1	0	8	1	0	34	37	7	86	86	0	86
5	A	ATCCG	0	0	1	0	3	2	7	1	24	38	0	2	13	0	38
5	B	ATCGG	0	0	0	0	1	2	7	1	31	26	0	0	13	0	31
6	a	AAAAAC	3	1	1	13	46	11	0	0	25	30	0	0	18	0	46
6	A	AAAAAG	2	0	4	57	163	1	0	2	8	8	2	49	703	0	703
6	B	CTTTTT	2	0	0	86	143	1	0	0	6	5	0	50	656	0	656
6	b	ATTTTT	1	0	0	77	94	1	0	0	39	33	0	34	379	0	379
6	a	AAAAAGC	0	0	1	0	7	2	6	0	20	17	0	0	2	0	20
6	a	AAATAC	0	0	0	0	3	1	1	0	11	10	1	0	9	0	11
6	A	AAATAT	0	0	0	2	2	3	1	0	21	20	0	29	376	0	376
6	B	ATATTT	0	0	0	4	4	1	1	0	18	26	0	30	358	0	358
6	a	AACAA	0	0	0	0	3	0	8	0	11	8	4	3	31	0	31
6	a	ACAGC	0	0	15	4	9	14	12	113	43	40	0	0	31	0	113
6	A	AACCCC	0	0	0	0	79	0	0	0	2	0	0	0	0	0	79
6	B	GGGGTT	0	0	0	1	75	0	0	0	1	3	0	0	0	0	75
6	a	AAGAGT	0	0	0	0	0	0	0	0	0	0	2	0	1	0	2
6	a	AAGCAG	0	0	1	3	3	1	2	3	12	5	0	5	13	0	13
6	a	AAGGCG	0	0	0	2	0	0	0	0	0	1	1	0	2	0	2
6	A	AATAGT	0	0	0	1	3	1	0	0	0	4	3	4	21	0	21
6	B	ACTATT	0	0	0	0	0	0	2	4	2	4	2	18	0	0	18
6	a	AATCGG	0	0	0	0	6	0	6	0	12	18	0	1	18	0	18
6	A	AATGAC	0	0	0	0	1	0	1	0	1	2	0	2	0	0	2
6	a	AATGAT	0	0	0	0	0	1	8	1	8	6	9	6	19	0	19
6	A	ACAGAT	0	0	0	0	0	4	0	0	150	99	0	1	150	0	150
6	B	ATGTGT	0	0	0	6	0	0	1	0	117	117	0	0	1	0	117
6	b	CGGTCT	0	0	0	0	1	0	0	0	0	2	1	0	4	0	4
6	b	ATCGTG	0	0	0	0	1	0	0	2	0	0	2	0	0	0	5
6	a	ATCCGC	0	0	0	0	0	2	6	13	19	26	0	0	0	0	29
7	a	AAAAAAC	1	0	1	21	43	8	2	0	21	24	0	1	20	0	43
7	A	AAAAAAG	0	0	0	36	88	0	2	0	5	2	2	45	533	0	533
7	B	CTTTTTT	0	0	0	40	63	0	0	0	0	4	1	62	616	0	616
7	A	AATATAT	0	0	0	2	0	0	0	0	18	28	0	41	558	0	558
7	B	ATATATT	0	0	0	4	5	2	0	0	9	23	0	43	530	0	530
8	A	AAAAAAG	0	0	0	18	42	2	2	0	12	4	1	37	403	0	403
8	B	CTTTTTTT	0	0	0	21	50	0	0	0	0	3	0	43	386	0	386
8	a	ACATATAT	0	0	0	2	0	7	1	0	14	19	0	9	123	0	123
9	b	CTTTTTTTT	0	1	0	10	18	0									

9	a	AACAGCAGC	0	0	4	2	5	2	3	53	13	14	1	0	18	0	53
9	a	AATAATCAT	0	0	0	0	1	0	0	0	3	1	0	1	4	0	4
9	b	ACTACTATT	0	0	0	0	1	0	0	0	0	0	2	0	4	0	4
9	a	AATATATAT	0	0	0	1	2	0	0	0	6	6	0	20	196	0	196
10	a	AAAGCTCGAG	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
10	b	AAAGTTCGCC	0	0	5	0	1	0	0	0	0	0	0	0	0	0	5
10	b	ACTGTGATGG	0	0	0	0	0	0	0	0	0	0	3	1	0	0	3
10	b	ATCGTGGTCC	0	0	0	0	0	0	0	0	0	0	2	1	0	0	2
10	a	ACCATGGACT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
10	b	ACGGTGGACT	0	0	0	0	0	0	0	0	0	0	2	0	2	0	2
10	a	ACGATGGACT	0	0	0	0	0	0	0	0	0	0	2	1	0	0	4
10	b	CGTGCCTCTGG	0	0	1	0	49	0	0	0	0	0	0	0	0	0	49
10	A	ACGCCAGTGC	0	0	5	0	3	0	0	0	0	0	0	0	0	0	5
10	B	ACTGGCGTGC	0	0	0	0	12	0	0	0	0	0	0	0	0	0	12
11	a	AAACAGCACTC	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
11	A	ACCAGTACGGG	0	0	0	0	0	0	0	0	1	55	0	0	0	0	55
11	B	ACTGGTCCCGT	0	0	0	0	0	0	0	2	5	57	0	0	0	0	57
12	a	AACAGCAGCAGC	0	0	3	3	2	1	0	32	6	5	1	0	4	0	32
12	b	ATGCTCTGGTGG	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
12	a	AATGATGATGAT	0	0	0	0	0	1	0	0	2	0	2	0	1	0	2
