

Supplementary Table 1. Sequencing and mapping statistics

Species	Flybase genome release	Sex	Reads	Auto. Depth	X Depth
<i>D. simulans</i>	r2.02	F	29287069	21.21	21.71
		M	25243382	19.19	10.21
<i>D. sechelia</i>	r1.3	F	26030971	18.26	17.13
		M	22024423	14.64	7.43
<i>D. melanogaster</i>	r6.03	F	18811547	14.01	14.20
		M	18552576	14.85	8.17
<i>D. erecta</i>	r1.3	F	20460077	16.56	16.57
		M	23801524	19.48	9.84
<i>D. ananassae</i>	r1.3	F	15862939	8.73	8.31
		M	20852751	12.48	6.47
<i>D. pseudoobscura</i>	r3.2	F	21585986	11.54	11.54
		M	18561056	11.30	5.94
<i>D. persimilis</i>	r1.3	F	17295743	10.38	9.38
		M	17555204	12.22	6.85
<i>D. mojavensis</i>	r1.3	F	17806801	11.50	10.81
		M	18100159	12.22	5.99
<i>D. virilis</i>	r1.2	F	20734250	11.73	10.27
		M	16986520	10.09	4.57

Supplementary Table 2. Satellites on the Y-chromosome

Species	Y-linked kmers*	Y-specific kmers**	No. of (%)	
			Y-linked †	Y-specific ‡
<i>D. melanogaster</i>	AATAT, AAGAC, AATATAT, AAGAGG, AATAC, AAAGAC, AATAGAC, AAGACATGAC, AATAG, AGATG, AAAAC, AAGACTAGAC, AAACAAT, AAAACAT, AAAGAG, AAAATAGAC, AAAAGAG, AAATTACT, AAAACATAT, ACATG, AAAAGAC, AAAAAC, AAGACAAGGAC, AAGACAAGACAC, AAT, AACAGAACATGTTTCG, AAATAT, AACAG, AACTTAAT	AAAAAC, AAAAC, AAAACAT, AAAACATAT, AAAAGAC, AAAATAGAC, AAACAAT, AAAGAC, AAT, AATTACT, AACAG, AACAGAACATGTTTCG, AACTTAAT, AAGACAAGACAC, AAGACAAGGAC, AAGACATGAC, AAGACTAGAC, AATAC, AATAGAC, ACATG	29 (34.9%)	20 (69.0%)
<i>D. simulans</i>	AATAT, AAACAAC, AAGAGAATAG, AAT, AATATAT, AACCAATC, AGATATAT, AATAGT, AAGAGAAGAGAG, AAACAAT, AATAGAATGG, AAACAAC, AAGAGAG, AAGAGAAGTG, AATAGAATCG, AAATAAC, AATGG, AG, AGATG, AATGT, AAAAGAG, AACCAATT, AACTTAAT	AAAACAAC, AAAAGAG, AAACAAT, AAATAAC, AACCAATC, AACCAATT, AACTTAAT, AAGAGAAGAGAG, AAGAGAAGTG, AAGAGAG, AATAGAATGG, AATAGT, AATGG, AATGT, AGATG	23 (45.1%)	15 (65.2%)
<i>D. sechelia</i>	AATAT, AAT, AATAATAT, AAAAC, AAATGT, AGATATAT, AATATAT, AAACATGTTCTGTTC, AAAAT, AACCAATT, AACTTAAT, AATATAATATAT, AACAGAACATGATCG, AATGT, AACATAGAAT, ACGAG, AACTTAC, AATAC, AAGAC, AACAC, AAGAT	AAAAC, AAAAT, AAATGT, AACCAATT, AACAC, AACAGAACATGATCG, AAGAC, AAGAT, AATAATAT, AATATAATATAT, AATGT, ACGAG	21 (35.0%)	12 (57.1%)
<i>D. erecta</i>	AAATAT, AACTTAC, AACATAGAAT, AATAT, AAGAG, AAGAC	AAGAC	6 (23.1%)	1 (16.7%)
<i>D. ananasae</i>	AAAGGT, AACATACAT, AAGACAGAC, AACATAGAAT, ACTGAG, AAGAG, AAGAC	AACATAGAAT, AAGAC, AAGACAGAC, AAGAG	7 (18.4%)	4 (57.1%)
<i>D. persimilis</i>	AAATAC		1 (5.9%)	0 (0%)
<i>D. pseudoobscura</i>	ACGG		1 (5.3%)	0 (0%)
<i>D. mojavensis</i>	AAAAT, AAAAC, ACTGATAT, AAATG, AAGAG, AACATAGAAT, AAGAC	AAAAC, AAATG, AACATAGAAT, AAGAC	7 (10.3%)	4 (57.1%)
<i>D. virilis</i>	ACAG, AACTTAT, AC, AAAC, AACTATT, ACACAT, AACCAATCC, AATAATAG, AAATCAAC, AATAGATT, ACAGACAGACCAG, ACAGACAGG, AAGACAGAC, AAATCAACAATCCAAC, AATCAATT, ACAGACAGGCCAG, ACACACAT, AAACATG, ACAGGCAG, ACAGACCAG, AATCTAT, AAACAAGC, ACAGACAGACAGG, AACACAGACAGACAGAC, ACAGACAGACAGAGAG, AAAACAAC, ACAGACAGAGAG, AAACAC, AACTACT, AAATCAT, AAAAC, AACACAGAC, ACACACAG, AACACAGACAGAC, ACTC, AAACCAT, AACAGAACATGTTTCG, ACTAGAG, ACAGAGAG, AAAAC	AAAAC, AAAACAAC, AAAAC, AAAC, AAACAAGC, AAACAC, AAACAGAC, AAACCAT, AAATCAAC, AAATCAACAATCCAAC, AAATCAT, AACCAATCC, AACACAGACAGAC, AACACAGACAGACAGAC, AACTATT, AAGACAGAC, AATAATAG, AATAGATT, AATCAATT, AATCTAT, ACACACAG, ACACACAT, ACAGACAGACAGAGAG, ACAGACAGACAGG, ACAGACAGACCAG, ACAGACAGAGAG, ACAGACAGG, ACAGACAGGCCAG, ACAGACCAG, ACAGAGAG, ACAGGCAG, ACTC	40 (44.4%)	32 (80.0%)

