

Figure S1. Pathophysiological evidence of OVA-induced asthma. (A) Histology for lung tissue, (B) eosinophils count in BALF and (C) IL-4 level in BALF. Scale bar, 50  $\mu$ m.  $^{##}P < 0.01$  vs. NC. OVA, ovalbumin; NC, normal control; IL, interleukin; BALF, bronchoalveolar lavage fluid.

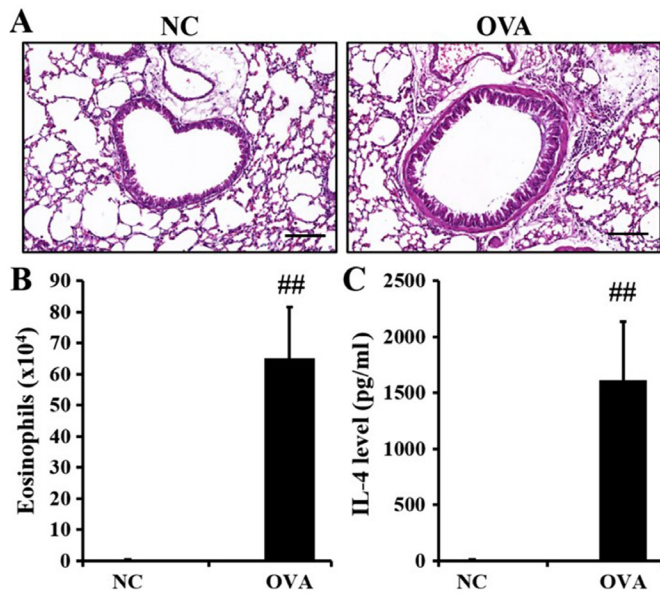


Table S1. Hyper-KEGG pathway functional annotation of DEGs and gene expression.

Term	Count	%	P-value	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
mmu04510: Focal adhesion	24	3.283173735	1.94x10 <sup>-6</sup>	224	198	5738	3.104978355	2.81x10 <sup>-4</sup>	2.81x10 <sup>-4</sup>	0.002298853
mmu04512: ECM-receptor interaction	12	1.641586867	3.26x10 <sup>-4</sup>	224	83	5738	3.703528399	0.046199094	0.023372689	0.386513354
mmu04666: Fc gamma R-mediated phagocytosis	13	1.778385773	3.72x10 <sup>-4</sup>	224	98	5738	3.398050292	0.052510261	0.017819053	0.440642841
mmu04914: Progesterone-mediated oocyte maturation	12	1.641586867	4.03x10 <sup>-4</sup>	224	85	5738	3.616386555	0.056718967	0.014491725	0.476924273
mmu04070: Phosphatidylinositol signaling system	11	1.504787962	5.79x10 <sup>-4</sup>	224	75	5738	3.75702381	0.080612469	0.01666902	0.685760966
mmu00562: Inositol phosphate metabolism	9	1.23119015	0.001018121	224	54	5738	4.269345238	0.137312489	0.024316595	1.202005187
mmu04810: Regulation of actin cytoskeleton	19	2.599179207	0.001799596	224	217	5738	2.24288183	0.229854989	0.036623446	2.115631468
mmu04930: Type II diabetes mellitus	8	1.094391245	0.002600114	224	49	5738	4.182215743	0.314431972	0.046092377	3.043494008
mmu04020: Calcium signaling pathway	17	2.325581395	0.002904479	224	191	5738	2.279964473	0.344110017	0.045781376	3.394157488
mmu04912: GnRH signaling pathway	11	1.504787962	0.004174862	224	97	5738	2.904915317	0.454810699	0.058858916	4.845282988
mmu04270: Vascular smooth muscle contraction	12	1.641586867	0.006658712	224	120	5738	2.561607143	0.620439831	0.084300906	7.625007583
mmu05414: Dilated cardiomyopathy	10	1.367989056	0.009058717	224	92	5738	2.78435559	0.732730948	0.104128496	10.24006457
mmu04621: NOD-like receptor signaling pathway	8	1.094391245	0.009725005	224	62	5738	3.305299539	0.757566356	0.103271461	10.95393476
mmu04062: Chemokine signaling pathway	15	2.051983584	0.010896598	224	182	5738	2.111214678	0.795804631	0.107275274	12.19659821
mmu04710: Circadian rhythm	4	0.547195622	0.01240693	224	13	5738	7.881868132	0.836388093	0.113685896	13.77511641
mmu04150: mTOR signaling pathway	7	0.957592339	0.017524805	224	54	5738	3.320601852	0.922975091	0.148049328	18.93281671
mmu05221: Acute myeloid leukemia	7	0.957592339	0.022377366	224	57	5738	3.145833333	0.962430885	0.175545814	23.56063983
mmu04722: Neurotrophin signaling pathway	11	1.504787962	0.029242219	224	130	5738	2.167513736	0.986476857	0.212644294	29.69509961
mmu05410: Hypertrophic cardiomyopathy	8	1.094391245	0.043938939	224	84	5738	2.43962585	0.998519473	0.29030042	41.3411804
mmu05200: Pathways in cancer	20	2.735978112	0.045067727	224	323	5738	1.586134454	0.998752551	0.284184432	42.15810861