12	A	ACCGAGTACGGG	0	0	0	0	0	0	0	0	2	21	0	0	0	0	21
12	B	ACTCGGTCCCGT	0	0	0	0	0	0	0	0	4	22	0	0	0	0	22
12	a	ACGAGCCTATCC	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
15	a	AAAAATAGTGGACCG	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
15	a	AAAAGTCTACTGATT	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
15	b	AACCTAGTTATTTTG	0	0	0	0	0	0	0	0	0	0	4	2	0	0	4
15	b	AACCTAGTCAITTTG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
15	b	ACATTTGCTCCGCCG	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
15	a	AAACCAGCCTGACCC	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
15	a	AAGTCACGGAGGAGC	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
15	b	ACGATGGTGTCCGATG	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
16	a	AAAAATCTCAAAGACC	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
16	a	AAATTCGAAGGCATCC	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
17	A	AAAAGTAGAACCTTTCT	0	0	0	0	30	0	0	0	0	0	0	0	0	0	30
17	B	AAAAGTCTACTTTTAG	0	0	0	0	15	0	0	15	0	0	0	0	0	0	15
17	A	AAAAGTTCAACTTTTATG	0	0	0	0	53	0	0	0	0	0	0	0	0	0	53
17	B	AAAAGTTGAACTTTTTAT	0	0	0	0	82	0	0	0	0	0	0	0	0	0	82
17	b	AAAAGTAGAACCTTTTGTG	0	0	0	0	15	0	0	0	0	0	0	0	0	0	15
18	a	AAAGAAGAGAGAGAGAGG	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
18	a	AAATTTCAAGGAACGTGC	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
18	b	ACGGTGTGGACTCGGTT	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
18	a	AACGTGAAGCTGATCGTG	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
19	a	AAGAAGTAGAATAAGAGCT	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
20	b	ACGTCCATCTGGTGCATCT	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
21	a	AAAATGATGAAATCAGGACG	0	0	0	0	0	0	0	0	0	0	3	0	0	0	3
21	a	AATAATAATAATGATGATGAT	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
21	a	AATAGTAGTAGTAGTAGTAGT	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
21	b	ACTGGTCCCGTACTGGTCCGT	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
22	b	AACACTACATTTTACTTTT	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
22	a	AAAAGAATCGTGGAGAATCGTC	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
22	a	ACCAGTACGGGACGAGTACGGG	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
23	a	ACCAGTACGGGACCCAGTACGGG	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
23	A	ACCAGTACGGGACCGAGTACGGG	0	0	0	0	0	0	0	0	0	3	0	0	0	0	3
23	B	ACTCGGTCCCGTACTGGTCCCGT	0	0	0	0	0	0	0	0	1	0	0	0	0	0	4
24	b	AAATTTTAGTTATATTGAAGTTC	0	0	0	0	0	0	0	0	0	3	1	1	0	0	3
24	b	CGGTGTTGTCTGTCTGTGGCTT	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
24	a	AAGGCAGCGGAGTACTACACCACC	0	0	10	3	8	0	0	0	0	0	0	0	0	0	10
24	a	ACCCTGTCTCGCCCGGCCAGCC	0	0	13	1	5	0	0	0	0	0	0	0	0	0	13
26	b	AAATTTCCGTGTGAAGGAATGAT	0	0	0	0	0	0	0	0	0	3	4	0	0	0	4
