

Supplementary Table 6. Partitioned heritability analysis using functional annotation categories

Category	Prop_SNPs	Prop_h2	Prop_h2_std_error	Enrichment	Enrichment_std_error	Enrichment_p	Enrichment_fdr	Coefficient	Coefficient_std_error	Coefficient_z-score
MAFbin5L2_0	0.098	-0.282	0.356	-2.867	3.626	0.023	0.797	-4.94E-08	2.98E-08	-1.657
H3K27ac_HnizL2_0	0.389	1.252	0.734	3.217	1.886	0.030	0.797	6.21E-08	4.43E-08	1.400
WeakEnhancer_HoffmanL2_0	0.021	0.943	0.855	45.088	40.888	0.031	0.797	6.45E-07	3.10E-07	2.083
non_synonymousL2_0	0.003	-0.264	0.256	-97.369	94.241	0.037	0.797	-1.12E-06	8.24E-07	-1.353
SuperEnhancer_HnizL2_0	0.167	0.603	0.389	3.606	2.325	0.062	0.797	1.19E-08	3.80E-08	0.313
Human_Promoter_Villar.flanking.500L2_0	0.004	0.354	0.353	98.716	98.495	0.081	0.797	1.31E-06	8.93E-07	1.470
Ancient_Sequence_Age_Human_PromoterL2_0	0.004	-0.263	0.276	-63.162	66.290	0.081	0.797	-1.40E-06	6.40E-07	-2.194
MAFbin6L2_0	0.100	0.409	0.320	4.105	3.208	0.102	0.797	5.09E-08	3.39E-08	1.502
TSS_Hoffman.flanking.500L2_0	0.017	-0.530	0.605	-32.032	36.589	0.104	0.797	-5.91E-07	3.34E-07	-1.770
Intron_UCSCL2_0	0.387	0.889	0.503	2.295	1.298	0.105	0.797	1.26E-08	1.46E-08	0.861
H3K4me1_Trynka.flanking.500L2_0	0.182	1.666	1.489	9.144	8.170	0.106	0.797	1.14E-07	8.66E-08	1.311
Promoter_UCSCL2_0	0.046	0.701	0.700	15.138	15.101	0.122	0.797	2.91E-07	1.46E-07	1.990
Human_Promoter_VillarL2_0	0.015	-0.286	0.336	-18.771	22.066	0.130	0.797	4.97E-08	2.95E-07	0.169
Ancient_Sequence_Age_Human_Enhancer.flanking.500L2_0	0.009	0.359	0.363	39.761	40.251	0.140	0.797	5.58E-07	4.15E-07	1.345
Conserved_LindbladTohL2_0	0.025	-0.644	0.711	-26.090	28.832	0.151	0.797	-8.04E-07	4.79E-07	-1.677
Human_Promoter_Villar_ExtAC.flanking.500L2_0	0.001	0.105	0.108	182.017	187.237	0.154	0.797	1.56E-06	1.88E-06	0.827
BivFlnk.flanking.500L2_0	0.018	0.489	0.452	27.765	25.633	0.155	0.797	3.94E-07	2.87E-07	1.371
MAFbin2L2_0	0.100	-0.131	0.267	-1.314	2.677	0.171	0.797	-2.47E-08	2.93E-08	-0.843
MAFbin4L2_0	0.101	0.354	0.270	3.517	2.683	0.172	0.797	4.35E-08	3.20E-08	1.359
Nucleotide_Diversity_10kblL2_0	4.609	6.094	1.726	1.322	0.375	0.182	0.797	8.22E-09	4.34E-09	1.894
Transcr_Hoffman.flanking.500L2_0	0.417	1.603	1.340	3.847	3.215	0.189	0.797	1.05E-07	5.32E-08	1.975
MAFbin10L2_0	0.098	0.341	0.297	3.466	3.015	0.189	0.797	4.24E-08	3.09E-08	1.373
