Enrichment analysis for Asthma

1, Download the Chip data related to asthma from GEO.
2, Collect the differential gens (p<0.05, logFC<-1 or logFC>1)
3, Intersection of differential gens
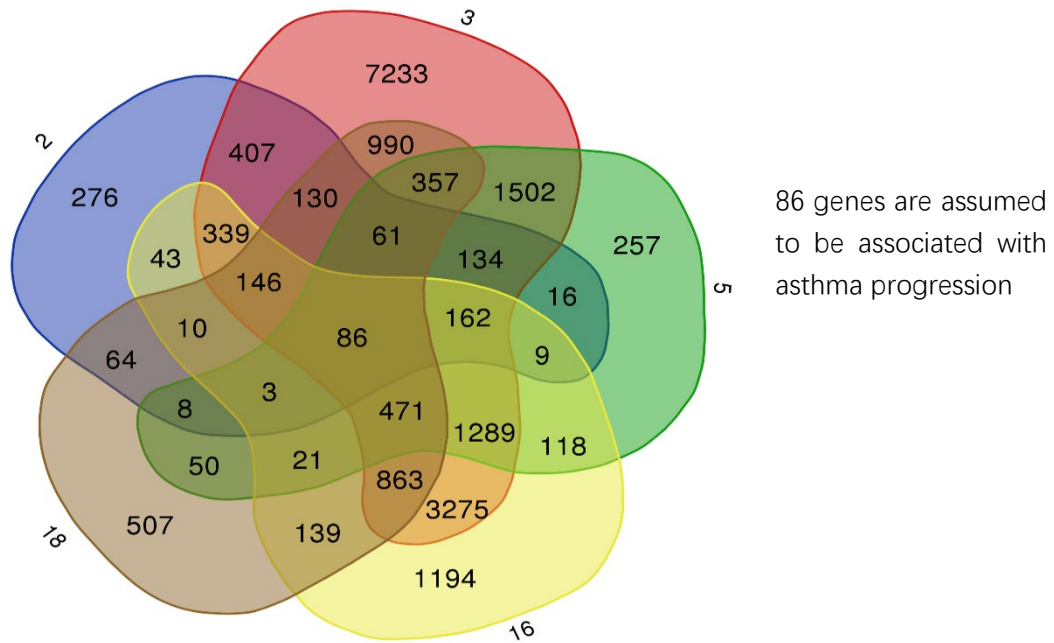

86 genes are assumed to be associated with asthma progression

Figure 1. Intersection set of gene list.

