

Figure S1 Multivariate statistical analysis of proteomics data. (A) Principal component analysis score plot of DEPs between preschool Asthma and Health subjects, AsthmaY and HealthY represented Asthma and Health subjects under 5 years old, respectively. R2X[1] and R2X[2] are the explanatory rates of the corresponding principal components t[1] and t[2]; (B) OPLS-DA model of DEPs between Asthma and Health subjects; (C) 200 permutation tests score plot of DEPs between Asthma and Health subjects, R2X[1] and R2Xo[1] are the explanatory rates of the t[1] and to[1]; (D) 200 permutation tests score plot of DEPs between preschool Asthma and Health subjects, The Q2 value represents the proportion of data variance that can be predicted by the current model, The R2 value is the cumulative variance value of the model. DEP, differentially expressed proteins; OPLS-DA, orthonormal partial least squares discriminant analysis.

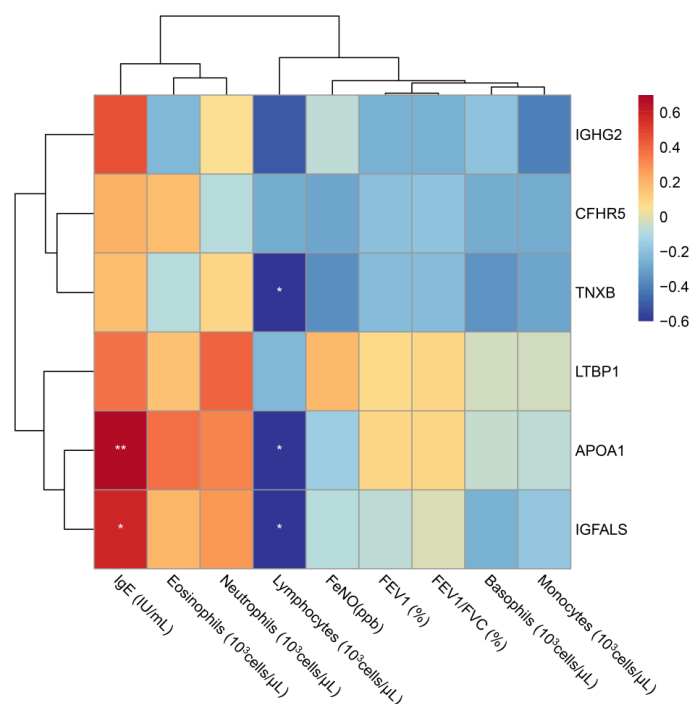


Figure S2 Correlation analysis between clinical indicators and candidate biomarkers. Different colors indicate different correlations, red for positive correlation, blue for negative correlation, and the depth of color for the strength of the correlation. *, P < 0.05, **, P < 0.01. IgE, immunoglobulin E; FEV1, forced expiratory volume in one second; FVC, forced vital capacity.

Table S1 The result of GO enrichment analysis of the DEPs

GO terms level 1	GO terms description	GO terms level	GO Terms ID	Mapping	Background	All mapping	All background	Fold enrichment	Fisher's exact test P value	-log10 (P value)	Related proteins	Q value
Cellular component	Sarcoplasmic reticulum	6	GO:0016529	2	2	35	335	9.57	0.010635	1.97	O43852 P07996	0.015953
	Growth cone	4	GO:0030426	2	3	35	335	6.38	0.029798	1.53	P03950 P16035	0.029798
	Site of polarized growth	3	GO:0030427	2	3	35	335	6.38	0.029798	1.53	P03950 P16035	0.029798
	Sarcoplasm	5	GO:0016528	2	3	35	335	6.38	0.029798	1.53	O43852 P07996	0.029798
Molecular function	CXCR chemokine receptor binding	7	GO:0045236	3	3	41	356	8.68	0.00143	2.84	P02775 P02776 P10720	0.008578
	Chemokine receptor binding	6	GO:0042379	3	4	41	356	6.51	0.005257	2.28	P02775 P02776 P10720	0.010514
	Chemokine activity	6	GO:0008009	3	4	41	356	6.51	0.005257	2.28	P02775 P02776 P10720	0.010514
	G-protein coupled receptor binding	5	GO:0001664	4	9	41	356	3.86	0.012517	1.9	P01019 P02775 P02776 P10720	0.017672
	Heparin binding	4	GO:0008201	6	22	41	356	2.37	0.029426	1.53	E9PG40 P02776 P03950 P04114 P07996 P10720	0.029798
	Sulfur compound binding	3	GO:1901681	6	22	41	356	2.37	0.029426	1.53	E9PG40 P02776 P03950 P04114 P07996 P10720	0.029798
	Chemokine-mediated signaling pathway	6	GO:0070098	3	3	34	326	9.59	0.001046	2.98	P02775 P02776 P10720	0.008578
Biological process	Positive regulation of leukocyte chemotaxis	7	GO:0002690	4	6	34	326	6.39	0.00129	2.89	P02775 P02776 P07996 P10720	0.008578
	Regulation of granulocyte chemotaxis	7	GO:0071622	4	6	34	326	6.39	0.00129	2.89	P02775 P02776 P07996 P10720	0.008578
	Positive regulation of leukocyte migration	6	GO:0002687	4	7	34	326	5.48	0.002785	2.56	P02775 P02776 P07996 P10720	0.010514
	Positive regulation of neutrophil migration	7	GO:1902624	3	4	34	326	7.19	0.003883	2.41	P02775 P02776 P10720	0.010514
	Regulation of neutrophil migration	6	GO:1902622	3	4	34	326	7.19	0.003883	2.41	P02775 P02776 P10720	0.010514
	Regulation of neutrophil chemotaxis	7	GO:0090022	3	4	34	326	7.19	0.003883	2.41	P02775 P02776 P10720	0.010514
	Regulation of leukocyte chemotaxis	6	GO:0002688	4	8	34	326	4.79	0.005157	2.29	P02775 P02776 P07996 P10720	0.010514
	Positive regulation of chemotaxis	6	GO:0050921	4	8	34	326	4.79	0.005157	2.29	P02775 P02776 P07996 P10720	0.010514
	Regulation of nucleotide metabolic process	7	GO:0006140	3	5	34	326	5.75	0.00901	2.05	P02776 P07996 P16035	0.015953
	Regulation of organic acid transport	6	GO:0032890	2	2	34	326	9.59	0.01059	1.98	P01019 P07996	0.015953
	Negative regulation of cell cycle	6	GO:0045786	2	2	34	326	9.59	0.01059	1.98	P07996 P16035	0.015953
	Protein-lipid complex remodeling	6	GO:0034368	4	10	34	326	3.84	0.01326	1.88	P01019 P02647 P04114 P04180	0.017733
	Positive regulation of lipase activity	7	GO:0060193	3	6	34	326	4.79	0.016729	1.78	P01019 P02647 P03950	0.021132

