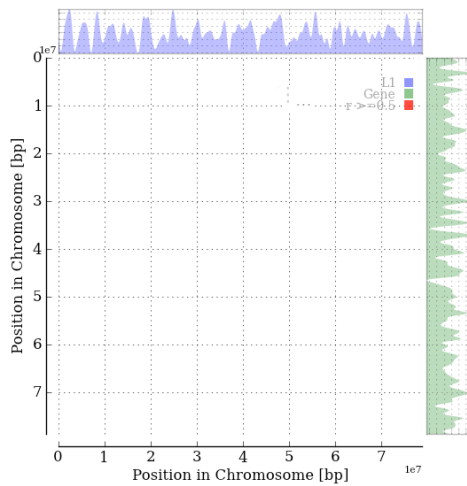


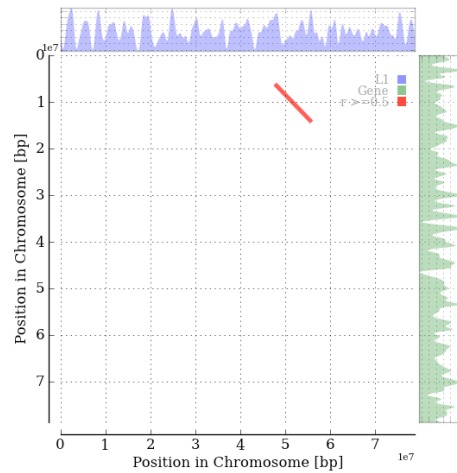
Supplementary Information

This file contains supplementary information on alignment of the genomic landscapes.

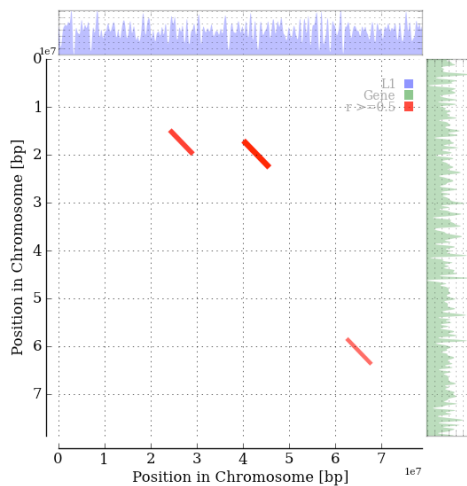
1Mbp



0.5 Mbp



0.25 Mbp



0.1 Mbp

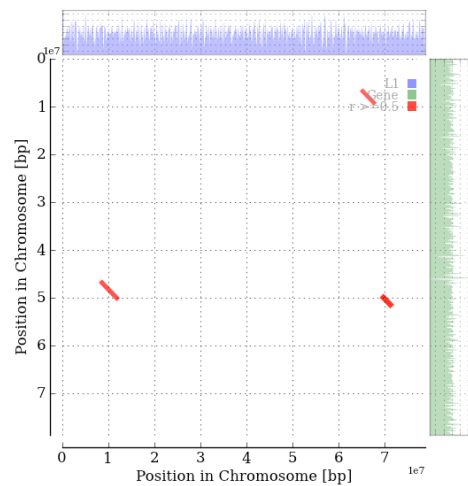


Figure S1 Dot plot representation of the alignment between LINE-1 and gene density at 4 different scales (chromosome 17). Unlike the H3K4me2/H3K9ac alignment, almost no similarity is detected along the diagonal.

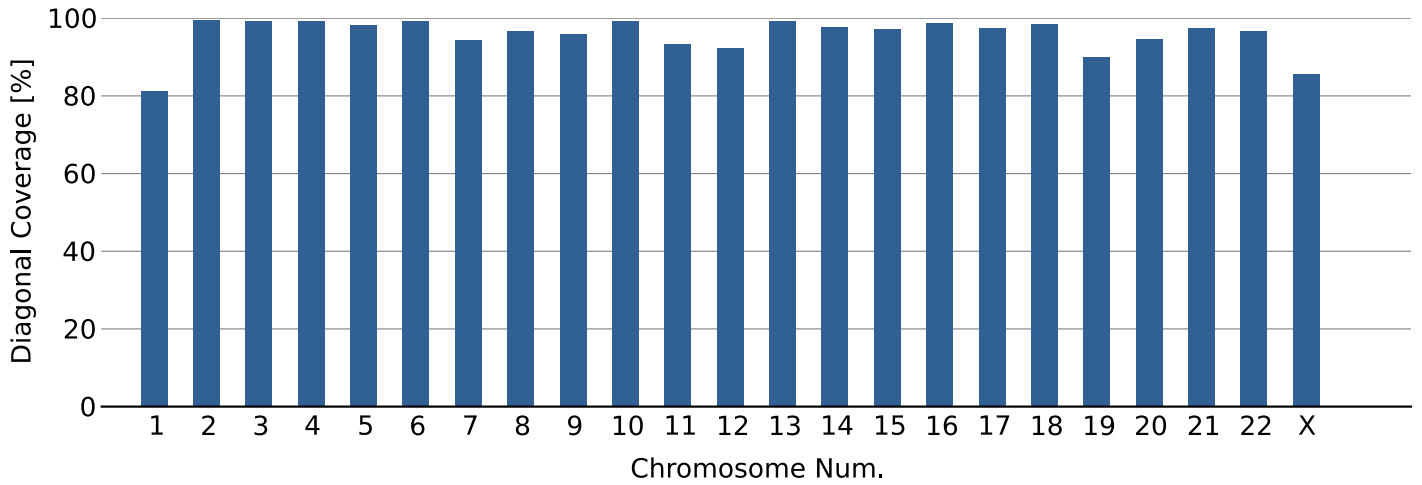


Figure S2. Aligned coverage between replication timing data (in ES cells) and the density of Alu elements for all chromosomes at the 1Mbp scale.

