

A

Metabolism	P Value	Enrichment Ratio
Threonine & 2-Oxobutanoate Degradation	9.0355E-4	4.757
Phosphatidylethanolamine Biosynthesis	0.014279	4.057
Homocysteine Degradation	0.014407	4.036
Selenoamino Acid Metabolism	0.014687	3.620
Biotin Metabolism	0.014849	4.039
Lysine Degradation	0.016517	3.403
Methionine Metabolism	0.016937	3.106
Glycine & Serine Metabolism	0.023257	2.599
Catecholamine Biosynthesis	0.038154	3.494
Thyroid Hormone Synthesis	0.038154	3.494
Carnitine Synthesis	0.24275	1.494
Ammonia Recycling	0.25056	1.533

B

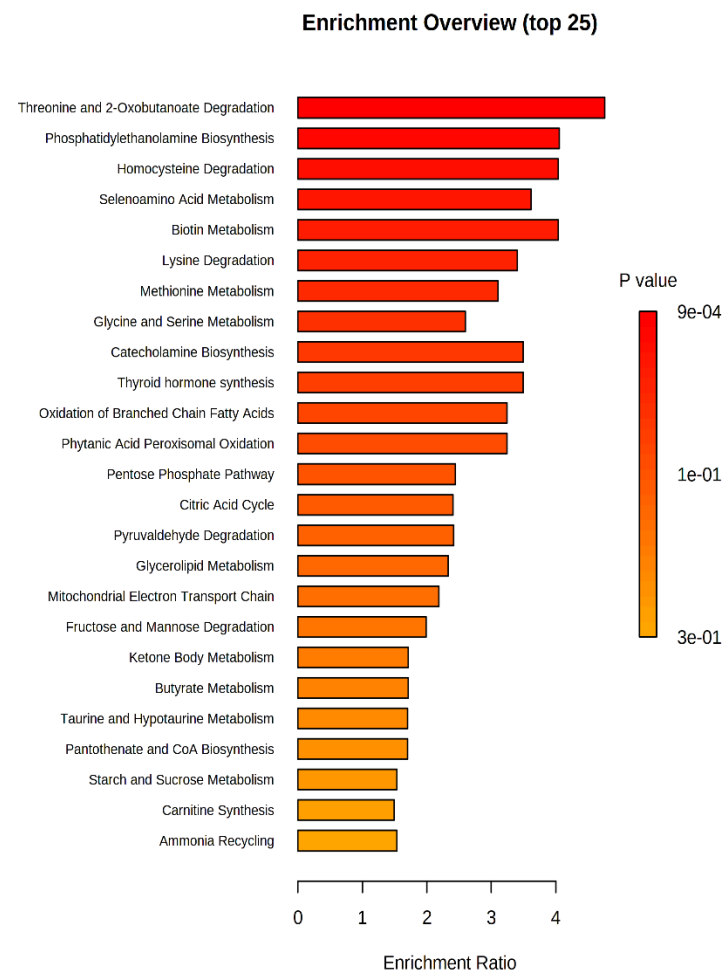
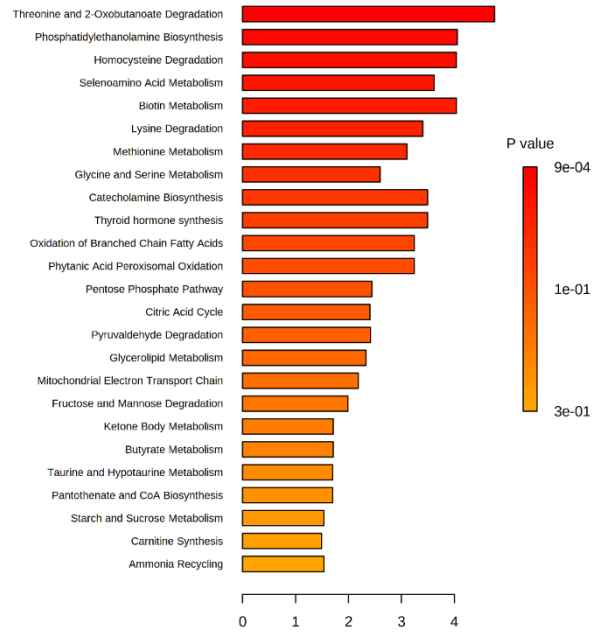


Figure S1. PFAS exposure upregulates mitochondrial dependence (citric acid cycle, PPP), and altered amino acid metabolism (serine & lysine) . Metabolic pathways that were upregulated in the PFAS-treated group compared to a non-treated control group were cross referenced and pathways that were upregulated in the PFAS group were listed based on enrichment ratio.