4. Enrichment analysis (www.metascape.com)
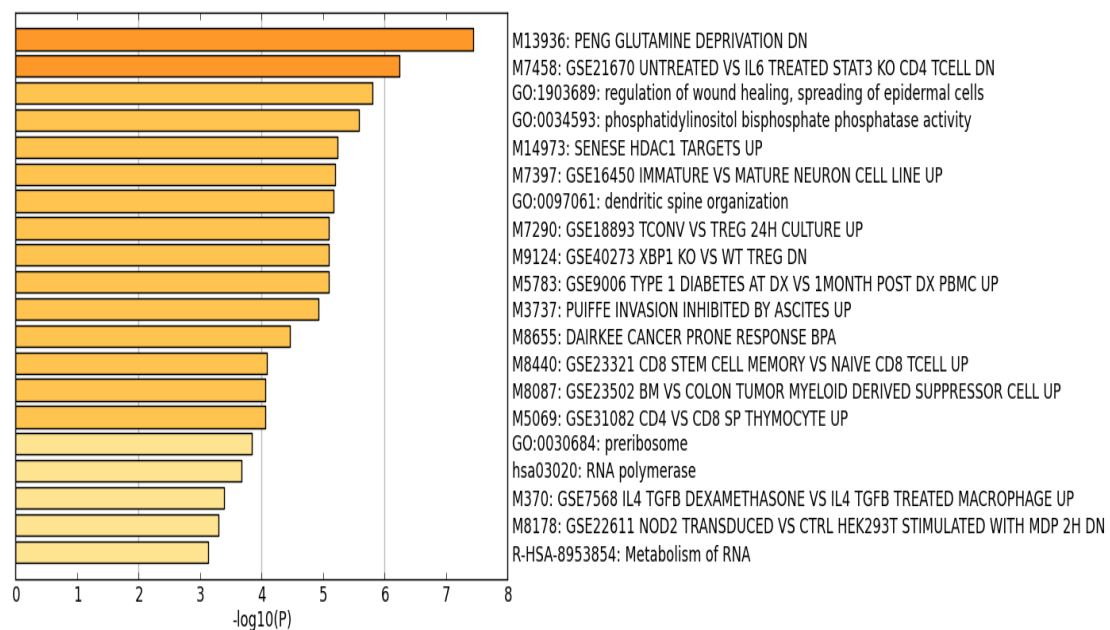
Figure 2. Enrichment summary

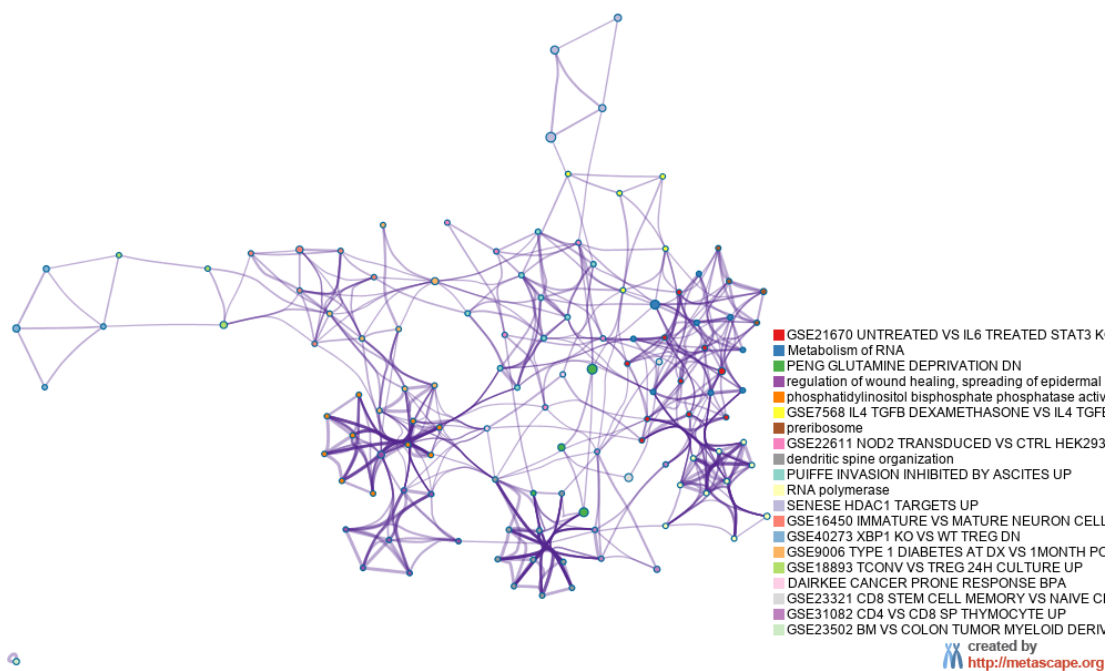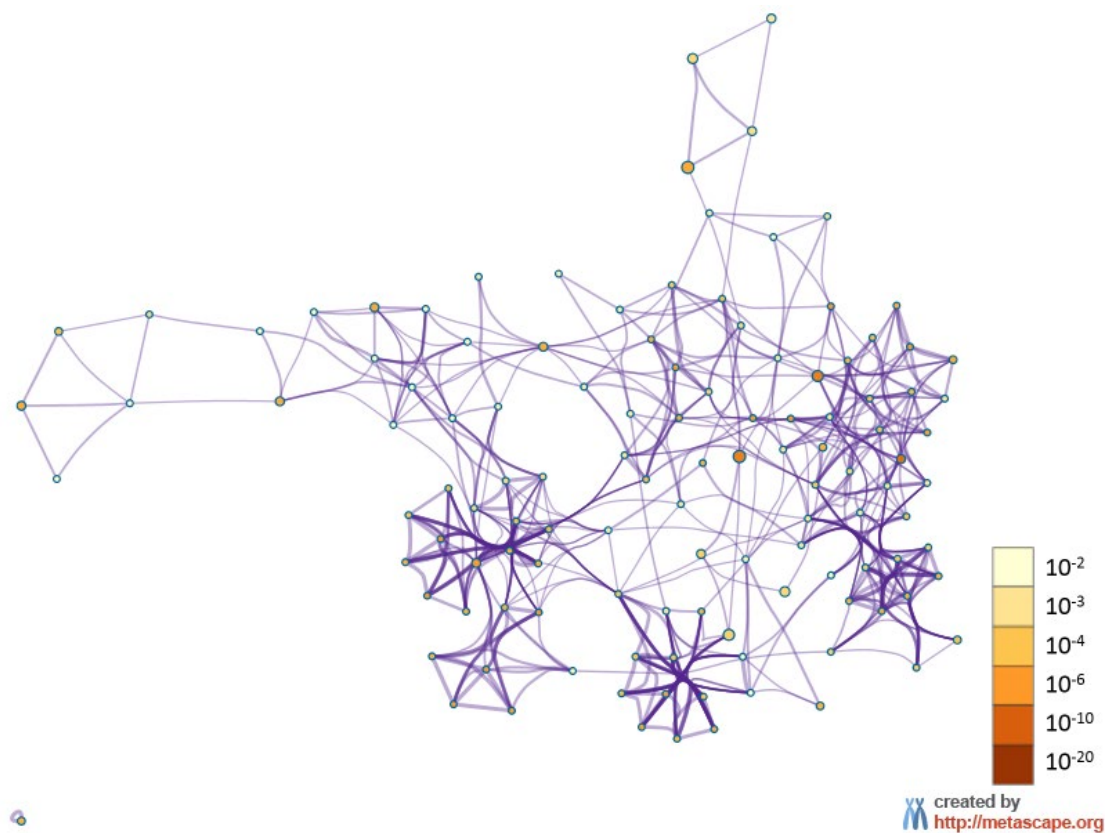**Figure 3.** Enriched ontology clusters. Colored by cluster ID.

