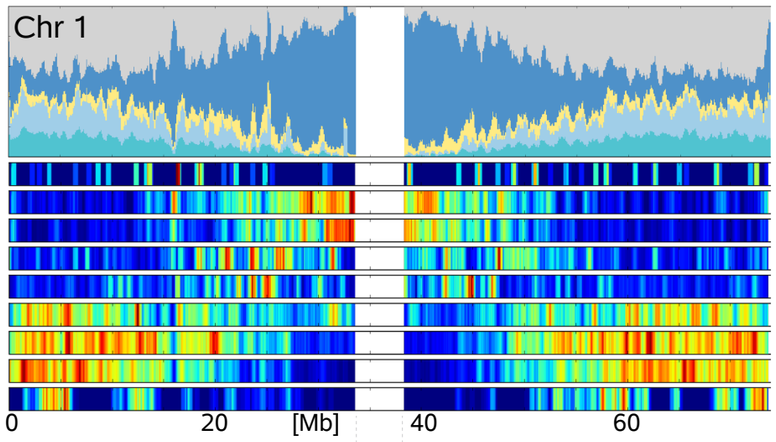
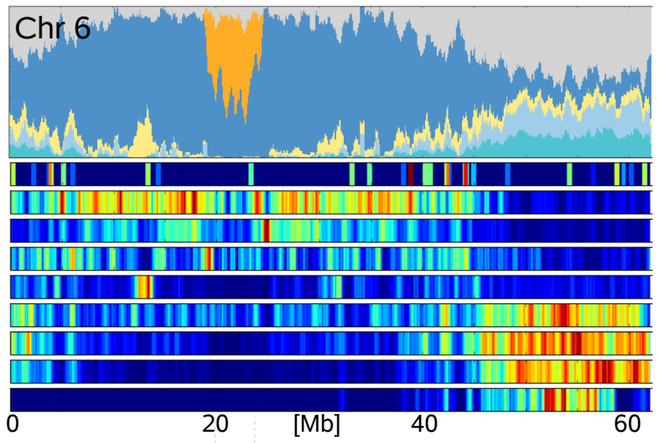
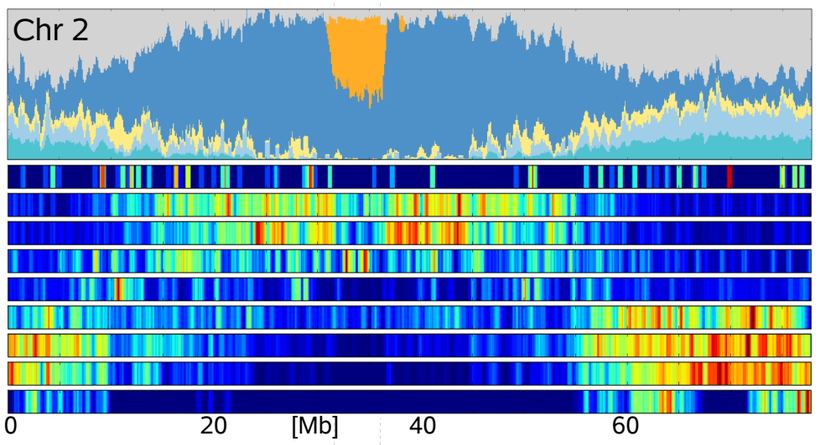


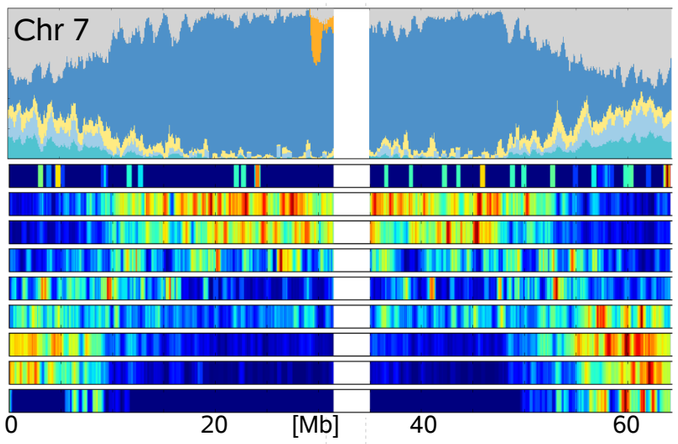
Cen38	0 - 0.2	0.0
RTs	8.5 - 94.8	39.5
DNA-TEs	1.4 - 20.4	7.3
genes (introns)	0 - 32.2	12.5
genes (exons)	0 - 20.5	9.7
	range	avg
LTR-RTs <=0.01 mya	0 - 6.9	0.76
full length LTR-RTs	0 - 46.4	13.9
LTR-RTs/ gypsy	0.3 - 49.8	12.9
LTR-RTs/ copia	0.2 - 15.7	4.4
DNA-TEs/ CACTA	0.6 - 18.4	4.5
CpG islands	0.3 - 5.6	2.5
DNA-TEs/ MITE	0.1 - 4.8	2.5
genes (exons)	0 - 19.7	8.9
paralogs (exons)	0 - 6.1	1.2