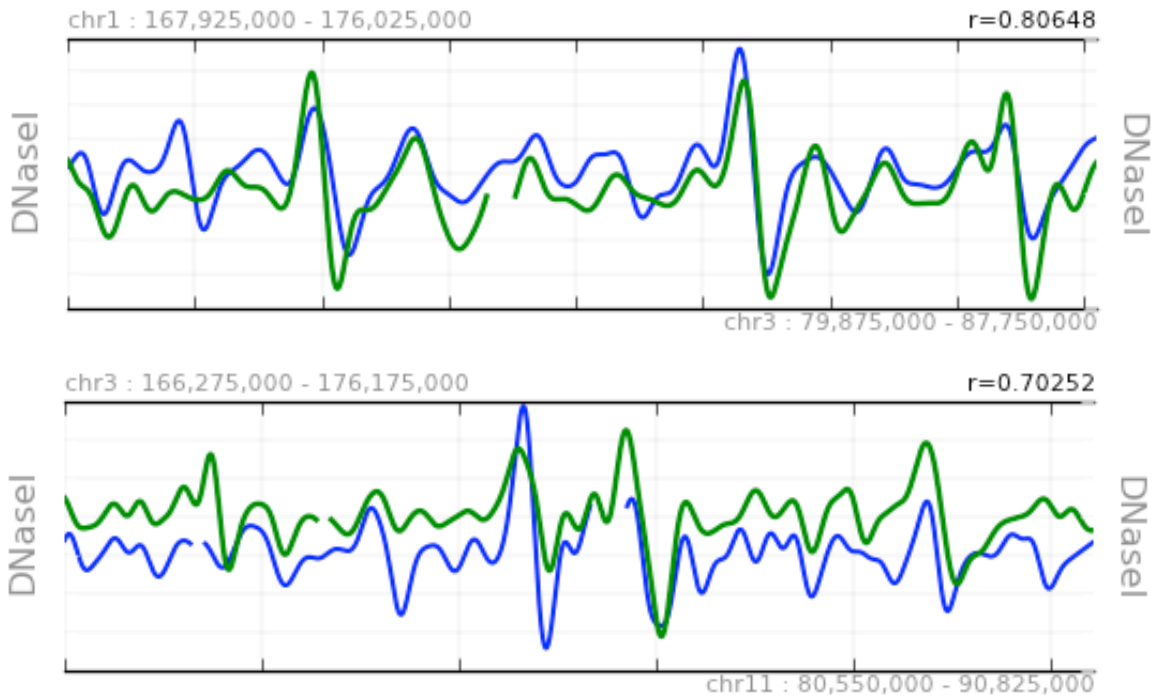


Figure S3. Examples of self-aligned pairs in DNase I data at 0.1 Mbp scale. Self alignment can detect those regions with similar landscapes within itself. Note that detection of these pairs do not necessary indicate they are biologically meaningful. However, they could be used to compare the regions with different factors to detect commonalities. See Table S4 for processing time.

Table S1. All-to-all Inter-chromosomal comparison. Processing time (in seconds) of each step in four scales.

Scale [Mbp]	1	0.5	0.25	0.1	Total
Wavelet Transformation	68.08	72.16	69.92	67.15	277.31
Symbol Representation	27.90	28.50	29.81	32.93	119.14
Sequence Alignment	2,547.30	2,535.16	2,558.35	2,829.16	10,469.97
Filtering	7,466.42	9,436.31	9,780.91	14,732.04	41,415.68
Total	10,109.7	12,072.13	17,390.12	17,922.41	52,282.10

The processing time was measured with all-to-all inter-chromosomal comparison of DNaseI self-alignment , for chromosome 1-23 and X . We used an Intel(R) Xeon(R) CPU X5550 machine with a Linux OS, where the clock of CPU is 2.67GHz and the size of memory is 24 GByte.

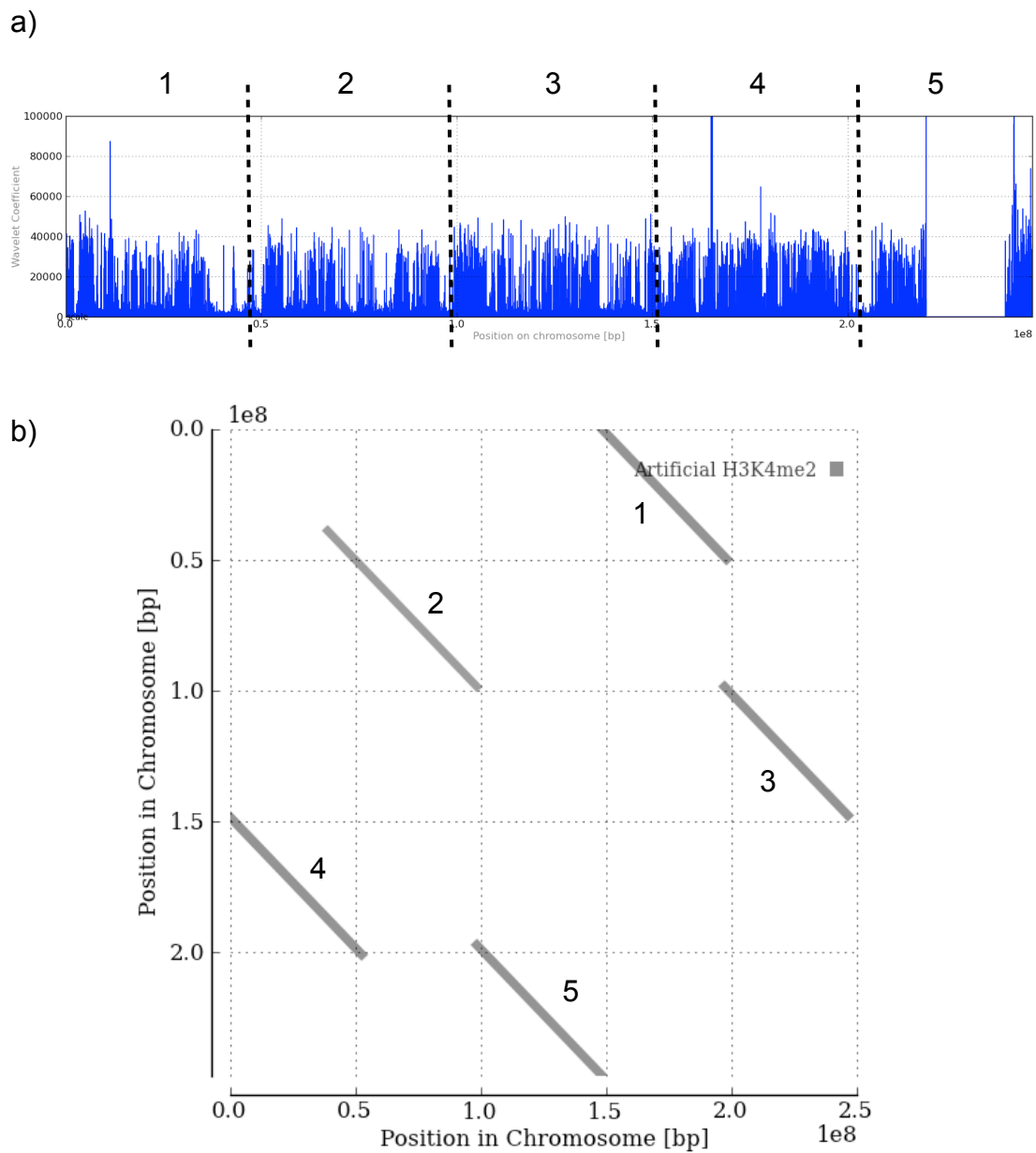


Figure S4. a) Artificial data created from H3K4me2 of human chromosome 1. The enrichment landscape of H3K4me2 is divided into five segments and shuffled. b) Dot plot representation that detected all the regions indicating that similar regions that do not match at exact positions can also be aligned.

