

Supplement Figure

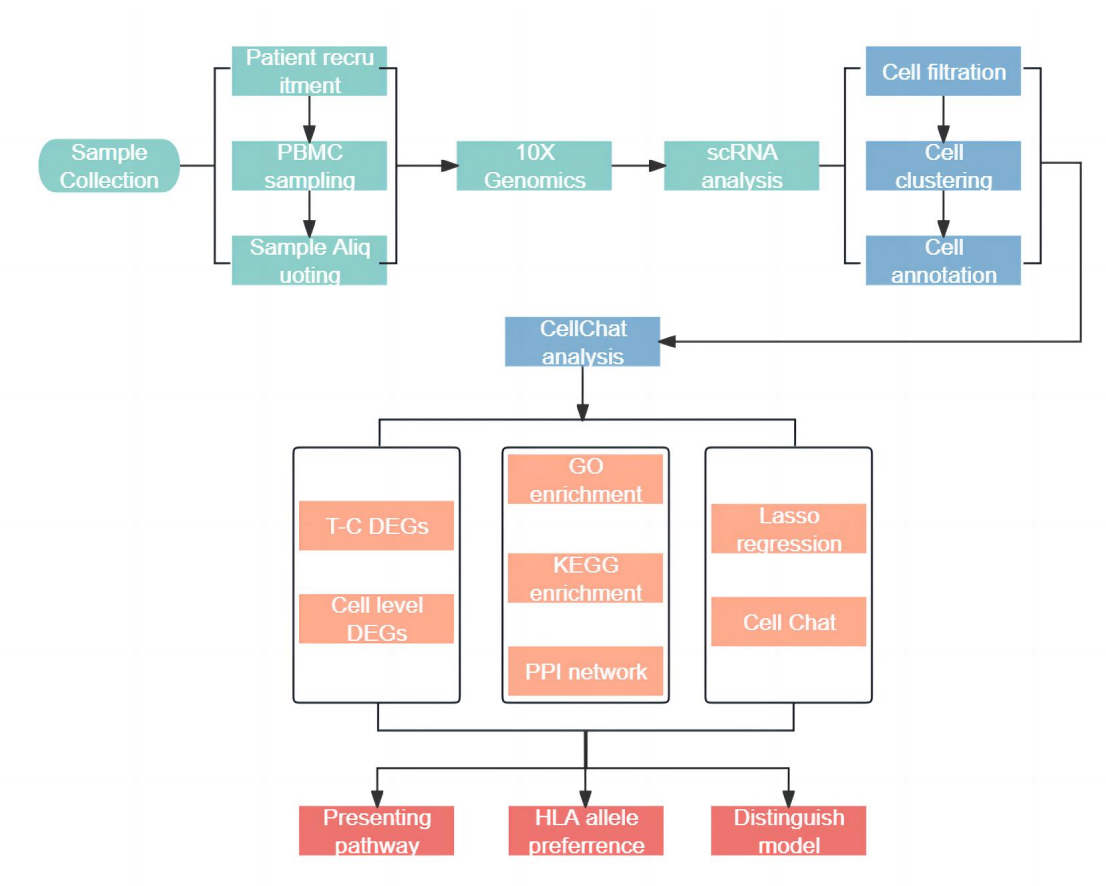


Fig. S1. Workflow of the Study. We initially collected eight asthma samples from Shenzhen Baoan Women's and Children's Hospital. All eight samples underwent 10X Genomics single-cell sequencing. Subsequently, we employed the Seurat R package to filter and cluster cells, annotating clusters based on Cellmarker2.0. Following this, differential expression analyses were performed for the T-C group at both the overall cell and separate cell-typ. Further analyses included enrichment analysis, construction of a protein-protein interaction (PPI) network, and implementation of a lasso regression model based on the DEGs. Simultaneously, cell-cell communication analysis was conducted.