28	a	AAATAACTTATCAATTCCTCGGACG	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
30	b	AAATACGTGCGTTTGAAGAAATCCAGAAATC	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
30	b	ATGATGATGATGATGATGATGATGAT	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
30	b	AGTCCATGTAGTCACTATGTCCATCGT	0	0	0	0	0	0	0	0	0	0	2	0	0	0	2
30	a	ACATAGATGGACTACGATGGGCTACGATGG	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
31	a	AAAAATAAATTATTTGTTGCCACCCTTT	0	0	0	0	0	0	0	0	0	5	0	0	0	0	10
31	b	AAACGAATAAATTAATTTTAAAGGGTGGC	0	0	0	0	0	0	0	0	4	2	0	0	0	0	4
31	a	AACAGTAGTAGTAGTAGTAGTAGTAGTAGT	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
33	b	ACTCGGTCCCGTACTGGTCCCGTACTGGTCCGT	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
34	b	ATCGTTCCTGTGGCTTTATGCCGGCTTCGTGCC	0	0	3	0	1	0	0	0	0	0	0	0	0	0	3
34	b	ACTCGGTCCCGTACTGGTCCCGTACTGGTCCCGT	0	0	0	0	0	0	0	0	0	2	0	0	0	0	2
35	b	ACTCGGTCCCGTACTGGTCCCGTACTGGTCCCGT	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
36	b	AAATTGAAGTTACAATTTTGTATATTGAAGTTC	0	0	0	0	0	0	0	0	0	2	0	1	0	0	2
36	b	AAAATTTTGTATATTGAAGTTCAAGTTGAAGTT	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
36	b	AAAATTTTGTATATCTGAAGTTCAAAATGAAGTT	0	0	0	0	0	0	0	0	0	2	0	6	5	0	6
36	b	AAAATTTTGTATATCTGAAGTTCAAAATGAAGTT	0	0	0	0	0	0	0	0	0	2	0	1	0	0	2
36	b	ACCTCTCCGCTCTTCTCTCTCAGCTTCATCTTC	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1
39	a	AAACCAACTGAGGGACGAGTGCCAAAGCCAACACTTTG	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
45	b	AAATATTCCCAAGTATCAAGATCGAAGTAAGTTGAGTAGATTGAG	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
45	a	AACGACGACCACTCCAGCAGCAGCACTCCACGCCGACACCCGAC	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1
45	a	ACCAGTACGGGACAGTACGGGACCCAGTACGGGACCGAGTACGGG	0	0	0	0	0	0	0	0	2	0	0	0	0	0	2
46	a	ACCAGTACGGGACAGTACGGGACCGAGTACGGGACCGAGTACGGG	0	0	0	0	0	0	0	0	2	0	0	0	0	0	2
47	b	AACACTCTCTCTCCGGATGATTTGACACAGTTGGAACTGGAAGAG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
47	b	AACACTCTCTCTCCGGATGATTTGACACAGTTGGAACTGGAAGAG	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2
48	a	AAAAATGTCAAAGATTGTTGATAAGGGATAAATTGATTATTGTAAG	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
48	a	AACCAACAACCTTCCACAAAGTGCCCAACGACAACTACTCTAGATCCAC	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
48	a	ACCAGTACGGGACCGAGTACGGGACCGAGTACGGGACCTAGTACGGG	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1

Additional file 7: (d) Mean perfection of repeat motifs in different genomic regions of *Daphnia pulex* (Dappu), *Drosophila melanogaster* (DroMel) and *Apis mellifera* (ApiMel). A=normal B=reverse complement of repeat motif A; "-." denotes palindromic motifs; a and b are used if only the normal form (a) OR its reverse complement (b) were found.