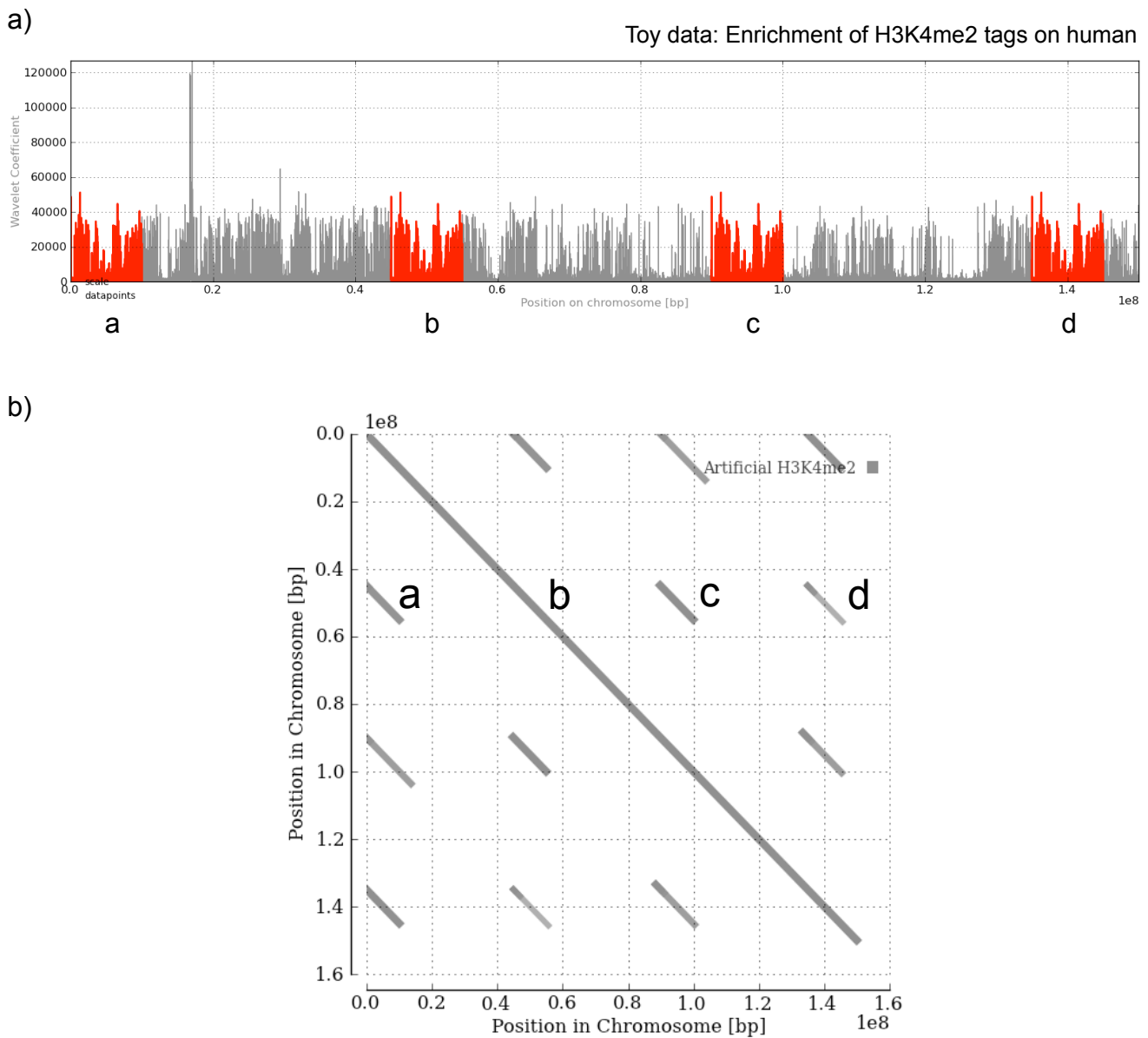


Figure S5. a) Artificial data created from H3K4me2 of human chromosome 1. Four motifs are embedded sparsely in the raw data before the wavelet transformation. b) We checked that 16 regions are correctly detected on the dot plot. Although further process is needed to cut out the common regions, the method can successfully align artificial motifs.

Table S2. Diagonal coverage was calculated between 13 samples for full genome-wide dataset. Higher percentage indicate that the two landscapes are highly correlated at the exact position. Internal parameters were set as follows: 5, 7 and 9 symbols, and 0.75, 1.0 and 1.25 for distance of single symbol representation relative to the scale were used internally. All the results were merged in order to minimize the effect of parameters. See Method section for calculation of the diagonal coverage.

(a) Scale: 0.75 Mbp

	Gene	GC	CTCF	PhyloP	Alu	LINE	RT-ESC	RT-NPC	H3K4me2	H3K27me3	H3K9ac	DNaseI	DNAmeth.
Gene	-	28.86	29.55	7.35	86.69	2.71	67.86	35.99	66.89	4.4	61.32	56.87	0.29
GC	28.86	-	34.98	27.54	55.78	6.55	39.0	39.35	89.96	38.3	90.13	95.54	45.23
CTCF	29.55	34.98	-	2.69	26.86	2.91	29.32	23.55	50.84	14.03	24.32	85.28	0.0
Cons.	7.35	27.54	2.69	-	6.45	7.08	3.15	5.51	23.11	6.63	16.16	10.62	60.88
Alu	86.69	55.78	26.86	6.45	-	5.63	93.8	52.13	90.11	14.32	85.12	75.25	5.3
LINE	2.71	6.55	2.91	7.08	5.63	-	0.0	0.37	2.64	2.75	3.59	4.73	6.3
RT-ESC	67.86	39.0	29.32	3.15	93.8	0.0	-	92.28	91.66	5.93	77.23	58.57	1.37
RT-NPC	35.99	39.35	23.55	5.51	52.13	0.37	92.28	-	62.79	5.05	57.89	44.05	4.36
H3K4me2	66.89	89.96	50.84	23.11	90.11	2.64	91.66	62.79	-	75.33	99.36	95.39	11.08
H3K27me3	4.4	38.3	14.03	6.63	14.32	2.75	5.93	5.05	75.33	-	52.97	54.52	2.56
H3K9ac	61.32	90.13	24.32	16.16	85.12	3.59	77.23	57.89	99.36	52.97	-	82.11	11.43
DNaseI	56.87	95.54	85.28	10.62	75.25	4.73	58.57	44.05	95.39	54.52	82.11	-	11.42
DNAmeth.	0.29	45.23	0.0	60.88	5.3	6.3	1.37	4.36	11.08	2.56	11.43	11.42	-

