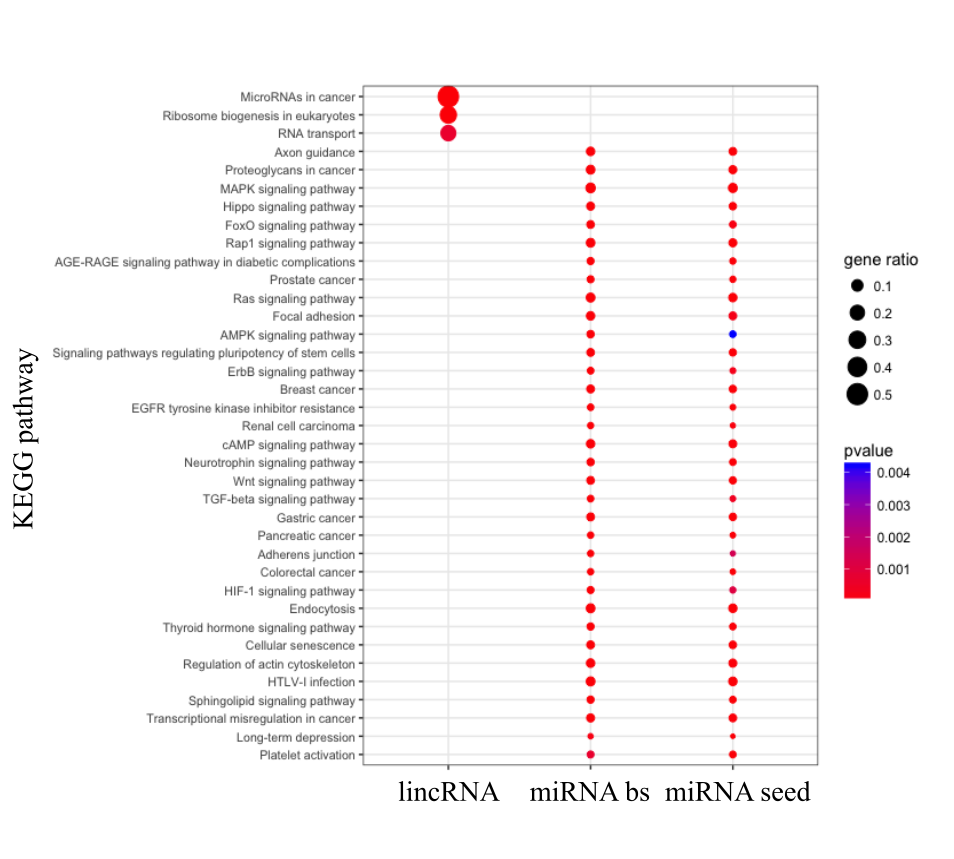
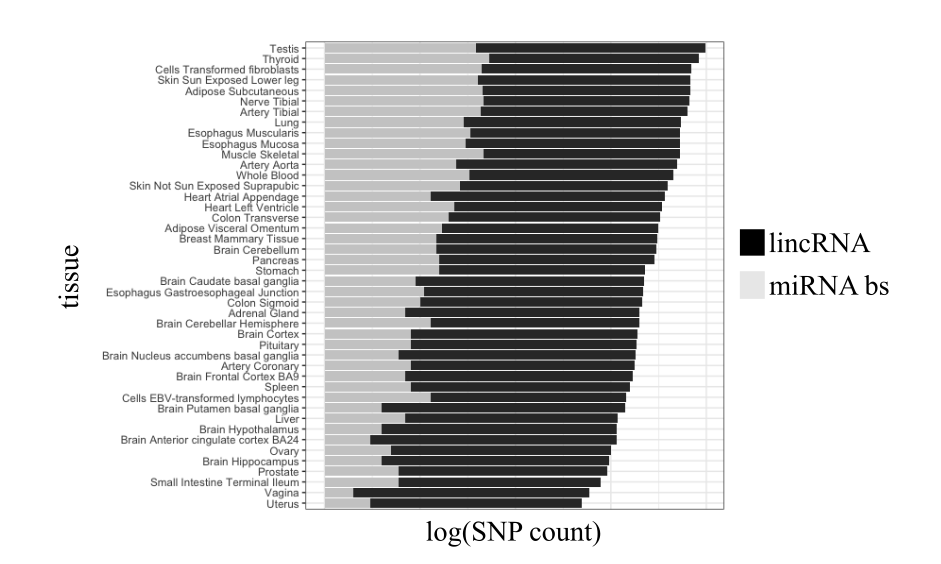
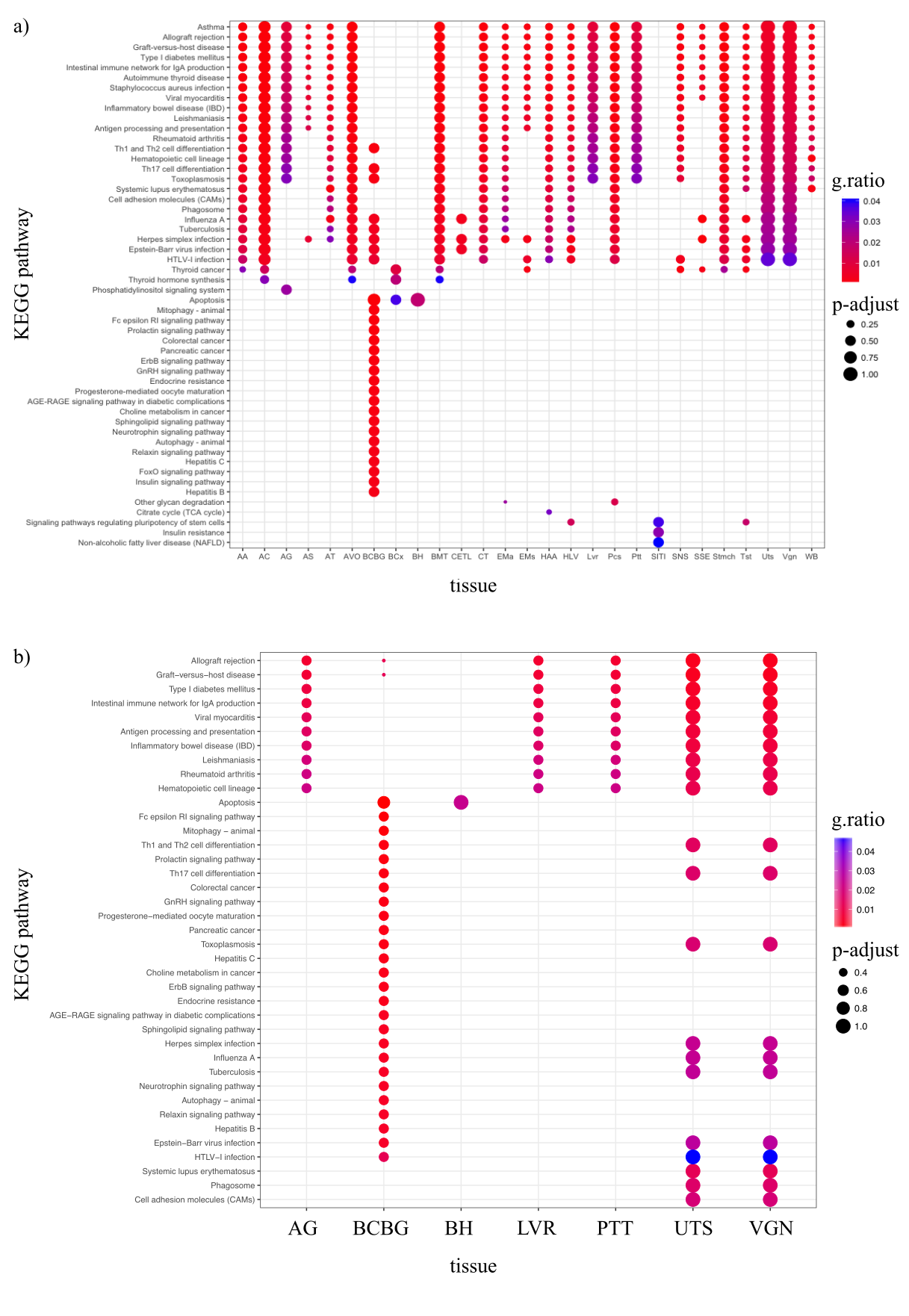