The legend for Figure 3 contains:
- GSE21670 UNTREATED VS IL6 TREATED STAT3 K
- Metabolism of RNA
- PENG GLUTAMINE DEPRIVATION DN
- regulation of wound healing, spreading of epidermal
- phosphatidylinositol bisphosphate phosphatase activ
- GSE7568 IL4 TGFB DEXAMETHASONE VS IL4 TGFI
- preribosome
- GSE22611 NOD2 TRANSDUCED VS CTRL HEK293
- dendritic spine organization
- PUIFFE INVASION INHIBITED BY ASCITES UP
- RNA polymerase
- SENESE HDAC1 TARGETS UP
- GSE16450 IMMATURE VS MATURE NEURON CELL
- GSE40273 XBP1 KO VS WT TREG DN
- GSE9006 TYPE 1 DIABETES AT DX VS 1MONTH PO
- GSE18893 TCONV VS TREG 24H CULTURE UP
- DAIRKEE CANCER PRONE RESPONSE BPA
- GSE23321 CD8 STEM CELL MEMORY VS NAIVE CI
- GSE31082 CD4 VS CD8 SP THYMOCYTE UP
- GSE23502 BM VS COLON TUMOR MYELOID DERIV

created by
http://metascape.org

Figure 4. Enriched ontology clusters. Colored by p-value.

