**Identification of Biomarkers and Pathogenesis in Severe Asthma by Co-expression Network Analysis**

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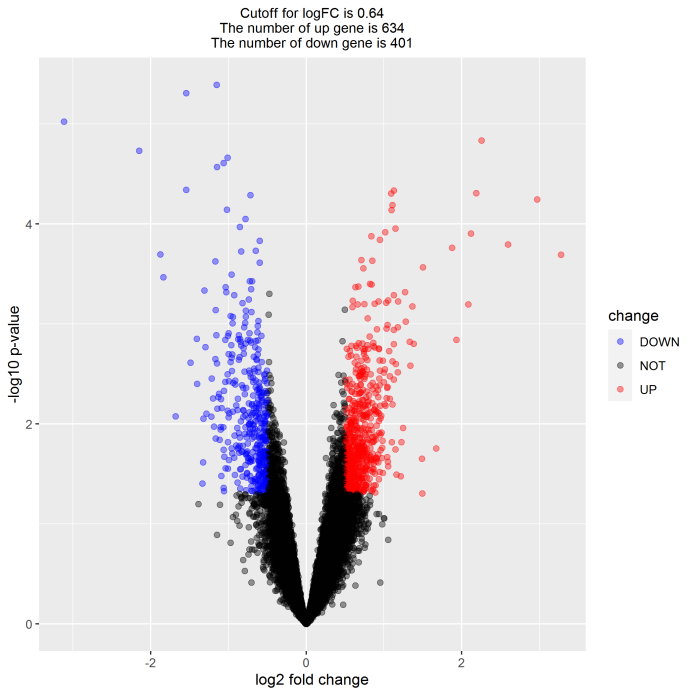
\*Correspondence: Chen Ou