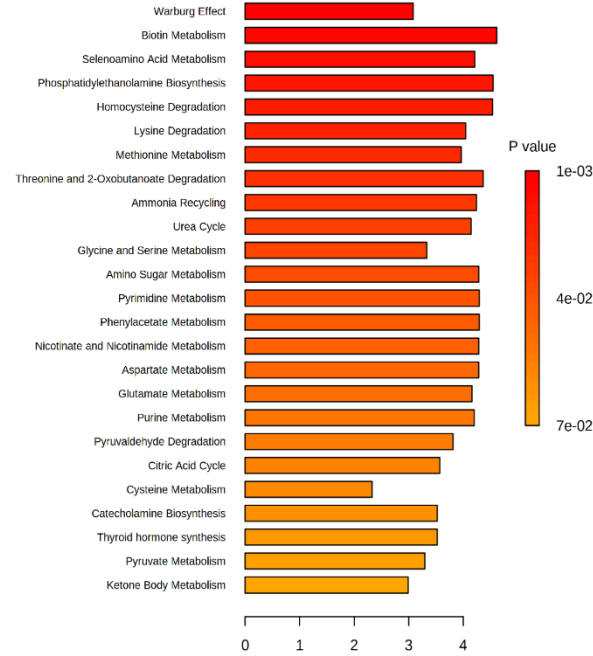
Veh vs. PFOS

Enrichment Overview (top 25)



Veh vs. DHT

Enrichment Overview (top 25)



DHT vs. DHT/PFOS

Enrichment Overview (top 25)

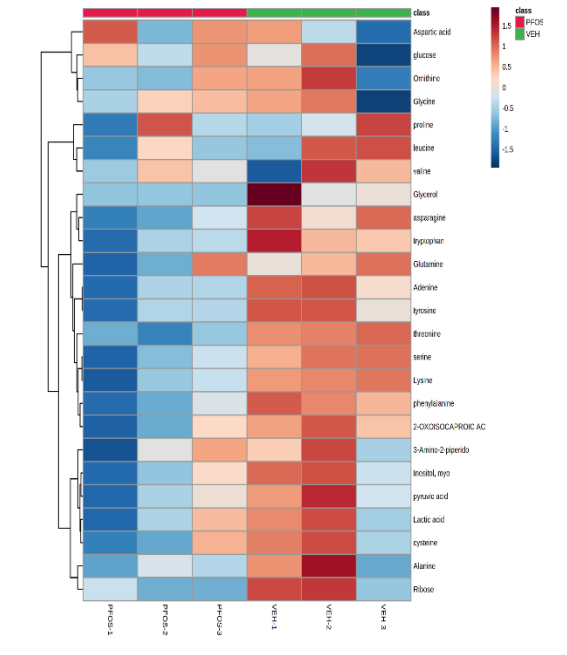
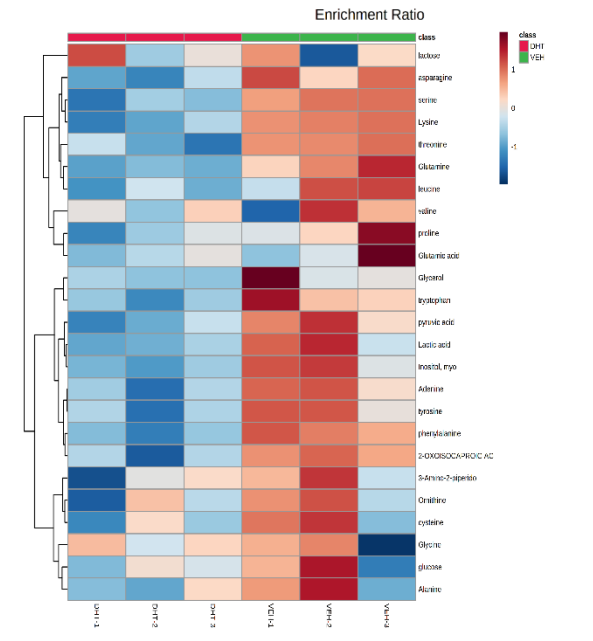
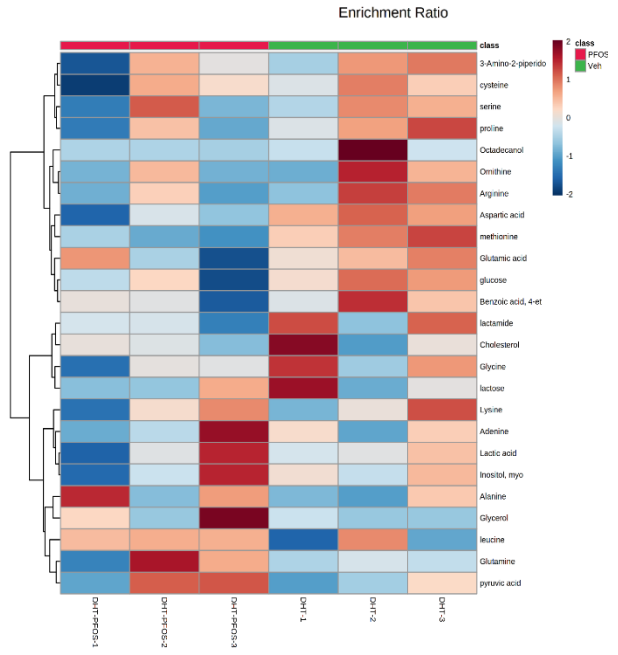
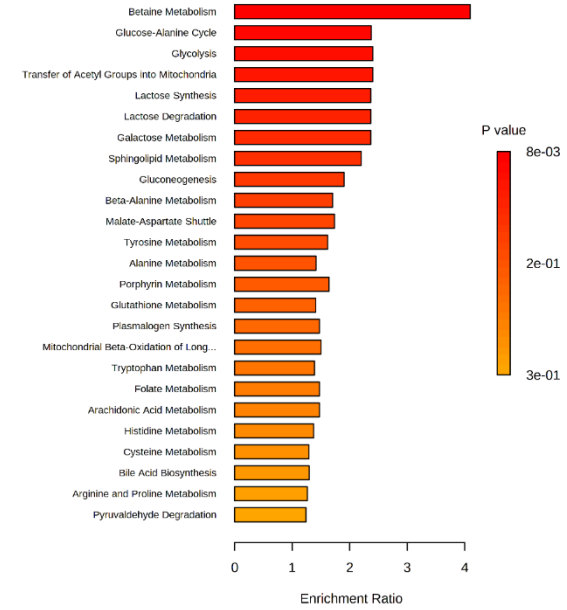


