Supplemental Material to:

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Retrotransposon Alu is enriched in the epichromatinof HL-60 cells

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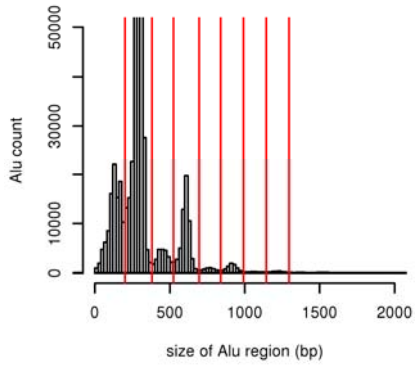
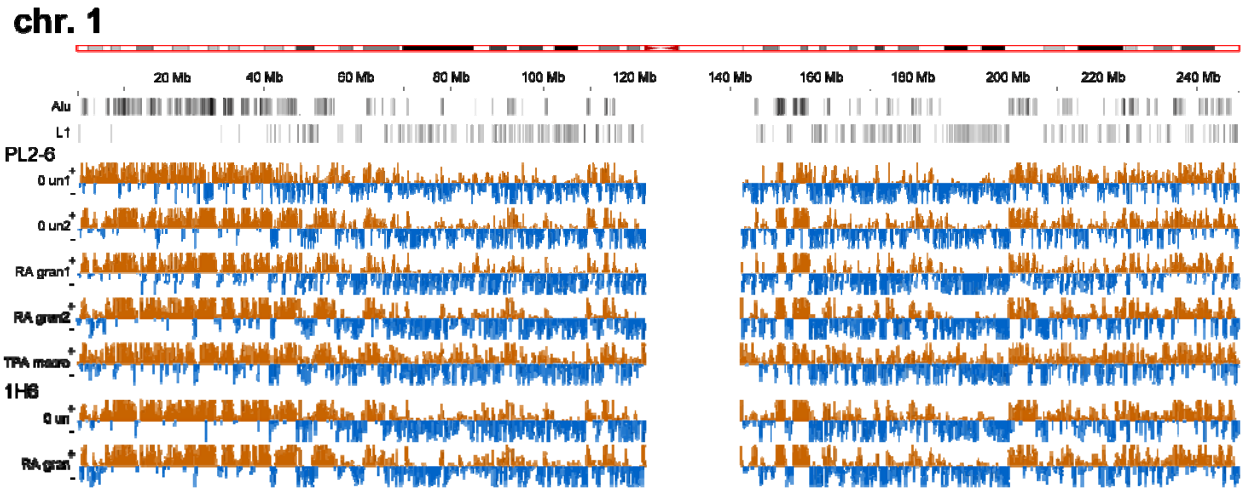
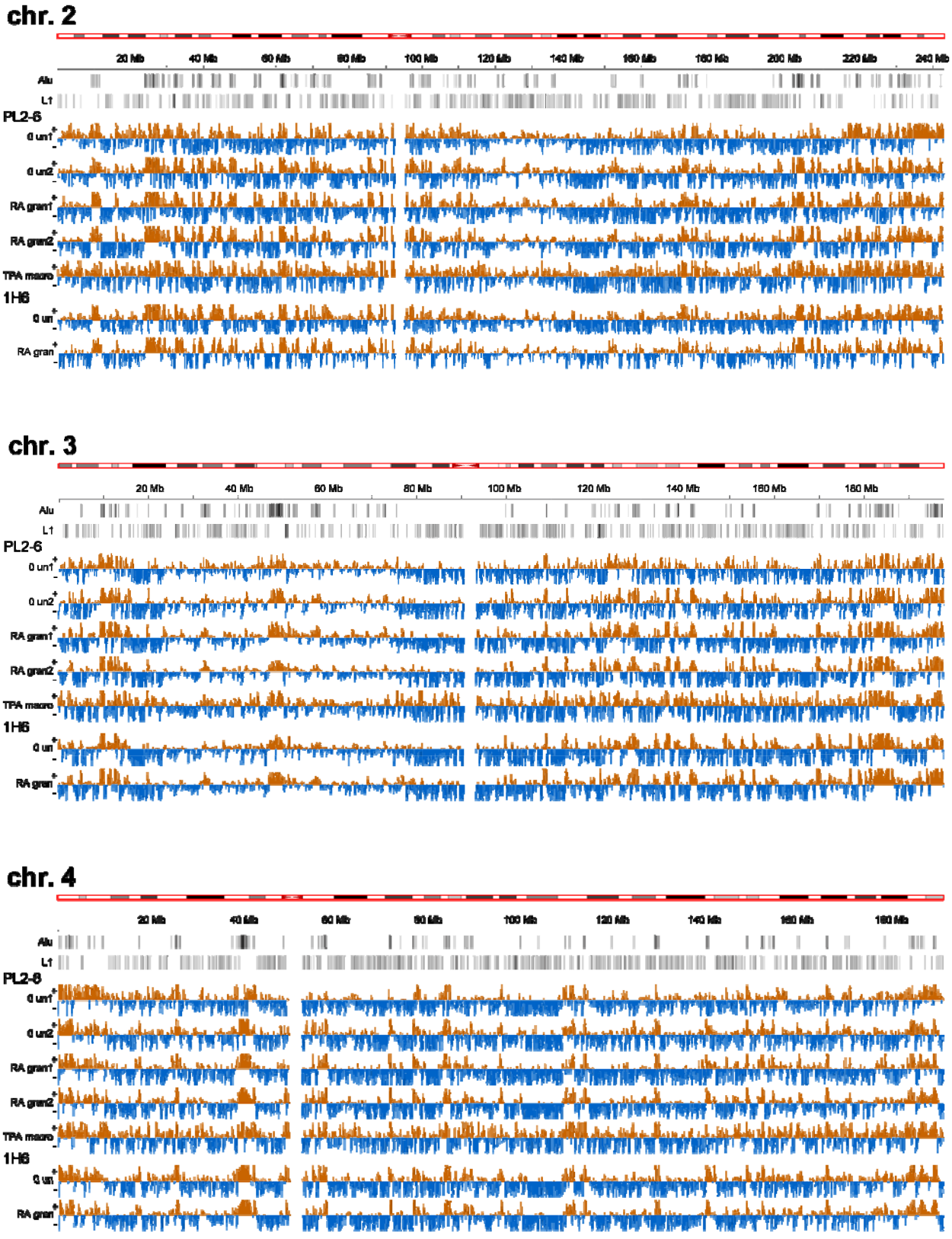