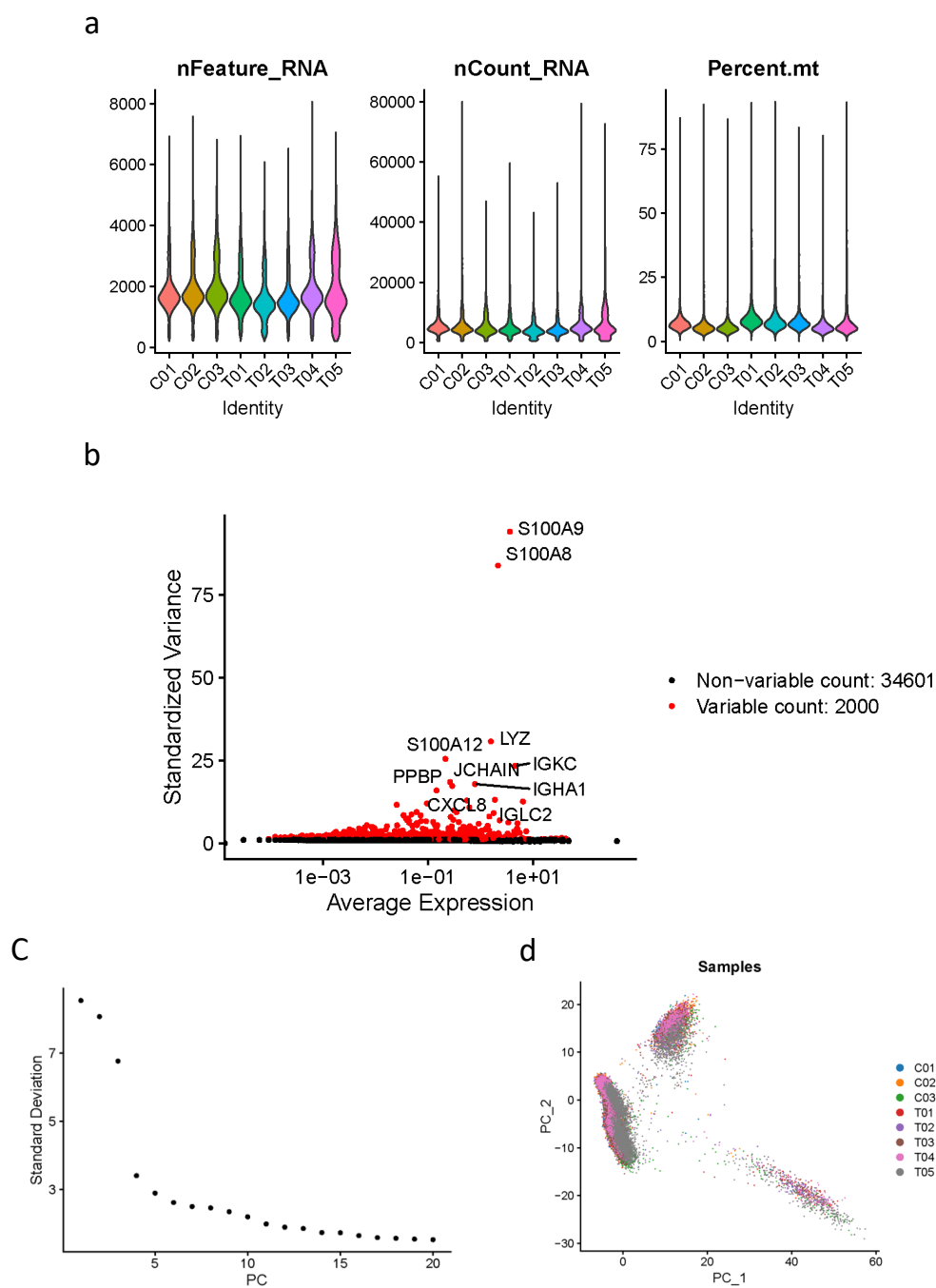


Fig. S2. Quantitative Control in scRNA Analysis.

- (a) Distribution of RNA features, cell counts, and mitochondrial gene ratios in samples.
- (b) Dot plot of top 2000 highly variable genes.
- (c) Standard deviations of the principal components.
- (d) Dot plot of cells after PCA dimensional reduction.

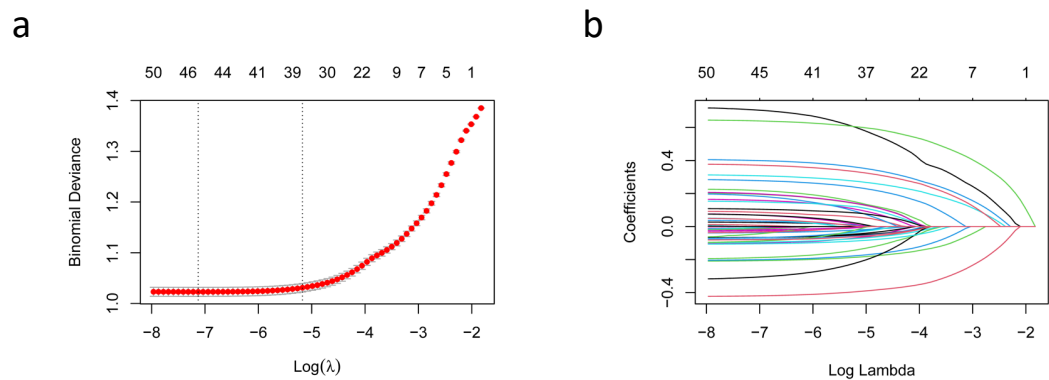


Fig. S3. Parameter Control in Lasso Model Construction.