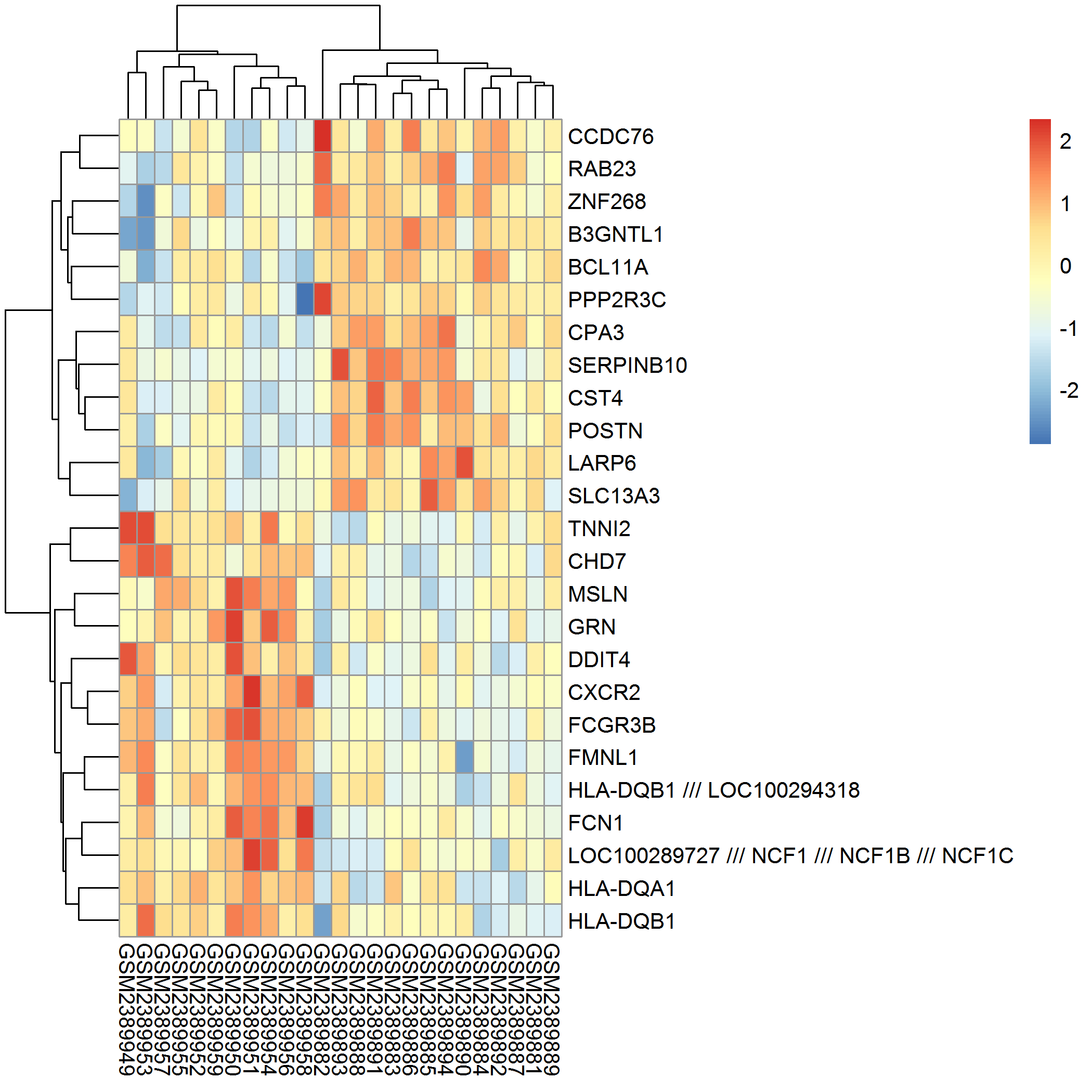
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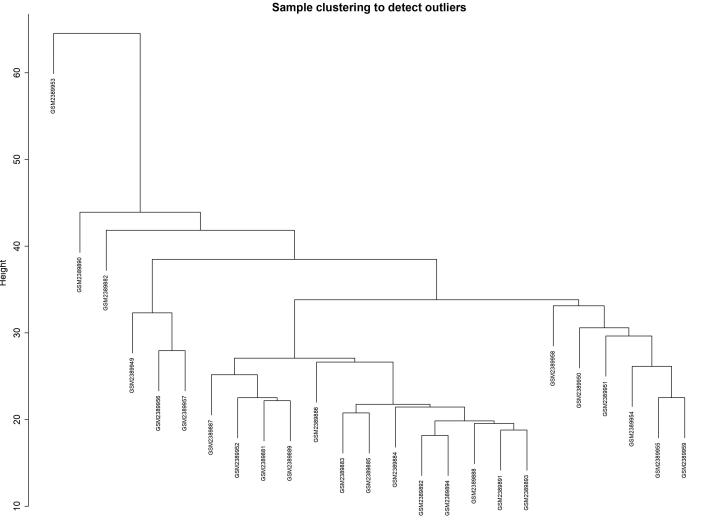
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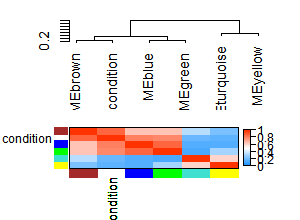
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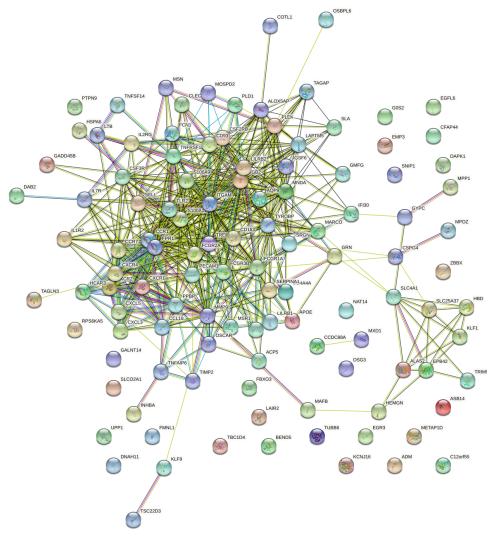
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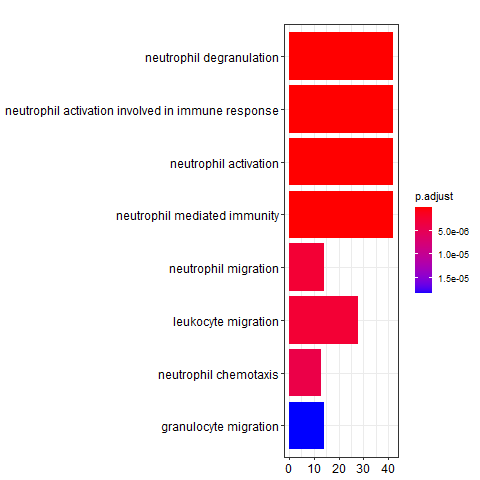
Figure S1. Volcano plot of all probesets