Figure S2

GSEA Dotplot for Prostate – HF against HF+PFOS, Prostate

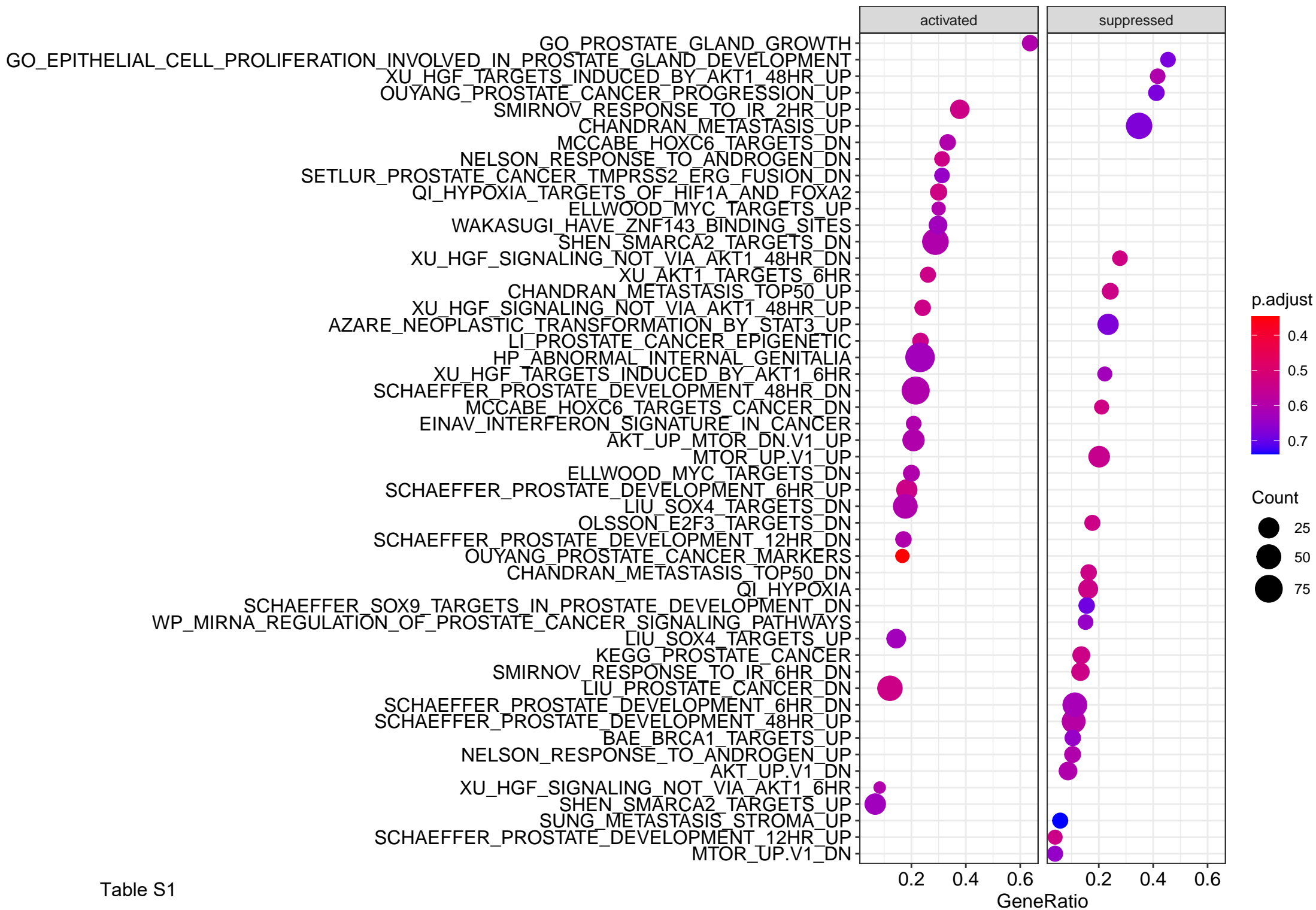
