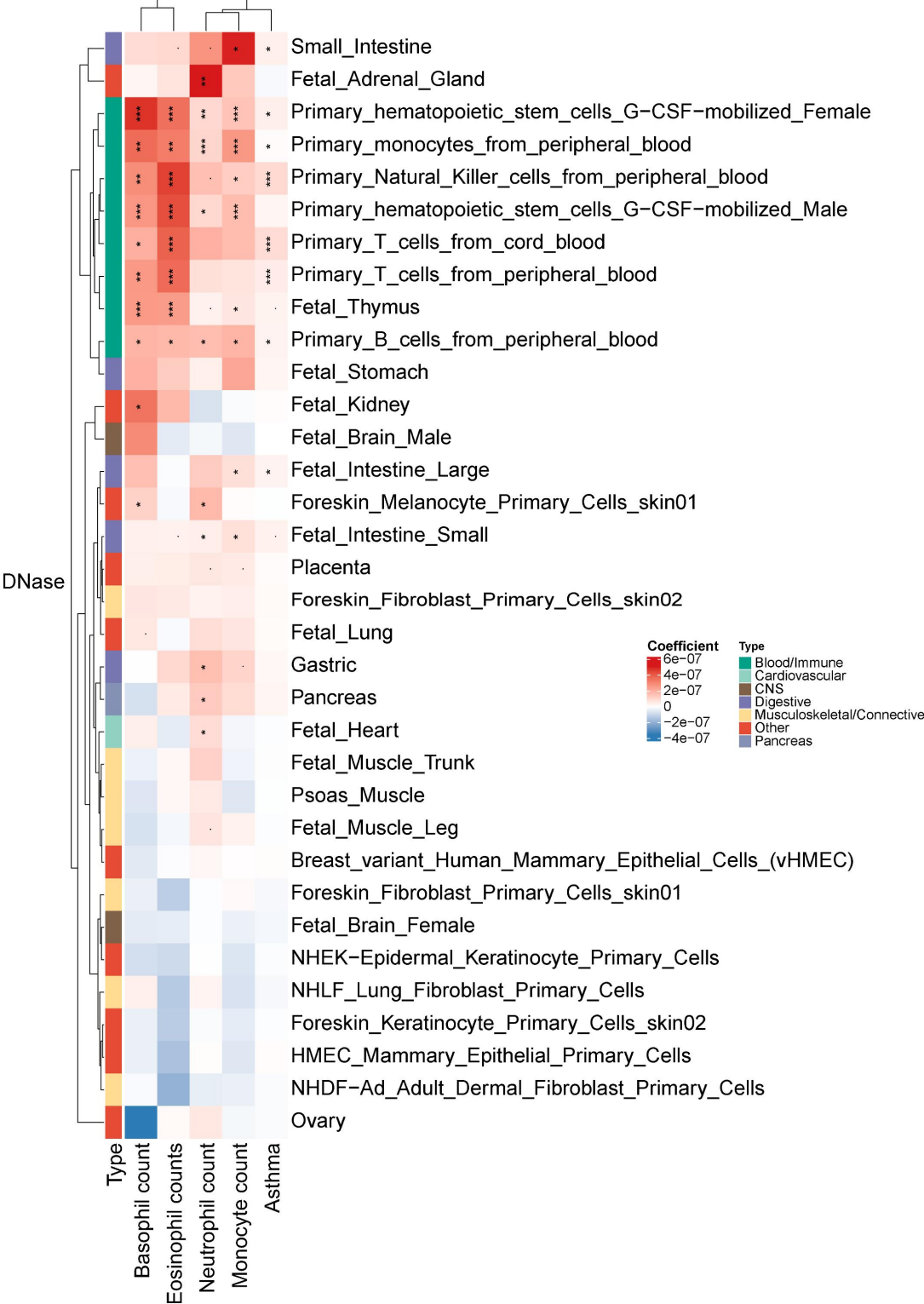


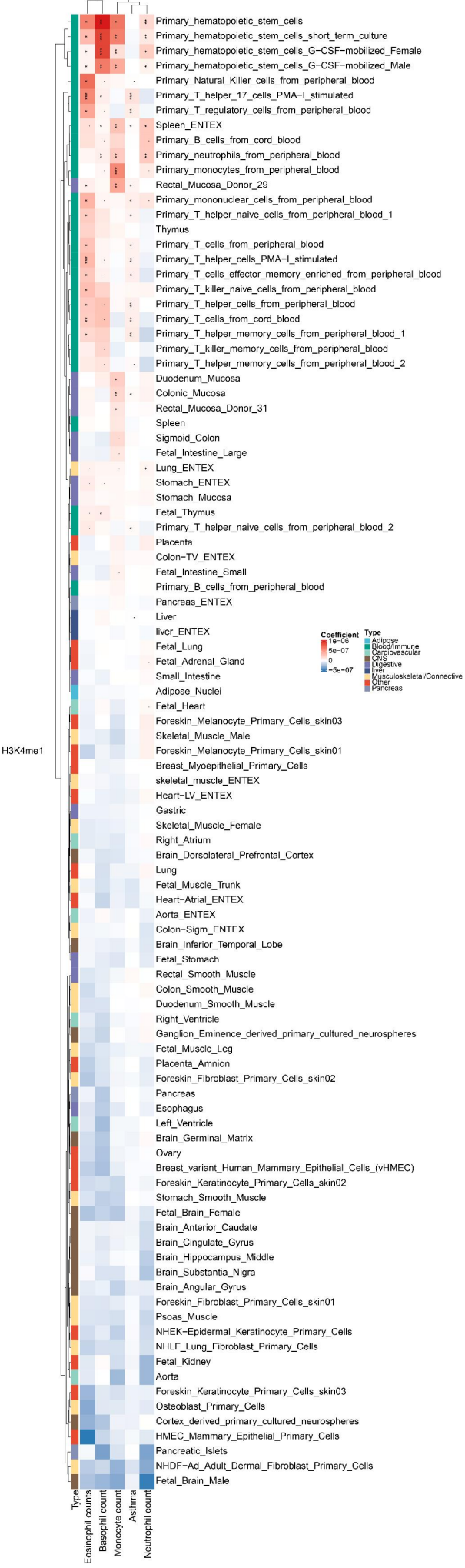
Online Supplement

Supplementary Figure S1. Heat maps showing patterns of cell-type-specific enrichments of SNP-heritability for genetically associated traits across 88 cell types- or tissues-specific annotations. Each checkered rectangle reflects the z-score, scaled by traits. Red indicates enrichment, blue indicates depletion. Deeper color represents stronger magnitude of effects. Asterisks represent statistical significance. The category of cell-types is color coded to the left. A) DNase (DNase I hypersensitive sites), B) H3K27ac, C) H3K36me3, D) H3K4me1, E) H3K4me3, and F) H3K9ac. Sample sizes: Asthma (GBMI): 341,204 (18,549 cases, 322,655 controls); Basophil count: 81,042; Eosinophil count: 86,890; Lymphocyte count: 89,266; Monocyte count: 88,929; Neutrophil count: 78,744; Leukocyte count: 151,807; Platelet count: 145,648; Erythrocyte count: 150,708. All GWAS were conducted in East Asian populations.