unit size	motif	unit	Dappu v1.1 3UTR	Dappu v1.1 5UTR	Dappu v1.1 CDS	Dappu v1.1 introns	Dappu v1.1 intergenic	DroMel-5.5 3UTR	DroMel-5.5 5UTR	DroMel-5.5 CDS	DroMel-5.5 introns	DroMel-5.5 intergenic	ApiMel-2.0 CDS	ApiMel-2.0 introns	ApiMel-2.0 intergenic	min	max	
(bp)	form		[%]	[%]	[%]	[%]	[%]	[%]	[%]	[%]	[%]	[%]	[%]	[%]	[%]	[%]	[%]	
1	A		99.3	99.6	98.5	99.4	99.3	99.5	99.3	99.4	99.3	99.4	98.9	99.0	99.4	98.6	99.6	
1	B	T	99.2	100.0	98.4	99.2	99.2	99.3	99.7	99.0	99.4	99.4	98.3	99.0	99.1	98.3	100.0	
1	A	C	100.0	100.0	100.0	99.9	99.9	100.0	100.0		99.9	99.9	100.0	100.0	99.8	99.8	100.0	
1	B	G	99.7	100.0	100.0	99.9	99.9	100.0			99.9	99.9	100.0	100.0	99.8	99.7	100.0	
2	A	AC	99.3	100.0	99.5	99.4	99.4	98.7	98.6	100.0	98.9	98.9	100.0	99.1	98.6	98.6	100.0	
2	B	GT	99.8	97.5	98.5	99.5	99.4	98.2	99.2	99.2	99.0	98.9		98.6	98.9	97.5	99.8	
2	A	AG	100.0	100.0	99.6	99.5	99.5	98.3	98.9	98.2	98.5	98.9	98.4	98.8	98.7	98.2	100.0	
2	B	CT	99.6	99.3	99.0	99.5	99.5	99.1	98.8	100.0	98.7	98.7	98.0	98.5	98.7	98.0	100.0	
-	A	AT	98.6	100.0	100.0	99.2	98.9	97.9	97.8		98.0	97.9	95.5	98.5	98.5	95.5	100.0	
3	A	AAC	99.4	97.8	98.8	99.0	98.9	97.6	98.6	98.5	98.2	98.7	97.9	99.4	98.9	97.6	99.4	
3	B	GTT	99.3	96.8	99.3	99.4	99.2	98.5	98.9	95.8	98.6	98.5	98.4	99.1	98.7	95.8	99.4	
3	A	AAG	99.4	100.0	98.7	99.5	99.4	95.2	99.5	98.5	99.4	99.6	98.2	99.0	98.7	95.2	100.0	
3	B	CTT	98.7		99.1	99.4	99.4	100.0	95.2	95.2	99.1	99.2	98.9	98.7	98.9	95.2	100.0	
3	A	AAT	100.0	100.0	99.0	99.1	99.4	98.1	98.5	98.8	98.1	97.5	96.7	97.8	98.3	96.7	100.0	
3	B	ATT	100.0	100.0	98.1	99.2	99.3	98.1	98.2	100.0	98.1	97.3	97.9	98.5	98.3	97.3	100.0	
3	A	ACC	98.3	100.0	99.4	99.9	99.5	98.0	98.8	98.4	99.0	99.0	97.2	97.8	98.4	97.2	100.0	
3	B	GGT	98.5		99.5	99.5	99.6	95.5	97.5	98.8	99.0	98.6	96.9	99.6	98.3	95.5	100.0	
3	A	ACG	100.0		99.2	99.7	99.6	98.4	99.3		99.2	98.6	96.9	99.2	98.3	96.9	100.0	
3	B	CGT		100.0	99.5	99.7	99.6	100.0	98.7	99.0	99.5	99.2	93.7	98.8	98.3	93.7	100.0	
3	A	ACT	97.3	96.7	98.9	98.8	99.0	98.0	100.0		98.6	98.8	93.1	96.5	97.3	93.1	100.0	
3	B	AGT			98.6	99.0	99.2	96.2	98.2	98.2	98.9	98.3	95.1	96.6	97.5	95.1	99.2	
3	A	AGC	100.0	98.5	99.6	99.6	99.6	98.2	97.7		97.3	97.6	97.6	97.8	98.2	97.3	100.0	