(b) Scale: 0.5 Mbp

	Gene	GC	CTCF	PhyloP	Alu	LINE	RT-ESC	RT-NPC	H3K4me2	H3K27me3	H3K9ac	DNaseI	DNAmeth.
Gene	-	7.95	7.64	3.39	45.13	2.02	22.82	1.58	36.81	2.52	36.03	31.4	0.0
GC	7.95	-	30.21	21.94	31.69	4.69	22.11	17.68	62.83	28.13	72.73	96.22	22.93
CTCF	7.64	30.21	-	1.39	5.7	1.52	15.23	5.64	20.61	4.51	7.47	65.24	0.7
Cons.	3.39	21.94	1.39	-	6.83	9.62	4.37	1.13	13.62	4.99	12.91	6.6	57.61
Alu	45.13	31.69	5.7	6.83	-	3.53	82.6	13.79	64.74	3.27	69.67	55.42	3.8
LINE	2.02	4.69	1.52	9.62	3.53	-	0.07	1.43	1.48	0.3	1.89	4.42	7.89
RT-ESC	22.82	22.11	15.23	4.37	82.6	0.07	-	72.92	71.61	4.48	52.49	41.51	0.81
RT-NPC	1.58	17.68	5.64	1.13	13.79	1.43	72.92	-	19.41	3.79	25.65	12.98	0.5
H3K4me2	36.81	62.83	20.61	13.62	64.74	1.48	71.61	19.41	-	61.05	99.61	90.82	2.38
H3K27me3	2.52	28.13	4.51	4.99	3.27	0.3	4.48	3.79	61.05	-	41.35	49.69	3.2
H3K9ac	36.03	72.73	7.47	12.91	69.67	1.89	52.49	25.65	99.61	41.35	-	71.62	5.32
DNaseI	31.4	96.22	65.24	6.6	55.42	4.42	41.51	12.98	90.82	49.69	71.62	-	2.17
DNAmeth.	0.0	22.93	0.7	57.61	3.8	7.89	0.81	0.5	2.38	3.2	5.32	2.17	-

(c) Scale: 0.1 Mbp

	Gene	GC	CTCF	PhyloP	Alu	LINE	RT-ESC	RT-NPC	H3K4me2	H3K27me3	H3K9ac	DNaseI	DNAmeth.
Gene	-	0.92	2.17	3.49	6.59	0.0	1.01	0.28	10.88	0.35	10.41	6.18	0.1
GC	0.92	-	13.81	12.59	16.51	0.0	6.38	9.09	33.87	16.76	52.95	83.89	9.5
CTCF	2.17	13.81	-	0.3	0.2	0.3	2.21	0.31	5.73	1.77	2.27	28.04	0.0
Cons.	3.49	12.59	0.3	-	0.68	3.45	1.34	0.31	6.49	0.57	10.96	4.9	32.2
Alu	6.59	16.51	0.2	0.68	-	1.59	6.89	2.47	25.34	2.58	46.81	22.93	0.18
LINE	0.0	0.0	0.3	3.45	1.59	-	0.0	1.69	0.05	1.27	0.61	2.27	0.24
RT-ESC	1.01	6.38	2.21	1.34	6.89	0.0	-	70.62	9.56	1.62	11.35	4.16	0.6
RT-NPC	0.28	9.09	0.31	0.31	2.47	1.69	70.62	-	0.61	1.21	3.84	0.61	1.15
H3K4me2	10.88	33.87	5.73	6.49	25.34	0.05	9.56	0.61	-	60.08	99.25	86.08	1.84
H3K27me3	0.35	16.76	1.77	0.57	2.58	1.27	1.62	1.21	60.08	-	23.4	45.06	0.35
H3K9ac	10.41	52.95	2.27	10.96	46.81	0.61	11.35	3.84	99.25	23.4	-	49.89	3.86
DNaseI	6.18	83.89	28.04	4.9	22.93	2.27	4.16	0.61	86.08	45.06	49.89	-	0.77
DNAmeth.	0.1	9.5	0.0	32.2	0.18	0.24	0.6	1.15	1.84	0.35	3.86	0.77	-

Table S3. Table of diagonal coverage with ‘reversed’ landscapes in four different scales. To check how reliable and significant the values of diagonal coverages are, we calculated all the landscape pairs with one of two samples in reversed direction. If the diagonal coverage is caused due to a false-positive, it is likely to also show up in pairs of reversed direction as they have the same complexity and composition of symbols. As a result, all pairs showed significantly low diagonal coverage in every scales studied, which indicates that values of diagonal coverage is not caused by random effects.

(a) Scale: 1 Mbp

	Gene	GC	CTCF	Conservation	Alu	LINE	RT-ESC	RT-NPC	H3K4me2	H3K27me3	H3K9ac	DNaseI	DNAmethyl
revGene	2.82	0.55	0.0	0.0	1.35	1.63	0.0	1.61	1.31	0.66	2.03	1.09	0.2
revGC	2.13	1.06	0.0	0.0	4.84	1.64	2.74	0.55	1.47	5.08	1.1	2.36	0.72
revCTCF	0.0	0.0	2.89	2.63	4.4	0.0	2.47	0.7	3.55	0.0	1.26	3.04	0.28
revConservation	1.73	1.42	2.92	0.68	1.42	0.43	2.03	0.0	0.0	0.44	1.21	0.77	0.0
revAlu	1.35	4.29	4.45	0.0	1.6	2.06	0.5	0.5	4.3	4.46	3.59	6.29	0.0
revLINE	0.65	1.22	0.2	0.0	2.06	0.0	0.0	2.75	0.0	1.41	0.41	1.3	0.69
revRT-ESC	0.0	2.45	3.0	1.12	0.46	0.29	1.12	0.43	3.97	0.46	0.63	1.52	0.72
revRT-NPC	1.91	0.55	0.41	0.0	0.0	2.36	0.89	0.85	1.19	0.51	0.39	0.88	2.69
revH3K4me2	1.11	0.65	3.98	0.0	5.46	0.0	1.69	2.11	4.67	3.76	0.88	0.81	0.23
revH3K27me3	1.03	5.03	0.0	1.13	4.43	2.02	0.0	1.91	5.17	8.84	4.96	3.59	1.58
revH3K9ac	2.03	0.51	1.08	0.0	3.91	0.4	0.83	0.0	1.25	6.09	2.75	0.73	0.0
revDNaseI	1.09	2.75	3.06	0.77	6.06	1.3	2.05	0.88	0.7	3.86	1.1	3.98	0.0
revDNAmethyl	0.21	0.0	0.0	0.0	0.29	0.29	1.32	2.65	0.3	1.16	1.48	0.69	0.0