Fig. S1. Distribution of the sizes of Alu elements in the human genome. All Alu elements within 30bp of each other were merged. The red vertical bars (200, 381, 525, 695, 839, 991, 1144, 1296 bp) were manually selected for segmentation of the Alu multimers. The first peak in the histogram corresponds to "half Alu" elements (~150 bp). The second peak (truncated in the Y-axis) represents the distribution of Alu monomers (~305 bp). The peaks representing multiples of whole Alu (e.g. monomers, dimers, trimers) are typically higher than their neighboring "half Alu" elements. The increasing orders of multimers and neighboring "half Alu" show exponentially fewer elements. This segmentation enabled estimation of the number and percentage of each repeat size in the human genome (**Tables S2 and S3**).

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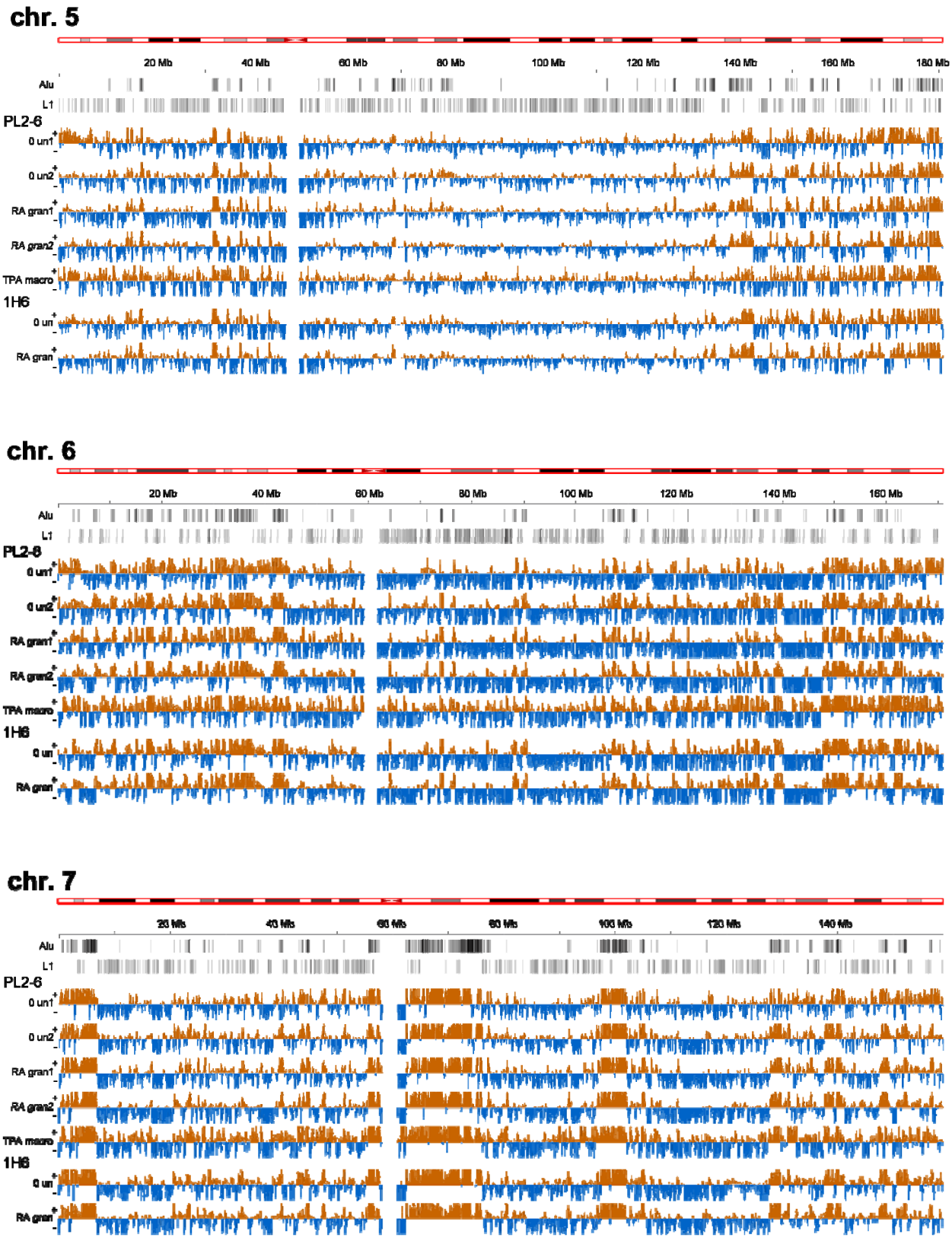
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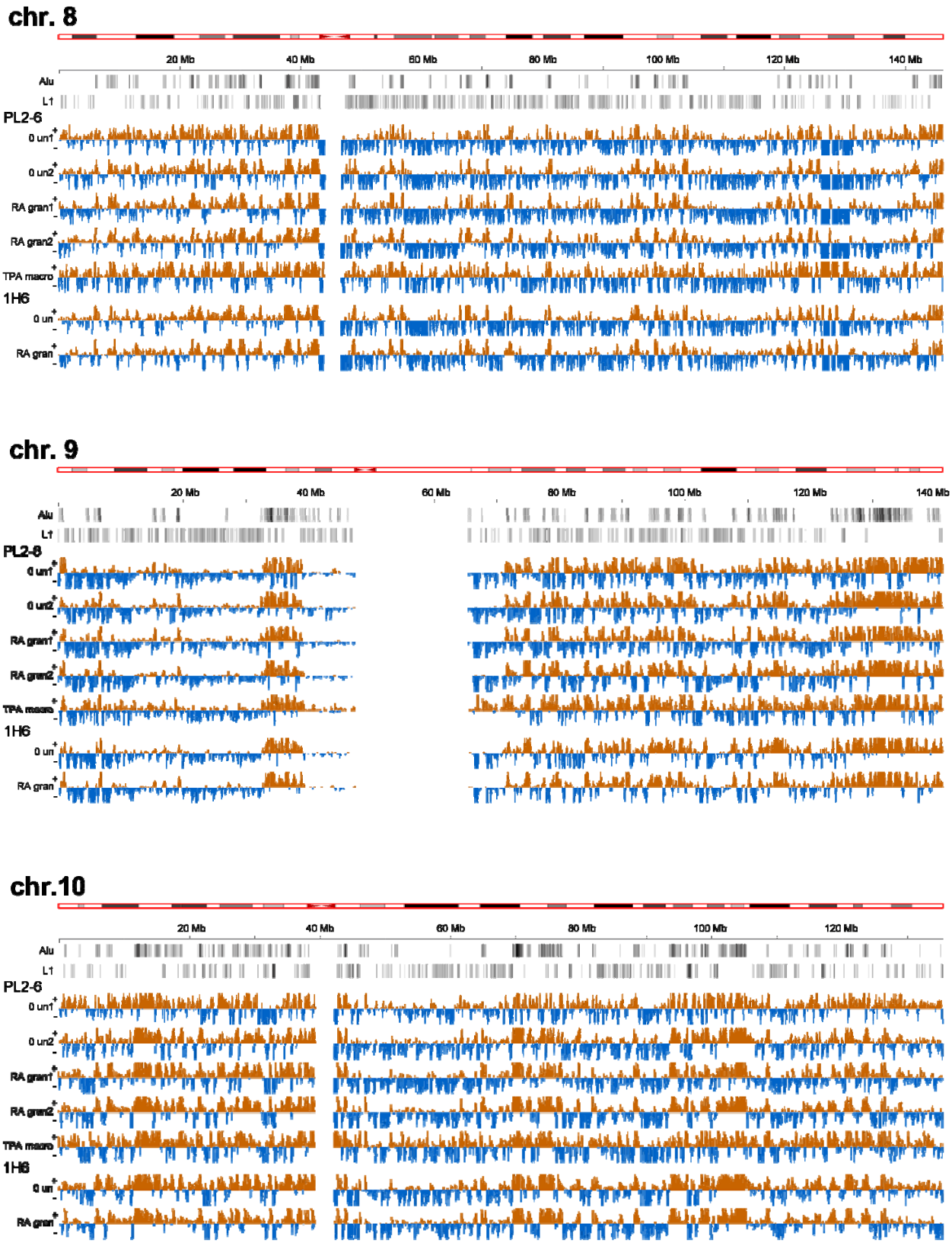
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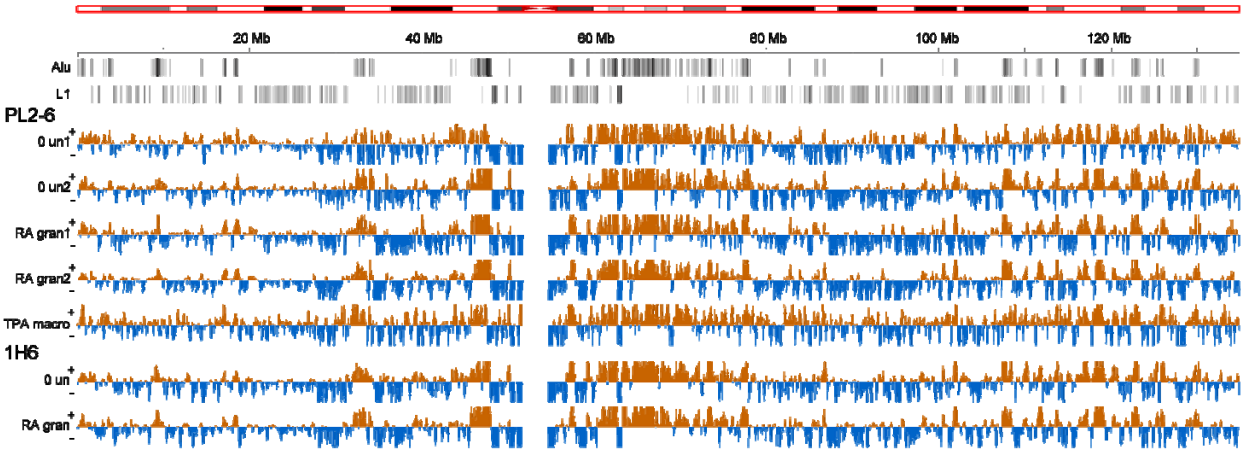

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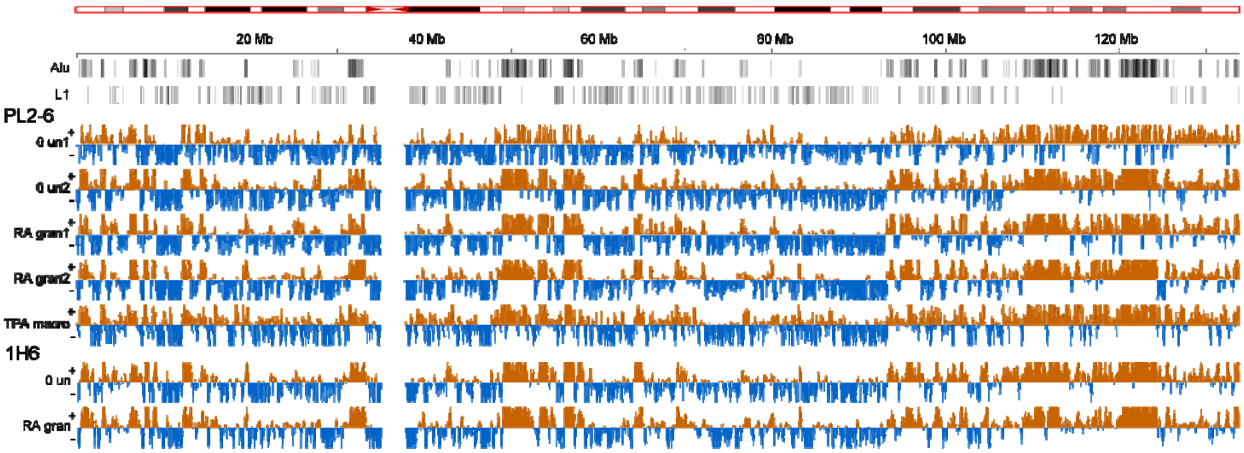