3	B	CTG	100.0	100.0	99.5	99.5	99.5	100.0	98.7		98.4	98.0	98.6	100.0	98.0	98.0	100.0	
3	A	AGG			99.4	99.6	99.6	98.7	99.2	98.2	98.4	98.8	98.0	99.0	98.9	98.0	99.6	
3	B	CCT	100.0	100.0	99.1	99.7	99.5	99.0	100.0	99.4	98.4	98.3	99.1	99.0	98.8	98.3	100.0	
3	A	ATG	100.0	100.0	99.5	99.5	99.5	98.4	99.1	98.9	98.9	98.4	98.7	98.7	98.4	98.4	100.0	
3	B	ATG	97.7		98.6	99.8	99.5	98.0	100.0	99.1	98.8	98.7	97.1	97.8	98.5	97.1	100.0	
3	A	CCG	100.0		98.7	99.5	99.3	100.0	99.0	99.2	100.0	99.6	98.7	99.5	98.7	98.7	100.0	
3	B	CGG			98.9	99.4	99.4	98.5	100.0	98.1	99.7	99.7	98.7	99.7	99.1	98.1	100.0	
4	A	AAAC	98.9	100.0	97.6	98.7	98.8	97.6	98.7		98.8	98.9	98.9	97.6	98.9	97.6	100.0	
4	B	GTTT	100.0		98.8	98.8	98.6	95.7	98.7		98.7	98.7	100.0		99.5	95.7	100.0	
4	A	AAAG	95.7		100.0	99.1	98.9	99.4	98.0		99.5	99.5	98.5	98.1	98.5	95.7	100.0	
4	B	CTTT	100.0	95.5	100.0	98.9	98.9	98.9		98.9	98.9	97.2	100.0		98.5	95.5	100.0	
4	A	AAAT			99.0	98.6	99.0	98.5	98.9		99.2	98.7	98.5	97.5	98.5	97.5	99.2	
4	B	ATTT	100.0		100.0	98.9	99.0	99.2	98.0		99.2	98.1	100.0		98.8	98.5	100.0	
4	a	AACCC	100.0			99.1	99.4	97.9	99.3	100.0	98.6	98.6		100.0	98.9	97.9	100.0	
4	A	AAGG			97.7	100.0	99.1	100.0		99.3		98.1	100.0		98.9	99.1	97.7	100.0
4	B	CCTT			100.0	99.5	99.4	98.2		99.4	98.2	99.4		99.0	99.4	99.0	98.2	100.0
-	A	AATT				98.4	99.7	98.9	97.7		98.8	98.6		99.0	98.6	97.7	99.7	100.0
4	A	ACAT			100.0	98.4	98.7	99.4	97.9		99.2	99.0		97.8	98.4	97.8	100.0	
4	B	ATGT				99.6	99.0	99.8	100.0		99.1	99.1		96.9	98.4	96.9	100.0	
4	a	AGCC		100.0	100.0	99.5	99.5	99.4	97.3	100.0	98.6	98.6		98.4	98.8	97.3	100.0	
4	A	AGCG				98.8	99.8	99.0			98.6	98.6	100.0		99.2	99.2	100.0	
4	B	CCCT				99.5	99.8	99.1			98.6	94.1	100.0		99.4	94.1	100.0	
4	a	ATCC	100.0		100.0	99.2	99.3	100.0			98.1	97.6		99.0	99.3	97.6	100.0	
5	A	AAAC	98.5		100.0	99.0	98.4	98.3	94.9		98.1	98.8		100.0	98.9	94.9	100.0	
5	B	TTTT	100.0	100.0	99.5	98.8	99.5	98.7	95.7		98.9	98.9		99.6	95.7	95.7	100.0	
5	A	AAAAG	100.0	100.0	98.2	99.0	98.6	100.0	100.0		96.8	99.1	97.8	97.6	98.0	96.8	100.0	
5	B	CTTTT	98.0	95.8		98.9	98.9	95.8		98.1	98.6	98.6	89.8	97.7	98.0	89.8	98.9	
5	A	AAAAT	100.0	98.0		99.3	99.0	99.0	96.5		97.8	98.2		98.2	98.4	96.5	100.0	