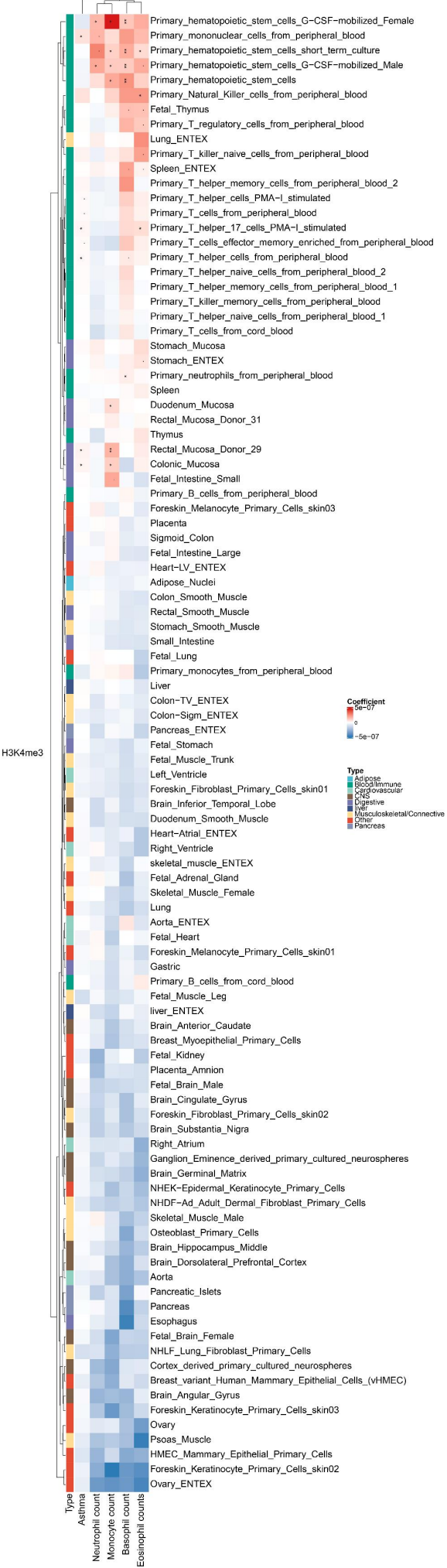
A) DNase



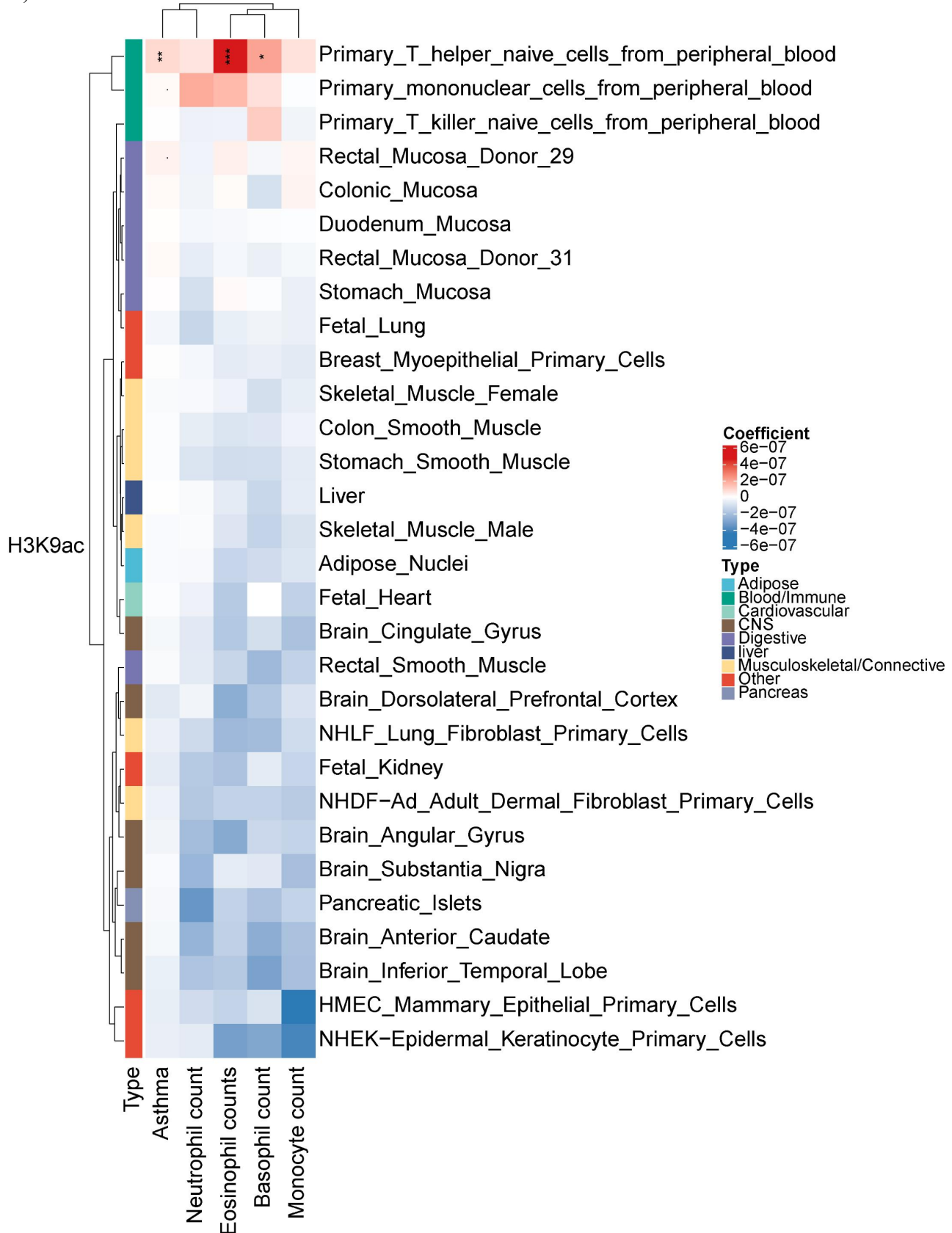
B) H3K4me1



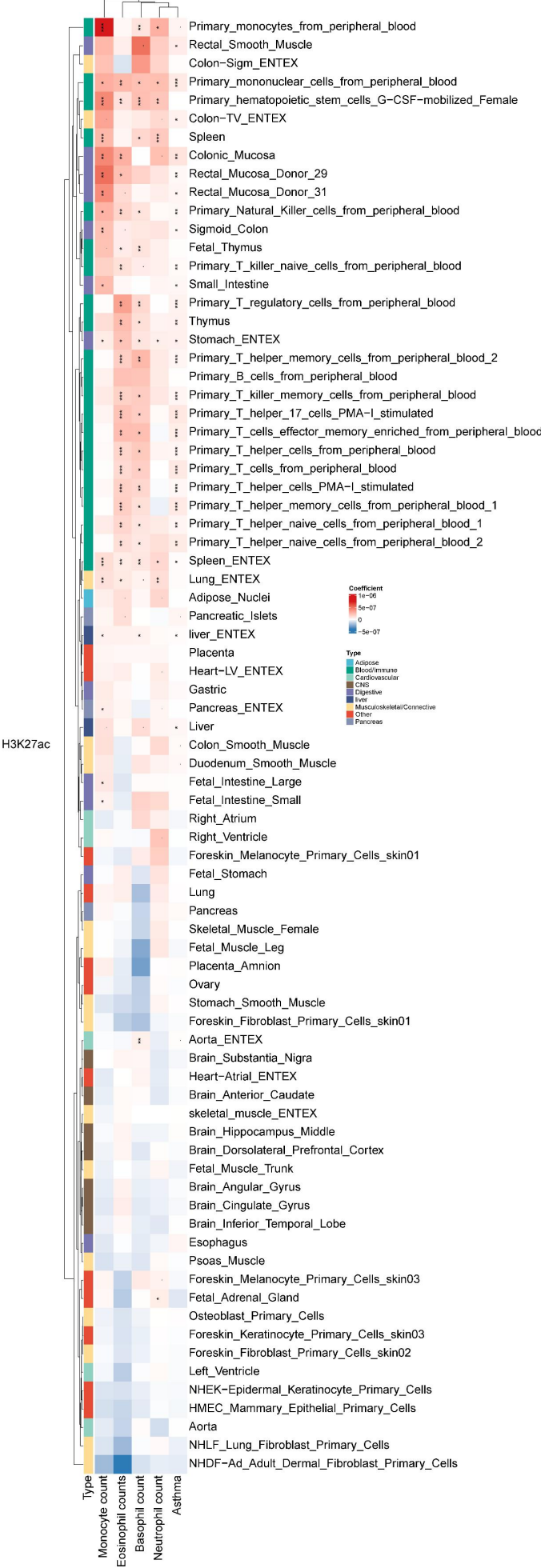
C) H3K4me3



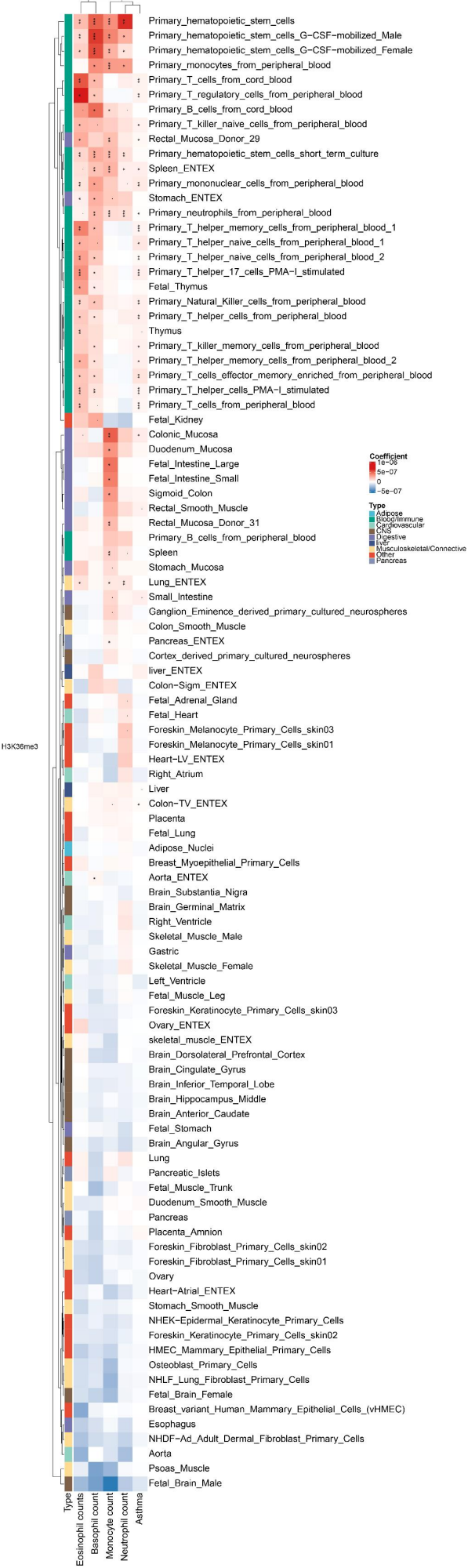
D) H3K9ac



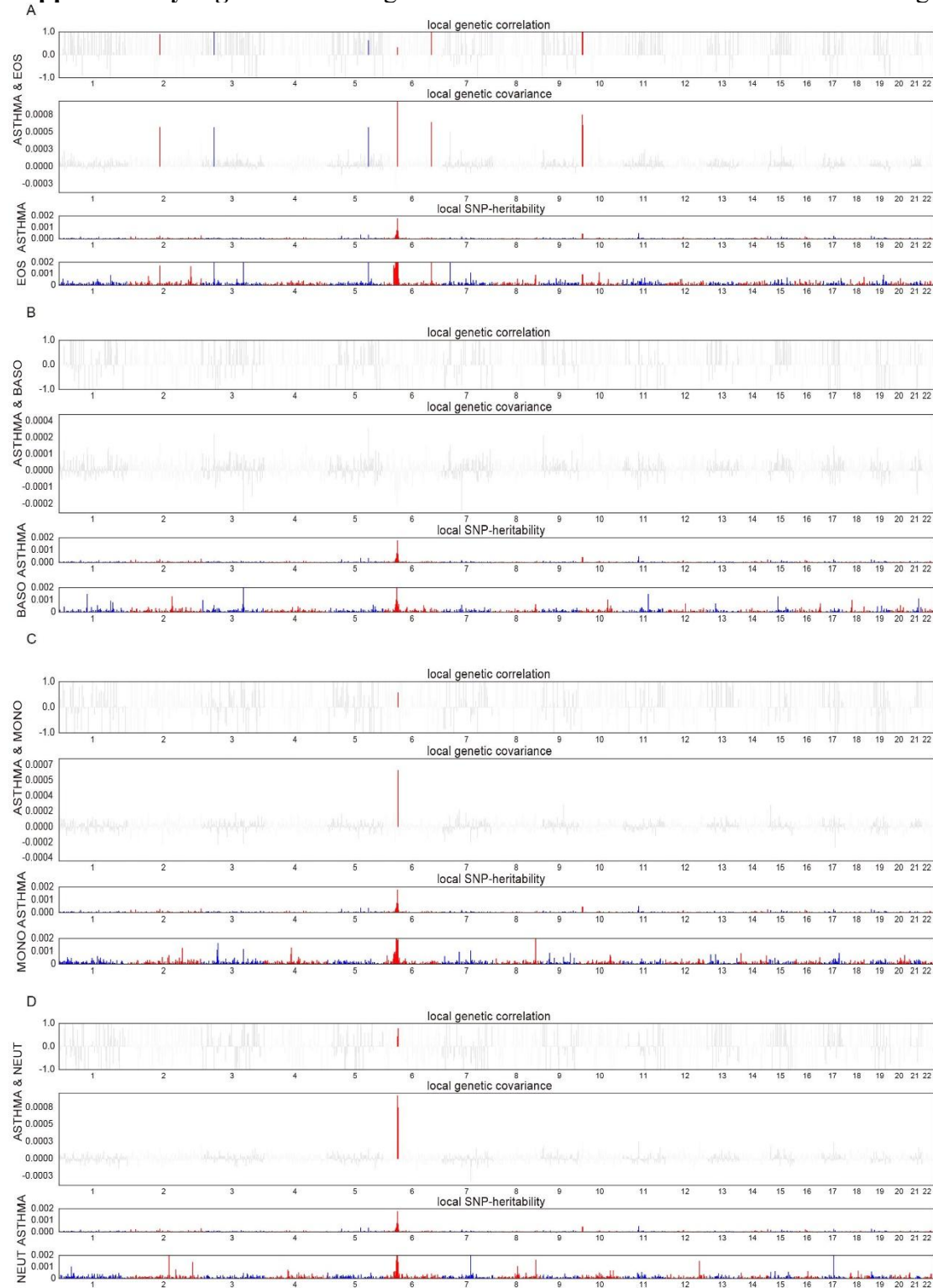
E) H3K27ac



F) H3K36me3

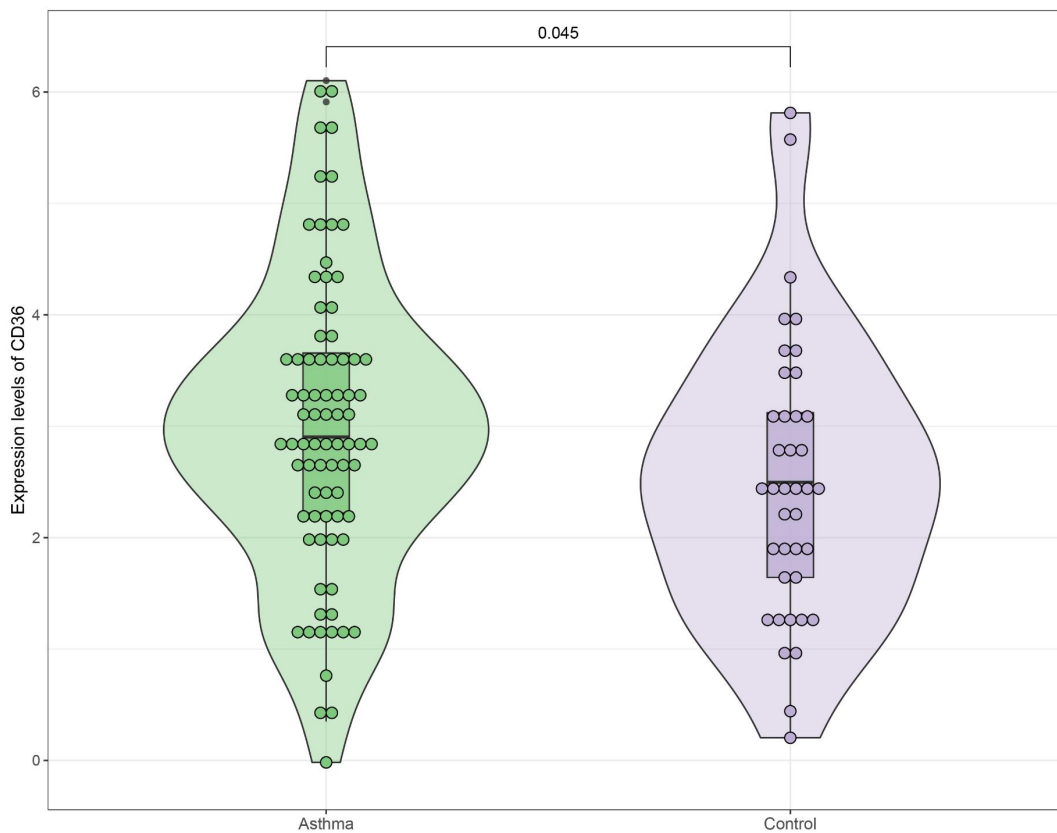


Supplementary Figure S2. Local genetic correlation between asthma and hematological traits.



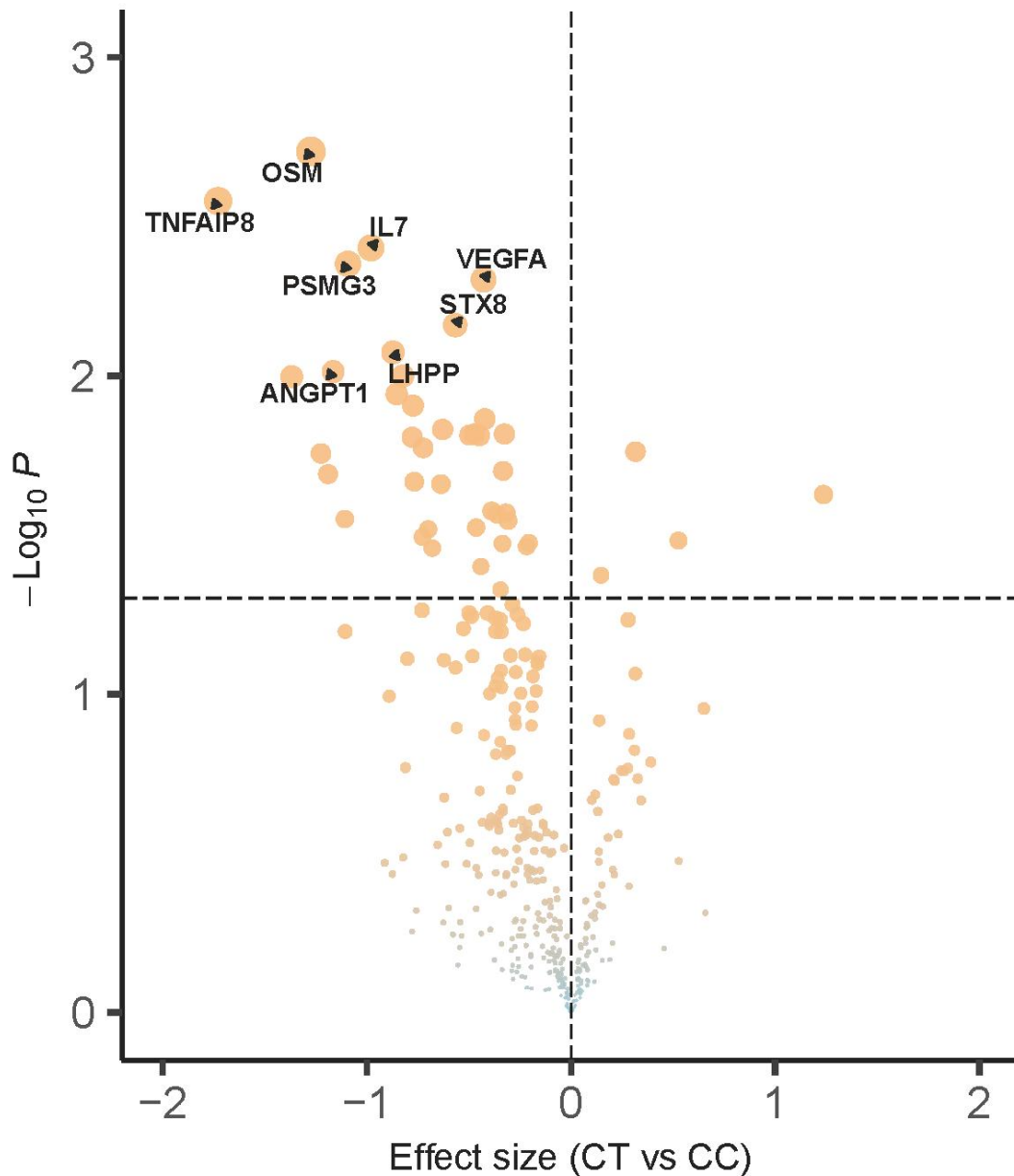
(A) Manhattan plot showing the estimates of local genetic correlation, genetic covariance, and SNP heritability between asthma and eosinophils. (B) Manhattan plot showing the estimates of local genetic correlation, genetic covariance, and SNP heritability between asthma and basophils. (C) Manhattan plot showing the estimates of local genetic correlation, genetic covariance, and SNP heritability between asthma and monocytes. (D) Manhattan plot showing the estimates of local genetic correlation, genetic covariance, and SNP heritability between asthma and neutrophils. Red bars represent loci showing significant local genetic correlation after multiple testing adjustment ($p < 0.05/1,703$). Sample sizes: Asthma (GBMI): 341,204 (18,549 cases, 322,655 controls); Basophil count: 81,042; Eosinophil count: 86,890; Lymphocyte count: 89,266; Monocyte count: 88,929; Neutrophil count: 78,744; Leukocyte count: 151,807; Platelet count: 145,648; Erythrocyte count: 150,708. All GWAS were conducted in East Asian populations.

Supplementary Figure S3. Differential expression analysis of the *CD36* gene in asthmatic patients compared to healthy controls.