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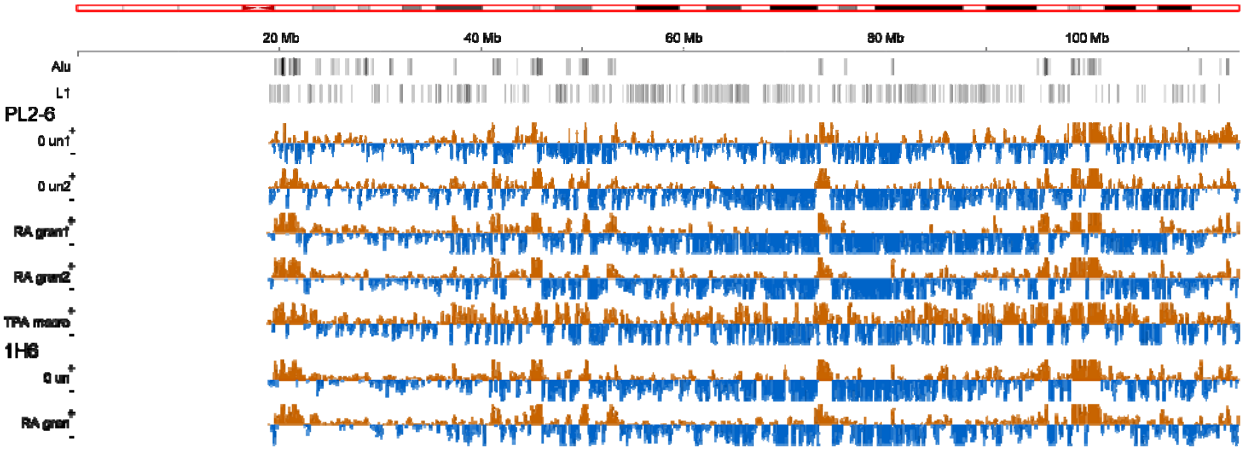

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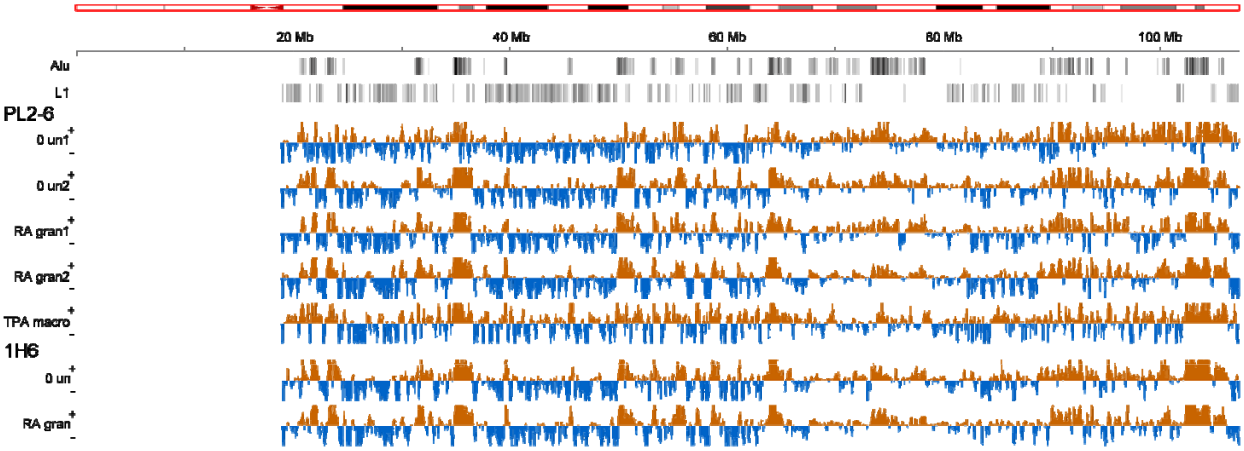

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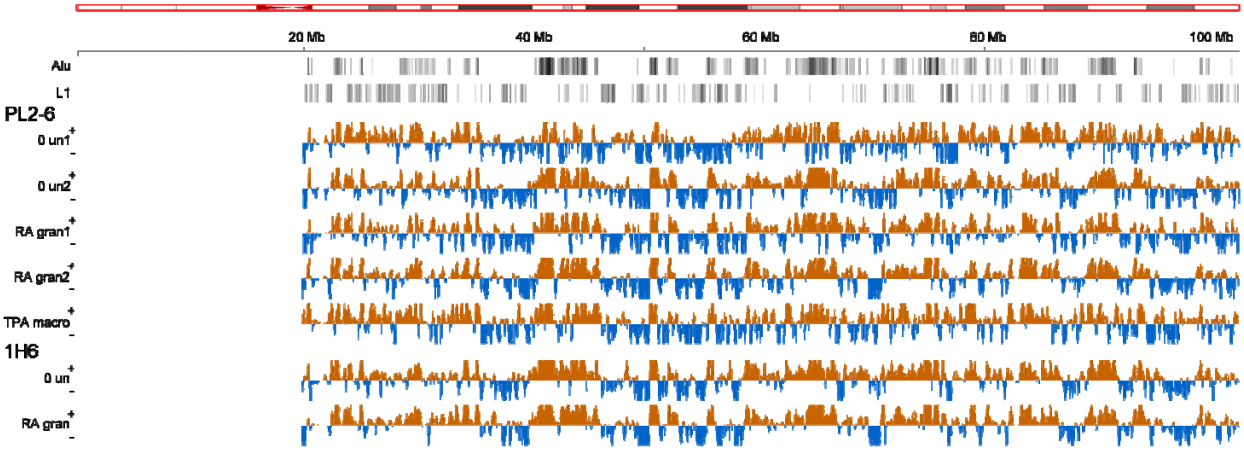

