Table S5 Normalized abundance of polymorphic and fixed TEs in several sizes of genomic regions around "500 kB" clusters. Normalized abundance of TEs was calculated by dividing the abundance of each element with that found in random regions. Test regions corresponded to those containing cis-eQTLs (either clustered or single) or control clusters, each region being augmented by flanking regions of either 250, 500, 1000 kb.

		Polymorphic				Total	
		full LINEs	**LINE frag.**	**LTR-TEs**	**SINEs**	**LTR-TEs**	**SINEs**
Size of flanking regions	250 kB						
Mean numbers of elements /MB (fold diff vs random mean)	Cis-eqtl clusters (n=53)	0.66 ± 1.33	0.96 ± 1.59	2.24 ± 1.73	4.00 ± 2.84	1.57 ± 1.99	2.85 ± 2.8
	CTL clusters (n=59)	0.89 ±1.71	0.72 ± 0.9	1.08 ± 1.1	1.29 ± 1.48	1.36 ± 1.17	1.91 ± 1.43
	Single cis-eQTL regions (n=232)	0.69±1.26	0.97±1.19	1.69±1.29	1.76±1.6	1.43±1.14	1.64±1.6
	Random regions (n=500)	1 ± 1.9	1 ± 1.56	1 ± 1.28	1 ± 1.6	1 ± 1.19	1 ± 1.33
Anova P values		0.099	0.56	8.05E-16	3.05E-32	9.33E-06	1.16E-18
Post-hoc Tukey P values	Cis-eqtl clusters vs CTL	0.88	0.8	2.00E-05	<e-5	0.81	0.0078
	Cis-eqtl clusters vs single cis-eQTL regions	0.99	1	0.028	<e-5	0.88	<e-5
	Cis-eqtl clusters vs random	0.5	0.99	<e-5	<e-5	0.008	<e-5
	Control and single cis-eQTL regions	0.84	0.63	0.0071	0.22	0.98	0.62
	CTL vs random	0.96	0.48	0.97	0.59	0.14	0.00012
	Random vs single cis-eQTL regions	0.09	0.99	<e-5	<e-5	8.00E-05	<e-5

		Polymorphic				Total	
		full LINEs	**LINE frag.**	**LTR-TEs**	**SINEs**	**LTR-TEs**	**SINEs**
Size of flanking regions	500 kB						
Mean numbers of elements /MB (fold diff vs random mean)	Cis-eqtl clusters (n=53)	0.69 ± 1.38	1.08 ± 1.73	1.80 ± 1.32	3.41 ± 2.19	1.36 ± 1.16	2.39 ± 1.77
	CTL clusters (n=59)	1.10 ± 1.9	0.88 ± 1.05	1.08 ± 1.07	1.14 ± 1.16	1.32 ± 1.1	1.60 ± 1.28
	Single cis-eQTL regions (n=232)	0.8±1.2	1±1.11	1.56±1.1	1.58±1.25	1.36±1.06	1.49±1.41
	Random regions (n=500)	1 ± 1.67	1 ± 1.49	1 ± 1.15	1 ± 1.54	1 ± 1.03	1 ± 1.22
Anova P values		0.19	0.8	2.65E-11	5.09E-27	3.93E-05	2.80E-14
Post-hoc Tukey P values	Cis-eqtl clusters vs CTL	0.49	0.86	0.0046	<e-5	0.99	0.0092
	Cis-eqtl clusters vs single cis-eQTL regions	0.96	0.97	0.51	<e-5	0.99	5.00E-05
	Cis-eqtl clusters vs random	0.50	0.97	1.00E-05	<e-5	0.088	<e-5
	Control and single cis-eQTL regions	0.52	0.93	0.019	0.17	0.99	0.93
	CTL vs random	0.96	0.91	0.96	0.9	0.117	0.0054
	Random vs single cis-eQTL regions	0.35	0.99	<e-5	1.00E-05	9.00E-05	2.00E-05

		Polymorphic				Total	
		full LINEs	LINE frag.	LTR-TEs	SINEs	LTR-TEs	SINEs
Size of flanking regions	1 MB						
Mean numbers of elements /MB (fold diff vs random mean)	Cis-eqtl clusters (n=53)	0.76 ± 1.21	1.06 ± 1.34	1.58 ± 1.04	2.93 ± 1.87	1.18 ± 0.86	2.02 ± 1.45
	CTL clusters (n=59)	1.01 ± 1.43	0.94 ± 1.08	1.03 ± 0.91	1.06 ± 1.02	1.16 ± 0.85	1.31 ± 0.95
	Single cis-eQTL regions (n=232)						
	Random regions (n=500)	1 ± 1.4	1 ± 1.36	1 ± 0.99	1 ± 1.35	1 ± 0.84	1 ± 1.07
Anova P values		1.97E-05	0.42	8.00E-10	3.84E-26	3.43E-13	4.94E-19
Post-hoc Tukey P values	Cis-eqtl clusters vs CTL	0.78	0.97	0.16	1.00E-05	0.9	0.04
	Cis-eqtl clusters vs single cis-eQTL regions	0.47	0.7	0.9	0.75	0.012	0.99
	Cis-eqtl clusters vs random	0.65	0.99	0.022	<e-5	0.65	<e-5
	Control and single cis-eQTL regions	0.034	0.9	0.004	0	0.0047	0.0036
	CTL vs random	0.99	0.99	0.99	0.99	0.72	0.39
	Random vs single cis-eQTL regions	1.00E-05	0.39	<e-5	<e-5	<e-5	<e-5