Conserved_LindbladToh.flanking.500L2_0	0.306	1.204	0.891	3.939	2.917	0.191	0.797	2.84E-08	5.87E-08	0.485
H3K4me1_TrynkaL2_0	0.423	-0.556	1.146	-1.312	2.706	0.214	0.828	-1.18E-07	7.97E-08	-1.484
Conserved_Primate_phastCons46way.flanking.500L2_0	0.157	1.004	0.980	6.414	6.262	0.219	0.828	7.97E-08	9.95E-08	0.801
BivFlnkL2_0	0.014	-0.304	0.357	-22.437	26.317	0.242	0.828	-2.80E-07	3.04E-07	-0.922
MAFbin9L2_0	0.101	-0.123	0.248	-1.212	2.449	0.248	0.828	-2.66E-08	3.07E-08	-0.866
CTCF_HoffmanL2_0	0.024	-0.486	0.608	-20.421	25.544	0.249	0.828	-2.66E-07	2.81E-07	-0.949
UTR_3_UCSCL2_0	0.011	0.236	0.290	21.102	26.009	0.255	0.828	4.31E-07	3.59E-07	1.201
Enhancer_AnderssonL2_0	0.004	-0.219	0.268	-50.825	62.197	0.275	0.828	-8.27E-07	6.77E-07	-1.221
WeakEnhancer_Hoffman.flanking.500L2_0	0.068	-0.532	0.765	-7.849	11.275	0.275	0.828	-1.17E-07	1.37E-07	-0.854
Coding_UCSC.flanking.500L2_0	0.049	0.399	0.428	8.074	8.662	0.276	0.828	1.25E-07	1.18E-07	1.065
H3K4me3_TrynkaL2_0	0.133	0.690	0.730	5.191	5.492	0.342	0.928	1.65E-07	1.02E-07	1.611
Intron_UCSC.flanking.500L2_0	0.009	-0.242	0.337	-25.858	36.042	0.351	0.928	-2.56E-07	4.59E-07	-0.559
Promoter_UCSC.flanking.500L2_0	0.011	-0.330	0.493	-31.201	46.597	0.352	0.928	-4.83E-07	5.07E-07	-0.953
Enhancer_Hoffman.flanking.500L2_0	0.048	0.527	0.622	11.016	12.994	0.357	0.928	1.32E-07	1.75E-07	0.755
Human_Enhancer_Villar_Species_Enhancer_CountL2_0	0.066	0.735	0.897	11.096	13.531	0.371	0.928	2.89E-08	4.05E-08	0.713
Backgrd_Selection_StatL2_0	0.178	0.125	0.048	0.701	0.271	0.382	0.928	-3.18E-08	2.33E-08	-1.365
Conserved_Primate_phastCons46wayL2_0	0.019	-0.332	0.495	-17.206	25.665	0.383	0.928	-1.72E-07	3.81E-07	-0.452
TFBS_ENCODEL2_0	0.131	-0.724	1.232	-5.526	9.407	0.401	0.928	-1.67E-07	1.50E-07	-1.108
H3K27ac_PG2L2_0	0.269	0.834	0.815	3.107	3.035	0.405	0.928	3.64E-08	6.57E-08	0.554
Human_Enhancer_Villar.flanking.500L2_0	0.010	0.227	0.316	23.124	32.283	0.417	0.928	1.96E-07	4.00E-07	0.490
DHS_Trynka.flanking.500L2_0	0.330	-0.636	1.568	-1.927	4.752	0.422	0.928	-2.51E-08	9.63E-08	-0.261
H3K9ac_peaks_TrynkaL2_0	0.038	0.510	0.726	13.355	19.016	0.425	0.928	3.12E-07	3.32E-07	0.939
TSS_HoffmanL2_0	0.018	0.264	0.394	14.800	22.110	0.442	0.935	4.06E-07	3.15E-07	1.287
H3K9ac_Trynka.flanking.500L2_0	0.104	0.597	0.754	5.719	7.221	0.459	0.935	3.27E-08	1.09E-07	0.300