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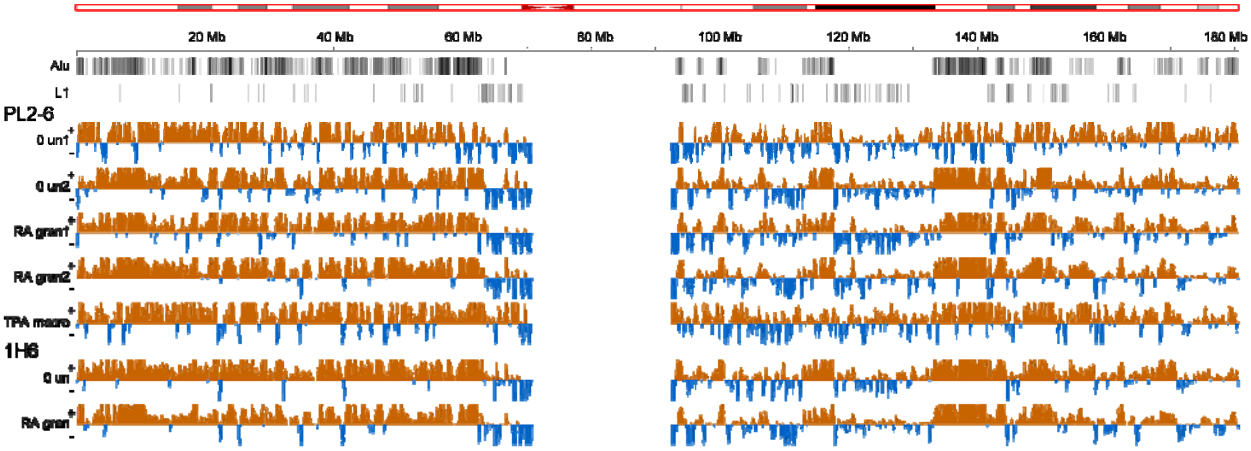

