Table S7 Comparisons for respective normalized abundance of binding sites for regulatory factors in several sizes of genomic regions around "250 kB" clusters. Normalized abundances of binding sites for regulatory factors was calculated in regions containing cis-eQTL cluster, control cluster, single cis-eQTL region or random regions, and augmented by flanking region of either 250, 500, 1000 kb.

		CTSF	h3ac	gata4	MEF2A	NKX2_5	SRF	TBX5	P300
Size of flanking regions	250 kB								
Normalized abundance of TFs / MB (mean ± SD)	Cis-eqtl clusters (n=42)	2.81 ± 0.94	4.20 ± 2.89	2.10 ± 1.65	2.67 ± 4.8	2.11 ± 1.65	4.02 ± 2.92	3.65 ± 2.52	2.43 ± 2.22
	CTL clusters (n=188)	1.76 ±0.69	1.85 ± 1.19	1.72 ± 1.29	1.47 ± 3.27	1.86 ± 1.62	1.87 ± 1.51	1.91 ± 1.67	1.64 ± 1.8
	Single cis-eQTL regions (n=232)	1.63±0.73	1.81±1.6	1.68±1.4	1.34±2.53	1.64±1.41	1.9±1.85	1.85±1.73	1.7±1.89
	Random regions (n=500)	1 ± 0.89	1 ± 1.57	1 ± 1.46	1 ± 4.16	1 ± 1.63	1 ± 1.58	1 ± 1.57	1 ± 1.61
Anova P values		4.4E-56	7.65E-37	6.20E-14	0.026	8.29E-13	5.89E-31	3.68E-27	1.48E-10
Post-hoc Tukey P values	Cis-eqtl clusters vs CTL	<e-5	<e-5	0.40684	0.22	0.77	<e-5	<e-5	0.039
	Cis-eqtl clusters vs single cis-eQTL regions	<e-5	<e-5	0.29376	0.140	0.27	<e-5	<e-5	0.059
	Cis-eqtl clusters vs random	<e-5	<e-5	1.00E-05	0.025	7.00E-05	<e-5	<e-5	<e-5
	Control and single cis-eQTL regions	0.41	0.99	0.98	0.98	0.49	0.99	0.97	0.98
	CTL vs random	<e-5	<e-5	<e-5	0.44	<e-5	<e-5	<e-5	0.00014
	Random vs single cis-eQTL regions	<e-5	<e-5	<e-5	0.65	<e-5	<e-5	<e-5	<e-5
	Cis-eqtl clusters vs CTL	<e-5	<e-5	0.4	0.22	0.77	<e-5	<e-5	0.039

		CTSF	h3ac	gata4	MEF2A	NKX2_5	SRF	TBX5	P300
Size of flanking regions	500 kB								
Normalized abundance of TFs / MB (mean ± SD)	Cis-eqtl clusters (n=42)	2.43 ± 0.78	3.60 ± 2.36	2.06 ± 1.5	2.67 ± 4.69	2.06 ± 1.69	3.47 ± 2.58	3.24 ± 2.17	2.03 ± 1.64
	CTL clusters (n=188)	1.57 ± 0.59	1.63 ± 1.14	1.60 ± 1.07	1.42 ± 3.16	1.79 ± 1.56	1.69 ± 1.33	1.72 ± 1.54	1.33 ± 1.27
	Single cis-eQTL regions (n=232)	1.5±0.67	1.61±1.33	1.59±1.18	1.26±2.11	1.58±1.32	1.7±1.65	1.66±1.56	1.4±1.3
	Random regions (n=500)	1 ± 0.84	1 ± 1.42	1 ± 1.26	1 ± 3.44	1 ± 1.44	1 ± 1.47	1 ± 1.48	1 ± 1.31
Anova P values		1.88E-41	1.06E-30	9.36E-15	0.0081	5.40E-13	6.99E-25	6.61E-22	1.34E-07
Post-hoc Tukey P values	Cis-eqtl clusters vs CTL	<e-5	<e-5	0.12	0.099	0.69	<e-5	<e-5	0.0094
	Cis-eqtl clusters vs single cis-eQTL regions	<e-5	<e-5	0.1	0.04	0.195	<e-5	<e-5	0.02
	Cis-eqtl clusters vs random	<e-5	<e-5	<e-5	0.0063	4.00E-05	<e-5	<e-5	1.00E-05
	Control and single cis-eQTL regions	0.76	0.99	0.99	0.95	0.45	0.99	0.979	0.94
	CTL vs random	<e-5	<e-5	<e-5	0.41	0<e-5	<e-5	<e-5	0.019
	Random vs single cis-eQTL regions	<e-5	<e-5	<e-5	0.73	<e-5	<e-5	<e-5	8.00E-04
	Cis-eqtl clusters vs CTL	<e-5	<e-5	0.12	0.099	0.690	<e-5	<e-5	0.009

		CTSF	**h3ac**	**gata4**	**MEF2A**	**NKX2_5**	**SRF**	**TBX5**	**P300**
Size of flanking regions	1 MB								
Normalized abundance of TFs / MB (mean ± SD)	Cis-eqtl clusters (n=42)	2.15 ± 0.7	3.16 ± 1.98	1.87 ± 1.18	2.63 ± 5.5	1.82 ± 1.43	2.99 ± 2.2	2.90 ± 1.94	1.69 ± 1.11
	CTL clusters (n=188)	1.45 ± 0.56	1.48 ± 0.97	1.45 ± 0.87	1.38 ± 3.2	1.59 ± 1.33	1.51 ± 1.19	1.53 ± 1.35	1.23 ± 0.96
	Single cis-eQTL regions (n=232)	1.4±0.6	1.44±1.12	1.44±0.96	1.16±1.71	1.45±1.13	1.49±1.35	1.47±1.34	1.29±0.95
	Random regions (n=500)	1 ± 0.76	1 ± 1.27	1 ± 1.01	1 ± 2.92	1 ± 1.17	1 ± 1.32	1 ± 1.34	1 ± 1.08
Anova P values		4.82E-33	4.59E-27	7.69E-14	0.004	6.77E-11	1.98E-20	2.12E-18	5.31E-06
Post-hoc Tukey P values	Cis-eqtl clusters vs CTL	<e-5	<e-5	0.05	0.05	0.65	<e-5	<e-5	0.038
	Cis-eqtl clusters vs single cis-eQTL regions	<e-5	<e-5	0.04	0.013	0.25	<e-5	<e-5	0.087
	Cis-eqtl clusters vs random	<e-5	<e-5	<e-5	0.0028	0.00014	<e-5	<e-5	0.00017
	Control and single cis-eQTL regions	0.82	0.97	0.99	0.86	0.65	0.99	0.97	0.92
	CTL vs random	<e-5	3.00E-05	<e-5	0.42	<e-5	6.00E-05	4.00E-05	0.05
	Random vs single cis-eQTL regions	<e-5	5.00E-05	<e-5	0.9	2.00E-05	4.00E-05	9.00E-05	0.002
	Cis-eqtl clusters vs CTL	<e-5	<e-5	0.059	0.056	0.65	<e-5	<e-5	0.038