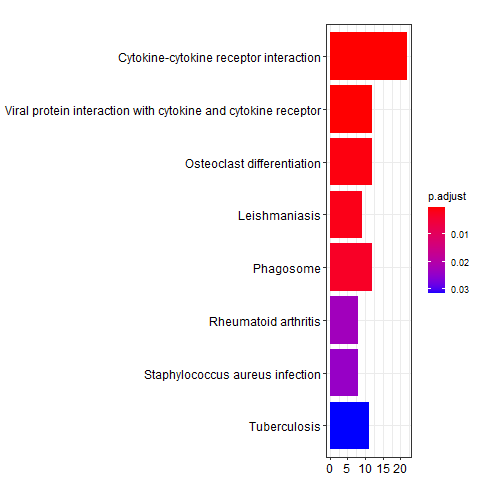
Figure S2. Heatmap of the top 25 changed genes

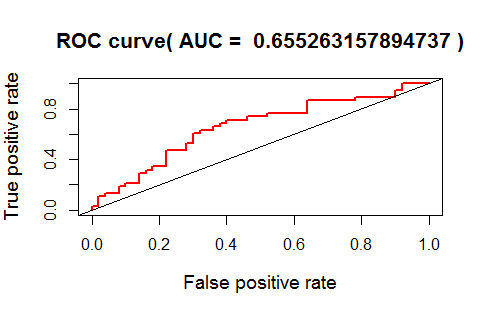
Figure S3. Hierarchical clustering analysis

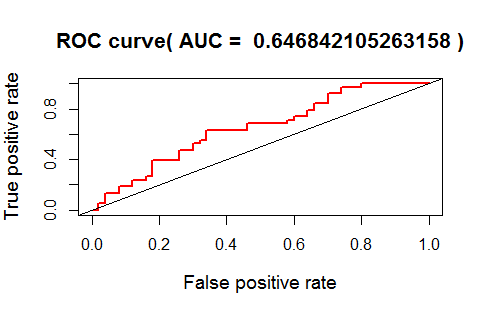
Figure S4. The eigengene dendrogram and heatmap

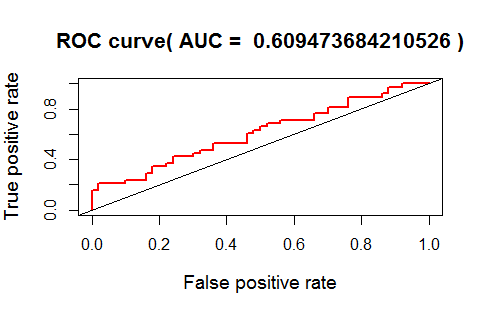
Figure S5. Brown module visualized in String database

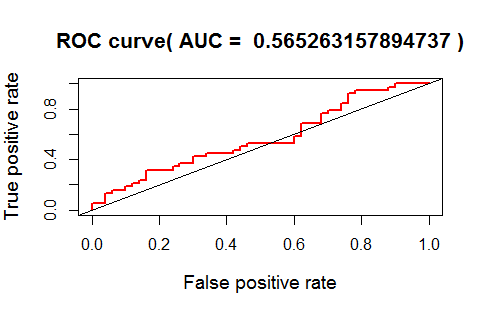
Figure S6. GO enrichment analysis of genes in modules positively related to asthma severity