\*listed in decreasing order of abundance

\*\* Y-specific kmers are a subset of Y-linked kmers

† % represents the fraction of total number of kmers

‡ % represents the fraction of Y-linked kmers

Supplementary table 3. Parallel gains and ambiguous simple satellites

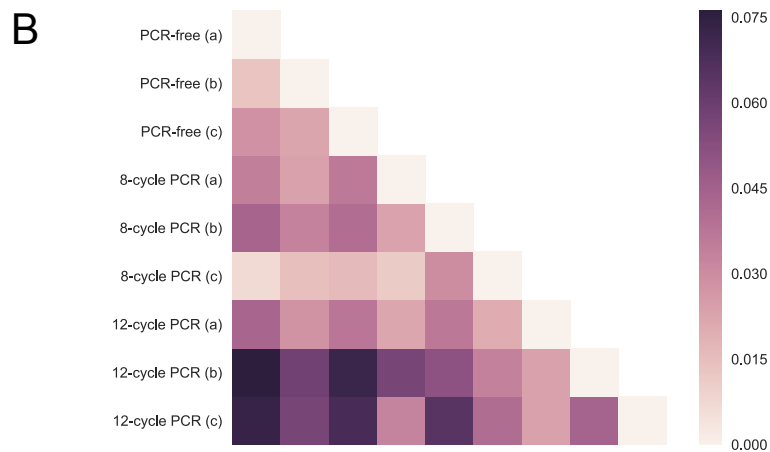
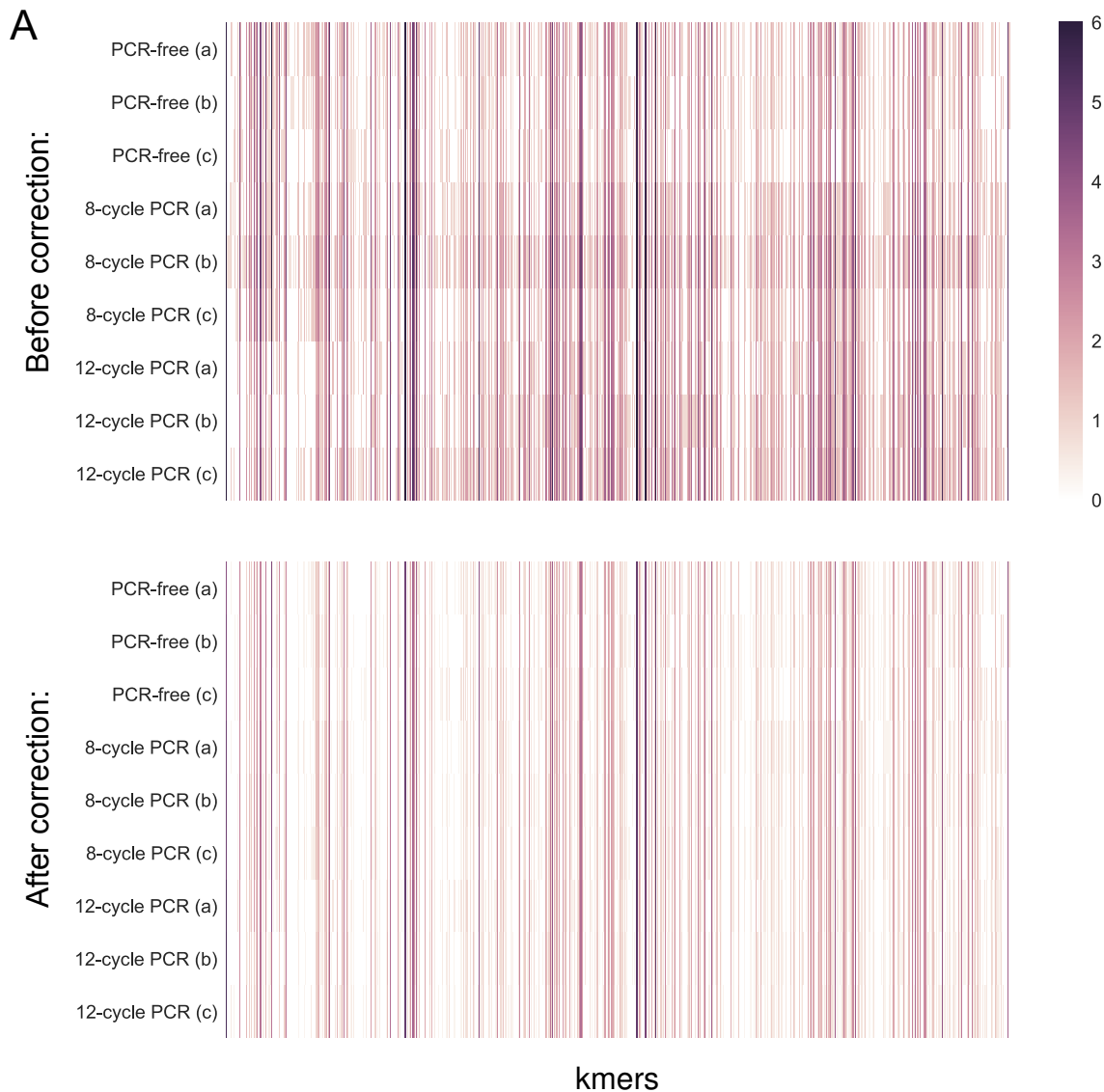
Parallel gains		Ambiguous		both	
kmer	species	kmer	species	kmer	species
AAAAAC	<i>mel, vir</i>	AAATTAT	<i>mel, ere</i>	AAAAC	<i>mel, sec, moj</i>
AAACAC	<i>mel, vir</i>	AACAC	<i>mel, sec</i>	AAAAG	<i>mel, sec, moj</i>
ACAGACCAG	<i>mel, vir</i>	AACAGAG	<i>mel, sec</i>	AGATG	<i>mel, sim, moj</i>
AAAAT	<i>sec, moj</i>	AAGAGAAGAGAG	<i>mel, sim</i>	AATACT	<i>mel, sec, moj, vir</i>
AAATGT	<i>sec, moj</i>	AAGAGAG	<i>mel, sim</i>		
AAACAAC	<i>sim, vir</i>	AATAC	<i>mel, sec</i>		
AAAGAC	<i>mel, moj</i>	AATGT	<i>mel, sec</i>		
AAAGAG	<i>mel, moj</i>	ACGAG	<i>mel, sec</i>		
AAGAGG	<i>mel, moj</i>	AAACAAT	<i>mel, sim, ana</i>		
AAGGAG	<i>mel, moj</i>	AAATAAT	<i>mel, ana, moj</i>		
ACTG	<i>sec, vir</i>	AAGAC	<i>mel, sec, ana</i>		
AACTATT	<i>ana, vir</i>	AAAT	<i>mel, pse, moj, vir</i>		
AAGACAGAC	<i>ana, vir</i>	AAATAT	<i>mel, ere, moj, vir</i>		
ACAGACAGACAGG	<i>ana, vir</i>	ACAGACGG	<i>ana, per, pse, moj</i>		
ACAGACAGG	<i>ana, vir</i>	ACAT	<i>ere, per, moj, vir</i>		
ACAGAGAG	<i>ana, vir</i>	AGATAT	<i>mel, ana, per, moj, vir</i>		
ACAGAG	<i>ana, moj</i>				
ACTGAG	<i>ana, moj</i>				
AAATAC	<i>sec, per, pse</i>				
AAGTAT	<i>ana, moj, vir</i>				
ACTCTCT	<i>ana, moj, vir</i>				
ACTCTAT	<i>ana, moj, vir</i>				
AAAATAT	<i>mel, sim, sec, moj</i>				
AGATATAT	<i>sim, sec, moj, vir</i>				
AATAG	<i>mel, sim, sec, ere, vir</i>				
AATAGT	<i>sim, ere, vir</i>				
AACATAT	<i>mel, moj, vir</i>				