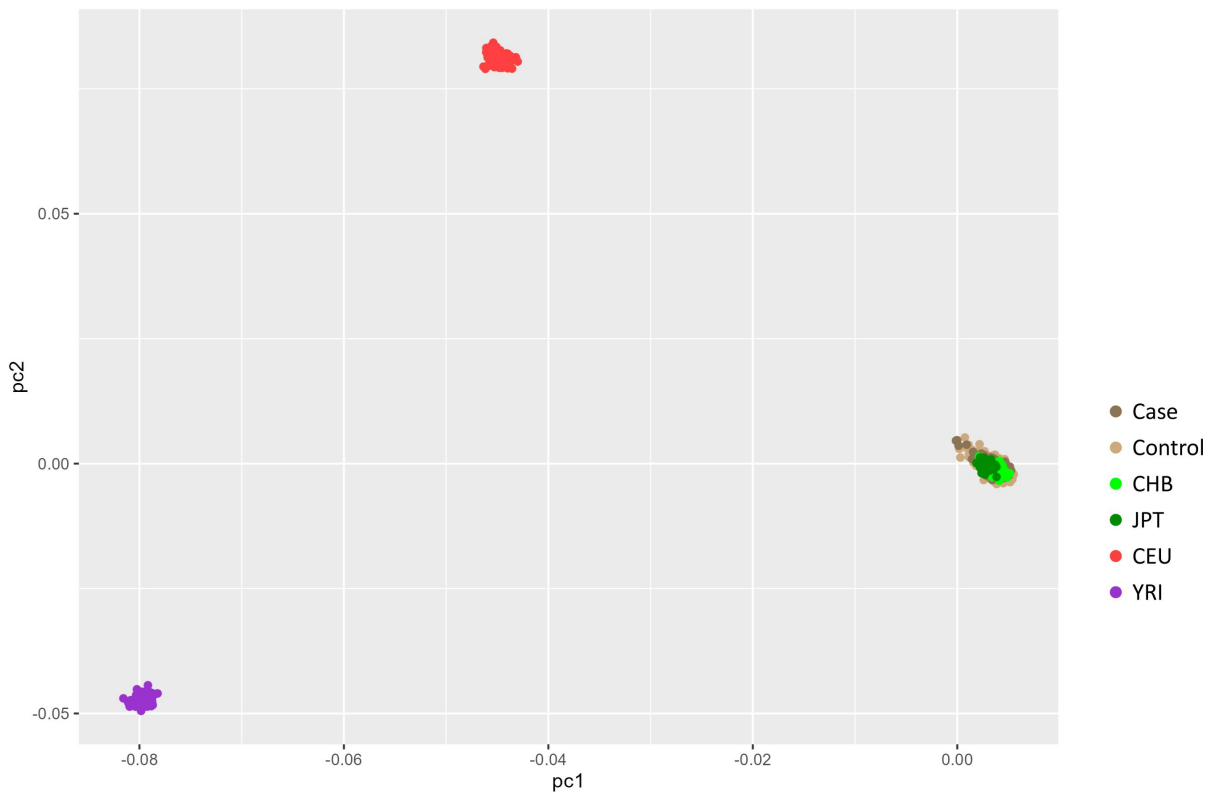
Violin plots show the distribution and density of *CD36* expression levels, with overlaid boxplots summarizing key statistics. The y-axis indicates *CD36* expression levels, while the x-axis distinguishes between asthma patients and healthy controls. Wilcoxon test revealed a significant increase in *CD36* expression among asthmatic patients. The analysis was based on 79 asthmatic patients and 39 controls. Statistical significance was assessed using a two-sided Wilcoxon rank-sum test without correction for multiple comparisons.

Supplementary Figure S4. Volcano plot showing differentially expressed proteins between CT (*CD36* missense variant rs75326924 carrier) and CC (non-carrier) groups.



The x-axis represents the effect size (log fold-change) of protein expression between CT and CC, while the y-axis represents the statistical significance ($-\log_{10}$ P-value) of the observed changes. Proteins with significant changes are highlighted in orange, with names labeled for those with the most notable differences. The dashed horizontal line indicates the threshold for statistical significance ($P < 0.05$), and the vertical dashed lines mark the threshold for effect size. Plasma proteins were measured in the CAS cohort 1K multi-omics subgroup ($n=1,056$) using the Olink Explore 384 Inflammation panel. Significant differentially expressed proteins include OSM, TNFAIP8, IL7, VEGFA, STX8, PSMG3, ANGPT1, and LHPP. The analysis was based on 1,100 asthmatic patients and 2,506 controls of East Asian ancestry. Statistical significance was assessed using a two-sided Wilcoxon rank-sum test without correction for multiple comparisons.

Supplementary Figure S5. Principal component analysis of Chinese study samples and reference populations.



This PCA plot shows the genetic clustering of Chinese study participants (asthma cases and controls) relative to reference populations from the 1000 Genomes Project. The study cohort, consisting of asthma cases (brown) and controls (light brown), clusters closely with Han Chinese in Beijing (CHB, light green) and Japanese in Tokyo (JPT, dark green), confirming their East Asian ancestry. In contrast, reference populations from European (CEU, Utah residents of Northern and Western European ancestry, red) and African (YRI, Yoruba in Ibadan, purple) backgrounds form distinct, separate clusters.

Supplementary Table S1. Details on the characteristics of GWAS datasets of Asthma and hematological traits in this study.

Phenotype	Data source	Phenotype Definitions	Total sample size	N _{case}	N _{control}	SNP Count	Source ID or Source link
Asthma	GWAS Catalog	Defined using curated past medical history and text-mined EMR. Cases had physician-confirmed asthma, and controls excluded asthma or related diseases based on PheCode 495.	175,948	13,015	162,933	12,045,483	GCST90018575
Asthma	GBMI	Asthma cases were defined using PheCode mappings of ICD-9/ICD-10 codes (e.g., UKBB, BBJ, UCLA, BioMe) or self-reported physician-diagnosed asthma (e.g., TWB, CKB, QSKIN). Original data were contributed by multiple biobanks, including BBJ, CKB, TWB, UKBB, UCLA, and others. Controls excluded participants with asthma or related PheCodes.	341,204	18,549	322,655	12,219,296	https://gbmi-sumstats.s3.amazonaws.com/
Basophil count	GWAS Catalog	Calculated as the product of total white blood cell count ($10^9/L$) and the percentage of basophils, providing the absolute count.	81,042			16,286,709	GCST90002293
Eosinophil counts	GWAS Catalog	Determined by multiplying the total white blood cell count ($10^9/L$) by the percentage of eosinophils, representing the absolute count. The same exclusion criteria as listed above were applied.	86,890			16,279,099	GCST90002299
Lymphocyte count	GWAS Catalog	Measured as the total white blood cell count ($10^9/L$) multiplied by the percentage of lymphocytes, indicating the absolute count. The same exclusion criteria as listed above were applied.	89,266			16,289,068	GCST90002317
Monocyte count	GWAS Catalog	Obtained by multiplying the total white blood cell count ($10^9/L$) with the percentage of monocytes, reflecting the absolute count. The same exclusion criteria as listed above were applied.	88,929			16,289,044	GCST90002341
Neutrophil count	GWAS Catalog	Derived from the product of the total white blood cell count ($10^9/L$) and the percentage of neutrophils, representing the absolute count. The same exclusion criteria as listed above were applied.	78,744			16,289,068	GCST90002352
Platelet count	GWAS Catalog	Measured directly as the number of platelets per unit volume of blood ($10^9/L$), indicating platelet abundance. The same exclusion criteria as listed above were applied.	145,648			16,710,488	GCST90002358
Erythrocyte count	GWAS Catalog	Measured as the number of red blood cells per unit volume of blood ($10^{12}/L$). The same exclusion criteria as listed above were applied.	150,708			16,709,798	GCST90002364
Leukocyte count	GWAS Catalog	Measured as the aggregate number of white blood cells per unit volume of blood ($10^9/L$). The same exclusion criteria as listed above were applied.	151,807			16,710,636	GCST90002375

Note: For all blood cell count data, samples were excluded if they lacked study agreement, had hematologic malignancies, an eGFR < 15 or were on hemodialysis, were under EPO treatment, had cirrhosis, were phenotypic outliers, were related to other samples with PI_HAT > 0.125, or were identified as East Asian (EAS) outliers in PCA plots.