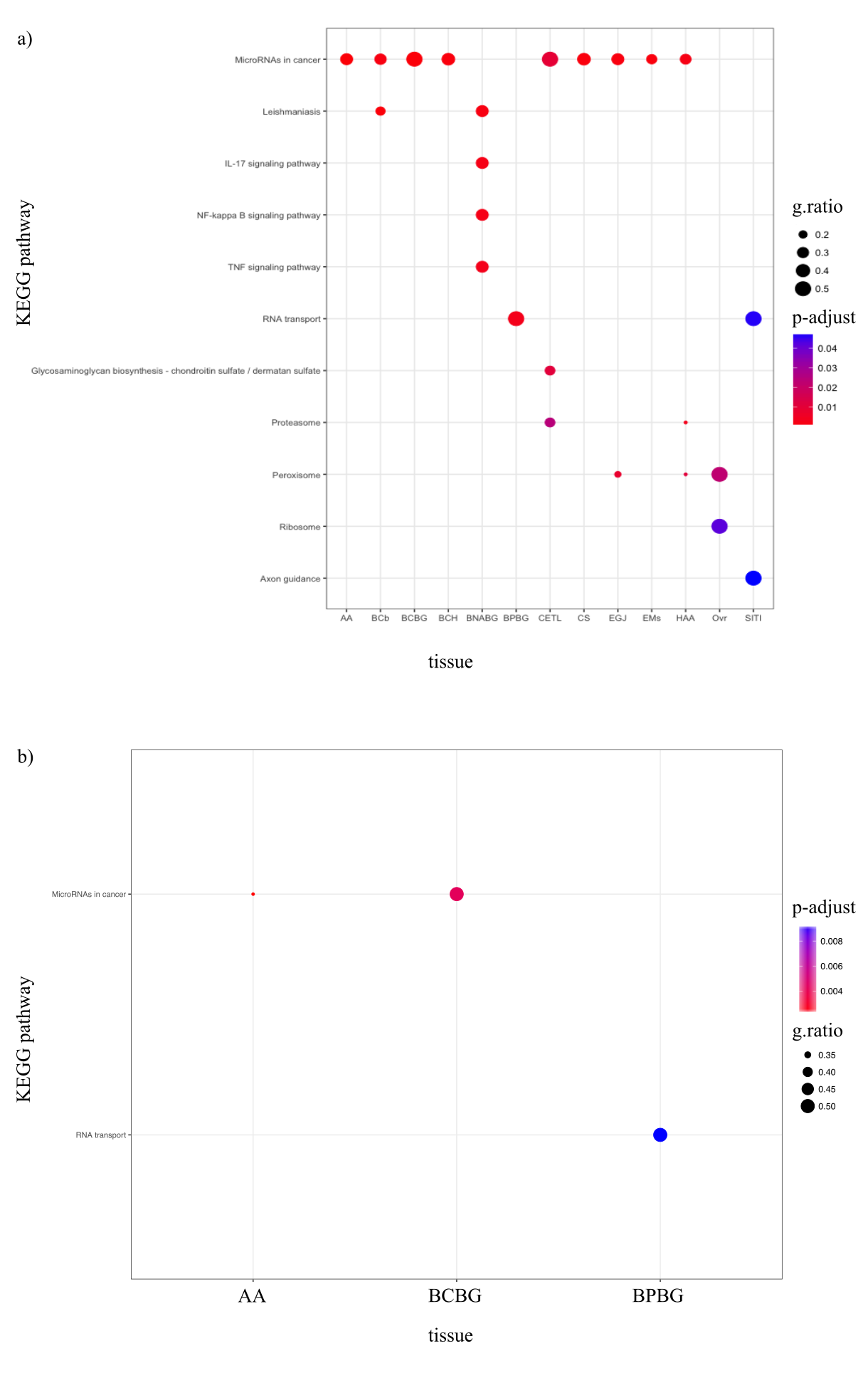
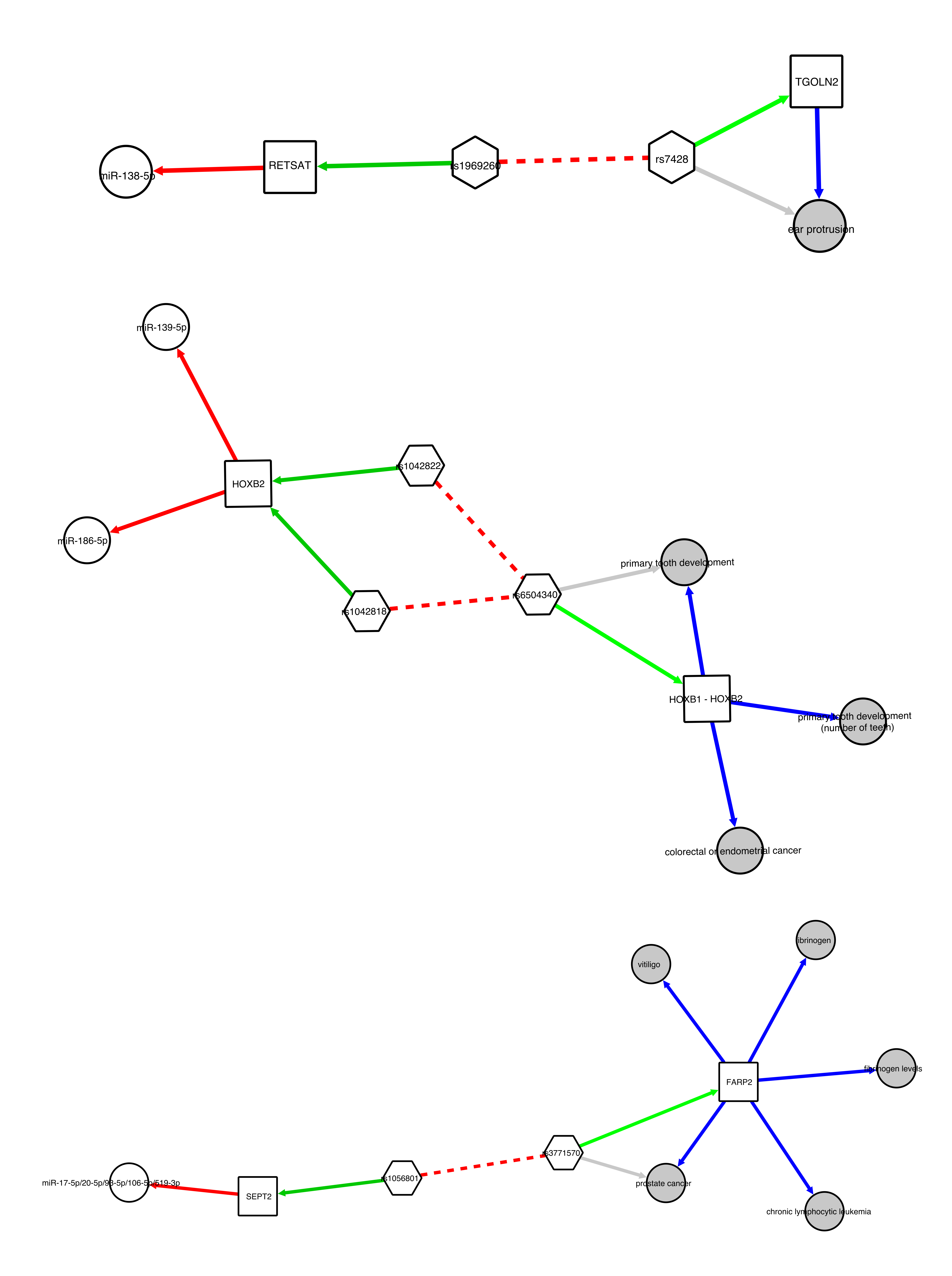
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**Figure S1.** KEGG enrichment analysis of genes where SNPs mapped to miRNA seeds (right column), miRNA binding sites (middle column) and lincRNAs (left column) are located.