Recomb_Rate_10kblL2_0	1.552	3.639	2.250	2.344	1.450	0.488	0.935	3.92E-09	7.75E-09	0.506
MAF_Adj_ASMCL2_0	0.000	-0.393	0.701	1.68E+13	-2.99E+13	0.496	0.935	-1.39E-08	1.28E-08	-1.087
BLUEPRINT_H3K4me1QTL_MaxCPPL2_0	0.013	-0.078	0.149	-5.807	11.126	0.499	0.935	-2.75E-07	4.35E-07	-0.775
PromoterFlanking_HoffmanL2_0	0.008	-0.160	0.288	-19.320	34.746	0.499	0.935	-3.47E-07	3.43E-07	-0.802
GERP_RSsup4L2_0	0.008	0.208	0.344	25.521	42.236	0.506	0.935	6.95E-07	6.03E-07	1.153
DHS_TrynkaL2_0	0.166	0.853	1.249	5.145	7.535	0.524	0.935	2.40E-07	2.11E-07	1.137
UTR_5_UCSC.flanking.500L2_0	0.021	-0.129	0.276	-6.013	12.897	0.539	0.935	-2.34E-07	1.85E-07	-1.263
MAFbin8L2_0	0.100	0.216	0.218	2.154	2.170	0.543	0.935	2.30E-08	3.26E-08	0.705
MAF_Adj_LLD_AFRIL2_0	0.003	-0.383	0.399	-137.016	142.559	0.543	0.935	2.99E-09	8.63E-09	0.346
CpG_Content_50kblL2_0	0.010	0.011	0.002	1.135	0.179	0.545	0.935	-1.10E-06	1.86E-06	-0.592
Enhancer_HoffmanL2_0	0.042	-0.228	0.494	-5.430	11.780	0.561	0.936	7.25E-10	1.78E-07	0.004
FetalDHS_Trynka.flanking.500L2_0	0.200	-0.370	1.224	-1.855	6.136	0.575	0.936	-4.94E-08	9.98E-08	-0.495
Coding_UCSCL2_0	0.014	-0.141	0.310	-9.890	21.766	0.582	0.936	-1.25E-07	4.81E-07	-0.261
Conserved_Mammal_phastCons46way.flanking.500L2_0	0.318	0.740	0.778	2.327	2.447	0.592	0.936	1.25E-07	1.33E-07	0.940
H3K4me1_peaks_TrynkaL2_0	0.169	0.662	1.096	3.921	6.491	0.626	0.936	8.79E-08	1.53E-07	0.576
MAFbin7L2_0	0.100	0.013	0.184	0.129	1.843	0.631	0.936	-5.01E-09	2.78E-08	-0.180
Ancient_Sequence_Age_Human_Promoter.flanking.500L2_0	0.005	-0.079	0.193	-14.928	36.353	0.635	0.936	-8.47E-07	6.18E-07	-1.371
GERP_NSL2_0	1.745	2.608	1.868	1.494	1.071	0.636	0.936	1.46E-08	1.89E-08	0.773
PromoterFlanking_Hoffman.flanking.500L2_0	0.025	0.200	0.392	8.053	15.759	0.642	0.936	4.07E-08	2.43E-07	0.167
H3K9ac_TrynkaL2_0	0.125	-0.122	0.627	-0.976	5.002	0.673	0.936	-1.74E-07	1.28E-07	-1.363
GTEx_eQTL_MaxCPPL2_0	0.010	0.065	0.136	6.246	13.133	0.675	0.936	1.25E-07	3.25E-07	0.383
TFBS_ENCODE.flanking.500L2_0	0.210	0.677	1.213	3.221	5.774	0.691	0.936	1.48E-08	9.82E-08	0.151
Repressed_Hoffman.flanking.500L2_0	0.258	-0.101	0.948	-0.390	3.668	0.692	0.936	3.19E-09	6.12E-08	0.052
BLUEPRINT_H3K27acQTL_MaxCPPL2_0	0.017	0.080	0.169	4.852	10.186	0.704	0.936	1.47E-07	3.32E-07	0.443