5	B	ATTTT	97.8	100.0		99.0	99.1	98.6			97.8	98.3		98.3	98.4	97.8	100.0	
5	A	AACCT			98.9	98.9	98.9	98.0			98.7	98.0		98.7	98.0	98.9		
5	B	AGGTT			98.1	98.2								98.3	98.8	98.1	98.8	
5	A	AAGAT			97.4	98.0					100.0	97.9		100.0	99.4	97.4	100.0	
5	B	ATCTT			98.5	98.3					99.1	99.2		100.0	98.9	98.3	100.0	
5	A	AATAG			98.4	98.8		100.0	98.4		98.4	98.9	95.5		98.8	95.5	100.0	
5	B	ATTCT			99.2	99.2		100.0			98.1	96.5		97.4	98.6	96.5	100.0	
5	A	AATAT			100.0	97.8		96.3			96.8	96.8		96.3	96.4	96.3	100.0	
5	B	ATATT	100.0			98.2	97.8	93.7	90.9		97.1	97.6	100.0		96.8	90.9	100.0	
5	A	ATTCG			100.0	97.1	94.2	97.1	97.6		97.5	98.5		99.5	94.2	94.2	100.0	
5	B	ATTCG				100.0		94.2	96.9	100.0	97.7	97.4		100.0	99.3	96.9	100.0	
5	A	ATCCG			100.0		100.0	97.9	98.3	100.0	98.9	98.5		100.0	99.7	97.9	100.0	
5	B	ATCCG				100.0		97.9	98.2	100.0		98.1			98.3	97.9	100.0	
6	a	AAAAAC	100.0	100.0	100.0	98.1	97.8				98.1	97.9			98.8	95.3	100.0	
6	A	AAAAAG	98.0		96.5	98.0	98.3	100.0			98.6	97.5	97.1	96.5	97.2	96.5	100.0	
6	B	CTTTTT	97.9			97.4	97.7	100.0			98.8	97.6		96.9	97.4	96.9	100.0	
6	b	ATTTTT	100.0			98.6	99.0	95.8			98.1	97.6		98.1	98.2	95.8	100.0	
6	a	AAAAGC			96.6	99.1	95.4	97.6			97.9	97.9			100.0	95.4	100.0	
6	A	AAATAC				97.3	100.0	98.2	100.0		98.2	98.2	100.0		99.3	97.3	100.0	
6	A	AAATAT				97.9	92.2	98.2			99.0	98.1		97.5	97.3	92.2	100.0	
6	B	ATATTT				96.7	99.0	100.0			99.3	97.1		97.8	97.1	96.7	100.0	
6	a	AACAAT			96.5	98.6	99.0	98.6		98.5	99.4	97.7	94.9	94.1	99.0	94.1	99.4	
6	a	AACAGC				99.0	99.0	97.2	97.1	96.4	97.9	98.8	98.7		96.4	93.5	99.0	
6	A	AACCCC				99.4						98.2				98.2	99.4	
6	B	GGGGTT			100.0	99.6					100.0	100.0				99.6	100.0	
6	a	AAGAGT											92.4		100.0	92.4	100.0	
6	A	AAGCAG			100.0	100.0	100.0	98.7	100.0	100.0	100.0	98.0		94.3	94.3	91.4	100.0	
6	a	AAGGCG				100.0	100.0					94.1		100.0	100.0	94.1	100.0	
6	A	AATAGT			100.0	97.5		100.0				96.0		93.8	96.4	93.8	100.0	
6	B	ACTATT						100.0				97.6		90.0	96.7	97.1	90.0	100.0
6	a	AATCGG							98.1			98.5			100.0	98.1	100.0	
6	A	AATGAC						100.0	96.2			93.9		98.1	93.6	96.6	100.0	
6	A	AATGAT				96.2		100.0	97.3			97.7		96.4	98.0	96.2	100.0	
6	A	ACAGAT							97.8			97.5		100.0	100.0	95.		

[illegible]