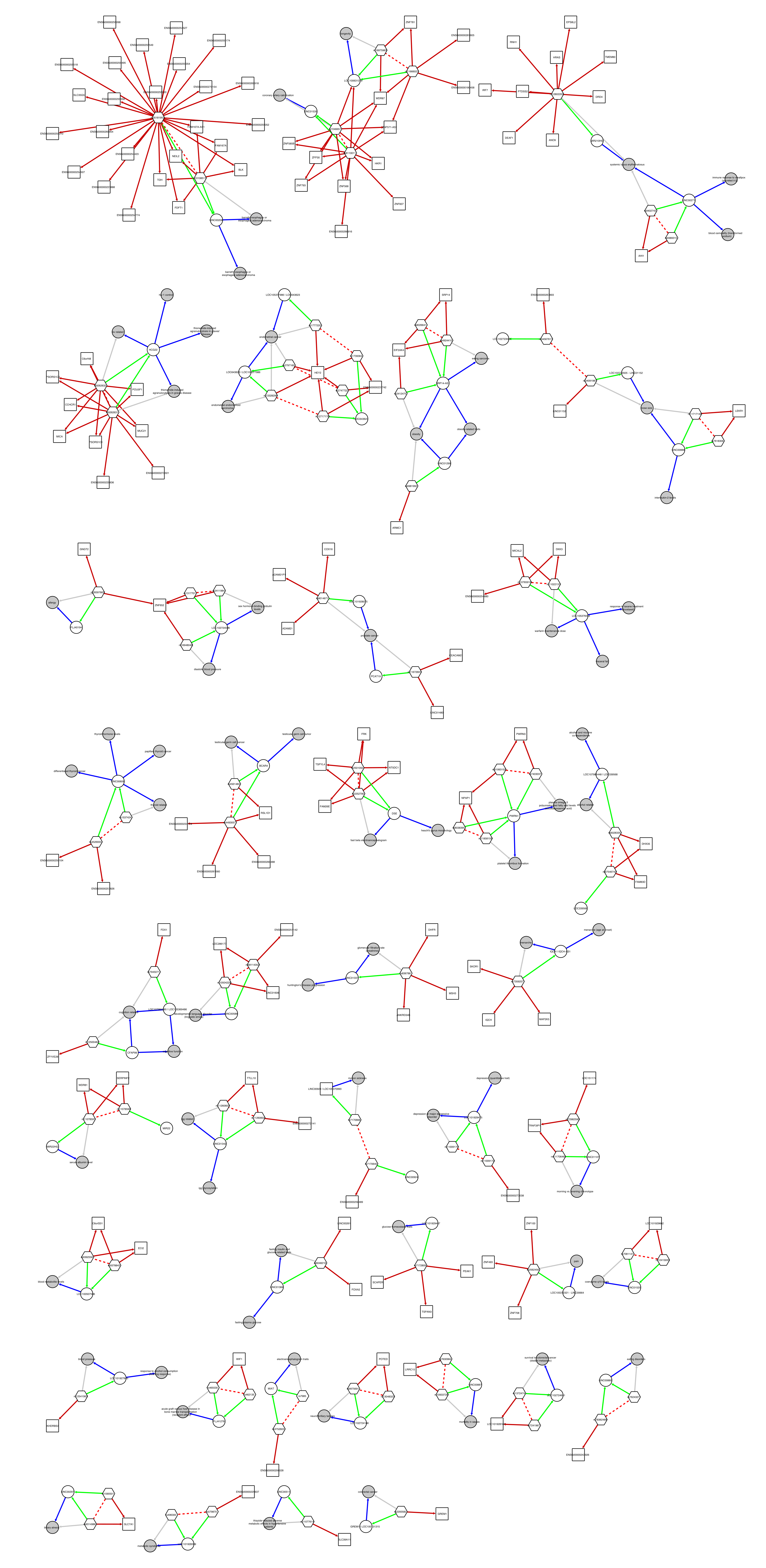
**Figure S2.** GTEX eQTL analysis results. The amount of SNPs (log) for each tissue.

**Figure S3.** KEGGenrichment analysis plot for GTEx eQTL analysis on miRNA binding sites. X-axis represents the tissues and y-axis represents the KEGG pathways. a) All genes are used as the control universe. b) Control universe is composed by genes selected based on all SNPs mapped to the studied regions.

**Figure S4.** KEGGenrichment analysis plot for GTEx overlapping lincRNAs. X-axis represents the tissues and y-axis represents the KEGG pathways. a) All genes are used as the control universe. b) Control universe is composed by genes selected based on all SNPs mapped to the studied regions.

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**Figure S5.** Smaller miRNA association sub-networks. The largest sub-network is shown as Figure 6C in the main text.



**Figure S6.** Smaller lincRNA association sub-networks. The largest sub-network is shown in Figure 7C in the main text.