Conserved_Vertebrate_phastCons46wayL2_0	0.029	-0.145	0.503	-4.923	17.094	0.709	0.936	-6.12E-08	3.26E-07	-1.188
Human_Enhancer_VillarL2_0	0.033	0.127	0.265	3.828	7.975	0.711	0.936	-1.57E-07	1.55E-07	-1.015
Conserved_Mammal_phastCons46wayL2_0	0.021	-0.141	0.458	-6.590	21.376	0.716	0.936	5.18E-07	6.23E-07	0.831
Conserved_Vertebrate_phastCons46way.flanking.500L2_0	0.378	0.087	0.889	0.231	2.355	0.723	0.936	-1.84E-07	1.16E-07	-1.583
CTCF_Hoffman.flanking.500L2_0	0.047	0.223	0.534	4.742	11.370	0.731	0.936	4.35E-08	1.66E-07	0.262
Enhancer_Andersson.flanking.500L2_0	0.015	0.102	0.304	6.952	20.642	0.772	0.975	5.74E-08	3.06E-07	0.187
Repressed_HoffmanL2_0	0.460	0.686	0.856	1.492	1.861	0.786	0.980	-1.33E-11	5.00E-08	-2.7E-04
DGF_ENCODE.flanking.500L2_0	0.403	0.072	1.367	0.179	3.394	0.800	0.980	-1.75E-08	7.45E-08	-0.235
FetalDHS_TrynkaL2_0	0.084	0.295	0.916	3.527	10.946	0.809	0.980	2.26E-08	2.54E-07	0.089
Human_Promoter_Villar_ExtACL2_0	0.002	0.022	0.091	8.951	36.602	0.824	0.980	6.66E-07	5.50E-07	1.211
MAF_Adj_Predicted_Allele_AgeL2_0	0.000	-0.167	0.728	-4.93E+04	2.15E+05	0.828	0.980	-4.18E-09	1.38E-08	-0.303
H3K27ac_PG2C.flanking.500L2_0	0.067	0.209	0.717	3.138	10.758	0.843	0.980	2.80E-08	1.67E-07	0.168
DHS_peaks_TrynkaL2_0	0.110	-0.084	1.070	-0.760	9.731	0.854	0.980	-2.37E-07	2.79E-07	-0.848
UTR_3_UCSC.flanking.500L2_0	0.015	0.050	0.205	3.267	13.418	0.864	0.980	-1.89E-08	2.13E-07	-0.089
Transcr_HoffmanL2_0	0.345	0.248	0.703	0.719	2.037	0.890	0.980	4.29E-08	4.11E-08	1.044
H3K4me3_peaks_TrynkaL2_0	0.041	-0.029	0.521	-0.713	12.606	0.893	0.980	-1.48E-07	2.67E-07	-0.553
UTR_5_UCSCL2_0	0.005	0.031	0.191	5.671	34.995	0.893	0.980	1.57E-07	5.21E-07	0.301
DGF_ENCODEL2_0	0.135	0.285	1.185	2.102	8.758	0.898	0.980	2.32E-08	1.64E-07	0.141
BLUEPRINT_DNA_methylation_MaxCPPL2_0	0.032	0.048	0.209	1.520	6.598	0.937	0.987	-3.61E-09	2.04E-07	-0.018
H3K4me3_Trynka.flanking.500L2_0	0.122	0.177	0.745	1.448	6.102	0.941	0.987	2.37E-08	9.95E-08	0.238
MAFbin1L2_0	0.102	0.112	0.181	1.094	1.769	0.957	0.987	1.09E-08	3.21E-08	0.340
synonymousL2_0	0.003	0.012	0.177	0.910	56.654	0.959	0.987	6.29E-07	9.79E-07	0.642
MAFbin3L2_0	0.100	0.091	0.180	3.904	1.804	0.960	0.987	5.15E-09	3.00E-08	0.172
SuperEnhancer_Hniz.flanking.500L2_0	0.003	0.010	0.170	3.260	53.534	0.966	0.987	-2.25E-08	7.77E-07	-0.029
Ancient_Sequence_Age_Human_EnhancerL2_0	0.005	0.001	0.187							