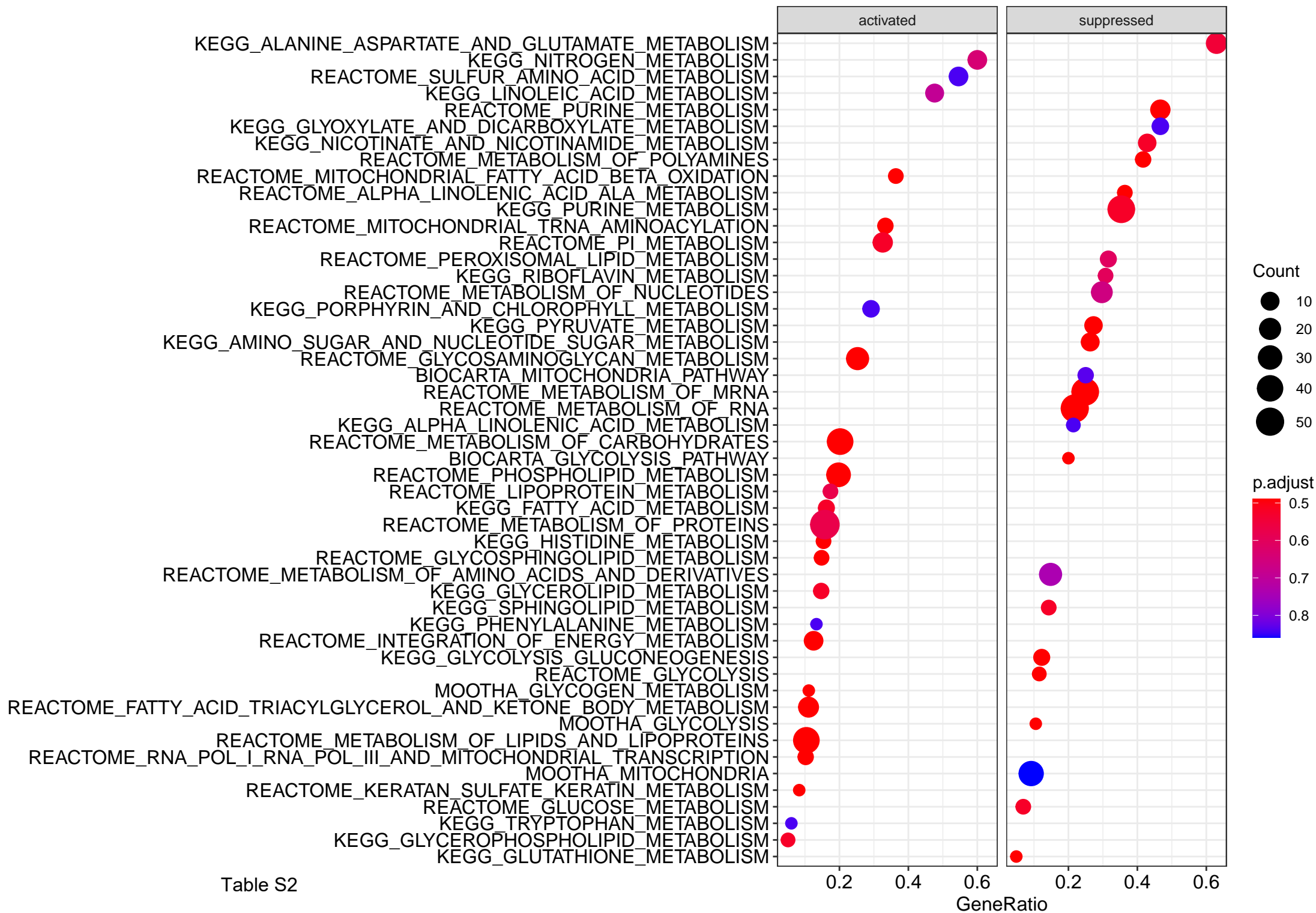
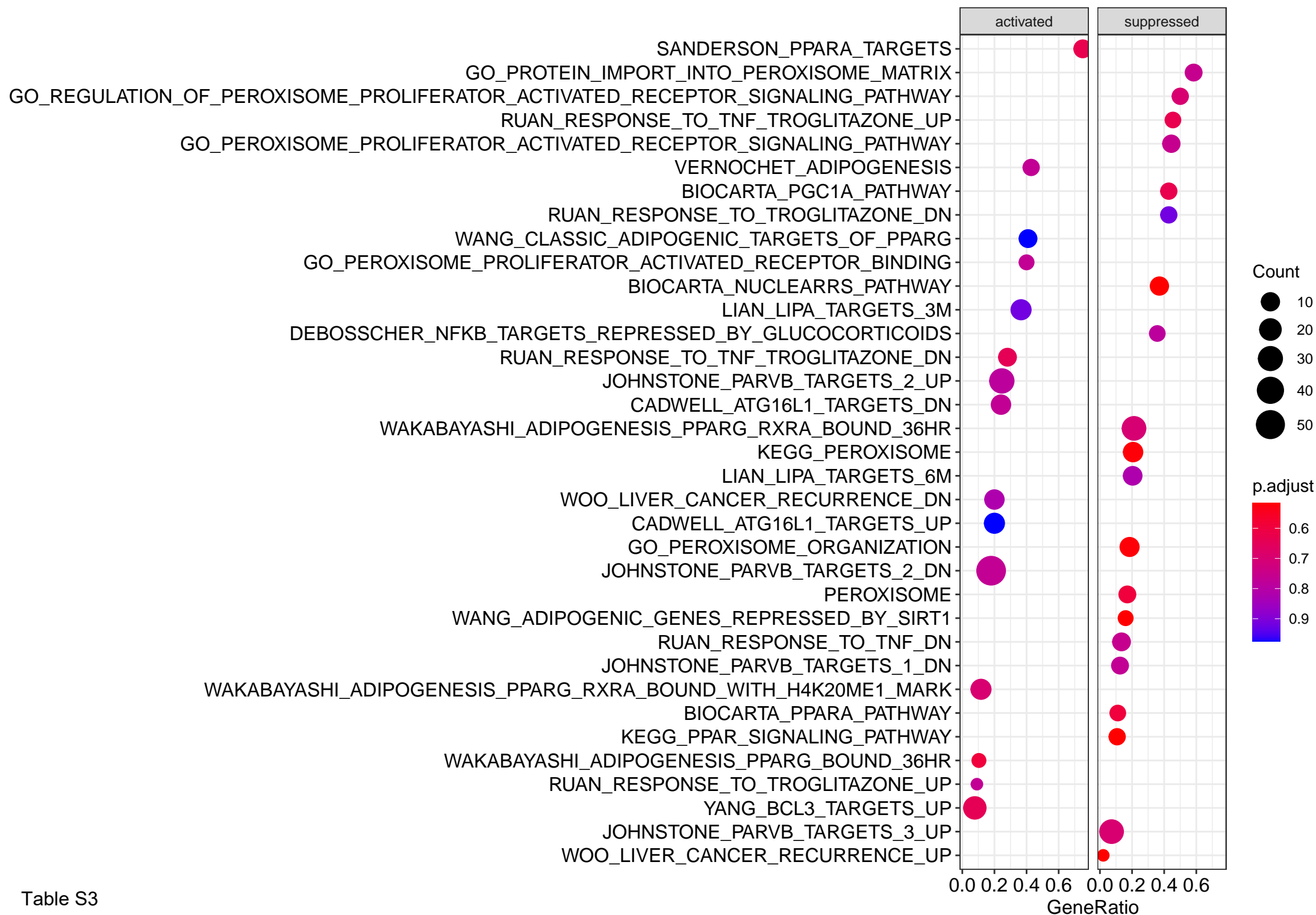