Supplementary Table 4. Satellites presence and abundance across species

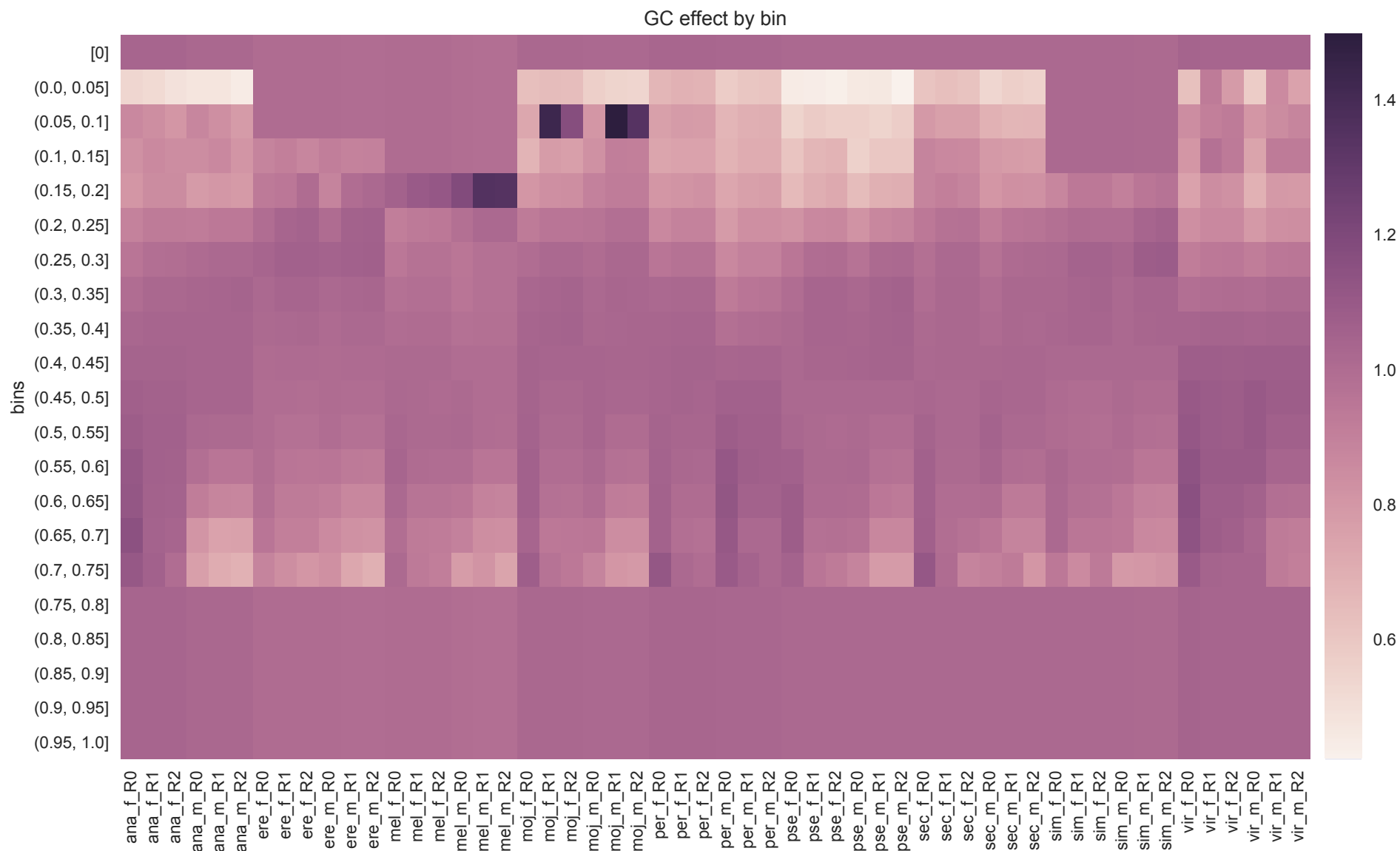
Simple satellites	No. of species present	Species names	<i>mel</i>	<i>sim</i>	<i>sec</i>	<i>ere</i>	<i>ana</i>	<i>pse</i>	<i>per</i>	<i>moj</i>	<i>vir</i>
AAAGGT	1	<i>ana</i>	2.6	0.0	0.0	0.0	1.3	16465.2	2.9	0.0	0.0
AAAGGTC	1	<i>ana</i>	0.0	1.5	0.0	0.0	0.0	24503.0	2.4	0.0	0.0
AAATGCTGTGCGGT	1	<i>ana</i>	0.0	0.0	0.0	0.0	1.7	2827.1	2.4	0.0	0.0
AACATACAT	1	<i>ana</i>	0.0	0.0	0.0	0.0	0.0	1488.7	0.0	0.0	0.0
AAGGTC	1	<i>ana</i>	69.1	38.7	9.9	32.5	262747.0	36.3	12.9	40.6	31.5
ACAGACAGAG	1	<i>ana</i>	2.9	0.0	3.0	4.9	29845.8	0.0	0.0	0.0	17.2
ACAGACATG	1	<i>ana</i>	0.0	0.0	0.0	0.0	2282.9	0.0	0.0	0.0	0.0
AAGAGT	1	<i>ere</i>	0.0	0.0	0.0	8454.0	28.1	0.0	0.0	14.3	60.3
AAGT	1	<i>ere</i>	6.0	0.0	0.0	33417.9	28.2	9.8	0.0	4.0	0.0
AAAACAT	1	<i>mel</i>	4966.1	0.0	2.0	17.1	0.0	0.0	0.0	10.1	4.4
AAAACATAT	1	<i>mel</i>	3260.2	0.0	0.0	20.4	20.6	0.0	0.0	0.0	0.0
AAAAGAC	1	<i>mel</i>	2136.7	1.5	0.0	0.0	5.2	0.0	0.0	9.3	6.3
AAAAGAG	1	<i>mel</i>	6334.8	128.0	7.4	5.1	3.7	0.0	0.0	2.4	0.0
AAAAGAGAAG	1	<i>mel</i>	5928.6	2.9	3.5	1.8	0.0	0.0	4.8	0.0	0.0
AAAAGAGAAGAG	1	<i>mel</i>	1164.4	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AAAAGG	1	<i>mel</i>	7181.9	0.0	1.8	0.0	9.5	4.0	3.8	0.0	10.8
AAAAGGAAAAGGAG	1	<i>mel</i>	2007.7	0.0	2.2	0.0	0.0	0.0	0.0	3.4	2.9
AAAATAGAC	1	<i>mel</i>	4455.2	1.9	7.1	5.5	5.2	0.0	0.0	11.8	0.0
AAATATAT	1	<i>mel</i>	3584.6	11.2	0.0	2.3	69.7	2.4	4.6	0.0	75.6
AAATTACT	1	<i>mel</i>	4319.3	0.0	0.0	21.8	4.5	0.0	6.3	4.6	8.6
AACATTGAAT	1	<i>mel</i>	982.7	0.0	0.0	2.1	0.0	0.0	0.0	0.0	0.0
AAGAAGAGAG	1	<i>mel</i>	1393.7	0.0	3.3	0.0	0.0	0.0	0.0	0.0	5.2
AAGACAAGACAC	1	<i>mel</i>	510.7	0.0	2.0	1.8	0.0	0.0	0.0	0.0	0.0
AAGACAAGGAC	1	<i>mel</i>	677.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AAGACATGAC	1	<i>mel</i>	15576.5	59.8	54.3	22.4	33.8	0.0	0.0	4.1	17.6
AAGACTAGAC	1	<i>mel</i>	8445.5	13.1	5.3	26.2	9.1	0.0	0.0	6.1	4.1
AAGAGAAGAGAAGAG	1	<i>mel</i>	1258.0	13.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AAGAGAAGAGG	1	<i>mel</i>	950.8	0.0	1.5	0.0	3.5	0.0	0.0	0.0	0.0
AAGAGAAGAT	1	<i>mel</i>	4571.2	0.0	11.0	0.0	4.0	0.0	0.0	0.0	0.0
AAGAGAAGCG	1	<i>mel</i>	989.4	0.0	2.3	0.0	0.0	0.0	0.0	0.0	4.8
AAGAGATGAG	1	<i>mel</i>	1890.0	120.2	0.0	0.0	0.0	0.0	0.0	4.1	0.0
AAGAT	1	<i>mel</i>	58652.7	10.1	142.8	16.8	8.0	34.8	6.3	18.1	19.3
AAGCAC	1	<i>mel</i>	1045.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	19.6
AAGGC	1	<i>mel</i>	1920.0	0.0	8.1	0.0	3.0	0.0	8.9	35.2	22.2
ACACG	1	<i>mel</i>	5588.9	0.0	13.0	1.5	0.0	6.0	0.0	2.2	2.6
ACATAG	1	<i>mel</i>	6897.4	11.5	5.6	5.8	4.9	4.3	0.0	42.0	20.9
ACATG	1	<i>mel</i>	3064.1	6.5	7.5	5.9	0.0	0.0	2.9	5.7	0.0
AGAGG	1	<i>mel</i>	2325.4	1.5	0.0	5.2	0.0	19.5	18.4	0.0	3.0
AGATGG	1	<i>mel</i>	18662.3	5.7	12.3	18.3	7.1	0.0	0.0	9.7	39.2
AAAAAGTTATCGAAATCGAT	1	<i>moj</i>	0.0	2.4	0.0	0.0	0.0	8.1	0.0	1994.0	0.0
AAAGACT	1	<i>moj</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1132.0	0.0
AAATG	1	<i>moj</i>	0.0	2.0	0.0	0.0	0.0	0.0	0.0	938.9	0.0
AAGATAC	1	<i>moj</i>	0.0	0.0	0.0	1.5	0.0	0.0	0.0	3540.8	4.4
AAGATAT	1	<i>moj</i>	19.3	0.0	4.0	0.0	0.0	7.8	0.0	1291.3	4.5
AATGACT	1	<i>moj</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1862.6	0.0
AATGAGT	1	<i>moj</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1538.7	0.0
ACAGCAT	1	<i>moj</i>	76.5	74.2	26.6	55.9	155.6	130.3	87.1	20118.3	99.7
ACATAGAT	1	<i>moj</i>	3.2	0.0	0.0	1.6	0.0	0.0	0.0	9230.7	159.6
ACCTCT	1	<i>moj</i>	2.6	0.0	0.0	0.0	0.0	0.0	0.0	1723.7	0.0
ACTATCT	1	<i>moj</i>	0.0	0.0	0.0	0.0	27.8	0.0	0.0	1077.0	0.0
ACTGATAT	1	<i>moj</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2112.3	0.0
AGGATAT	1	<i>moj</i>	0.0	0.0	34.3	0.0	114.2	0.0	0.0	1151.7	176.6
AAAACATGTTCGAAC	1	<i>sec</i>	0.0	68.9	1195.2	0.0	0.0	0.0	0.0	0.0	3.4
AAAAGAAAAGAAATAG	1	<i>sec</i>	0.0	1.6	1521.9	0.0	0.0	0.0	0.0	0.0	0.0
AAAAGAATAG	1	<i>sec</i>	3.6	0.0	19415.4	0.0	7.8	0.0	0.0	7.3	3.2
AAAAGAATAGAAATAG	1	<i>sec</i>	0.0	0.0	1338.4	0.0	0.0	0.0	3.5	0.0	0.0
AACAGAACATGTTTC	1	<i>sec</i>	0.0	32.3	3429.3	0.0	0.0	0.0	3.1	0.0	0.0
AACAAGTCTGTTCG	1	<i>sec</i>	0.0	0.0	1281.3	0.0	0.0	0.0	0.0	0.0	2.7
AACAATT	1	<i>sec</i>	0.0	116.7	562.8	0.0	0.0	0.0	0.0	0.0	58.2
AACACAGAACAGAACAG	1	<i>sec</i>	0.0	0.0	1782.0	0.0	0.0	0.0	0.0	0.0	0.0
AACAGAACATGATCG	1	<i>sec</i>	0.0	3.0	637.2	0.0	0.0	0.0	0.0	0.0	0.0
AACAGAACATGTTCC	1	<i>sec</i>	0.0	1.7	2304.0	0.0	0.0	0.0	0.0	0.0	0.0
AACAGAACATGTTCGAATAG	1	<i>sec</i>	2.3	0.0	1345.1	0.0	0.0	0.0	0.0	0.0	0.0
AACAGAACCG	1	<i>sec</i>	0.0	0.0	2486.9	0.0	0.0	0.0	0.0	0.0	4.1
AACAGATCATGTTCCG	1	<i>sec</i>	0.0	0.0	1053.6	0.0	0.0	0.0	0.0	0.0	0.0
AACATGTTCTGACAG	1	<i>sec</i>	7.6	4.9	17796.7	6.2	0.0	3.2	6.3	2.5	14.3
AACCG	1	<i>sec</i>	0.0	0.0	862.6	0.0	0.0	0.0	0.0	2.6	0.0
AATATAATATAT	1	<i>sec</i>	97.9	71.4	545.3	6.0	0.0	0.0	0.0	0.0	0.0
AAAACAAC	1	<i>sim</i>	0.0	2266.4	14.1	0.0	0.0	0.0	0.0	0.0	0.0
AAATAAC	1	<i>sim</i>	4.2	875.6	0.0	2.4	0.0	0.0	0.0	0.0	16.3
AACAATC	1	<i>sim</i>	0.0	9308.4	2.5	0.0	0.0	0.0	0.0	3.4	18.8
AACAGAACATAATCG	1	<i>sim</i>	0.0	1900.1	145.8	0.0	0.0	0.0	0.0	0.0	2.9
AAGAGAAGTG	1	<i>sim</i>	117.2	952.0	0.0	0.0	0.0	0.0	0.0	0.0	5.1
AAGAGAATAG	1	<i>sim</i>	16.4	32479.6	0.0	0.0	0.0	8.4	0.0	3.3	10.4
AATAGAATCG	1	<i>sim</i>	2.4	1416.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0
AATAGAATGG	1	<i>sim</i>	0.0	2509.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0