(b) Scale: 0.75 Mbp

	Gene	GC	CTCF	Conservation	Alu	LINE	RT-ESC	RT-NPC	H3K4me2	H3K27me3	H3K9ac	DNaseI	DNAmethyl
revGene	0.3	0.24	0.66	1.37	0.36	0.92	2.37	0.0	0.63	0.94	0.98	0.0	0.0
revGC	0.0	0.31	0.0	0.37	0.94	0.32	0.3	0.64	0.94	1.32	0.53	2.72	0.25
revCTCF	0.66	0.0	1.21	0.11	0.44	0.38	0.0	0.0	1.71	0.11	0.0	0.0	0.53
revConservation	1.48	0.0	0.0	0.19	2.09	0.0	0.2	0.0	0.0	1.24	1.36	1.44	0.56
revAlu	0.93	2.42	0.44	0.91	0.0	0.66	0.56	0.98	0.16	3.65	0.0	3.28	0.54
revLINE	1.31	0.16	0.33	1.39	0.0	0.0	0.88	0.0	0.25	0.0	0.19	0.0	0.0
revRT-ESC	1.43	0.41	0.0	0.64	0.67	0.52	0.48	0.0	0.41	1.2	0.42	0.34	0.66
revRT-NPC	0.0	0.37	0.0	0.59	1.17	2.31	0.0	0.12	0.0	1.18	0.0	0.0	0.55
revH3K4me2	0.89	1.02	0.97	0.0	0.38	1.06	0.52	0.0	1.15	0.47	1.5	0.3	1.02
revH3K27me3	0.74	3.19	0.0	1.23	3.77	0.45	0.16	0.72	0.66	6.06	2.39	4.44	1.91
revH3K9ac	0.65	0.26	0.0	1.27	0.0	0.21	0.14	0.0	0.74	2.53	1.04	1.0	0.77
revDNaseI	0.31	2.99	0.0	1.25	3.07	0.0	0.39	0.16	1.99	4.32	1.99	3.41	0.2
revDNAmethyl	0.18	0.41	0.39	0.0	0.45	0.98	1.02	0.31	0.87	0.37	0.42	0.53	1.88

(c) Scale: 0.5 Mbp

	Gene	GC	CTCF	Conservation	Alu	LINE	RT-ESC	RT-NPC	H3K4me2	H3K27me3	H3K9ac	DNaseI	DNAmethyl
revGene	0.47	0.0	0.3	0.0	0.0	0.2	0.0	0.22	0.45	2.11	0.29	0.54	0.35
revGC	0.0	0.4	0.69	0.0	0.0	0.11	0.37	0.0	0.1	0.29	0.09	0.28	0.0
revCTCF	0.3	0.31	0.0	0.11	0.0	1.55	0.29	0.16	0.51	0.0	0.0	0.11	0.0
revConservation	0.0	0.0	0.0	0.19	0.11	0.42	0.62	0.28	0.0	0.83	0.0	0.2	0.77
revAlu	0.0	0.0	0.0	0.0	0.59	0.07	0.69	0.0	0.75	0.47	0.89	0.76	0.24
revLINE	0.2	0.0	1.47	0.44	0.26	0.0	0.09	0.05	0.0	0.0	0.06	0.0	0.29
revRT-ESC	0.35	0.99	0.26	0.37	0.65	0.07	0.18	0.09	0.42	0.23	0.0	0.37	0.16
revRT-NPC	0.21	0.0	0.05	0.16	0.0	0.0	0.09	0.75	0.15	0.0	0.0	0.0	0.07
revH3K4me2	0.53	1.05	0.42	0.14	0.3	0.0	0.42	0.2	0.45	0.52	1.59	0.45	0.21
revH3K27me3	1.47	0.56	0.0	0.65	0.57	0.55	0.19	0.0	0.86	2.74	0.56	1.92	1.37
revH3K9ac	0.35	0.21	0.0	0.0	0.58	0.16	0.35	0.0	1.27	0.38	0.49	0.28	0.0
revDNaseI	0.29	0.28	0.0	0.25	0.41	0.0	0.73	0.0	0.2	2.13	0.81	1.03	0.0
revDNAmethyl	0.25	0.0	0.0	0.5	0.25	0.61	0.16	0.46	0.11	1.03	0.08	0.0	0.21

(d) Scale: 0.1 Mbp

	Gene	GC	CTCF	Conservation	Alu	LINE	RT-ESC	RT-NPC	H3K4me2	H3K27me3	H3K9ac	DNaseI	DNAmethyl
revGene	0.16	0.03	0.0	0.53	0.04	0.0	0.12	0.1	0.59	0.42	0.59	0.14	0.06
revGC	0.0	0.33	0.25	0.0	0.57	0.0	0.0	0.0	0.29	0.24	0.13	0.23	0.21
revCTCF	0.0	0.33	0.43	0.13	0.16	0.11	0.0	0.21	0.3	0.27	0.08	0.0	0.25
revConservation	0.26	0.0	0.11	0.03	0.0	0.13	0.34	0.08	0.0	0.07	0.37	0.38	0.0
revAlu	0.13	0.29	0.18	0.0	0.73	0.07	0.24	0.33	0.23	0.26	1.48	0.44	0.08
revLINE	0.0	0.0	0.06	0.0	0.19	0.0	0.0	0.13	0.0	0.0	0.13	0.13	0.16
revRT-ESC	0.07	0.0	0.09	0.23	0.38	0.04	0.49	0.1	0.0	0.1	0.03	0.07	0.0
revRT-NPC	0.13	0.29	0.0	0.05	0.24	0.0	0.27	0.17	0.07	0.15	0.0	0.07	0.0
revH3K4me2	0.5	0.36	0.11	0.27	0.2	0.0	0.09	0.08	0.04	0.58	0.48	0.43	0.17
revH3K27me3	0.27	0.27	0.18	0.0	0.39	0.15	0.1	0.0	0.74	0.13	0.39	0.61	0.0
revH3K9ac	0.6	0.21	0.21	0.09	1.0	0.08	0.24	0.0	0.3	0.52	1.5	0.87	0.4
revDNaseI	0.29	0.0	0.21	0.33	0.4	0.09	0.0	0.0	0.63	0.86	1.18	0.72	0.13
revDNAmethyl	0.16	0.66	0.51	0.18	0.2	0.4	0.0	0.0	0.17	0.0	0.0	0.13	0.15