GO, Gene Ontology.

Table S2 The result of KEGG and Reactome enrichment analysis of the DEPs

Pathway name	Count	P value	-log10 (P value)	Related proteins	Q value
KEGG pathway					
Chemokine signaling pathway	3	0.000954	3.02	P02775 P02776 P10720	0.007632
Viral protein interaction with cytokine and cytokine receptor	3	0.00356	2.45	P02775 P02776 P10720	0.009492
Vitamin digestion and absorption	3	0.00356	2.45	P02647 P04114 P43251	0.009492
Cytokine-cytokine receptor interaction	3	0.01549	1.81	P02775 P02776 P10720	0.030981
p53 signaling pathway	2	0.028518	1.54	A6XND0 P07996	0.032592
TGF-beta signaling pathway	2	0.028518	1.54	P07996 Q14766	0.032592
Fat digestion and absorption	2	0.028518	1.54	P02647 P04114	0.032592
Cholesterol metabolism	4	0.042169	1.38	B0YIW2 P02647 P04114 P04180	0.042169
Reactome pathway					
Regulation of insulin-like growth factor (IGF) transport and uptake by insulin-like growth factor binding proteins (IGFBPs)	3	0.002077	2.68	P35858 P05019 P02647	0.031121
Post-translational protein phosphorylation	1	0.199025	0.7	P02647	0.199025
Platelet degranulation	4	0.000131	3.88	Q13201 P05019 P02647 P02776	0.006337
Response to elevated platelet cytosolic Ca ²⁺	4	0.000152	3.82	Q13201 P05019 P02647 P02776	0.006337
Platelet activation, signaling and aggregation	5	0.000182	3.74	P02452 Q13201 P05019 P02647 P02776	0.006337
Hemostasis	5	0.014857	1.83	P02452 Q13201 P05019 P02647 P02776	0.091538
Chylomicron assembly	1	0.020442	1.69	P02647	0.091538
Chylomicron remodeling	1	0.020442	1.69	P02647	0.091538
Plasma lipoprotein remodeling	2	0.002394	2.62	P04180 P02647	0.031121
HDL remodeling	2	0.000244	3.61	P04180 P02647	0.006337
RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	1	0.127721	0.89	P02776	0.127721

KEGG, Kyoto Encyclopedia of Genes and Genomes.

Table S3 The OPLS-DA VIPpreds of the DEPs

Proteins	Asthma vs. health VIPpred	AsthmaY vs. HealthY VIPpred
PCYOX1	2.83097	1.78946
ABHD12B	1.80749	1.81979
CFHR4	1.44895	1.24376
ANG	1.43256	1.02851
APOA1	1.37554	1.19251
LTBP1	1.34624	1.33773
TNXB	1.29098	0.894792
PZP	1.24422	0.860979
MMP14	1.19268	2.92587
IGHG4	1.07688	1.10475
IGFALS	1.07197	1.02818
CFHR5	1.05946	0.893787
PPBP	1.05215	0.990388
MMRN1	1.03436	0.986262
IGHG2	0.992135	0.98985
CALU	0.977326	1.0829
CD93	0.940778	0.74819
IGHV5-10-1	0.940242	1.10649
CNDP1	0.924339	0.836726
CDH5	0.898202	0.851741
APP	0.88369	1.05552
PF4	0.878734	0.811063
APOC3	0.866926	0.83721
ZNF831	0.861696	0.831826
IGHV3-49	0.856307	0.964003
IGFBP3	0.843854	0.556454
PF4V1	0.842137	0.756124
MADCAM1	0.841905	0.922295
PKM	0.832939	1.10255
IGKV3D-11	0.801736	0.787271
IGHA1	0.800188	0.780649
TF	0.786309	0.394046
IGLV1-47	0.75897	0.765378
APOB	0.755491	0.700089

Table S3 (continued)**Table S3** (continued)

Proteins	Asthma vs. health VIPpred	AsthmaY vs. HealthY VIPpred
AGT	0.752709	0.721844
GP5	0.750299	0.52642
TPM4	0.733293	1.36138
TIMP2	0.709115	0.760839
LCAT	0.70101	0.798153
BTD	0.692852	0.831114
PON1	0.680577	0.706046
COL1A1	0.591572	0.796639
TREML1	0.569582	0.445784
IGKV1D-33	0.566921	0.472392
IGHG1	0.548569	0.180366
ANTXR2	0.533689	0.396868
LGALS1	0.531774	0.70267
ITIH4	0.23506	0.0411886
MGP	0.22402	0.788555
PCDH12	0.142704	0.502253

VIPpred, predictive variable importance in projection.