AATAGAATTG	1	sim	4.5	30027.5	22.5	0.0	0.0	7.0	0.0	4.5	5.5
AATGG	1	sim	7.2	606.8	80.2	5.1	12.6	5.9	4.1	27.2	3.3
ACGGAGTACGGG	1	sim	0.0	1768.2	0.0	0.0	0.0	85.6	0.0	2.5	0.0
AAAAACAAAC	1	vir	0.0	0.0	10.2	0.0	0.0	6.2	0.0	0.0	1324.6
AAAAACT	1	vir	2.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	3479.1
AAAC	1	vir	0.0	12.8	2.9	0.0	7.4	0.0	4.4	21.5	27902.4
AAACAAGC	1	vir	0.0	0.0	2.7	0.0	0.0	0.0	0.0	0.0	1913.9
AAACAGAC	1	vir	2.1	0.0	2.2	0.0	0.0	0.0	3.9	3.1	840.9
AAACCAT	1	vir	17.5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	566.9
AAACTAG	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2903.6
AAACTAT	1	vir	39.8	17.9	34.5	48.6	25.8	94.7	76.1	47.3	490963.3
AAATCAAC	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5708.4
AAATCAACAATCCAAC	1	vir	3.1	0.0	0.0	0.0	2.6	0.0	0.0	0.0	2978.1
AAATCAT	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	934.0
AAATTAC	1	vir	50.5	20.7	36.8	34.6	68.7	109.0	62.6	47.7	540644.8
AACAAT	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	13.8	2120.1
AACAATCC	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6288.4
AACACAGACAGAC	1	vir	0.0	0.0	0.0	1.6	0.0	0.0	2.5	0.0	743.3
AACACAGACAGACAGAC	1	vir	1.8	0.0	0.0	0.0	0.0	2.9	0.0	7.7	1528.7
AACATAG	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	77.1	993.4
AACTACT	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1479.9
AAGTAC	1	vir	3.1	0.0	0.0	0.0	0.0	0.0	0.0	2.4	3037.3
AATAATAG	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6217.6
AATAGATT	1	vir	0.0	0.0	0.0	0.0	3.0	5.0	0.0	0.0	4231.0
AATATATC	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2896.2
AATATC	1	vir	0.0	0.0	2.0	3.3	0.0	0.0	0.0	58.6	13161.6
AATCAATT	1	vir	3.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2624.5
AATCTAT	1	vir	4.2	0.0	0.0	0.0	0.0	0.0	0.0	42.6	1923.3
ACACACAG	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.9	824.9
ACACACAT	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	2.7	2.4	2402.8
ACAGACAGACAGAGAGAG	1	vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1413.4
ACAGACAGACCCAG	1	vir	0.0	0.0	0.0	2.0	3.1	0.0	0.0	0.0	3708.5
ACAGACAGAGAG	1	vir	0.0	0.0	0.0	2.5	3.5	0.0	0.0	2.6	1171.3
ACAGACAGGCAG	1	vir	2.6	3.7	4.3	5.0	2.4	3.1	12.0	12.2	2588.3
ACAGGCAG	1	vir	0.0	7.0	2.4	0.0	12.9	0.0	5.7	0.0	2316.2
ACATACCT	1	vir	0.0	0.0	0.0	23.1	0.0	0.0	0.0	0.0	1127.7
ACTC	1	vir	0.0	0.0	0.0	0.0	17.9	29.2	7.4	77.2	635.3
ACTCAT	1	vir	0.0	1.9	2.0	5.0	56.8	4.3	0.0	65.5	23498.1
ACAGAG	2	ana moj	4.9	2.3	2.9	0.0	3878.8	0.0	4.4	280.4	22.2
ACTGAG	2	ana moj	0.0	0.0	0.0	0.0	386.1	0.0	0.0	1152.4	0.0
AACTATT	2	ana vir	0.0	0.0	0.0	0.0	206.4	0.0	0.0	0.0	12891.5
AAGACAGAC	2	ana vir	0.0	0.0	0.0	0.0	415.8	0.0	0.0	0.0	3054.2
ACAGACAGACAGG	2	ana vir	18.4	3.3	2.1	7.8	89885.2	0.0	0.0	2.8	1906.2
ACAGACAGG	2	ana vir	4.5	3.9	2.1	2.4	43607.6	0.0	5.1	8.6	3148.2
ACAGAGAG	2	ana vir	0.0	0.0	0.0	2.1	1691.7	0.0	0.0	0.0	322.1
AAATTAT	2	mel ere	1189.1	0.0	0.0	239.0	0.0	0.0	0.0	0.0	31.1
AAAGAC	2	mel moj	19269.7	8.5	23.2	15.2	19.7	4.3	0.0	364.6	13.3
AAAGAG	2	mel moj	5486.7	0.0	0.0	0.0	52.7	3.8	0.0	318.1	4.3
AAGAGG	2	mel moj	36660.2	12.9	13.4	16.2	29.4	7.9	0.0	226.4	34.9
AAGGAG	2	mel moj	23174.2	13.2	13.5	9.1	7.6	4.0	26.6	515.9	29.9
AAAC	2	mel sec	152057.0	135.6	239.4	120.0	99.0	20.2	47.3	98.5	94.8
AACAGAG	2	mel sec	11192.3	6.7	855.2	10.7	27.0	7.4	0.0	12.1	0.0
AATAC	2	mel sec	32452.9	58.3	308.8	89.0	27.0	0.0	0.0	40.8	4.8
AATGT	2	mel sec	1125.9	169.6	549.0	0.0	0.0	13.5	0.0	0.0	0.0
ACCACTACGGG	2	mel sec	65769.9	124.4	3875.2	60.7	60.5	13.3	15.1	43.3	25.1
ACGAG	2	mel sec	2016.5	2.4	279.3	0.0	0.0	2.7	0.0	0.0	3.3
AAGAGAAGAGAG	2	mel sim	7220.1	3238.2	10.6	1.9	9.2	6.2	0.0	0.0	20.4
AAGAGAG	2	mel sim	63244.3	1402.0	85.1	50.1	35.9	24.1	13.7	48.6	62.0
AAAAC	2	mel vir	881.0	0.0	2.3	0.0	3.1	0.0	6.8	0.0	842.2
AAACAC	2	mel vir	30850.7	6.2	39.6	16.2	34.1	0.0	3.8	6.9	1028.8
AATAGAC	2	mel vir	17625.2	11.5	44.2	15.5	6.6	4.7	13.7	18.5	822.4
ACAGACCAG	2	mel vir	978.2	3.7	0.0	0.0	0.0	0.0	0.0	0.0	2010.4
AAGTAG	2	maj vir	11.0	1.7	2.2	0.0	0.0	0.0	0.0	7795.3	2857.5
AATATAG	2	maj vir	8.5	22.2	6.0	4.7	0.0	0.0	0.0	1812.5	20562.1
AATATG	2	maj vir	0.0	4.7	3.0	0.0	0.0	0.0	0.0	4168.4	510.3
AATGAC	2	maj vir	9.3	9.3	4.4	0.0	0.0	24.7	9.3	21469.1	4375.3
ACACAT	2	maj vir	0.0	2.1	0.0	4.6	0.0	9.5	3.1	206.9	10176.6
ACTAGAG	2	maj vir	0.0	2.4	1.3	0.0	0.0	0.0	0.0	1974.4	535.5
ACTAGAT	2	maj vir	0.0	0.0	0.0	0.0	67.0	0.0	26.4	3149.1	643.4
AGAGAT	2	maj vir	12.6	2.1	0.0	0.0	0.0	0.0	0.0	8403.0	6236.4
AGCATAT	2	maj vir	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1114.7	457.9
ATATATC	2	maj vir	0.0	0.0	0.0	2.5	0.0	0.0	0.0	803.7	479.1
AAAAT	2	sec moj	15.3	17.7	740.9	2.3	5.5	9.3	2.9	7842.2	7.9
AAATGT	2	sec moj	0.0	19.9	3312.5	0.0	0.0	0.0	0.0	229.7	0.0
ACTG	2	sec vir	119.5	73.9	261.8	140.5	14.3	72.3	47.9	133.2	2633.9
AAACATGTTCTGTTC	2	sim sec	0.0	348.8	3051.3	0.0	0.0	0.0	0.0	0.0	0.0
AACAG	2	sim sec	188.1	57774.8	291904.7	36.2	33.5	17.8	43.5	50.6	162.7
AACAGAACAGAACATGTTCCG	2	sim sec	0.0	1222.9	4920.4	0.0	0.0	0.0	0.0	0.0	5.8
AACAGAATAG	2	sim sec	2.4	3583.3	2563.8	0.0	0.0	0.0	0.0	0.0	0.0