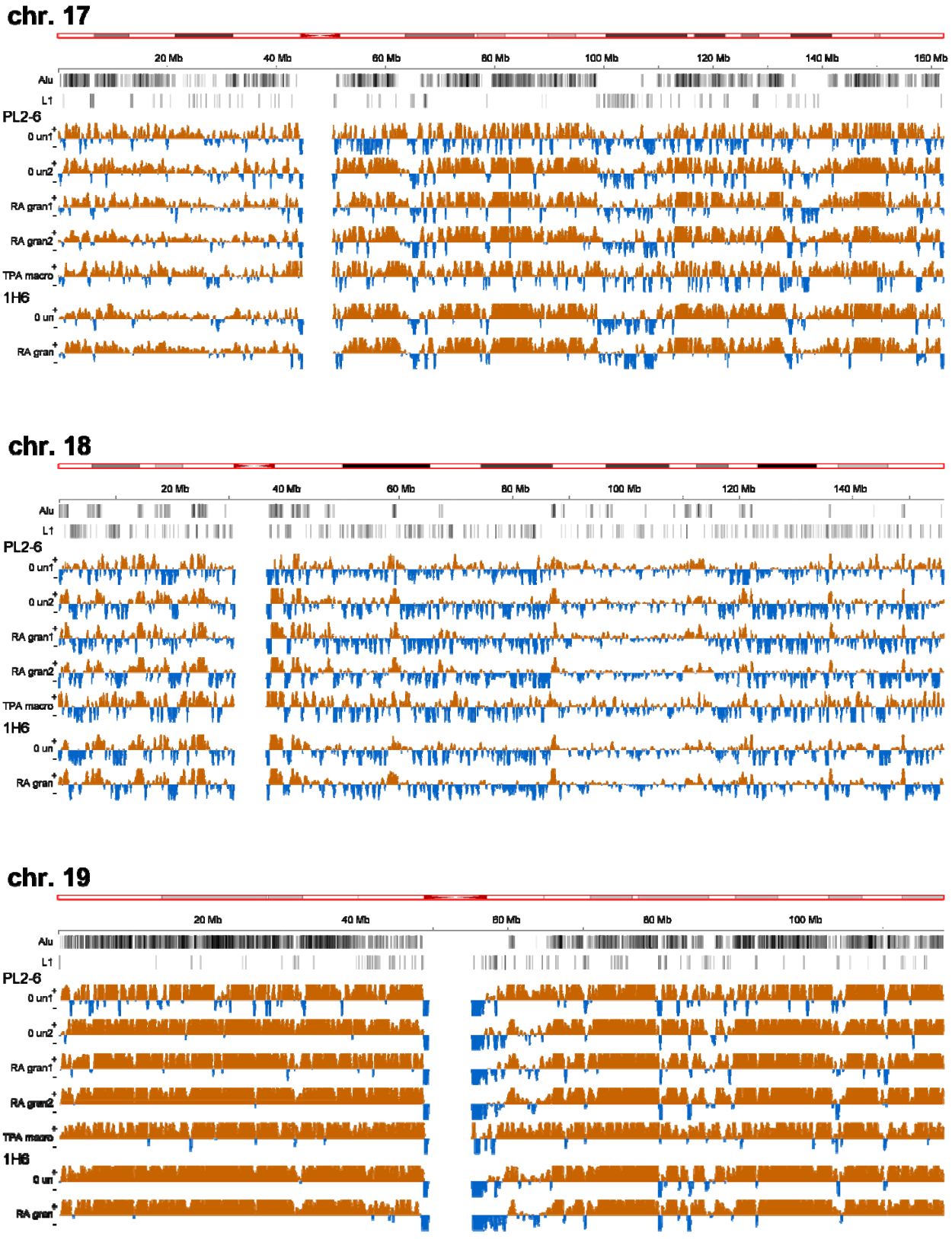
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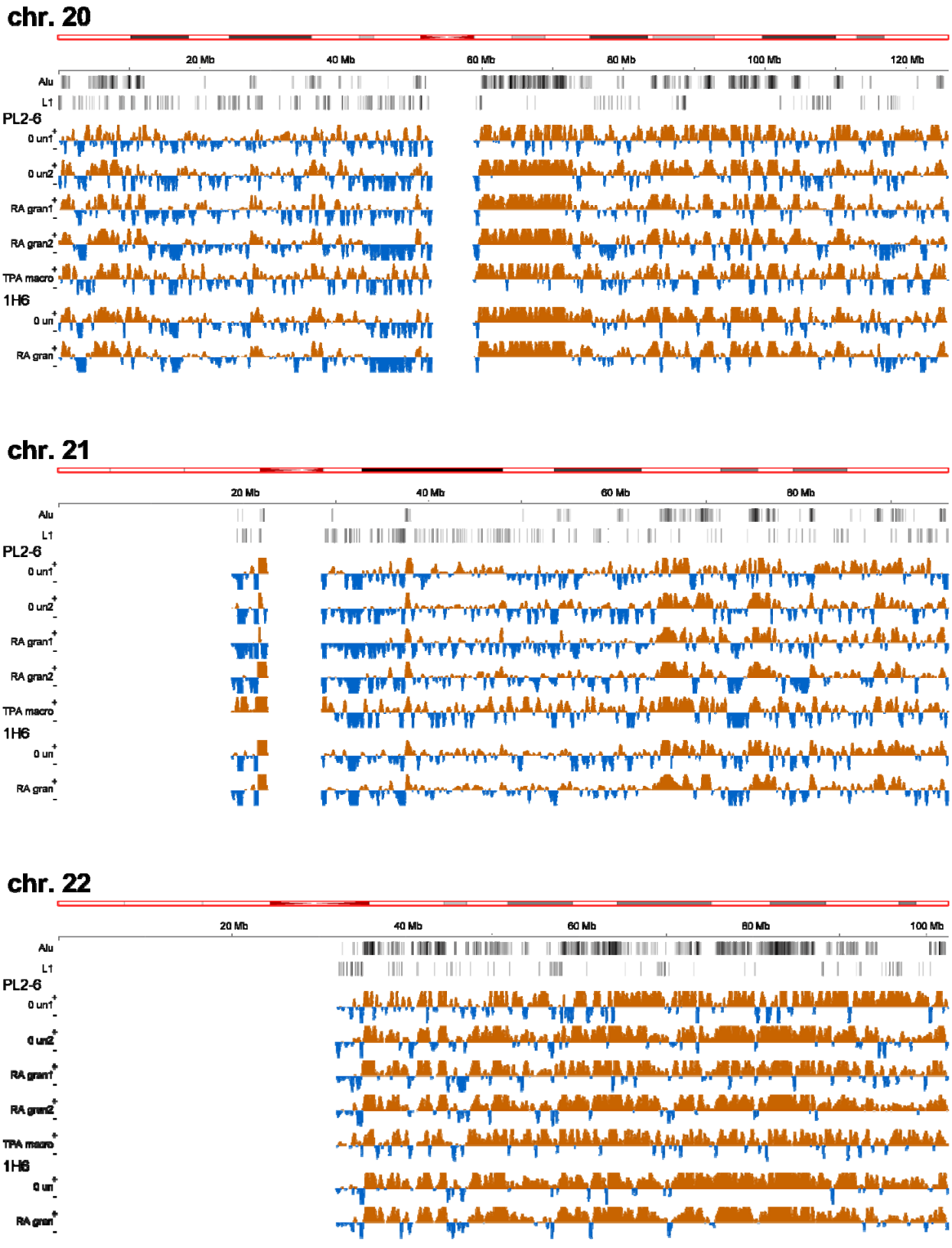
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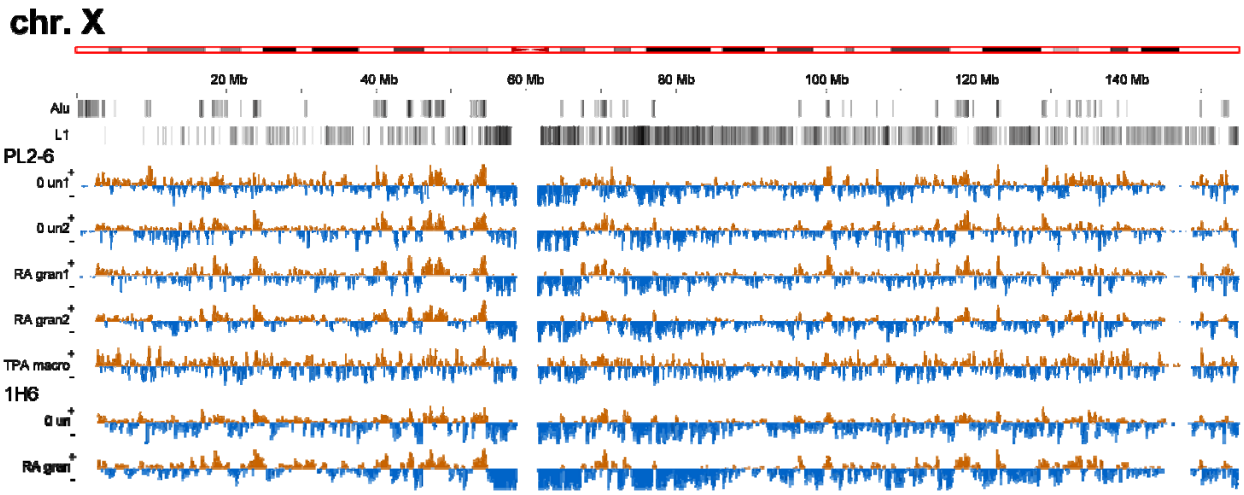