Supplementary Table S2. SNP based heritability estimated by LDSC.

Phenotype	h²	SE
Asthma	0.023	0.003
Basophils	0.093	0.021
Eosinophils	0.114	0.015
Neutrophils	0.115	0.014
Lymphocytes	0.088	0.009
Monocytes	0.092	0.012
Erythrocytes	0.126	0.013
Platelets	0.166	0.023

h² (heritability): the proportion of phenotypic variation explained by genetic variants

Supplementary Table S3. Genetic correlations between Asthma and hematological traits.

Phenotype1	Phenotype2	r_g	SE	<i>P</i>
Asthma	Platelet count	-0.038	0.050	0.450
	Leukocyte count	0.151	0.042	3.00E-04
	Neutrophil count	0.190	0.056	0.001
	Monocyte count	0.137	0.054	0.011
	Lymphocyte count	-0.004	0.055	0.938
	Eosinophil count	0.502	0.063	2.38E-15
	Basophil count	0.273	0.069	7.93E-05
	Erythrocyte count	0.060	0.044	0.174

r_g : Genetic correlation between asthma and hematological traits.

Statistical significance (two-sided) was determined using the Bonferroni correction to account for multiple testing, setting the threshold at $p < 0.00625$ ($0.05/8$).

Supplementary Table S4. Significant local genetic correlation regions between Asthma and hematological traits.

Phenotype1	Phenotype2	CHR	Start	End	local_rhog	SE	P
Asthma	Monocyte count	6	32682590	33209310	6.65E-04	1.50E-04	9.34E-06
	Eosinophil count	2	101557234	103759508	6.02E-04	1.32E-04	4.93E-06
	Eosinophil count	3	32845663	33989246	6.01E-04	1.32E-04	4.96E-06
	Eosinophil count	6	31571894	32682590	9.92E-04	2.03E-04	1.03E-06
	Eosinophil count	6	134243918	136223664	6.78E-04	1.33E-04	3.77E-07
	Eosinophil count	10	7227267	9038946	7.92E-04	1.30E-04	1.17E-09
	Eosinophil count	10	9038946	10631304	6.34E-04	1.29E-04	9.51E-07
	Neutrophil count	6	31571894	32682590	9.62E-04	1.98E-04	1.24E-06
	Neutrophil count	6	32682590	33209310	7.78E-04	1.53E-04	3.81E-07

local_rhog: local genetic correlation between pairs of traits within each of the 1703 pre- specified LD-independent segments.

Statistical significance (two-sided) using Bonferroni correction to account for multiple testing, setting threshold at $p < 0.05/1703$.

Note: Positions are reported based on the GRCh37 human genome assembly

Supplementary Table S5. Multi-trait meta-analysis between Asthma and Eosinophil counts.

Locus	Gene	SNP	CHR	BP (GRCh3 7)	A 1	A 2	gnomAD_AF							BETA					P					Annotation	
							ALL	AFR	AMR	ASJ	EAS	FIN	NFE	OTH	MTAG- BBJ	MTAG- GBMI	BBJ	GBMI	Eosinop hils	MTAG- BBJ	MTAG- GBMI	BBJ	GBMI		Eosinop hils
1p36.22‡	<i>TNFRSF8</i>	rs12024126	1	12100712	C	T	0.013	0.0001	0.001	0.003	0.243	0.003	3.00E-04	0.004	-0.062	-0.013	-0.053	-0.054	-0.031	1.43E-11	8.37E-07	6.04E-04	6.47E-05	5.75E-08	new
1p12	<i>WARS2</i>	rs12734353		119607194	G	A	0.180	0.134	0.117	0.110	0.227	0.249	0.189	0.185	0.055	0.009	0.058	0.034	0.024	1.28E-08	1.49E-03	4.13E-04	1.32E-02	6.13E-05	new
1q23.3#	<i>ADAMTS4</i>	rs33941127		161168004	C	T	0.275	0.376	0.344	0.258	0.503	0.234	0.200	0.229	0.045	0.011	0.054	0.046	0.018	1.35E-08	3.41E-06	7.08E-05	4.50E-05	3.01E-04	new
1q32.1†‡	<i>ADORA1</i>	rs56184464		203071529	G	A	0.977	0.936	0.968	1.000	0.933	1.000	1.000	0.996	-0.154	-0.034	-0.176	-0.072	-0.057	1.05E-12	4.01E-11	6.49E-07	3.08E-09	6.86E-06	known
2p25.1#	<i>LINC00299</i>	rs346835		8438693	T	C	0.607	0.426	0.649	0.801	0.717	0.639	0.682	0.682	-0.059	-0.019	-0.083	-0.035	-0.019	1.22E-10	2.94E-13	9.49E-08	5.86E-12	7.75E-04	known
2p25.1	<i>HPCAL1</i>	rs11885501	2	10331540	A	G	.	.	.	.	.	.	.	.	0.053	0.009	0.056	0.039	0.023	1.55E-08	1.98E-04	3.27E-04	2.19E-03	9.41E-05	new
2p23.3‡	<i>ADCY3</i>	rs11676272		25141538	A	G	0.562	0.848	0.327	0.368	0.410	0.404	0.470	0.487	0.055	0.010	0.068	0.041	0.021	4.34E-12	1.21E-05	5.87E-07	2.46E-04	1.86E-05	new