AACATGTTCCGTTCCG	2	sim	sec	2.1	458.3	2945.0	1.5	3.5	0.0	0.0	0.0	0.0							
AACATGTTCCG	2	sim	sec	33.0	42661.8	65746.5	8.2	0.0	7.6	12.4	5.0	34.8							
AATTC	2	sim	sec	25.4	8860.2	49597.2	52.4	0.0	6.2	4.2	2.7	7.0							
AAACAAC	2	sim	vir	5.7	25910.2	29.8	0.0	0.0	0.0	0.0	3.6	10421.0							
AAGTAT	3	ana	moj	vir	5.9	0.0	8.0	0.0	460.5	0.0	0.0	4934.8	735.3						
AATGAT	3	ana	moj	vir	0.0	0.0	0.0	0.0	293.9	0.0	0.0	614.1	3959.9						
ACTCTCT	3	ana	moj	vir	0.0	0.0	0.0	0.0	648.5	2.3	0.0	5937.5	393.8						
AAATAAT	3	mel	ana	moj	642.9	0.0	1.5	1.8	517.8	23.9	16.1	3319.5	107.1						
AACATAT	3	mel	moj	vir	2299.6	5.4	7.9	0.0	0.0	7.6	0.0	533.7	413.2						
AAGAC	3	mel	sec	ana	142243.5	84.2	248.7	140.4	208.0	31.7	36.5	150.1	56.9						
AAAAC	3	mel	sec	moj	9012.6	2.0	7572.3	2.8	0.0	11.9	17.1	1429.5	136.8						
AAAAG	3	mel	sec	moj	17765.5	4.9	289.6	15.6	8.9	13.9	7.4	1081.8	11.0						
AAACAAT	3	mel	sim	ana	6946.3	2569.4	6.8	16.5	365.8	5.5	0.0	6.6	19.1						
AGATG	3	mel	sim	moj	12665.5	233.1	2.0	20.4	6.4	7.5	0.0	1371.0	14.1						
AACTTAAT	3	mel	sim	sec	231.4	211.4	834.9	0.0	0.0	0.0	0.0	0.0	0.0						
AATAATAT	3	mel	sim	sec	20524.0	435.7	7812.8	21.4	54.2	8.5	11.2	71.3	22.4						
ACCGAGTACGGG	3	mel	sim	sec	10757.6	68974.0	15762.2	4.1	10.6	0.0	22.7	29.3	36.2						
ACTGGG	3	mel	sim	sec	985.0	500.8	756.6	2.0	130.2	0.0	28.4	0.0	0.0						
AAATAC	3	sec	pse	per	0.0	0.0	3705.0	0.0	0.0	1063.2	1720.4	182.9	28.5						
AATAGT	3	sim	ere	moj	0.0	4894.7	0.0	934.2	0.0	0.0	0.0	202.2	123.5						
ACTCTAT	3	sim	moj	vir	0.0	215.1	0.0	0.0	0.0	4.7	0.0	1018.0	590.2						
ACAGACGG	4	ana	pse	per	moj	2.3	1.7	0.0	84.1	2043.4	2154.0	1856.3	5751.0	15.6					
ACAT	4	ere	per	moj	vir	34.3	35.5	48.9	44313.1	135.5	30.9	257.8	986.1	29584.1					
AAATAT	4	mel	ere	moj	vir	318.8	0.0	0.0	9169.5	153.2	161.9	0.0	4846.6	7147.0					
AAAT	4	mel	pse	moj	vir	522.2	100.2	4.2	117.0	126.6	296.6	104.4	1910.7	16802.8					
AATACT	4	mel	sec	moj	vir	1058.2	4.0	4553.2	0.0	0.0	0.0	0.0	596.5	477.3					
AAAATAT	4	mel	sim	sec	moj	5867.0	1174.3	5179.4	117.8	4.3	14.0	29.7	5278.4	51.2					
AACAGAACATGTTCCG	4	mel	sim	sec	vir	509.4	503360.9	1159389.0	114.0	93.4	129.3	237.0	144.1	707.3					
ACGG	4	pse	per	moj	vir	0.0	2.8	0.0	42.9	32.2	519.1	618.6	5564.1	1115.0					
ATC	4	pse	per	moj	vir	61.9	6.2	70.3	37.0	113.0	262.2	345.1	675.0	1115.0					
AGATATAT	4	sim	sec	moj	vir	0.0	7538.6	2592.9	0.0	0.0	7.3	71.6	389.8	376.4					
AGATAT	5	mel	ana	per	moj	vir	288.4	5.4	5.8	144.0	293.2	124.5	410.0	20812.8	19896.9				
AACATAGAAT	5	mel	sec	ere	ana	moj	266251.0	115.5	569.6	500.2	434.3	102.4	36.2	283.6	125.6				
AATAG	5	mel	sim	sec	ere	vir	19464.8	63476.8	120924.0	12174.0	77.3	83.4	124.5	21.1	424.5				
ACATAT	6	ere	ana	pse	per	moj	vir	23.0	71.4	83.4	2483.1	702.2	483.6	379.6	4578.4	24824.3			
AATATAT	6	mel	sim	sec	ere	moj	vir	37435.5	11844.0	2696.7	704.1	198.3	96.4	16.9	931.6	241.1			
ACATATAT	6	mel	sim	sec	ere	moj	vir	42977.2	842.1	609.1	278.7	33.1	14.8	5.0	756.9	459.8			
ACT	7	mel	ere	ana	pse	per	moj	vir	273.3	164.1	131.7	720.7	606.0	296.5	208.8	9271.3	482.9		
ACAGAT	7	mel	sim	sec	ere	ana	moj	vir	1128.6	2292.1	429.1	783.8	276.5	156.3	91.1	107161.6	42925.7		
AATAT	8	mel	sim	sec	ere	ana	per	moj	vir	190434.3	119042.8	195483.8	383.4	326.1	87.9	286.7	630.2	498.1	
AAGAG	8	mel	sim	sec	ere	ana	pse	moj	vir	428334.6	26434.7	1289.4	285.1	285.4	222.9	121.8	1035.6	882.1	
A	9	mel	sim	sec	ere	ana	pse	per	moj	vir	202790.7	116912.0	155114.7	105529.2	202338.4	103320.7	144832.4	663993.5	325066.9
AAACTAC	9	mel	sim	sec	ere	ana	pse	per	moj	vir	598.1	398.0	419.2	572.5	467.7	585.1	637.4	734.8	7099097.1
AAC	9	mel	sim	sec	ere	ana	pse	per	moj	vir	868.4	643.6	435.6	417.3	1983.8	2517.2	2210.8	7975.9	16927.7
AAT	9	mel	sim	sec	ere	ana	pse	per	moj	vir	8596.4	15509.1	37205.6	3249.6	950.9	2237.1	1120.4	8924.9	18776.6
AC	9	mel	sim	sec	ere	ana	pse	per	moj	vir	1782.0	580.8	747.2	1707.6	1411.4	4789.3	5733.8	76098.8	191675.4
ACAG	9	mel	sim	sec	ere	ana	pse	per	moj	vir	318.6	264.5	299.2	243.2	51142.1	435.1	395.5	418.8	356835.7
AG	9	mel	sim	sec	ere	ana	pse	per	moj	vir	1032.6	539.5	364.5	1454.1	379.7	6132.6	8626.6	100593.8	51167.6
AGAT	9	mel	sim	sec	ere	ana	pse	per	moj	vir	33705.8	17899.9	159424.8	819.1	350.2	982.1	702.4	4112.2	1882.0
AGC	9	mel	sim	sec	ere	ana	pse	per	moj	vir	3972.1	3724.9	3380.2	7660.2	2995.7	7238.3	7395.0	20935.0	8379.8
AT	9	mel	sim	sec	ere	ana	pse	per	moj	vir	7373.0	6152.2	5515.9	3402.8	2481.9	4389.8	4094.1	61694.3	43027.9
C	9	mel	sim	sec	ere	ana	pse	per	moj	vir	12592.2	6005.6	8920.8	5944.0	8438.6	37373.7	32076.0	9994.3	20668.6