Program: David Functional Annotation tool; Input: DEG 841 genes (P<0.05 and logFC ≥ 11 and logCPM ≥ 11); KEGG\_PATHWAY (Top 20); KEGG, Kyoto Encyclopedia of Genes and Genomes; DEG, differentially expressed gene; FDR, false discovery rate; FC, fold change; CPM, counts per million.

Table SII. Hypo-KEGG pathway functional annotation of DEGs and gene expression.

Term	Count	%	P-value	List total	Pop hits	Pop total	Fold enrichment	Bonferroni	Benjamini	FDR
mmu03010: Ribosome	38	4.008438819	2.12x10 <sup>-21</sup>	379	89	5738	6.464202069	3.22x10 <sup>-19</sup>	3.22x10 <sup>-19</sup>	2.53x10 <sup>-18</sup>
mmu00190: Oxidative phosphorylation	25	2.637130802	2.99x10 <sup>-6</sup>	379	130	5738	2.911508017	4.54x10 <sup>-4</sup>	2.27x10 <sup>-4</sup>	0.003578335
mmu05010: Alzheimer's disease	27	2.848101266	1.28x10 <sup>-4</sup>	379	182	5738	2.24602047	0.019331732	0.006485887	0.153597442
mmu05012: Parkinson's disease	22	2.320675105	1.39x10 <sup>-4</sup>	379	133	5738	2.504334715	0.020883027	0.005262146	0.166043623
mmu04142: Lysosome	19	2.004219409	7.03x10 <sup>-4</sup>	379	119	5738	2.417285648	0.101408722	0.021158352	0.838446192
mmu04510: Focal adhesion	25	2.637130802	0.002506023	379	198	5738	1.911596173	0.317090908	0.061587432	2.95857873
mmu05016: Huntington's disease	23	2.426160338	0.004138336	379	183	5738	1.902821633	0.467585123	0.086112193	4.842292354
mmu00565: Ether lipid metabolism	8	0.843881857	0.006852658	379	35	5738	3.460535243	0.648374738	0.122473968	7.900613029
mmu04530: Tight junction interaction	18	1.898734177	0.007046512	379	135	5738	2.018645558	0.658654911	0.112573019	8.115550446
mmu04512: ECM-receptor interaction	12	1.265822785	0.019412292	379	83	5738	2.188892774	0.949191121	0.257675215	20.91372708
mmu00982: Drug metabolism	11	1.160337553	0.02426932	379	75	5738	2.220510114	0.976113416	0.28786971	25.47703692
mmu04666: Fc gamma R-mediated phagocytosis	13	1.371308017	0.026519321	379	98	5738	2.008346346	0.983182744	0.288546926	27.50806632
mmu04144: Endocytosis	21	2.215189873	0.042732132	379	202	5738	1.573943938	0.998690549	0.399880651	40.70891366

Program: David Functional Annotation tool; Input: DEG 1,061 genes (P<0.05 and logFC ≥ 11 and logCPM ≥ 11); KEGG\_PATHWAY: KEGG, Kyoto Encyclopedia of Genes and Genomes; DEG, differentially expressed gene; FDR, false discovery rate; FC, fold change; CPM, counts per million.