(a) The relationship between Binomial Deviance and cross-validation of lambda.

(b) Changes in the coefficients of feature genes with respect to lambda.

Table S1 S2 differentially expressed genes in PBMCs between HDM-sensitized group and non-HDM-sensitized group

p_val	avg_log2FC	pct. 1	pct. 2	p_val_adj	Change	gene
0	-0.595634222	0.868	0.94	0	DOWN	RPS26
3.8008995737167e-166	-0.578247277	0.368	0.504	1.39116725297605e-161	DOWN	XAF1
8.99095326878914e-147	-0.35067117	0.825	0.885	3.29077880590951e-142	DOWN	RNF213
1.3758944792631e-135	-0.46169314	0.576	0.69	5.03591138355088e-131	DOWN	SYNE2
3.65240190026804e-135	-0.379289967	0.703	0.801	1.33681561951711e-130	DOWN	ARL4C
3.00970952824841e-118	-0.570453194	0.364	0.489	1.1015837844342e-113	DOWN	CCL5
2.42633806523237e-117	-0.520289545	0.334	0.461	8.88063995255701e-113	DOWN	NKG7
7.84415638268231e-117	-0.495252327	0.298	0.42	2.87103967762555e-112	DOWN	CST7
1.34442999088893e-113	-0.457091487	0.3	0.426	4.92074820965256e-109	DOWN	GZMA
6.78748994029254e-99	-0.348319277	0.216	0.322	2.48428919304647e-94	DOWN	MT2A
1.26860101767268e-92	-0.425805873	0.23	0.337	4.64320658478376e-88	DOWN	PRF1
3.77573661523395e-90	-0.308276961	0.657	0.747	1.38195735854178e-85	DOWN	HCST
4.05299963207091e-90	-0.33686352	0.245	0.353	1.48343839533427e-85	DOWN	PYHIN1
6.6820225096576e-88	-0.434439173	0.311	0.413	2.44568696407598e-83	DOWN	ISG15
3.21496706535237e-86	-0.272119368	0.628	0.721	1.17671009558962e-81	DOWN	IL2RG
5.99284159770722e-86	-0.328851173	0.352	0.456	2.19343995317682e-81	DOWN	KLRK1
1.32617371564986e-83	-0.400576079	0.186	0.285	4.85392841665006e-79	DOWN	FGFBP2
1.22244080294359e-77	-0.309877444	0.187	0.276	4.47425558285383e-73	DOWN	EPSTI1
2.03648915749266e-75	-0.316831684	0.5	0.598	7.45375396533889e-71	DOWN	SYNE1
2.37344879114638e-73	-0.306106893	0.413	0.506	8.68705992047485e-69	DOWN	LYGE
2.80716500419353e-72	-0.387502921	0.187	0.277	1.02745046318487e-67	DOWN	GZMH
9.41612396352015e-72	-0.459665291	0.186	0.273	3.44639553188801e-67	DOWN	GZMB
3.55118622538242e-71	-0.36324268	0.229	0.323	1.29976967035222e-66	DOWN	XIST
3.36908400846817e-68	-0.256774054	0.662	0.737	1.23311843793944e-63	DOWN	PPP2R5C
7.7832302293928e-65	-0.31263371	0.57	0.65	2.84874009626006e-60	DOWN	PIK3R1
4.95260279509394e-61	-0.339906558	0.222	0.305	1.81270214903233e-56	DOWN	MYBL1
3.72888085561613e-60	-0.259888932	0.242	0.328	1.36480768196406e-55	DOWN	C12orf75
5.01993559771234e-58	-0.284423486	0.192	0.268	1.83734662811869e-53	DOWN	APOBEC3G
1.27003762328658e-57	-0.296677092	0.284	0.364	4.6484647049912e-53	DOWN	EIF2AK2
2.19653439404629e-55	-0.256945974	0.326	0.411	8.03953553564881e-51	DOWN	IQGAP2
7.91762791387025e-53	-0.260205048	0.48	0.559	2.89793099275565e-48	DOWN	FLNA
1.33745742722521e-52	-0.254092091	0.352	0.436	4.89522792938698e-48	DOWN	ITGAL
5.15782870823605e-51	-0.266218411	0.183	0.256	1.88781688550148e-46	DOWN	HOPX
4.05906350687357e-50	-0.260270644	0.259	0.343	1.48565783415079e-45	DOWN	KLRD1
1.67593229128484e-48	-0.309958875	0.32	0.393	6.13407977933164e-44	DOWN	PLEK
9.58772083096963e-46	-0.274327083	0.466	0.545	3.5092017013432e-41	DOWN	CD247
1.74560730859448e-45	-0.278041751	0.204	0.273	6.38909731018664e-41	DOWN	CEP78
4.17745636596439e-45	-0.279567829	0.216	0.285	1.52899080450662e-40	DOWN	DUSP2
1.27731998290733e-44	-0.434009265	0.236	0.31	4.67511886943912e-40	DOWN	GNLY
1.71402565727259e-33	-0.262213208	0.389	0.449	6.27350530818341e-29	DOWN	EFHD2
0	0.381600505499771	0.999	0.998	0	UP	RPS3A
0	0.394012766071985	1	1	0	UP	MT-ND4
5.71593071018522e-300	0.572412222204907	0.647	0.492	2.09208779923489e-295	UP	SNHG5
4.4062894301337e-264	0.64361458124767	0.31	0.143	1.61274599432323e-259	UP	AC253572.2
7.57247641822012e-246	0.262537175463589	0.999	0.997	2.77160209383275e-241	UP	RPL13A
2.7063120487674e-236	0.251431126894338	1	1	9.90537272969357e-232	UP	MT-ND1
3.48651903118512e-184	0.564340490862127	0.33	0.189	1.27610083060407e-179	UP	AC007952.4
1.22975278620433e-62	0.459969319002627	0.275	0.379	4.50101817278646e-58	UP	IGKC
3.26528079756032e-36	0.252245883086229	0.66	0.613	1.19512542471505e-31	UP	IRF1
1.4842266312901e-34	0.513032378902537	0.301	0.245	5.43241789318488e-30	UP	HLA-DRA
7.51469315789836e-08	0.293253508778651	0.397	0.375	0.00275045284272238	UP	HLA-DPB1
2.00685716863035e-07	0.383221088382854	0.535	0.524	0.00734529792290396	UP	CD74