Fig. S2. Epichromatin maps for all the human chromosomes (except Y) over their entire length with comparisons to the distribution of Alu and L1 retrotransposons, illustrating: 1) a genome wide association of epichromatin enriched regions with Alu elements and no clear association with L1 elements; 2) the locations of "internal Alu" and the existence of "constitutive" (common) epichromatin peak regions in undifferentiated, granulocytic and macrophage cells. The Alu and L1 tracks depict the density of elements per 10 kb window, where darker regions have greater density than lighter regions. The read enrichment tracks for PL2-6 and 1H6 ChIP-Seq experiments illustrate the following: 1) orange (+) sections of the tracks show regions with increased epichromatin read densities compared to input control; 2) blue (-) sections of the tracks show regions enriched in input control compared to the epichromatin read densities. These "epi-maps" are displayed with window step size of 25 kb and a smoothing bandwidth of 50 kb.

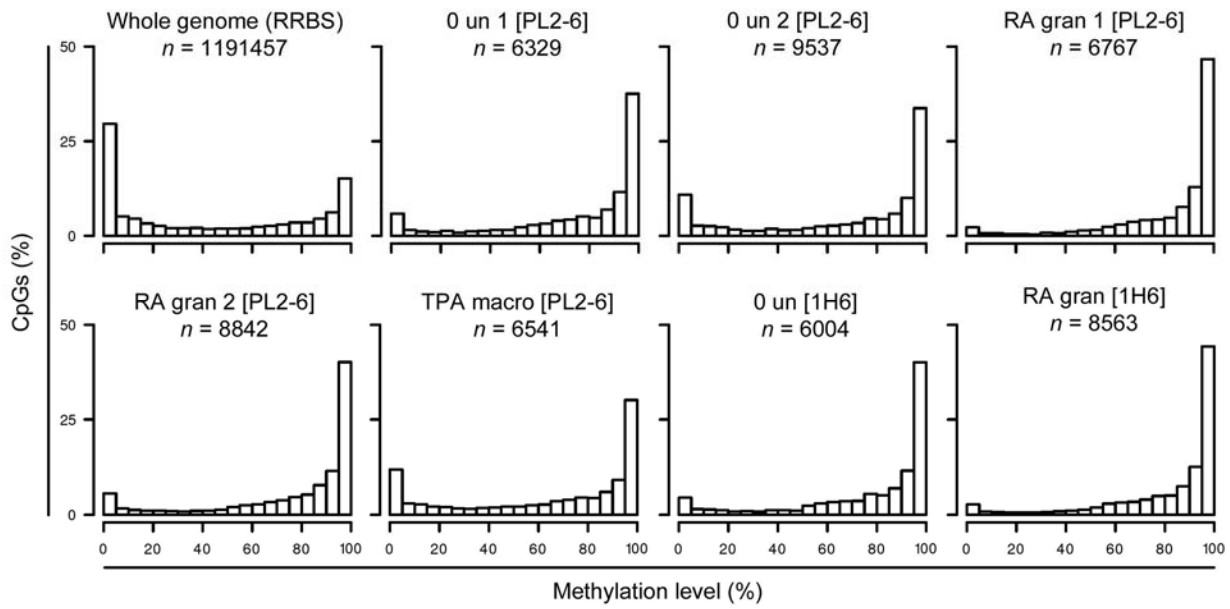

Fig. S3. CpG methylation profiles for individual epichromatin experiments. Histograms of the percentage of CpGs at different methylation levels in enriched epichromatin regions, showing an increased proportion of highly methylated CpGs in epichromatin compared to the background (whole genome). The whole genome methylation profile is for the second replicate of the ENCODE project HL-60 RRBS dataset[17] (which identified more CpGs than the first replicate). The individual experiments show overlapping of methylated CpG with enriched epichromatin peak predictions from the PL2-6 and 1H6 ChIP-Seq experiments. The epichromatin data are from undifferentiated HL-60/S4 (0 un 1 and 2), differentiated granulocytes (RA gran 1 and 2) and differentiated macrophages (TPA macro). Only positions with at least 10 reads covering a CpG were used. "*n*" denotes the number of CpGs covered by at least 10 reads that overlap with peak predictions.

Table S1. AluS and some AluY subfamilies are enriched in epichromatin regions.