The legend for Figure 4 shows a color scale:
- 10^{-2}
- 10^{-3}
- 10^{-4}
- 10^{-6}
- 10^{-10}
- 10^{-20}

created by
http://metascape.org

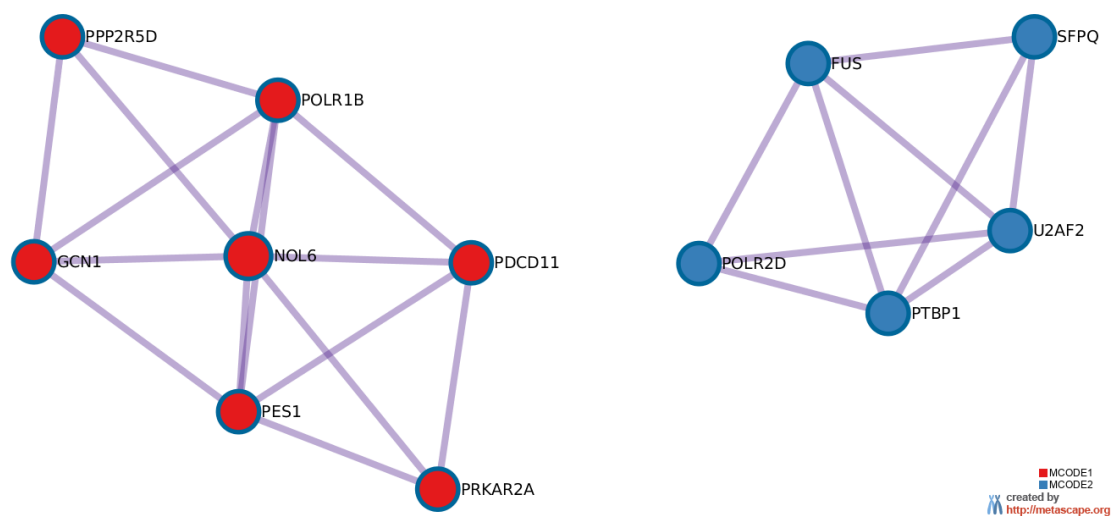5. Prediction of Protein-Protein Interaction (PPI) nectwork

Figure 5. PPI MCODE components
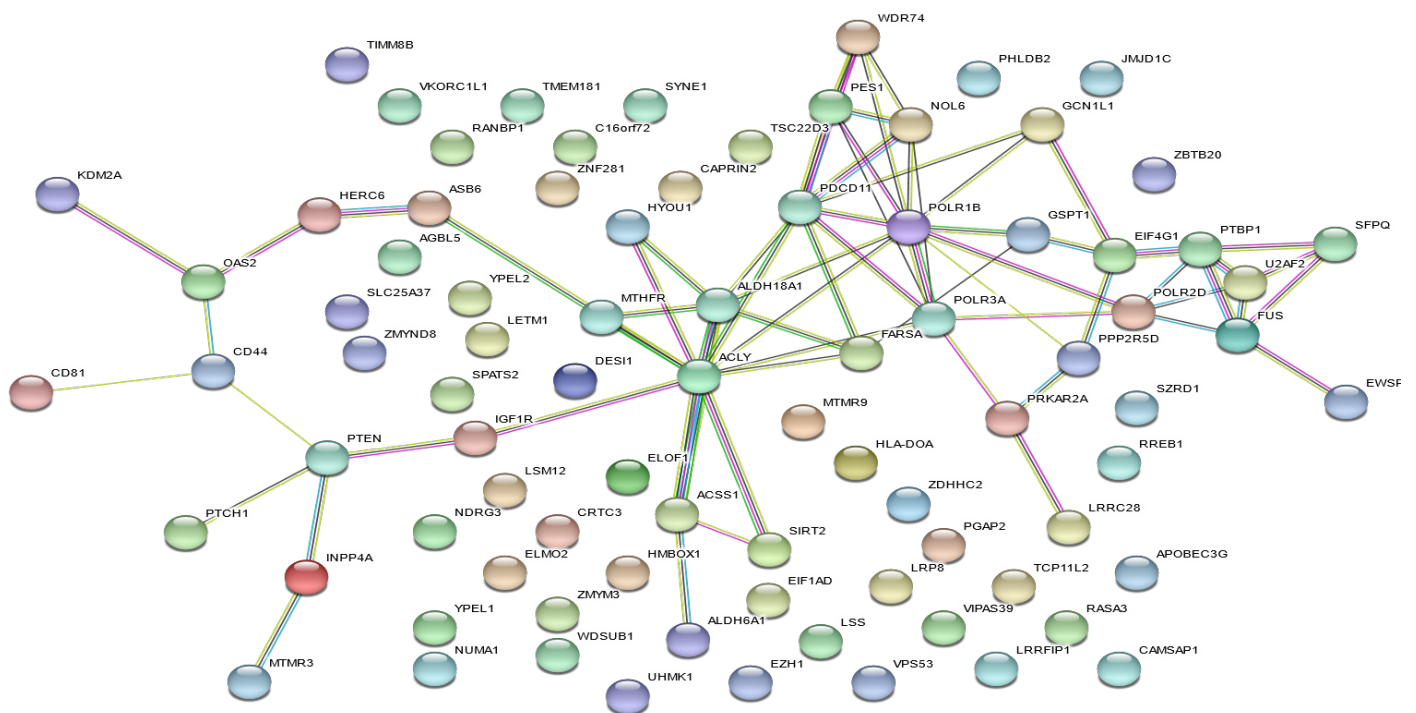
Figure 6. PPI network (www.string.com)