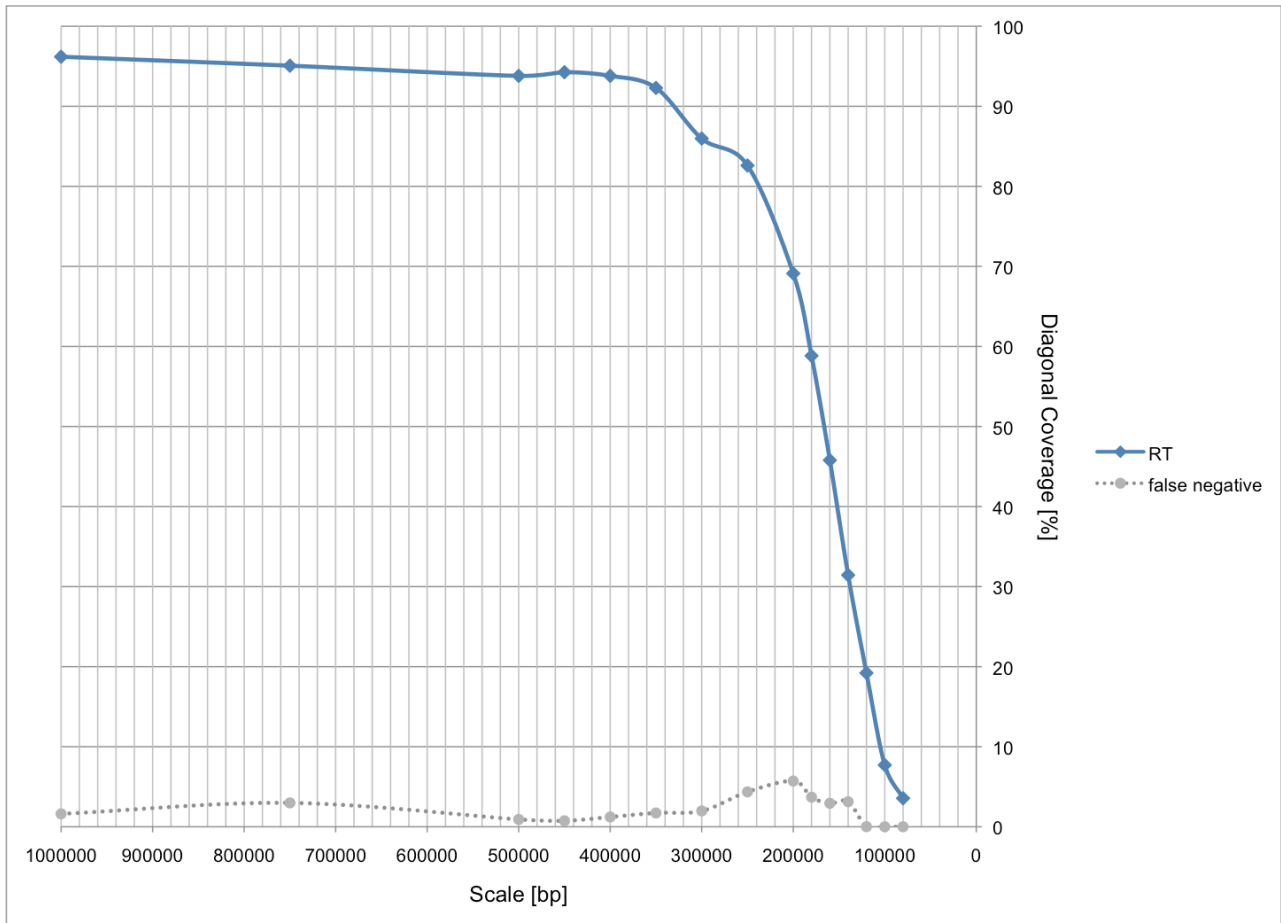


Figure S6. Transition of the diagonal coverage between density of Alu elements and replication timing with false-negative coverage plotted over 15 different scales. False-negative coverage is calculated by first obtaining the regions that come off the diagonal (unaligned region), then by calculating the Pearson correlation and obtaining the coverage that exceeded the threshold. The results show that it is kept small and they are no larger than 5-6 %. We therefore can assume that the scale-dependent difference is significant with 5% variability.

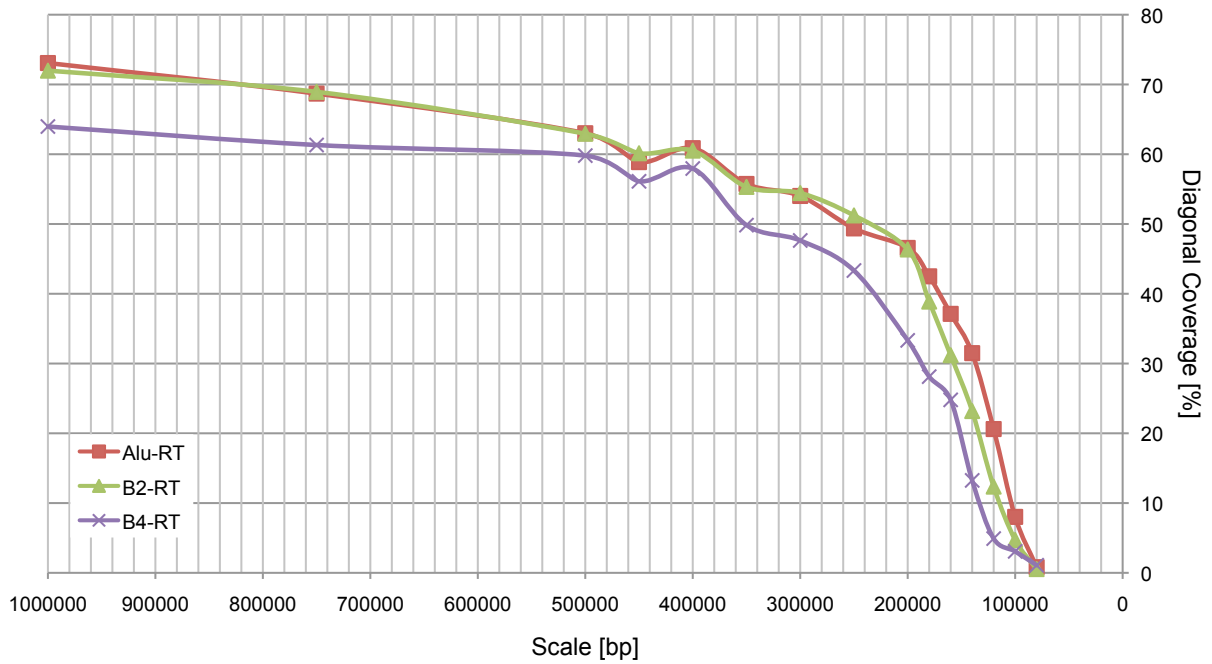


Figure S7. Transition of the diagonal coverage between replication timing and density of active SINE repeats in mouse genome (Alu, B2 and B4) over 15 different scales. All the diagonal coverage remains relatively high until around 0.25 Mbp scale and suddenly drops which is the same trend as human genome.

