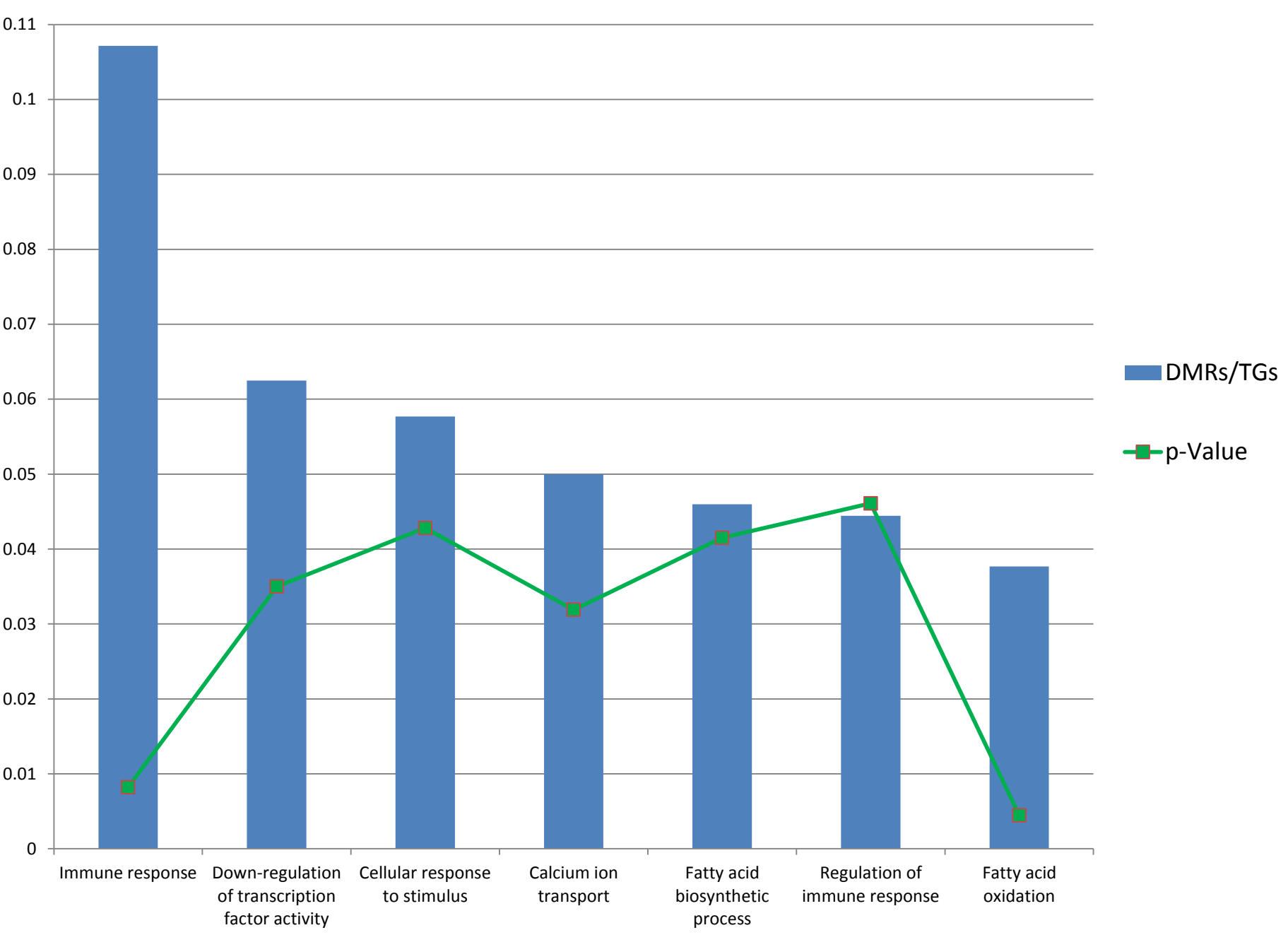
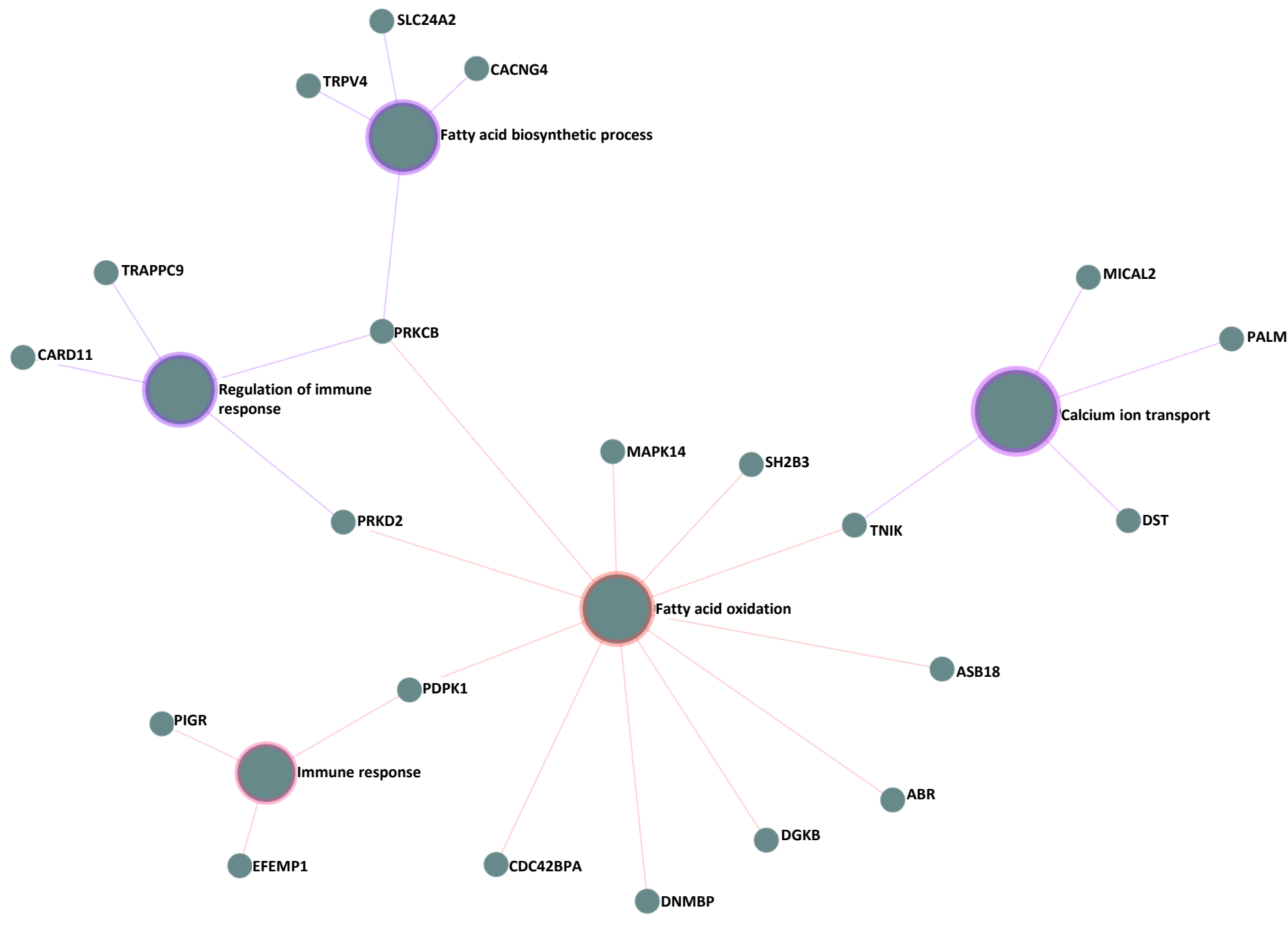
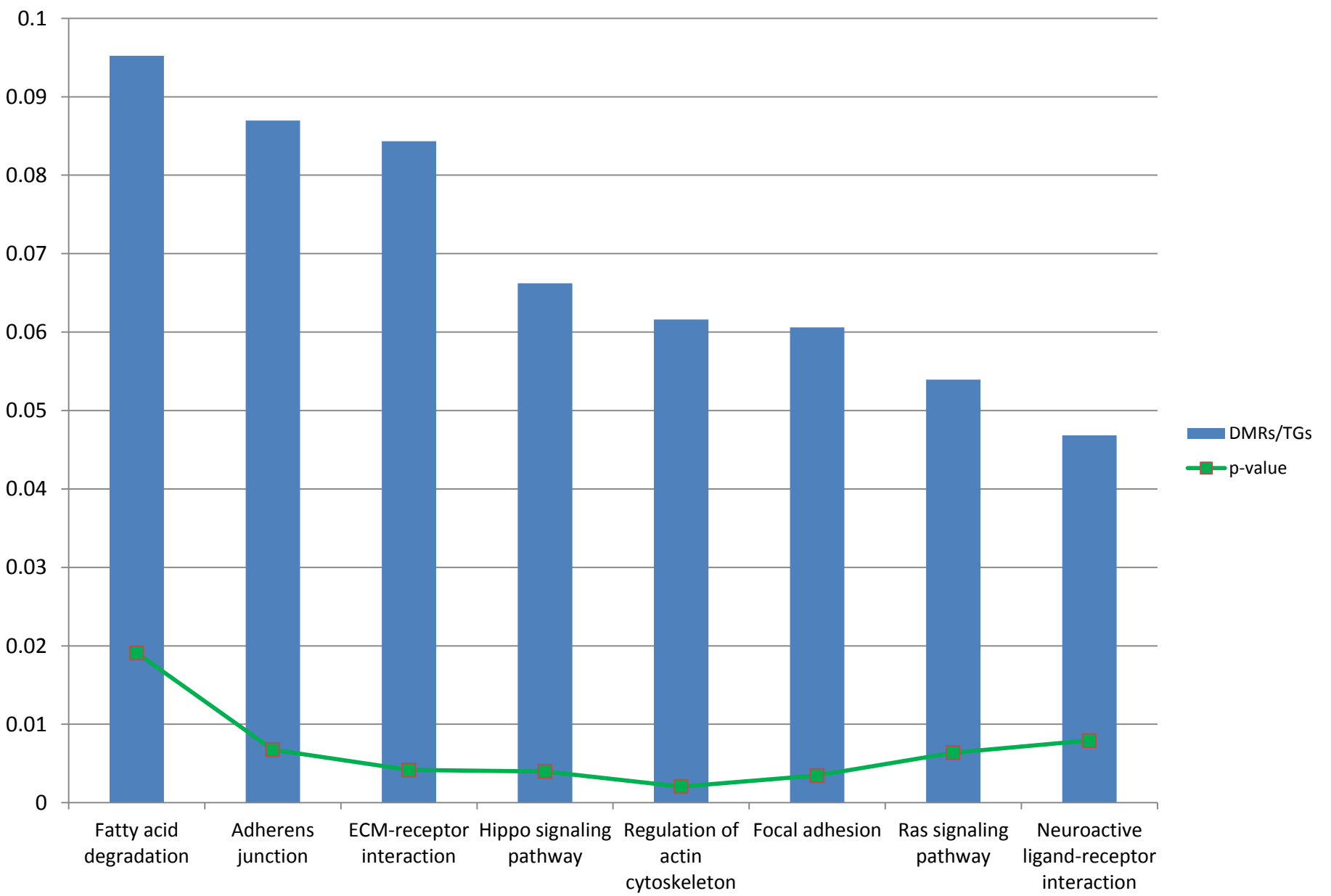
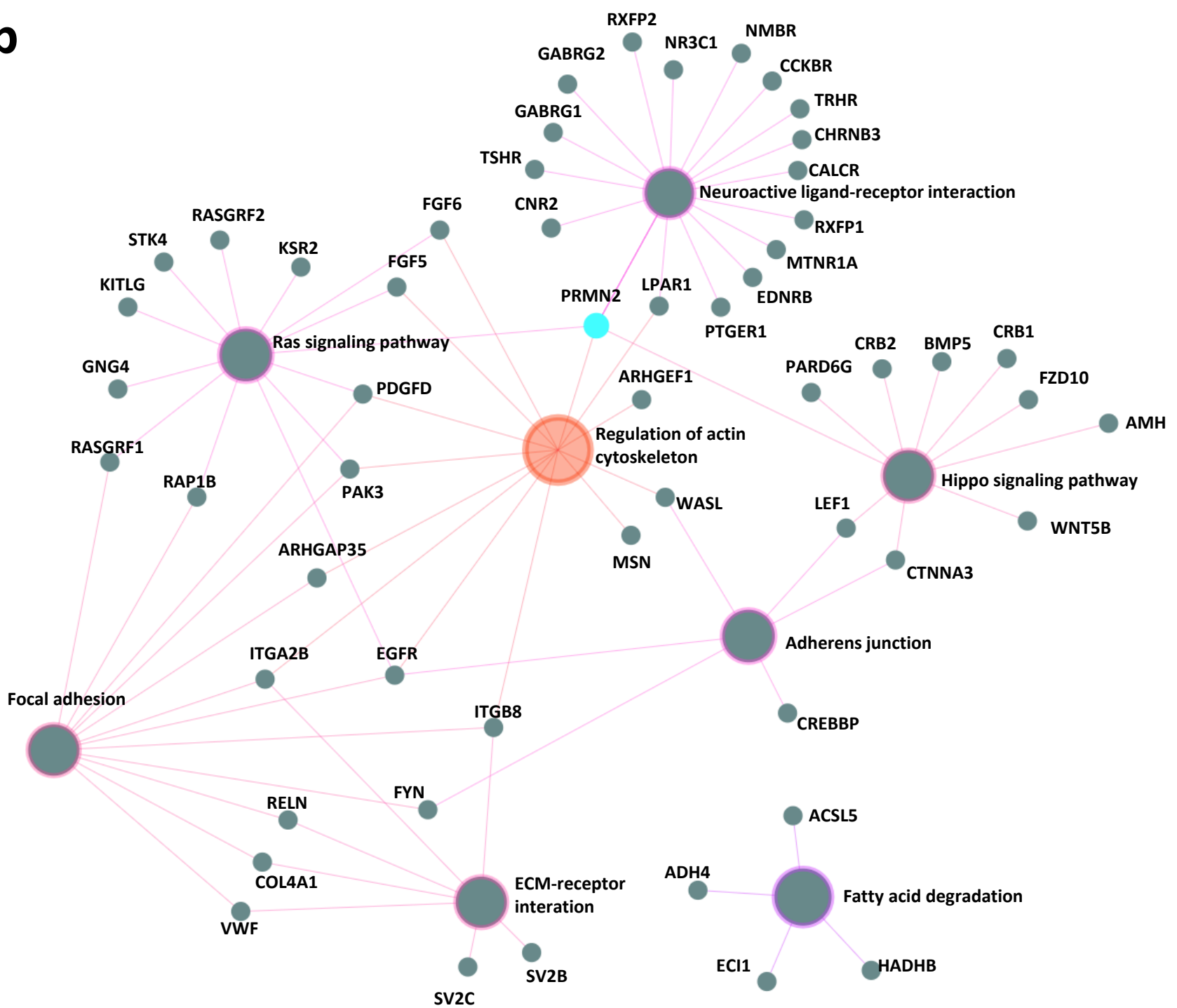


Metabolism-associated genome-wide epigenetic changes in bovine oocytes during early lactation

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a**b**

Supplemental figure 1. Functional annotation of mid postpartum (Mpp) specific DMRs. (a) Top biological processes enriched with the DMRs found in the Mpp group. (b) Biological processes network associated with DMRs from the Mpp group and their interaction. DMRs/TGs: Ratio of differentially methylated regions over the number of genes in the pathway. Pathways shown have p-values < 0.05.

a**b**

Supplemental figure 2. Functional annotation of cyclic heifer (CH) specific DMRs. (a) Top enriched KEGG pathways associated with the DMRs found in the CH group. (b) KEGG pathway network association with DMRs from the CH group and their interaction. DMRs/TGs: Ratio of differentially methylated regions over the number of genes in the pathway. Pathways shown have p-values < 0.05.