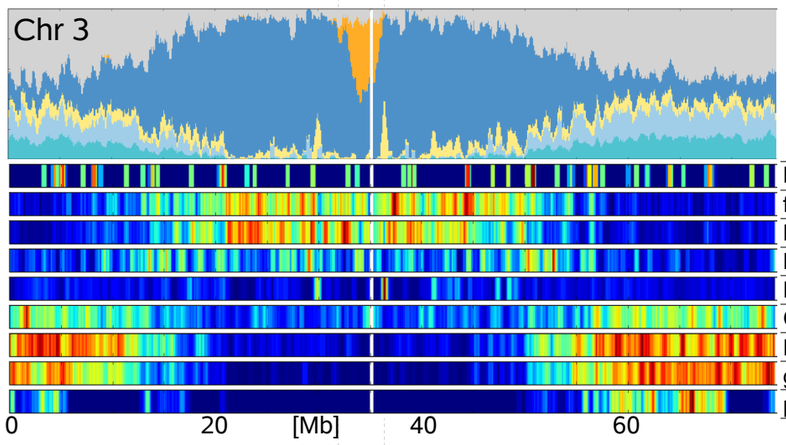
Cen38	0 - 67.5	3.7
RTs	7.6 - 98.9	56.6
DNA-TEs	0 - 33.3	6.5
genes (introns)	0 - 24.0	7.2
genes (exons)	0 - 20.7	5.7
	range	avg
LTR-RTs <=0.01 mya	0 - 5.0	0.45
full length LTR-RTs	0 - 44.3	19.8
LTR-RTs/ gypsy	0.4 - 84.4	20.3
LTR-RTs/ copia	0.1 - 19.4	4.9
DNA-TEs/ CACTA	0 - 33.3	4.8
CpG islands	0.1 - 5.4	1.9
DNA-TEs/ MITE	0 - 4.6	1.5
genes (exons)	0 - 20.1	5.1
paralogs (exons)	0 - 6.3	0.8



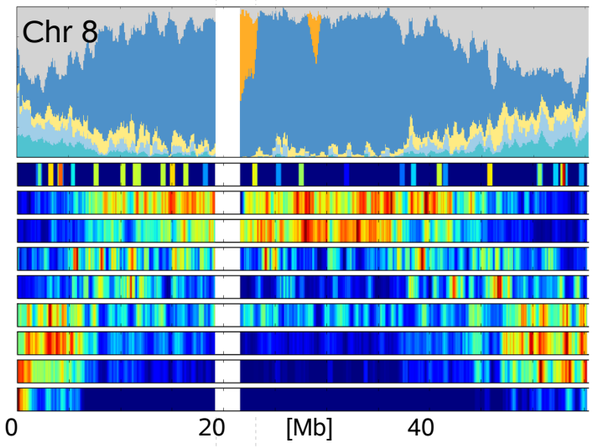
Cen38	0 - 59.9	3.2
RTs	8.0 - 97.3	51.0
DNA-TEs	0 - 27.2	6.4
genes (introns)	0 - 31.3	8.6
genes (exons)	0 - 19.7	6.7
	range	avg
LTR-RTs <=0.01 mya	0 - 5.7	0.66
full length LTR-RTs	0 - 48.1	17.2
LTR-RTs/ gypsy	0.3 - 51.8	16.6
LTR-RTs/ copia	0.2 - 19.8	5.3
DNA-TEs/ CACTA	0 - 26.1	4.4
CpG islands	0.1 - 5.7	1.9
DNA-TEs/ MITE	0 - 4.9	1.8
genes (exons)	0 - 19.3	6.0
paralogs (exons)	0 - 7.1	0.9