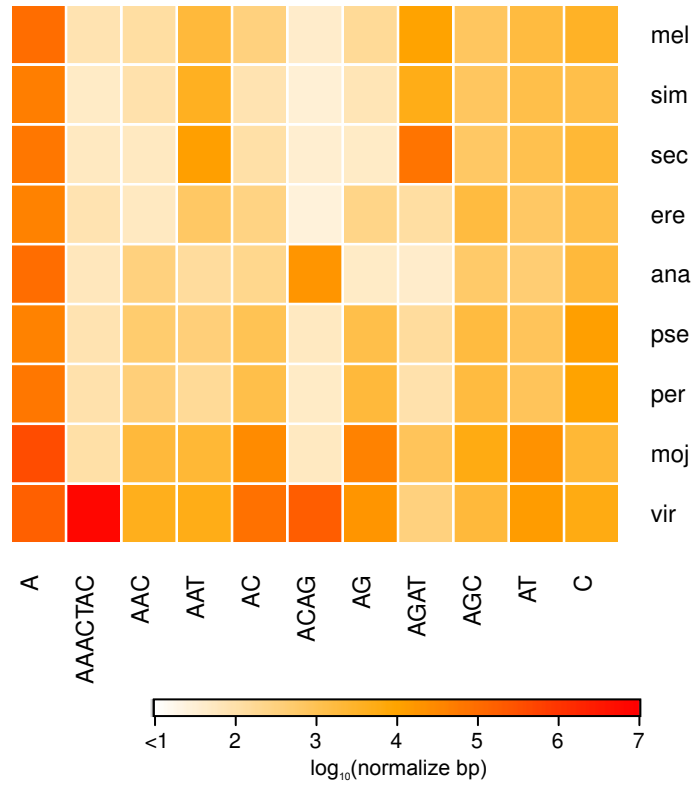
Supplementary Figure 1. Correction for GC bias for different library preparations. A. Heatmap of kmer log-abundances in base pairs, before (top) and after (bottom) correction for GC bias. B. Change in pairwise Spearman correlation coefficient among replicates for each library preparations after to GC correction.