Table S1

GSEA Dotplot for Prostate – HF against HF+PFOS, Metabolism



GSEA Dotplot for Prostate – HF against HF+PFOS, PPAR targets



GSEA Dotplot for Prostate – HF, Metabolism

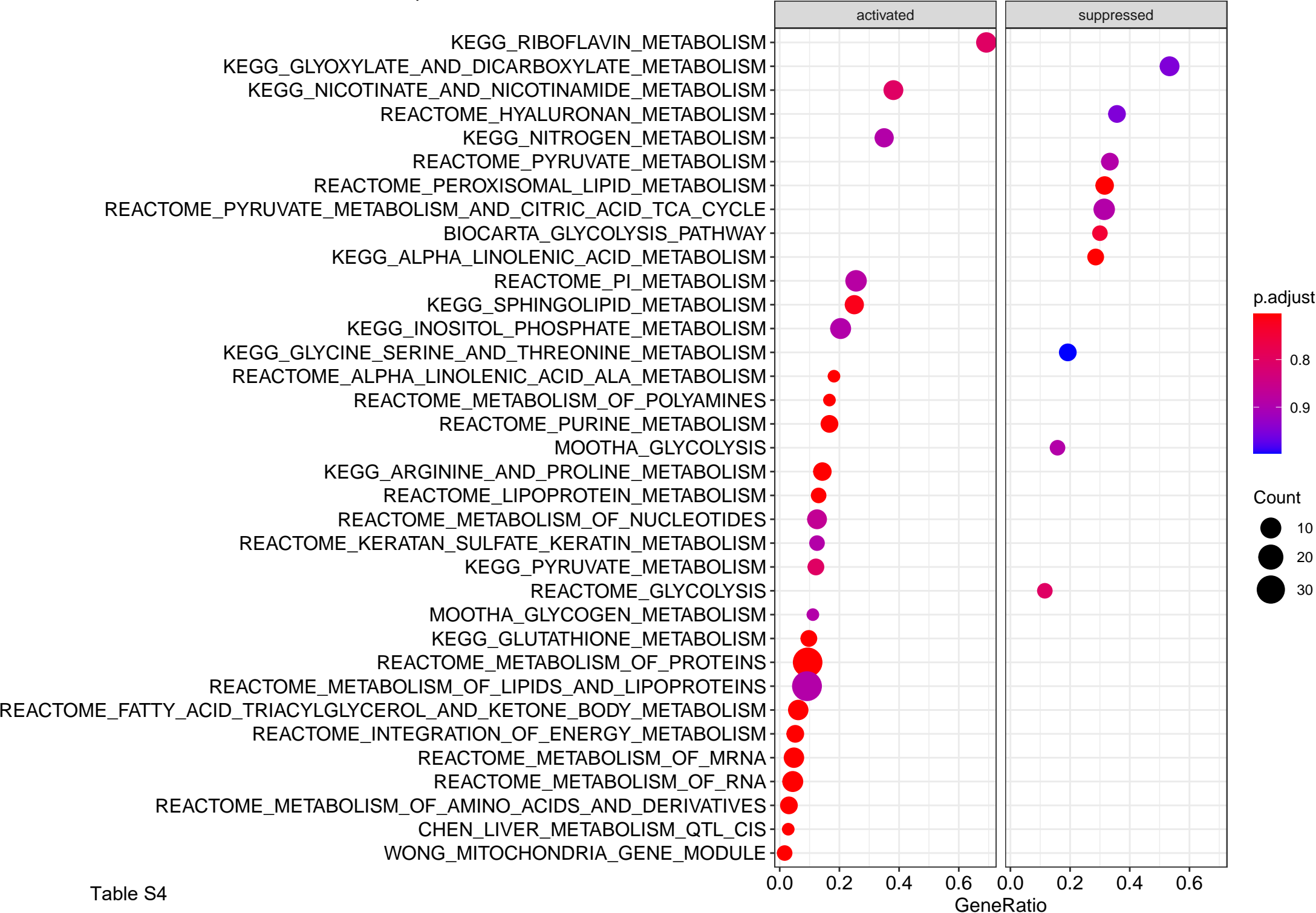
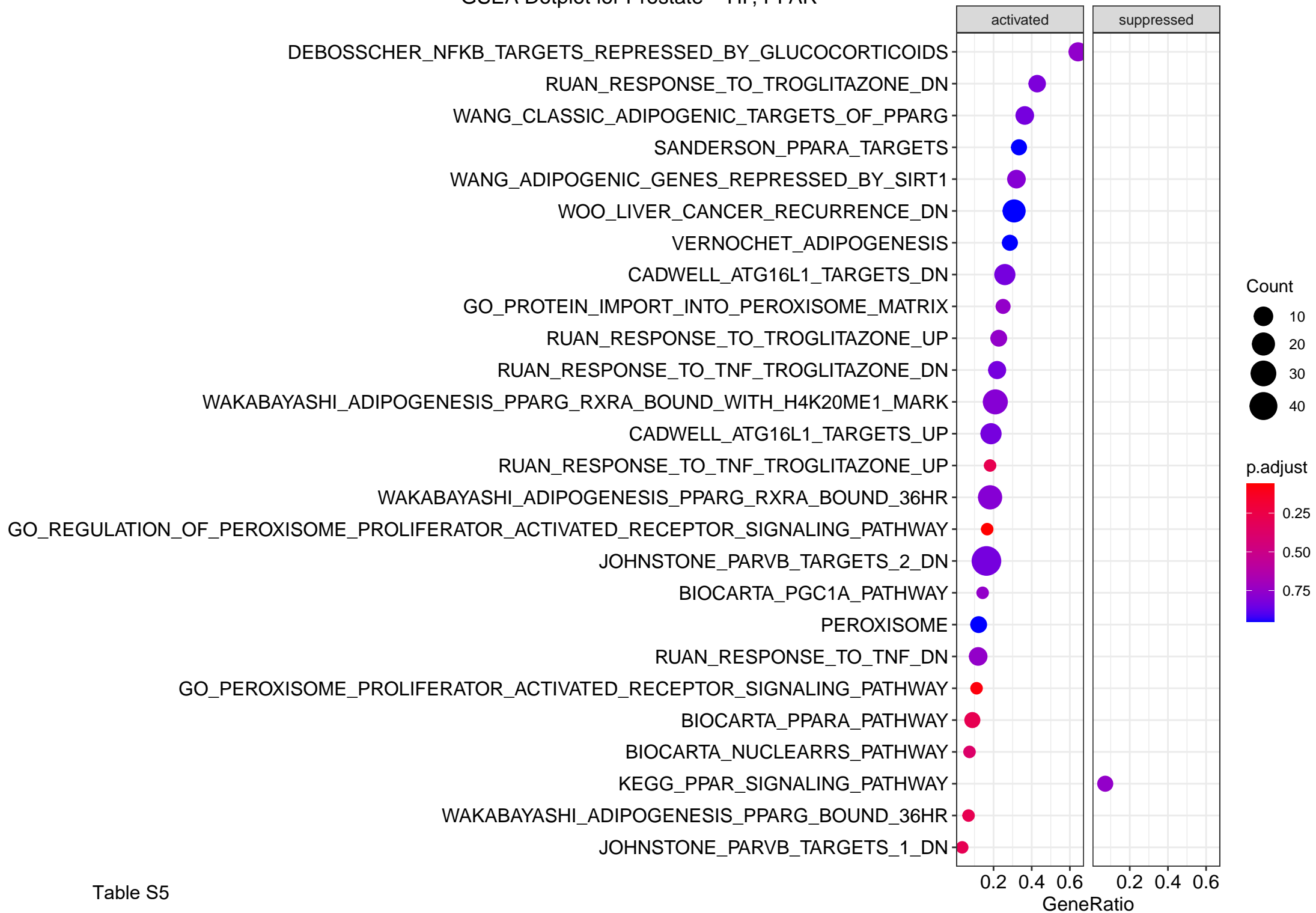