2q12.1#	<i>IL18R1</i>	rs17027258		103091540	G	A	0.739	0.819	0.802	0.834	0.575	0.715	0.713	0.697	0.098	0.023	0.078	0.026	0.050	1.41E-33	2.23E-21	2.56E-08	7.69E-15	2.58E-24	known
2q33.2‡	<i>CD28</i>	rs3181097		204570139	A	G	0.890	0.823	0.876	0.954	0.547	0.944	0.950	0.938	-0.075	-0.020	-0.088	-0.055	-0.029	3.17E-21	1.26E-16	8.38E-11	2.21E-13	8.95E-10	known
2q37.3#	<i>D2HGDH</i>	rs35305862		242700770	G	A	0.879	0.862	0.892	0.821	0.876	0.881	0.889	0.882	-0.106	-0.031	-0.135	-0.003	-0.037	2.76E-17	1.10E-19	3.82E-11	2.63E-17	2.85E-06	known
3p24.3	<i>SATB1</i>	rs13096484	3	18706969	T	C	0.541	0.417	0.458	0.500	0.397	0.579	0.623	0.574	-0.045	-0.012	-0.061	-0.052	-0.015	1.68E-08	5.30E-07	6.87E-06	4.98E-06	1.81E-03	new
3p22.3#	<i>GLB1</i>	rs35570272		33047662	T	G	0.636	0.746	0.611	0.566	0.516	0.659	0.586	0.574	0.094	0.018	0.066	0.058	0.051	2.66E-31	2.10E-14	1.78E-06	5.86E-09	4.79E-25	known
3q13.2†‡	<i>CD200R1</i>	rs12630906		112400097	C	T	0.031	0.004	0.152	0.007	0.279	0.049	0.009	0.038	0.056	0.006	0.053	0.037	0.026	5.28E-11	1.92E-02	2.65E-04	1.42E-03	5.90E-07	new
3q21.3‡	<i>KLF15</i>	rs76514276		126037434	G	A	0.001	0.001	0.000	0.000	0.003	0.001	0.000	0.001	-0.220	-0.071	-0.306	-0.306	-0.087	1.80E-10	3.35E-09	1.42E-07	7.23E-08	8.47E-04	new
3q28#	<i>LPP</i>	rs13098877		188133163	T	C	0.592	0.746	0.485	0.523	0.325	0.480	0.567	0.558	-0.061	-0.017	-0.084	-0.072	-0.020	4.05E-13	1.07E-12	2.92E-09	3.99E-11	1.27E-04	known
4q28.3	<i>SLC7A11</i>	rs35108180	4	139086246	A	G	0.170	0.039	0.289	0.123	0.557	0.237	0.181	0.211	-0.045	-0.009	-0.045	-0.034	-0.020	1.20E-08	2.15E-04	9.20E-04	2.88E-03	2.55E-05	new
5p13.3	<i>NPR3</i>	rs111545966		33360375	G	A	0.290	0.106	0.223	0.354	0.184	0.397	0.383	0.352	-0.051	-0.011	-0.060	-0.043	-0.020	3.16E-08	1.54E-04	1.31E-04	1.37E-03	3.76E-04	new
5p13.2#	<i>LOC105374724</i>	rs1961220		35844023	G	A	1.000	1.000	1.000	1.000	0.999	1.000	1.000	1.000	-0.055	-0.014	-0.062	-0.059	-0.023	4.56E-08	3.77E-06	3.61E-04	5.33E-05	2.12E-04	new
5q13.2	<i>ZNF366</i>	rs246579		71817018	A	G	0.760	0.668	0.782	0.815	0.560	0.827	0.815	0.784	-0.060	-0.015	-0.067	-0.062	-0.025	7.31E-14	3.52E-10	9.16E-07	4.28E-08	4.63E-07	known
5q22.1*#	<i>TSLP/WD R36</i>	rs1837253		110401872	C	T	0.288	0.267	0.296	0.328	0.628	0.237	0.275	0.283	0.074	0.028	0.122	0.090	0.019	4.10E-19	5.61E-30	1.16E-17	2.40E-28	2.10E-04	known
5q22.1#	<i>TSLP/WD R36</i>	rs10455025	5	110404999	C	A	0.772	0.928	0.759	0.667	0.957	0.703	0.683	0.720	0.109	0.039	0.149	0.085	0.037	1.28E-08	1.12E-10	5.83E-06	1.46E-09	1.66E-03	known
5q31.1*#	<i>IL13/RAD 50</i>	rs62383758		131961970	T	C	0.801	0.882	0.859	0.742	0.837	0.740	0.765	0.769	0.116	0.024	0.072	0.084	0.066	3.80E-33	2.73E-15	1.35E-05	3.08E-09	8.82E-29	known
5q31.3#	<i>NDIFPI</i>	rs13188700		141495139	T	C	0.665	0.746	0.691	0.719	0.652	0.659	0.618	0.669	0.059	0.014	0.061	0.058	0.026	2.89E-13	6.68E-09	1.41E-05	8.14E-07	1.10E-07	new
5q33.1‡	<i>G3BPI</i>	rs2053062		151169881	C	T	0.004	0.001	0.110	0.000	0.013	0.000	0.000	0.007	-0.077	-0.024	-0.093	-0.098	-0.034	2.34E-08	9.97E-07	5.98E-05	1.25E-05	5.62E-04	new
6p22.1*	<i>PPP1R11</i>	rs886997		29977869	C	T	0.131	0.216	0.219	0.318	0.083	0.048	0.100	0.094	0.021	0.024	0.107	0.102	0.003	2.26E-10	3.37E-09	2.13E-10	2.29E-11	5.95E-01	known
6p21.32*	<i>HLA-DQ42</i>	rs78218185	6	32432500	G	A	0.016	0.004	0.040	0.000	0.065	0.032	0.012	0.028	0.061	0.066	0.279	0.283	-0.035	1.65E-60	5.15E-46	4.12E-43	7.67E-58	1.30E-06	known
6q23.3*	<i>HBSIL</i>	rs7763883		135399243	C	T	0.160	0.180	0.236	0.126	0.229	0.153	0.139	0.160	0.021	0.023	0.066	0.079	-0.057	3.84E-13	3.14E-09	8.87E-05	1.60E-08	2.88E-20	known