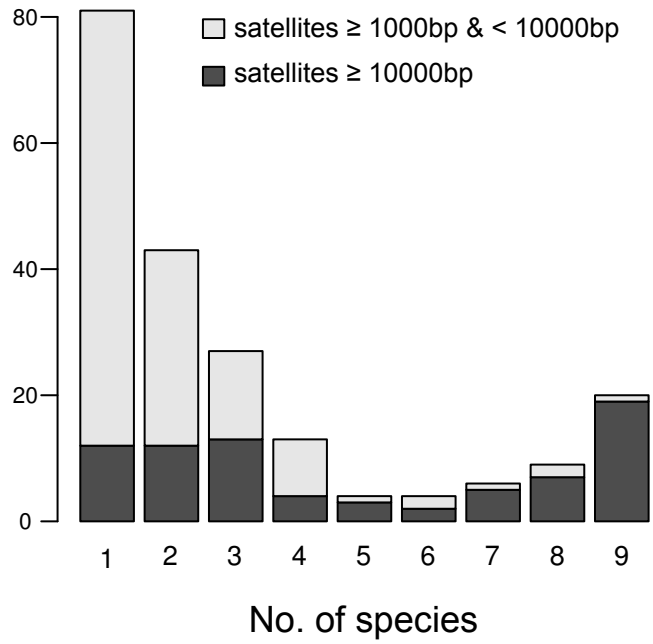
Supplementary Figure 2. Correction for GC bias across species samples and sequencings. The colors in the heatmap represent the over/under-representation of each GC bins (5% bins) of each sequenced sample (column). For each sample, there are three sequences: single end sequencing (R0), paired-end sequencing (R1 and R2).



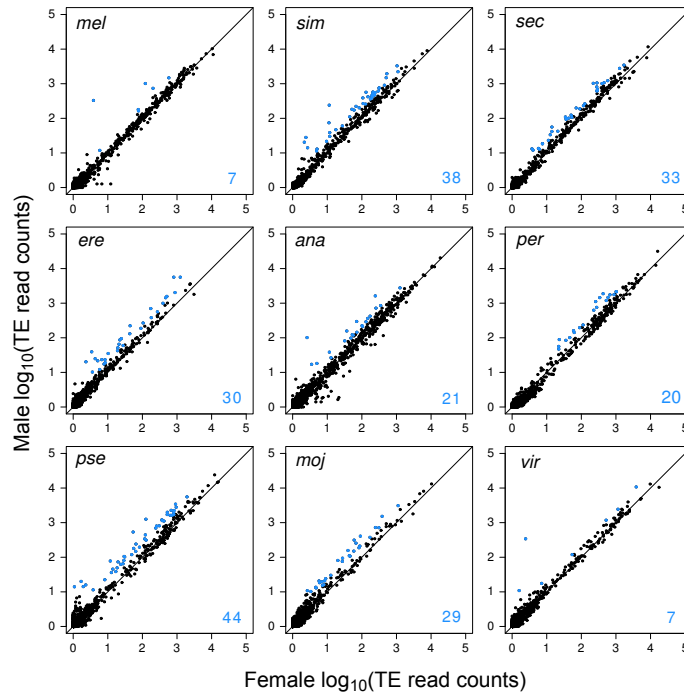




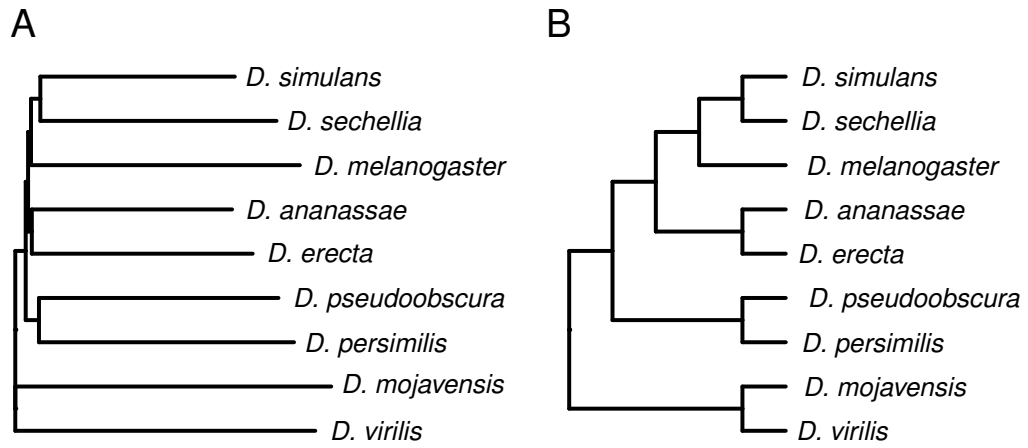
Supplementary Figure 4. Abundance of simple satellites present in all species.



Supplementary Figure 5. Distribution of simple satellite presence among species with lower absence cutoff of <5x copy number.

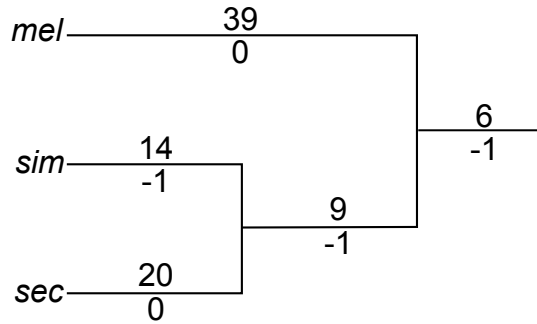


Supplementary Figure 6. Male-biased transposable elements. Y-linked TEs are those that are significantly more abundant in males than females by 1.5x (Fisher's Exact Test  $p < 0.005$ ). These TEs are plotted in blue dots and the number of them is labeled on the bottom right of each plot.

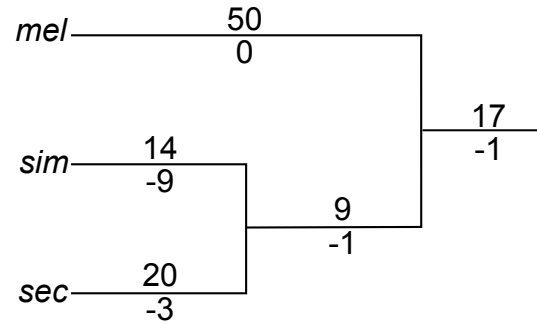


Supplementary Figure 7. Phylogeny inferred from kmer abundance. A. Neighbor-joining distance tree. B. Maximum parsimony tree.