5. Find the Hub gene by using different algorithm (Cytoscape)

name	Between	BottleN	Closene	Clusterir	Degree	DMNC	EcCentri	EPC	MCC	MNC	Radiality	Stress		
ACLY	715.5476	37	20.75	0.2	11	0.26253	0.25	16.94	28	9	7.02778	1472		10
POLR1B	350.1524	31	20.6	0.27273	11	0.358	0.2	17.506	66	9	6.91667	970		10
POLR3A	250.9714	4	18.6	0.42857	7	0.42794	0.2	16.727	33	6	6.80556	568		10
ALDH18A1	61.49048	5	17.68333	0.38095	7	0.2927	0.2	16.51	18	7	6.61111	238		9
PDCD11	93.01429	1	18.93333	0.44444	9	0.38186	0.2	17.193	68	9	6.72222	286		9
POLR2D	270.5238	6	16.21667	0.4	5	0.46346	0.16667	14.281	8	3	6.33333	756		8
PES1	1.3	1	15.21667	0.9	5	0.58344	0.16667	16.064	48	5	6.13889	6		7
NOL6	1.3	1	15.21667	0.9	5	0.58344	0.16667	15.826	48	5	6.13889	6		7
FARSA	26.2	1	15.63333	0.5	4	0.46346	0.2	14.882	7	3	6.38889	90		6
IGF1R	320	7	14.73333	0	2	0	0.2	8.756	2	1	6.44444	572	6	5
FUS	87.57143	2	13.52857	0.5	5	0.47366	0.14286	11.365	13	4	5.55556	238	6	5
PTBP1	47.04762	1	14.1119	0.5	5	0.47366	0.14286	12.19	13	4	5.66667	152		5
WDR74	0	1	14.46667	1	4	0.56839	0.16667	14.981	24	4	6.05556	0		5
ASB6	158	4	14.1	0	2	0	0.2	8.256	2	1	6.27778	284	5	4
PTEN	314	6	13.58333	0	4	0	0.16667	6.106	4	1	5.88889	524		3
ACSS1	71	2	14.58333	0.33333	4	0.30898	0.2	12.432	5	3	6.16667	172		3
U2AF2	17.57143	2	13.02857	0.83333	4	0.47366	0.14286	11.313	12	4	5.52778	102	5	3

Figure 7. Evaluation of differential genes

6.Verification by wet experiment like qPCR and WB