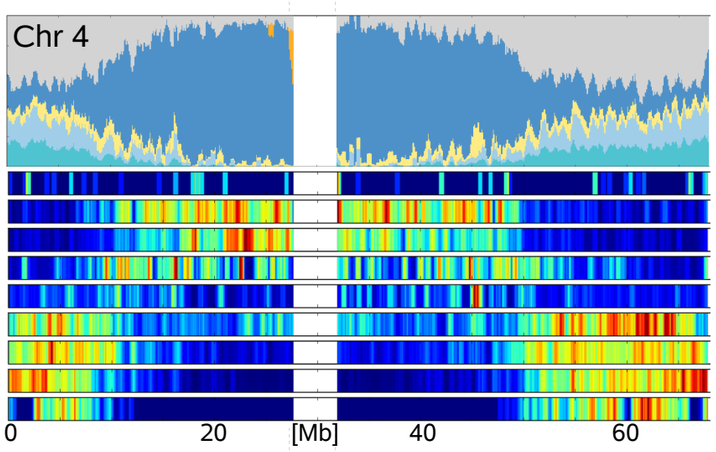
Cen38	0 - 31.0	0.6
RTs	10.1 - 96.5	64.2
DNA-TEs	0.3 - 18.2	5.9
genes (introns)	0 - 21.7	5.5
genes (exons)	0 - 18.9	4.6
	range	avg
LTR-RTs <=0.01 mya	0 - 5.8	0.54
full length LTR-RTs	0 - 45.8	22.6
LTR-RTs/ gypsy	0.8 - 59.3	23.5
LTR-RTs/ copia	0.2 - 18.2	5.7
DNA-TEs/ CACTA	0 - 16.4	4.2
CpG islands	0.2 - 5.2	1.8
DNA-TEs/ MITE	0 - 4.9	1.5
genes (exons)	0 - 18.4	4.0
paralogs (exons)	0 - 5.5	0.7



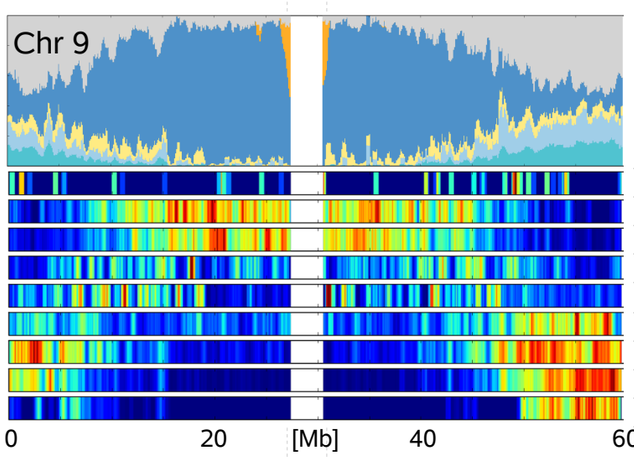
Cen38	0 - 53.7	1.5
RTs	7.5 - 96.1	50.6
DNA-TEs	0 - 38.6	6.5
genes (introns)	0 - 26.7	9.4
genes (exons)	0 - 20.0	7.4
	range	avg
LTR-RTs <=0.01 mya	0 - 5.0	0.76
full length LTR-RTs	0 - 43.6	16.3
LTR-RTs/ gypsy	0.2 - 53.0	18.3
LTR-RTs/ copia	0 - 18.5	4.8
DNA-TEs/ CACTA	0 - 38.4	4.3
CpG islands	0.3 - 6.3	2.1
DNA-TEs/ MITE	0 - 4.6	2.0
genes (exons)	0 - 18.1	6.7
paralogs (exons)	0 - 7.1	1.0



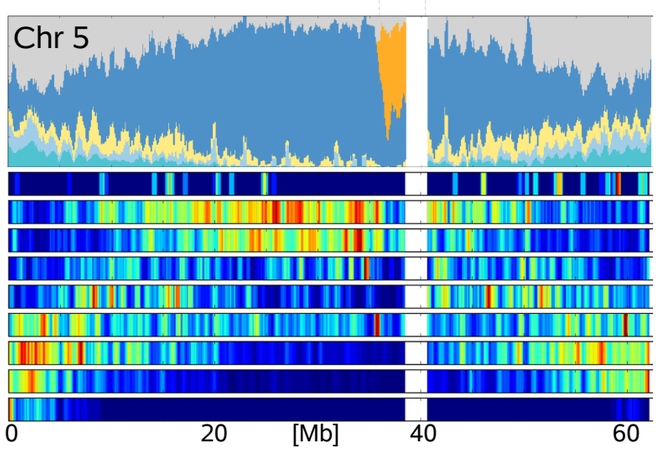
Cen38	0 - 57.7	1.4
RTs	13.5 - 95.7	61.0
DNA-TEs	0 - 20.5	6.6
genes (introns)	0 - 29.5	6.0
genes (exons)	0 - 18.0	4.8
	range	avg
LTR-RTs <=0.01 mya	0 - 4.2	0.50
full length LTR-RTs	0 - 41.0	21.1
LTR-RTs/ gypsy	0.5 - 51.5	21.5
LTR-RTs/ copia	0 - 17.0	5.8
DNA-TEs/ CACTA	0 - 19.4	5.1
CpG islands	0.1 - 4.3	1.6
DNA-TEs/ MITE	0 - 4.2	1.3
genes (exons)	0 - 17.2	3.8
paralogs (exons)	0 - 10.6	0.7