Table S4. Correlation between replication timing and various classes of repeat elements.

(a) Scale: 0.75 Mbp

		RT					SINE					LINE	
		ESC	ESC2	iPS	NPC	Lympho.	Alu	AluJ	AluS	AluY	MIR	L1	L2
RT	ESC	-	99.24	99.21	93.9	81.3	95.07	94.43	89.85	56.93	7.9	0.0	7.89
	ESC2	99.24	-	99.23	95.01	86.64	93.33	92.0	91.67	53.43	7.75	0.0	2.1
	iPS	99.21	99.23	-	90.31	75.37	95.37	93.32	93.24	59.23	8.92	0.0	3.71
	NPC	93.9	95.01	90.31	-	71.31	62.3	67.73	62.55	20.48	11.1	0.27	9.55
	LYMPHO	81.3	86.64	75.37	71.31	-	77.56	78.19	71.79	32.77	5.18	0.91	2.2
SINE	Alu	95.07	93.33	95.37	62.3	77.56	-	99.14	99.26	98.97	17.09	4.47	13.71
	AluJ	94.43	92.0	93.32	67.73	78.19	99.14	-	98.24	91.09	15.59	2.51	16.11
	AluS	89.85	91.67	93.24	62.55	71.79	99.26	98.24	-	96.61	11.13	4.55	8.62
	AluY	56.93	53.43	59.23	20.48	32.77	98.97	91.09	96.61	-	3.88	9.17	5.05
	MIR	7.9	7.75	8.92	11.1	5.18	17.09	15.59	11.13	3.88	-	0.82	95.44
LINE	L1	0.0	0.0	0.0	0.27	0.91	4.47	2.51	4.55	9.17	0.82	-	2.9
	L2	7.89	2.1	3.71	9.55	2.2	13.71	16.11	8.62	5.05	95.44	2.9	-

(b) Scale: 0.5 Mbp

		RT					SINE					LINE	
		ESC	ESC2	iPS	NPC	Lympho.	Alu	AluJ	AluS	AluY	MIR	L1	L2
RT	ESC	-	99.49	99.49	92.28	80.46	93.8	94.9	91.02	39.92	3.49	1.08	3.71
	ESC2	99.49	-	99.23	94.55	85.95	94.16	94.21	88.23	38.29	2.94	0.39	1.73
	iPS	99.49	99.23	-	88.49	76.51	91.77	92.43	88.33	51.05	1.56	0.58	4.26
	NPC	92.28	94.55	88.49	-	69.35	52.7	57.21	48.49	10.25	5.41	0.52	3.01
	LYMPHO	80.46	85.95	76.51	69.35	-	68.28	77.03	62.41	25.52	1.77	0.63	1.74
SINE	Alu	93.8	94.16	91.77	52.7	68.28	-	99.35	99.49	98.3	7.07	4.52	9.07
	AluJ	94.9	94.21	92.43	57.21	77.03	99.35	-	99.17	90.41	10.02	2.22	8.67
	AluS	91.02	88.23	88.33	48.49	62.41	99.49	99.17	-	97.87	6.47	3.88	7.78
	AluY	39.92	38.29	51.05	10.25	25.52	98.3	90.41	97.87	-	4.7	4.21	4.51
	MIR	3.49	2.94	1.56	5.41	1.77	7.07	10.02	6.47	4.7	-	0.13	93.05
LINE	L1	1.08	0.39	0.58	0.52	0.63	4.52	2.22	3.88	4.21	0.13	-	3.8
	L2	3.71	1.73	4.26	3.01	1.74	9.07	8.67	7.78	4.51	93.05	3.8	-

(c) Scale: 0.1 Mbp

		RT					SINE					LINE	
		ESC	ESC2	iPS	NPC	Lympho.	Alu	AluJ	AluS	AluY	MIR	L1	L2
RT	ESC	-	99.87	99.76	70.62	77.77	7.71	8.14	4.9	0.23	0.56	0.27	1.0
	ESC2	99.87	-	99.72	70.16	79.92	10.98	9.61	6.26	0.26	0.13	0.82	0.38
	iPS	99.76	99.72	-	60.64	73.29	7.53	3.99	5.33	0.27	0.13	0.09	0.09
	NPC	70.62	70.16	60.64	-	56.84	2.52	0.2	1.05	0.22	0.91	1.8	1.03
	LYMPHO	77.77	79.92	73.29	56.84	-	4.65	4.65	3.15	0.48	0.4	1.11	1.11
SINE	Alu	7.71	10.98	7.53	2.52	4.65	-	99.45	99.89	95.51	4.67	2.38	1.99
	AluJ	8.14	9.61	3.99	0.2	4.65	99.45	-	92.03	31.39	5.34	0.53	4.14
	AluS	4.9	6.26	5.33	1.05	3.15	99.89	92.03	-	71.41	3.57	2.01	2.97
	AluY	0.23	0.26	0.27	0.22	0.48	95.51	31.39	71.41	-	0.26	1.03	1.9
	MIR	0.56	0.13	0.13	0.91	0.4	4.67	5.34	3.57	0.26	-	0.0	48.86
LINE	L1	0.27	0.82	0.09	1.8	1.11	2.38	0.53	2.01	1.03	0.0	-	0.31
	L2	1.0	0.38	0.09	1.03	1.11	1.99	4.14	2.97	1.9	48.86	0.31	-

Table S5. Correlation between replication timing and various classes of repeat elements in Mouse genome.