Table S2 List of gene sets

The 52 DGEs between group T and C	The 35 shared DEGs across comparisons (T vs. C and O vs. T)	29 overlapping genes
RPS3A	HLA-DPB1	GZMH
MT-ND4	EFHD2	AC253572.2
SNHG5	HLA-DRA	PRF1
AC253572.2	GNLY	CST7
RPL13A	DUSP2	HLA-DRA
MT-ND1	KLRD1	AC007952.4
AC007952.4	HOPX	RPS3A
IGKC	FLNA	EFHD2
IRF1	EIF2AK2	FLNA
HLA-DRA	APOBEC3G	SNHG5
HLA-DPB1	C12orf75	RPL13A
CD74	IGKC	APOBEC3G
RPS26	XIST	ISG15
XAF1	GZMB	EIF2AK2
RNF213	GZMH	CCL5
SYNE2	LY6E	HOPX
ARL4C	EPSTI1	GZMB
CCL5	FGFBP2	HLA-DPB1
NKG7	ISG15	XIST
CST7	HCST	C12orf75
GZMA	PRF1	RNF213
MT2A	MT2A	GNLY
PRF1	GZMA	LY6E
HCST	CST7	KLRD1
PYHIN1	NKG7	DUSP2
ISG15	CCL5	MT-ND4
IL2RG	RNF213	NKG7
KLRK1	XAF1	GZMA
FGFBP2	AC007952.4	FGFBP2
EPSTI1	RPL13A	
SYNE1	AC253572.2	
LY6E	SNHG5	
GZMH	MT-ND4	
GZMB	RPS26	
XIST	RPS3A	
PPP2R5C		
PIK3R1		
MYBL1		
C12orf75		
APOBEC3G		
EIF2AK2		
IQGAP2		
FLNA		
ITGAL		
HOPX		
KLRD1		
PLEK		
CD247		
CEP78		
DUSP2		
GNLY		
EFHD2		