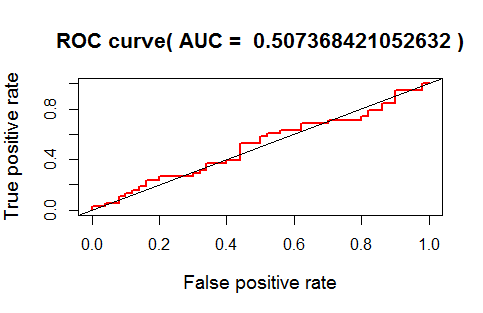
Figure S7. KEGG enrichment analysis of genes in modules positively related to asthma severity

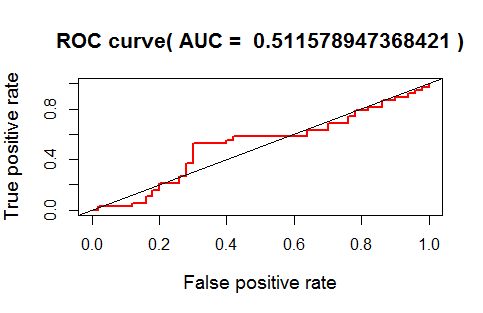
Figure S8. Receiver operating characteristics curve analyses of CXCR2

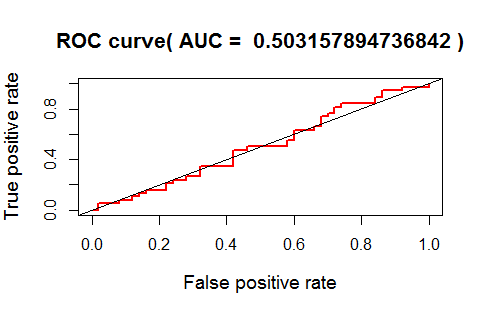
Figure S9. Receiver operating characteristics curve analyses of CXCR1

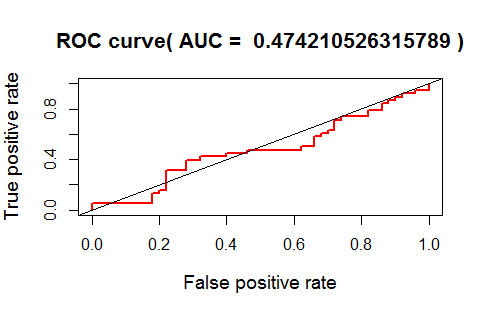
Figure S10. Receiver operating characteristics curve analyses of TLR2

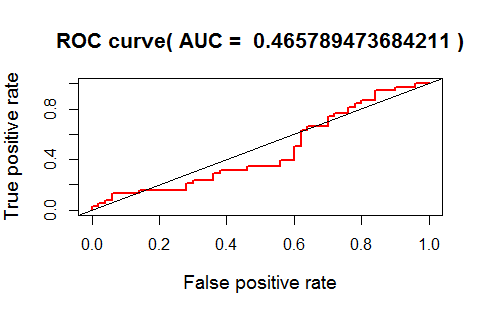
Figure S11 Receiver operating characteristics curve analyses of FPR1

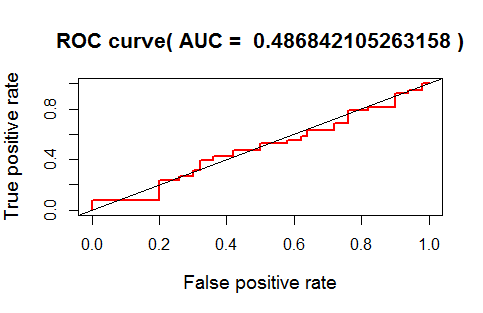
Figure S12. Receiver operating characteristics curve analyses of CCR1

Figure S13. Receiver operating characteristics curve analyses of FCGR3B

Figure S14. Receiver operating characteristics curve analyses of ITGAM

Figure S15. Receiver operating characteristics curve analyses of FCGR2A

Figure S16. Receiver operating characteristics curve analyses of CCR7

Figure S17. Receiver operating characteristics curve analyses of PLEK