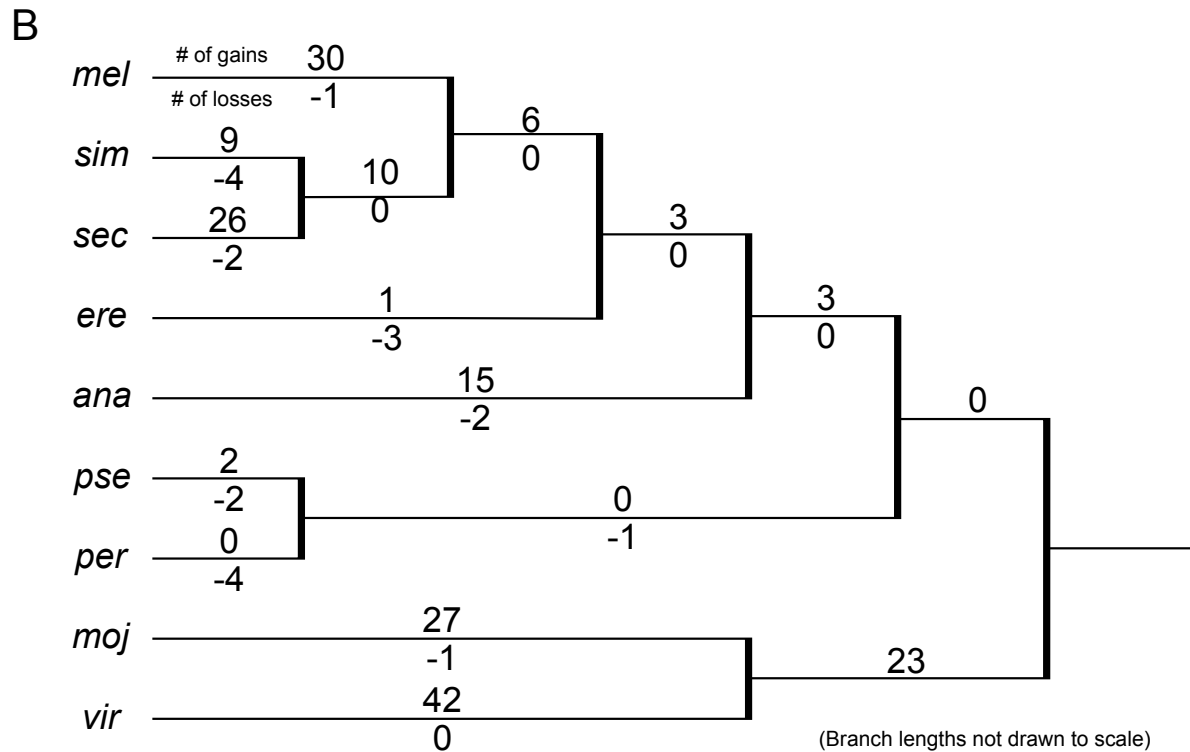
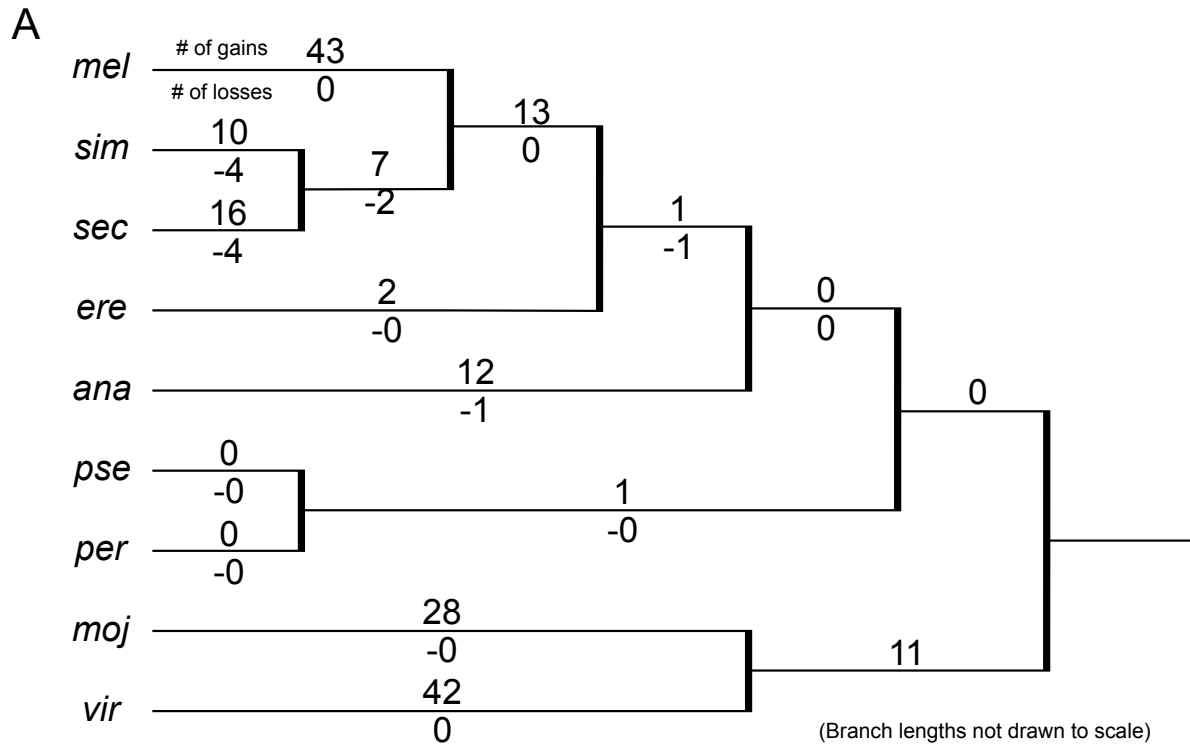
A



B



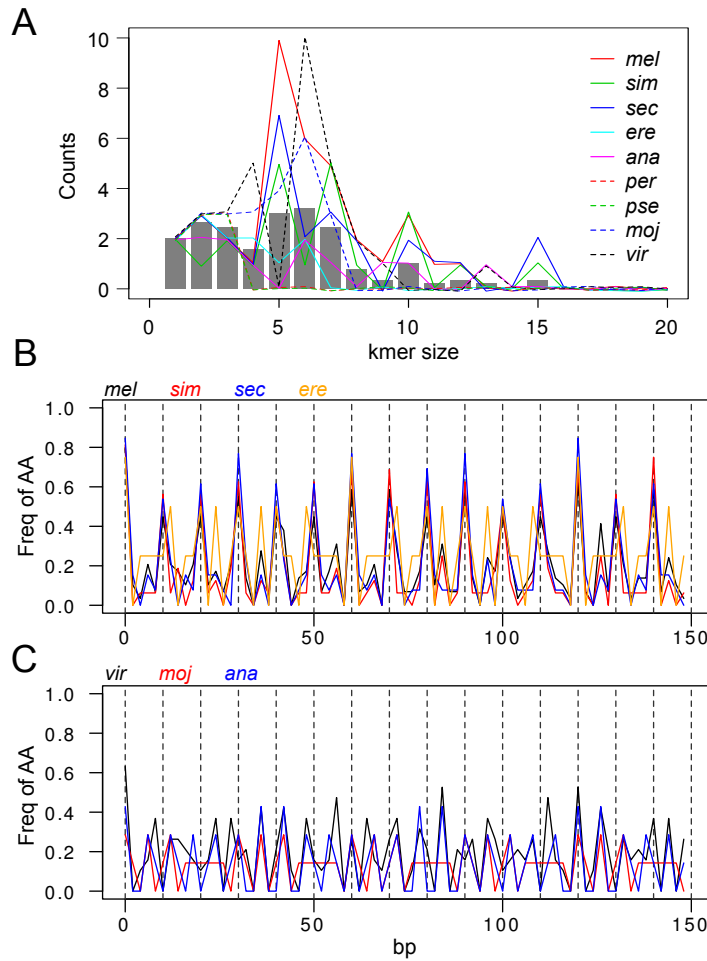
Supplementary Figure 8. Gain and losses within the melanogaster subgroup. 11 simple satellites are present in *D. melanogaster* but absent in either *D. simulans* or *D. sechellia*. Because they can either be parallel gains or gains in the branches leading up to the group followed by losses in either *D. simulans* or *D. sechellia*, they were classified as ambiguous and excluded from the tree in A (same as in the main text). In B, these satellites are counted as gains followed by losses.



Supplementary Figure 9. Losses and gains inference with different presence cutoffs. A. Same analysis as with Figure 4A but satellites  $\geq 1000$  bp were deemed present. B. Same but, satellites with copy number  $\geq 5$  were deemed present. For both A and B, ambiguities were resolved in favor of losses instead of multiple gains.







Supplementary Figure 11. Length and dinucleotide distribution of satellites. A. The distribution of kmer length is plotted for each species. Gray bars depict the average across the species. B. For each of the species of the melanogaster subgroup, the AA-dinucleotide frequency is plotted across 150bp which is roughly the length of DNA wrapping around a single nucleosome. Gray dotted lines mark every 10bp. Only kmer greater than 10kb are used to calculate the dinucleotide frequency as to capture satellites that have expanded. C. Same as B, but for *D. ananassae*, *D. virilis*, and *D. mojavensis*.