Table S4 Normalized abundance of polymorphic and fixed TEs in several sizes of genomic regions around "250 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				**Fixed**	
		full LINEs	**LINE frag.**	**LTR-TEs**	**SINEs**	**LTR-TEs**	**SINEs**
Size of flanking regions	250 kB						
Normalized abundance of TEs / MB (mean ± SD)	Cis-eqtl clusters (n=42)	0.51 ± 1.39	0.77 ± 1.42	2.27 ± 1.75	4.78 ± 3.51	1.55 ± 2.17	2.85 ± 3.01
	CTL clusters (n=188)	0.46 ± 1.16	0.55 ± 1.01	1.28 ± 1.58	1.45 ± 2.07	1.53 ± 1.3	2.05 ± 1.62
	Single cis-eQTL regions (n=232)	0.59 ± 1.32	0.94 ± 1.33	1.8± 1.53	1.97±1.84	1.53±1.26	1.71±1.78
	Random regions (n=500)	1 ± 2.04	1 ± 1.72	1 ± 1.39	1 ± 1.72	1 ± 1.27	1 ± 1.42
Anova P values		0.00039	0.0059	1.22E-13	1.11E-33	3.15E-08	4.40E-20
Post-hoc Tukey P values	Cis-eqtl clusters vs CTL	0.99	0.83	0.00053	<e-5	0.99	0.02306
	Cis-eqtl clusters vs single cis-eQTL regions	0.99	0.90	0.22	<e-5	0.99	0.00023
	Cis-eqtl clusters vs random	0.28	0.77	<e-5	<e-5	0.048	<e-5
	Control and single cis-eQTL regions	0.8	0.042	0.0019	0.029	0.99	0.15
	CTL vs random	0.001	0.003	0.12	0.03	2.00E-05	<e-5
	Random vs single cis-eQTL regions	0.015	0.96	<e-5	<e-5	<e-5	<e-5

		Polymorphic				**Fixed**	
		full LINEs	**LINE frag.**	**LTR-TEs**	**SINEs**	**LTR-TEs**	**SINEs**
Size of flanking regions	500 kB						
Normalized abundance of TEs / MB (mean ± SD)	Cis-eqtl clusters (n=42)	0.54 ± 1.42	0.98 ± 1.69	1.88 ± 1.43	4.14 ± 2.84	1.39 ± 1.22	2.46 ± 1.86
	CTL clusters (n=188)	0.61 ± 1.16	0.65 ± 1.05	1.10 ± 1.25	1.27 ± 1.59	1.41 ± 1.10	1.79 ± 1.39
	Single cis-eQTL regions (n=232)	0.75±1.24	0.93±1.07	1.62±1.21	1.7±1.45	1.39±1.1	1.53±1.48
	Random regions (n=500)	1 ± 1.77	1 ± 1.51	1 ± 1.20	1 ± 1.6	1 ± 1.10	1 ± 1.29
Anova P values		0.0068	0.024	1.12E-11	2.22E-31	1.01E-06	6.32E-17
Post-hoc Tukey P values	Cis-eqtl clusters vs CTL	0.99	0.47	0.001	<e-5	0.99	0.024
	Cis-eqtl clusters vs single cis-eQTL regions	0.83	0.99	0.58	<e-5	1	0.00041
	Cis-eqtl clusters vs random	0.23	0.99	5.00E-05	<e-5	0.12352	<e-5
	Control and single cis-eQTL regions	0.75	0.13	8.00E-05	0.03	0.99	0.22
	CTL vs random	0.014	0.013	0.79	0.21	1.00E-04	<e-5
	Random vs single cis-eQTL regions	0.18	0.92	<e-5	<e-5	6.00E-05	1.00E-05

		Polymorphic				Fixed	
		full LINEs	**LINE frag.**	**LTR-TEs**	**SINEs**	**LTR-TEs**	**SINEs**
Size of flanking regions	1 MB						
Normalized abundance of TEs / MB (mean ± SD	Cis-eqtl clusters (n=42)	0.59 ± 1.25	0.93 ± 1.27	1.71 ± 1.17	3.47 ± 2.36	1.26 ± 0.93	2.12 ± 1.54
	CTL clusters (n=188)	0.76 ± 1.26	0.72 ± 1.02	1.06 ± 0.92	1.14 ± 1.17	1.33 ± 0.99	1.53 ± 1.1
	Single cis-eQTL regions (n=232)	0.48±1.71	0.81±1.91	1.76±2.28	2.69±3.3	1.7±1.58	2.02±2.02
	Random regions (n=500)	1 ± 1.47	1 ± 1.39	1 ± 1.03	1 ± 1.39	1 ± 0.87	1 ± 1.11
Anova P values		0.00013	0.1	4.95E-11	7.17E-31	1.75E-13	3.84E-20
Post-hoc Tukey P values	Cis-eqtl clusters vs CTL	0.91	0.82	0.037	<e-5	0.98	0.069
	Cis-eqtl clusters vs single cis-eQTL regions	0.96	0.96	0.99	0.1	0.083	0.97
	Cis-eqtl clusters vs random	0.32	0.99	0.011	<e-5	0.46	1.00E-05
	Control and single cis-eQTL regions	0.22	0.91	<e-5	<e-5	0.0034	0.0024
	CTL vs random	0.22	0.11	0.96	0.86	0.0034	6.00E-05
	Random vs single cis-eQTL regions	7.00E-05	0.37	<e-5	<e-5	<e-5	<e-5