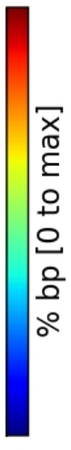
Cen38	0 - 35.3	0.2
RTs	7.2 - 96.8	53.7
DNA-TEs	0.5 - 22.3	6.3
genes (introns)	0 - 25.0	8.9
genes (exons)	0 - 21.4	6.9
	range	avg
LTR-RTs <=0.01 mya	0 - 6.9	0.48
full length LTR-RTs	0 - 44.9	17.6
LTR-RTs/ gypsy	0.4 - 60.6	18.6
LTR-RTs/ copia	0 - 16.1	5.3
DNA-TEs/ CACTA	0.1 - 21.4	4.1
CpG islands	0.3 - 4.9	2.1
DNA-TEs/ MITE	0 - 5.2	1.9
genes (exons)	0 - 20.2	6.3
paralogs (exons)	0 - 6.9	1.5

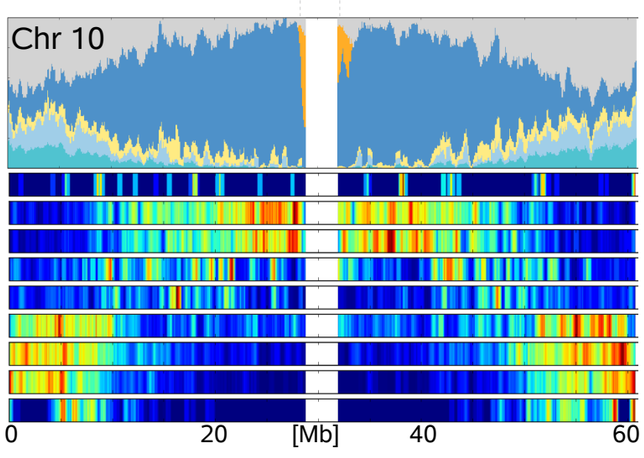


Cen38	0 - 49.1	0.7
RTs	8.6 - 95.6	59.0
DNA-TEs	0.2 - 15.0	6.1
genes (introns)	0 - 31.7	7.2
genes (exons)	0 - 19.1	5.4
	range	avg
LTR-RTs <=0.01 mya	0 - 5.9	0.63
full length LTR-RTs	0 - 46.5	20.8
LTR-RTs/ gypsy	0.2 - 55.7	21.8
LTR-RTs/ copia	0.3 - 17.8	4.9
DNA-TEs/ CACTA	0 - 14.9	4.3
CpG islands	0.2 - 5.8	1.9
DNA-TEs/ MITE	0.1 - 4.5	1.7
genes (exons)	0 - 18.0	4.8
paralogs (exons)	0 - 8.2	1.3



Cen38	0 - 71.0	2.2
RTs	14.9 - 95.0	58.1
DNA-TEs	0.1 - 24.3	8.3
genes (introns)	0 - 18.7	5.3
genes (exons)	0 - 19.5	4.9
	range	avg
LTR-RTs <=0.01 mya	0 - 7.9	0.61
full length LTR-RTs	0 - 43.1	19.7
LTR-RTs/ gypsy	0.9 - 55.0	19.0
LTR-RTs/ copia	0 - 22.1	5.7
DNA-TEs/ CACTA	0 - 22.6	6.8
CpG islands	0.1 - 4.7	1.7
DNA-TEs/ MITE	0 - 3.9	1.3
genes (exons)	0 - 19.2	3.7
paralogs (exons)	0 - 11.6	0.4





Cen38	0 - 61.1	0.9
RTs	12.3 - 96.5	56.8
DNA-TEs	0.4 - 23.1	6.6
genes (introns)	0 - 28.0	7.3
genes (exons)	0 - 20.1	6.0
	range	avg
LTR-RTs <=0.01 mya	0 - 7.8	0.65
full length LTR-RTs	0 - 49.9	20.6
LTR-RTs/ gypsy	0.4 - 51.7	19.8
LTR-RTs/ copia	0.1 - 18.2	5.4
DNA-TEs/ CACTA	0.2 - 21.7	4.7
CpG islands	0.2 - 5.6	2.0
DNA-TEs/ MITE	0 - 4.8	1.7
genes (exons)	0 - 19.9	5.1
paralogs (exons)	0 - 5.6	0.9