Alu family	*N*	0 un1 PL2-6	0 un2 PL2-6	RA gran1 PL2-6	RA gran2 PL2-6	TPA macro PL2-6	0 un 1H6	RA gran 1H6
AluJ	**312138**	**0.53**	**0.55**	**0.55**	**0.55**	**0.52**	**0.54**	**0.47**
AluJb	144945	0.65	0.68	0.67	0.67	0.62	0.65	0.57
AluJo	72303	0.46	0.47	0.46	0.47	0.45	0.46	0.41
AluJr	77205	0.43	0.43	0.43	0.42	0.42	0.43	0.38
AluJr4	17685	0.35	0.36	0.39	0.38	0.36	0.37	0.33
AluS	**686962**	**1.21**	**1.19**	**1.21**	**1.19**	**1.18**	**1.20**	**1.09**
AluSc	34517	1.22	1.17	1.24	1.24	1.29	1.22	1.20
AluSc5	6870	1.16	1.17	1.18	1.21	1.25	1.20	1.10
AluSc8	21943	1.22	1.24	1.24	1.24	1.28	1.26	1.33
AluSg	41617	1.38	1.34	1.36	1.33	1.34	1.34	1.28
AluSg4	7496	1.25	1.29	1.27	1.28	1.32	1.23	1.19
AluSg7	8418	1.26	1.23	1.22	1.20	1.24	1.24	1.12
AluSp	50221	1.28	1.26	1.25	1.25	1.21	1.27	1.24
AluSq	21900	1.26	1.26	1.23	1.22	1.24	1.25	1.17
AluSq10	2462	1.08	1.13	1.08	1.11	0.94	0.98	1.19
AluSq2	55327	1.30	1.25	1.29	1.26	1.27	1.27	1.17
AluSq4	1431	1.24	1.23	1.20	1.23	1.21	1.25	1.07
AluSx	144437	1.20	1.22	1.22	1.20	1.13	1.20	1.12
AluSx1	110831	1.28	1.21	1.24	1.21	1.22	1.23	1.09
AluSx3	29614	1.19	1.18	1.19	1.20	1.24	1.22	1.09
AluSx4	5782	1.21	1.14	1.19	1.16	1.20	1.12	1.02
AluSz	98343	1.15	1.12	1.16	1.12	1.11	1.15	0.91
AluSz6	45753	0.91	0.89	0.92	0.89	0.88	0.92	0.67
AluY	**143178**	**0.99**	**1.05**	**0.98**	**1.07**	**1.18**	**1.04**	**1.73**
AluY	120617	1.06	1.13	1.05	1.15	1.26	1.12	1.83
AluYa5	3918	0.37	0.57	0.42	0.55	0.69	0.55	1.47
AluYa8	338	0.53	0.62	0.51	0.49	0.62	0.48	0.78
AluYb8	2854	0.34	0.38	0.33	0.40	0.54	0.37	1.00
AluYb9	327	0.22	0.45	0.36	0.49	0.58	0.66	1.14
AluYc	8519	0.61	0.65	0.62	0.67	0.76	0.62	0.94
AluYc3	570	0.90	0.95	0.94	1.04	0.99	0.91	1.68
AluYc5	45	0.61	0.38	0.48	0.38	1.16	0.62	0.90
AluYd8	225	0.51	0.38	0.37	0.62	0.62	0.54	1.03
AluYf4	1379	0.79	0.81	0.68	0.73	0.90	0.78	1.51
AluYf5	180	1.25	1.14	0.89	1.13	1.35	1.14	2.01
AluYg6	797	0.51	0.65	0.52	0.54	0.71	0.51	1.00
AluYh9	272	0.44	0.44	0.53	0.57	0.57	0.50	0.67
AluYk11	1044	0.58	0.63	0.65	0.70	0.39	0.52	0.72
AluYk12	224	0.32	0.59	0.32	0.51	0.58	0.50	0.97
AluYk4	1869	0.96	0.98	0.88	0.97	1.22	1.05	1.79

Table S1. AluS and some AluY subfamilies are enriched in epichromatin regions. Annotations of Alu were obtained from the UCSC genome browser[48] RepeatMasker track, downloaded 4th July 2013. "*N*", the number of Alu in a family (bold) or subfamily. At least 50% of the Alu element must overlap an epichromatin peak to be counted. Each column entry represents the relative enrichment (or depletion) of a specific Alu subfamily in the epichromatin fragments derived from one experiment (column heading). Relative changes: >1.00, enrichment; <1.00, depletion.

Table S2. The total number of Alu multimers in the human genome.

Alu multimer	0.5	1.0	1.5	2.0	2.5	3.0	3.5	4.0	4.5	All
Total/genome	104479	784768	24211	56473	5104	7519	1193	1432	993	986172

Table S3. The percentage (%) of Alu multimers in the human genome.

Alu multimer	0.5	1.0	1.5	2.0	2.5	3.0	3.5	4.0	4.5	All
Total/genome	10.6	79.6	2.5	5.7	0.5	0.8	0.1	0.1	0.1	100

Table S4. The percentage (%) of Alu multimers in epichromatin.

Alu multimer	0.5	1.0	1.5	2.0	2.5	3.0	3.5	4.0	4.5	All
O un1 PL2-6	3.1	84.6	4.8	13.7	1.3	2.1	0.4	0.4	0.3	97.7
O un2 PL2-6	3.1	82.1	5.4	16.2	1.8	3	0.5	0.7	0.5	96.6
RA gran1 PL2-6	2.9	83.3	4.9	15	1.6	2.6	0.4	0.6	0.4	97
RA gran2 PL2-6	2.9	83.7	5	15	1.6	2.6	0.4	0.6	0.4	97.4
TPA macr PL2-6	2.9	63	2.8	8.6	0.9	1.6	0.3	0.4	0.3	76.9
0 un 1H6	3.3	78.7	4.2	12.5	1.4	2.2	0.4	0.5	0.4	93
RA gran 1H6	2.3	85.5	5.3	16.3	1.8	3	0.5	0.6	0.5	98.8

Table S5. The "fold" enrichment of Alu multimers in epichromatin.

Alu multimer	0.5	1.0	1.5	2.0	2.5	3.0	3.5	4.0	4.5	All
O un1 PL2-6	0.3	1.1	2	2.4	2.5	2.8	3.3	2.8	3	1
O un2 PL2-6	0.3	1	2.2	2.8	3.5	3.9	4.1	4.8	5	1
RA gran1 PL2-6	0.3	1	2	2.6	3.1	3.4	3.3	4.1	4	1
RA gran2 PL2-6	0.3	1.1	2	2.6	3.1	3.4	3.3	4.1	4	1
TPA macro PL2-6	0.3	0.8	1.1	1.5	1.7	2.1	2.5	2.8	3	0.8
0 un 1H6	0.3	1	1.7	2.2	2.7	2.9	3.3	3.4	4	0.9
RA gran 1H6	0.2	1.1	2.2	2.8	3.5	3.9	4.1	4.1	5	1

Table S6. Chromatin Features.

	CTCF	H3K9me3	H3K27me3	DHS	Pol2	H3K4me3
Epichromatin	2.8	19.6	20.8	3.4	6.2	1.2
Random	5.7	23.1	28.0	4.5	8.0	3.5

Table S6. The proximity of epichromatin regions to various chromatin features, compared to the predicted proximity of random sequence DNA to these features. Shown are the percentage overlap (without extension) of epichromatin and random sequence DNA with insulator elements (CTCF), repressive histone modifications (H3K9me3, H3K27me3) and active “open” chromatin markers (DNase I hypersensitive sites [DHS], RNA polymerase 2 [Pol2] and active promoters [H3K4me3].