(a) Scale: 1 Mbp

		RT						SINE				LINE	
		ESC-46C	ESC-D3	ESC-TT2	NPC-46C	NPC-D3	NPC-TT2	Alu	B2	B4	MIR	L1	L2
RT	ESC-46C	-	98.76	99.13	98.85	98.45	98.72	71.47	70.21	62.14	16.26	0.00	6.03
	ESC-D3	98.76	-	98.75	98.16	98.09	98.19	69.86	70.53	64.36	14.89	0.00	5.98
	ESC-TT2	99.13	98.75	-	98.83	98.37	98.88	73.07	71.98	63.97	18.5	0.00	8.92
	NPC-46C	98.85	98.16	98.83	-	98.86	98.59	65.14	64.59	68.34	16.86	0.00	12.23
	NPC-D3	98.45	98.09	98.37	98.86	-	98.59	65.12	65.14	71.85	27.00	0.00	11.53
	NPC-TT2	98.72	98.19	98.88	98.59	98.59	-	69.81	68.99	63.34	25.05	0.00	12.34
SINE	Alu	71.47	69.86	73.07	65.14	65.12	69.81	-	99.07	97.30	36.06	0.00	20.39
	B2	70.21	70.53	71.98	64.59	65.14	68.99	99.07	-	97.60	32.57	0.00	18.42
	B4	62.14	64.36	63.97	68.34	71.85	63.34	97.30	97.60	-	60.26	0.00	42.79
	MIR	16.26	14.89	18.50	16.86	27.00	25.05	36.06	32.57	60.26	-	0.00	95.23
LINE	L1	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	0.00
	L2	6.03	5.98	8.92	12.23	11.53	12.34	20.39	18.42	42.79	95.23	0.00	-

(b) Scale: 0.75 Mbp

		RT						SINE				LINE	
		ESC-46C	ESC-D3	ESC-TT2	NPC-46C	NPC-D3	NPC-TT2	Alu	B2	B4	MIR	L1	L2
RT	ESC-46C	-	95.37	96.3	96.86	96.61	96.29	70.15	68.68	60.73	7.51	0.32	0.86
	ESC-D3	95.37	-	95.23	95.13	95.23	94.93	69.41	70.28	60.56	4.18	1.3	0.0
	ESC-TT2	96.3	95.23	-	96.06	96.1	96.5	68.69	68.94	61.32	12.27	0.0	3.1
	NPC-46C	96.86	95.13	96.06	-	97.49	97.47	65.68	66.57	65.47	8.85	0.0	6.47
	NPC-D3	96.61	95.23	96.1	97.49	-	97.23	61.94	64.67	65.48	25.43	0.28	6.87
	NPC-TT2	96.29	94.93	96.5	97.47	97.23	-	65.65	66.74	63.4	14.08	0.0	6.37
SINE	Alu	70.15	69.41	68.69	65.68	61.94	65.65	-	99.33	97.06	25.29	0.31	12.06
	B2	68.68	70.28	68.94	66.57	64.67	66.74	99.33	-	96.8	24.71	0.29	11.7
	B4	60.73	60.56	61.32	65.47	65.48	63.4	97.06	96.8	-	46.2	0.0	30.71
	MIR	7.51	4.18	12.27	8.85	25.43	14.08	25.29	24.71	46.2	-	0.0	96.08
LINE	L1	0.32	1.3	0.0	0.0	0.28	0.0	0.31	0.29	0.0	0.0	-	0.21
	L2	0.86	0.0	3.1	6.47	6.87	6.37	12.06	11.7	30.71	96.08	0.21	-

(c) Scale: 0.5 Mbp

		RT						SINE				LINE	
		ESC-46C	ESC-D3	ESC-TT2	NPC-46C	NPC-D3	NPC-TT2	Alu	B2	B4	MIR	L1	L2
RT	ESC-46C	-	92.09	92.1	91.74	91.76	92.07	63.45	61.94	58.62	6.46	0.71	1.73
	ESC-D3	92.09	-	92.07	91.78	91.94	92.12	63.14	60.04	56.95	8.22	0.82	2.36
	ESC-TT2	92.1	92.07	-	91.9	92.05	92.13	63.01	62.94	59.8	6.16	0.35	2.68
	NPC-46C	91.74	91.78	91.9	-	92.12	92.15	61.07	58.32	60.0	4.38	1.42	4.07
	NPC-D3	91.76	91.94	92.05	92.12	-	92.15	56.95	55.71	60.63	9.16	0.67	3.92
	NPC-TT2	92.07	92.12	92.13	92.15	92.15	-	62.98	62.0	56.69	7.94	0.87	3.1
SINE	Alu	63.45	63.14	63.01	61.07	56.95	62.98	-	99.54	97.14	14.32	0.0	8.61
	B2	61.94	60.04	62.94	58.32	55.71	62.0	99.54	-	96.45	14.18	0.0	10.86
	B4	58.62	56.95	59.8	60.0	60.63	56.69	97.14	96.45	-	31.17	0.0	17.9
	MIR	6.46	8.22	6.16	4.38	9.16	7.94	14.32	14.18	31.17	-	0.0	98.87
LINE	L1	0.71	0.82	0.35	1.42	0.67	0.87	0.0	0.0	0.0	0.0	-	0.0
	L2	1.73	2.36	2.68	4.07	3.92	3.1	8.61	10.86	17.9	98.87	0.0	-

(d) Scale: 0.1 Mbp

		RT						SINE				LINE	
		ESC-46C	ESC-D3	ESC-TT2	NPC-46C	NPC-D3	NPC-TT2	Alu	B2	B4	MIR	L1	L2
RT	ESC-46C	-	90.55	90.61	87.07	88.33	89.85	3.43	3.41	1.12	0.0	0.35	0.0
	ESC-D3	90.55	-	90.56	79.37	89.45	82.05	1.16	1.09	0.34	0.22	0.69	0.07
	ESC-TT2	90.61	90.56	-	87.97	86.93	89.53	8.02	4.72	3.08	0.08	0.32	0.29
	NPC-46C	87.07	79.37	87.97	-	90.15	90.55	2.65	1.28	3.75	0.2	0.18	0.0
	NPC-D3	88.33	89.45	86.93	90.15	-	89.95	1.14	1.12	0.25	0.03	0.24	0.0
	NPC-TT2	89.85	82.05	89.53	90.55	89.95	-	11.16	7.78	6.84	0.0	0.14	0.05
SINE	Alu	3.43	1.16	8.02	2.65	1.14	11.16	-	97.89	84.09	2.51	0.03	2.11
	B2	3.41	1.09	4.72	1.28	1.12	7.78	97.89	-	73.52	1.07	0.0	1.17
	B4	1.12	0.34	3.08	3.75	0.25	6.84	84.09	73.52	-	4.41	0.28	3.36
	MIR	0.0	0.22	0.08	0.2	0.03	0.0	2.51	1.07	4.41	-	0.0	19.8
LINE	L1	0.35	0.69	0.32	0.18	0.24	0.14	0.03	0.0	0.28	0.0	-	0.09
	L2	0.0	0.07	0.29	0.0	0.0	0.05	2.11	1.17	3.36	19.8	0.09	-