Supplementary Table S5(continued). Multi-trait meta-analysis between Asthma and Eosinophil counts.

Locus	Gene	SNP	CHR	BP (GRCh37)	A1	A2	gnomAD_AF								BETA					P					Annotation
							ALL	AFR	AMR	ASJ	EAS	FIN	NFE	OTH	MTAG-BBJ	MTAG-GBMI	BBJ	GBMI	Eosinophils	MTAG-BBJ	MTAG-GBMI	BBJ	GBMI	Eosinophils	
7p21.1#	<i>ITGB8/ABCB5</i>	rs10280157		20535169	T	C	0.772	0.911	0.802	0.715	0.715	0.666	0.725	0.723	-0.128	0.023	-0.098	-0.158	-0.066	1.36E-42	6.32E-17	1.22E-09	3.33E-10	1.13E-31	known
7p21.11‡	<i>CD36</i>	rs75326924		80286003	C	T	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000	-0.127	-0.039	-0.138	-0.139	-0.054	1.25E-11	2.10E-07	2.16E-05	2.01E-05	2.12E-06	new
8q21.13#	<i>ZBTB10</i>	rs10957979	8	81289787	A	G	0.609	0.537	0.577	0.650	0.420	0.701	0.648	0.642	-0.047	-0.010	-0.053	-0.039	-0.019	3.81E-09	4.81E-05	1.19E-04	6.67E-04	6.63E-05	new
8q24.21†	<i>MYC</i>	rs16902875		129421904	G	A	0.108	0.235	0.196	0.040	0.270	0.039	0.033	0.071	-0.051	-0.014	-0.052	-0.060	-0.023	1.70E-09	2.88E-08	3.29E-04	1.16E-06	1.22E-05	new
9p24.1	<i>INSL4(JAK2)</i>	rs1555476	9	5233054	C	T	0.783	0.953	0.740	0.773	0.786	0.646	0.722	0.713	0.075	0.017	0.085	0.064	0.030	5.98E-13	6.64E-09	1.60E-06	4.66E-07	1.71E-06	known
10p14*#	<i>GATA3_1</i>	rs3802597	10	8114388	G	A	0.545	0.847	0.572	0.447	0.463	0.416	0.415	0.455	-0.069	-0.015	-0.074	-0.062	-0.030	6.48E-18	5.71E-10	6.38E-08	2.00E-07	1.68E-09	known
10p14#	<i>GATA3_2</i>	rs290901		8935933	A	C	0.319	0.375	0.325	0.271	0.651	0.328	0.248	0.316	0.105	0.030	0.133	0.105	0.038	1.46E-36	1.28E-33	3.73E-21	3.59E-28	6.76E-14	known
10p14*#	<i>GATA3_3</i>	rs2797288		9053173	A	G	0.189	0.133	0.112	0.093	0.214	0.288	0.198	0.238	-0.130	-0.035	-0.163	-0.116	-0.048	2.29E-37	1.49E-31	1.09E-20	6.30E-26	5.94E-15	known
10q21.2*#	<i>ZNF365</i>	rs16917546		64397538	C	T	0.697	0.878	0.813	0.606	0.373	0.639	0.638	0.666	-0.096	-0.018	-0.074	-0.035	-0.050	1.52E-33	2.96E-14	4.65E-08	7.00E-09	1.07E-24	known
10q26.13‡	<i>CTBP2</i>	rs1152690		126796382	T	C	0.188	0.363	0.265	0.166	0.301	0.101	0.094	0.129	-0.046	-0.008	-0.052	-0.031	-0.019	2.63E-08	1.06E-03	2.24E-04	8.38E-03	2.01E-04	new
11q13.1#	<i>OVOL1</i>	rs11227277	11	65493116	C	T	0.497	0.460	0.559	0.520	0.547	0.553	0.497	0.468	0.050	0.009	0.048	0.037	0.023	3.62E-10	5.88E-05	4.54E-04	1.40E-03	2.02E-06	new
11q13.5#	<i>C11orf30/LRRC32</i>	rs11236797		76299649	A	C	0.617	0.745	0.625	0.497	0.587	0.594	0.554	0.601	0.072	0.016	0.069	0.056	0.033	9.83E-18	2.42E-11	1.62E-06	2.13E-08	8.07E-11	known
11q23.3‡	<i>APOA5</i>	rs651821		116662579	C	T	0.892	0.851	0.851	0.861	0.710	0.922	0.931	0.897	0.056	0.013	0.067	0.055	0.022	3.31E-11	1.42E-07	2.82E-06	4.09E-06	2.92E-05	new
11q23.3	<i>TAGLN</i>	rs78135964		116971677	G	T	0.070	0.094	0.043	0.076	0.085	0.081	0.054	0.072	0.083	0.017	0.099	0.070	0.032	4.29E-10	1.55E-05	1.54E-05	2.50E-04	5.83E-05	new
12q13.2*#	<i>IKZF4</i>	rs1702877	12	56427808	T	C	0.746	0.883	0.797	0.629	0.796	0.678	0.680	0.703	0.079	0.022	0.117	0.068	0.024	4.34E-15	2.91E-14	1.39E-11	1.35E-12	9.57E-05	known
13q14.11	<i>COG6</i>	rs7986114	13	40514538	C	T	0.452	0.382	0.327	0.642	0.370	0.375	0.520	0.488	0.047	0.011	0.049	0.043	0.021	2.49E-09	8.92E-06	3.55E-04	1.93E-04	1.61E-05	new
13q14.11	<i>ELF1</i>	rs9566656		41581930	C	T	0.240	0.338	0.113	0.116	0.264	0.152	0.214	0.197	-0.055	-0.011	-0.080	-0.049	-0.017	2.08E-08	6.30E-05	2.50E-06	3.69E-04	3.87E-03	new
14q13.2#	<i>NFKB1A</i>	rs8015243	14	35881679	C	T	0.615	0.577	0.752	0.622	0.736	0.651	0.609	0.630	0.049	0.013	0.052	0.053	0.021	1.17E-08	9.45E-07	3.89E-04	1.99E-05	5.96E-05	new
15q21.2	<i>TRPM7</i>	rs8033532	15	50667421	G	T	.	.	.	.	.	.	.	.	-0.044	-0.009	-0.048	-0.039	#REF!	4.01E-08	6.96E-05	4.81E-04	8.04E-04	1.46E-04	new
15q22.2*#	<i>RORA</i>	rs34753162		61069177	C	T	0.762	0.559	0.847	0.818	0.808	0.839	0.847	0.823	-0.094	-0.026	-0.122	-0.109	-0.034	6.24E-23	1.30E-18	3.70E-14	1.48E-15	1.50E-08	known
16p12.1*#	<i>IL4R</i>	rs3024589	16	27360627	G	A	0.486	0.458	0.382	0.507	0.377	0.539	0.505	0.508	0.093	0.024	0.123	0.107	0.033	1.65E-26	7.59E-22	3.41E-16	3.28E-18	6.15E-10	known
16q13#	<i>CCL22</i>	rs223821		57396698	A	G									0.076	0.015	0.078	0.058	0.034	2.81E-11	1.68E-05	7.83E-05	5.11E-04	1.24E-06	new
17q21.33†	<i>ZNF652/PHB</i>	rs2671655	17	47468020	C	T	0.933	0.978	0.764	0.954	0.699	0.931	0.941	0.939	-0.049	-0.014	-0.059	-0.066	-0.018	2.22E-08	7.40E-09	5.31E-05	1.19E-07	5.81E-04	new
18q21.1‡	<i>SMAD2</i>	rs57631119	18	45473449	C	T	0.048	0.042	0.266	0.010	0.187	0.077	0.018	0.062	0.072	0.017	0.069	0.070	0.033	4.68E-14	2.82E-09	1.55E-05	5.29E-07	1.86E-08	new
18q21.2#	<i>SMAD4</i>	rs1942093		48517432	A	G	0.202	0.051	0.240	0.288	0.350	0.291	0.247	0.260	0.047	0.012	0.052	0.051	0.019	3.93E-09	6.23E-07	1.37E-04	1.36E-05	6.00E-05	new

Supplementary Table S5(continued). Multi-trait meta-analysis between Asthma and Eosinophil counts.

Locus	Gene	SNP	CHR	BP (GRCh37)	A1	A2	gnomAD_AF								BETA					P					Annotation
							ALL	AFR	AMR	ASJ	EAS	FIN	NFE	OTH	MTAG-BBJ	MTAG-GBMI	BBJ	GBMI	Eosinophils	MTAG-BBJ	MTAG-GBMI	BBJ	GBMI	Eosinophils	
19p13.3	<i>FUT5</i>	rs3760775	19	5841356	G	T	0.148	0.276	0.267	0.070	0.313	0.109	0.062	0.115	-0.046	-0.015	-0.063	-0.069	-0.016	2.94E-07	1.81E-08	4.53E-05	1.43E-07	4.67E-03	new
20q11.21	<i>ASXL1</i>	rs34310097	20	31055226	G	A	0.320	0.153	0.404	0.205	0.648	0.436	0.349	0.377	-0.054	-0.009	-0.051	-0.036	-0.026	4.55E-09	3.45E-04	9.19E-04	4.97E-03	1.01E-05	new
22q13.2#	<i>RANG API</i>	rs5758280	22	41675015	C	T	0.269	0.340	0.150	0.152	0.731	0.157	0.217	0.213	-0.057	-0.013	-0.060	-0.051	-0.025	1.83E-10	2.11E-06	9.88E-05	6.58E-05	5.40E-06	new

* Significant loci in the original Asthma GWAS of East Asians; # Loci reported in Asthma GWAS of Europeans; † genomic region reported in Asthma GWAS of Europeans; ‡ Asian specific loci

CHR: Chromosome. **BP (GRCh37):** The exact base-pair position of the SNP on the chromosome, based on the GRCh37 human genome assembly. **A1:** effect allele. **A2:** non-effect allele. **BETA:** effect size. **P:** statistical significance.

MTAG-BBJ: Multi-trait analysis of GWAS using asthma data from BioBank Japan. **MTAG-GBMI:** Multi-trait analysis of GWAS using asthma data from the Global Biobank Meta-analysis Initiative. **BBJ:** Single-trait GWAS results of asthma from BioBank Japan.

GBMI: Single-trait GWAS results of asthma from the Global Biobank Meta-analysis Initiative. **Eosinophils:** GWAS results for eosinophils. **ALL:** Overall allele frequency across all populations included.

gnomAD_AF: Represents allele frequency information obtained from the gnomAD (Genome Aggregation Database) annotations. Each column corresponds to a specific population or group. **AFR**: Allele frequency in African (AFR) populations, primarily representing Sub-Saharan African individuals.

AMR: Allele frequency in Admixed American (AMR) populations, including individuals from Latin America and the Caribbean with mixed ancestry. **ASJ:** Allele frequency in Ashkenazi Jewish (ASJ) populations, representing Jewish descendants primarily from Eastern and Central Europe

EAS: Allele frequency in East Asian (EAS) populations, including individuals from China, Japan, Korea, and other East Asian regions. **FIN:** Allele frequency in Finnish (FIN) populations, a genetically unique European population.

NFE: Allele frequency in Non-Finnish European (NFE) populations, representing Europeans excluding Finnish individuals. **OTH:** Allele frequency in Other (OTH) populations, representing individuals who do not fall into any of the defined population groups.