Table S4

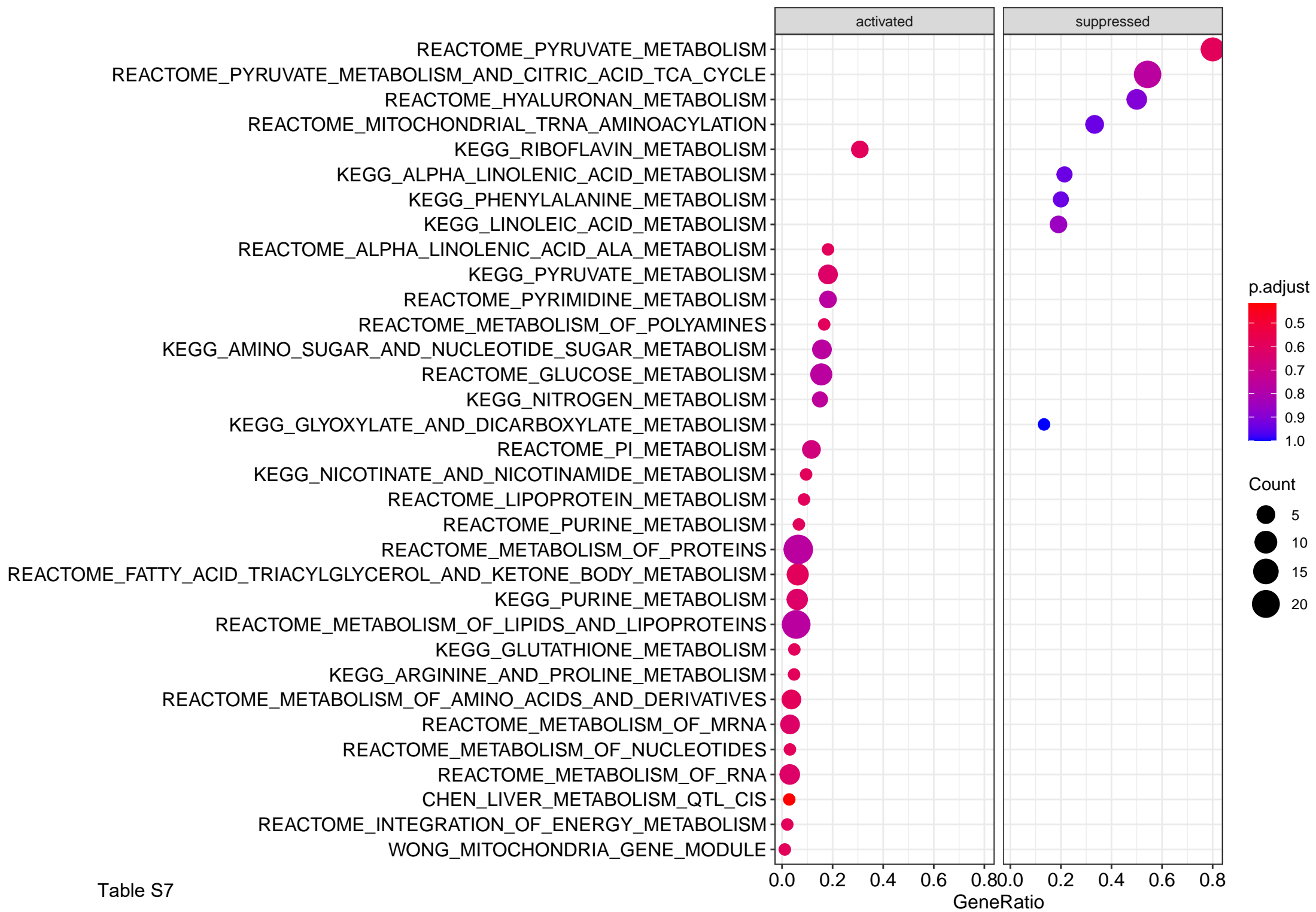
GSEA Dotplot for Prostate – HF, PPAR



GSEA Dotplot for Prostate – HF, Prostate



GSEA Dotplot for Prostate – PFOS, Metabolism



GSEA Dotplot for Prostate – PFOS, PPAR

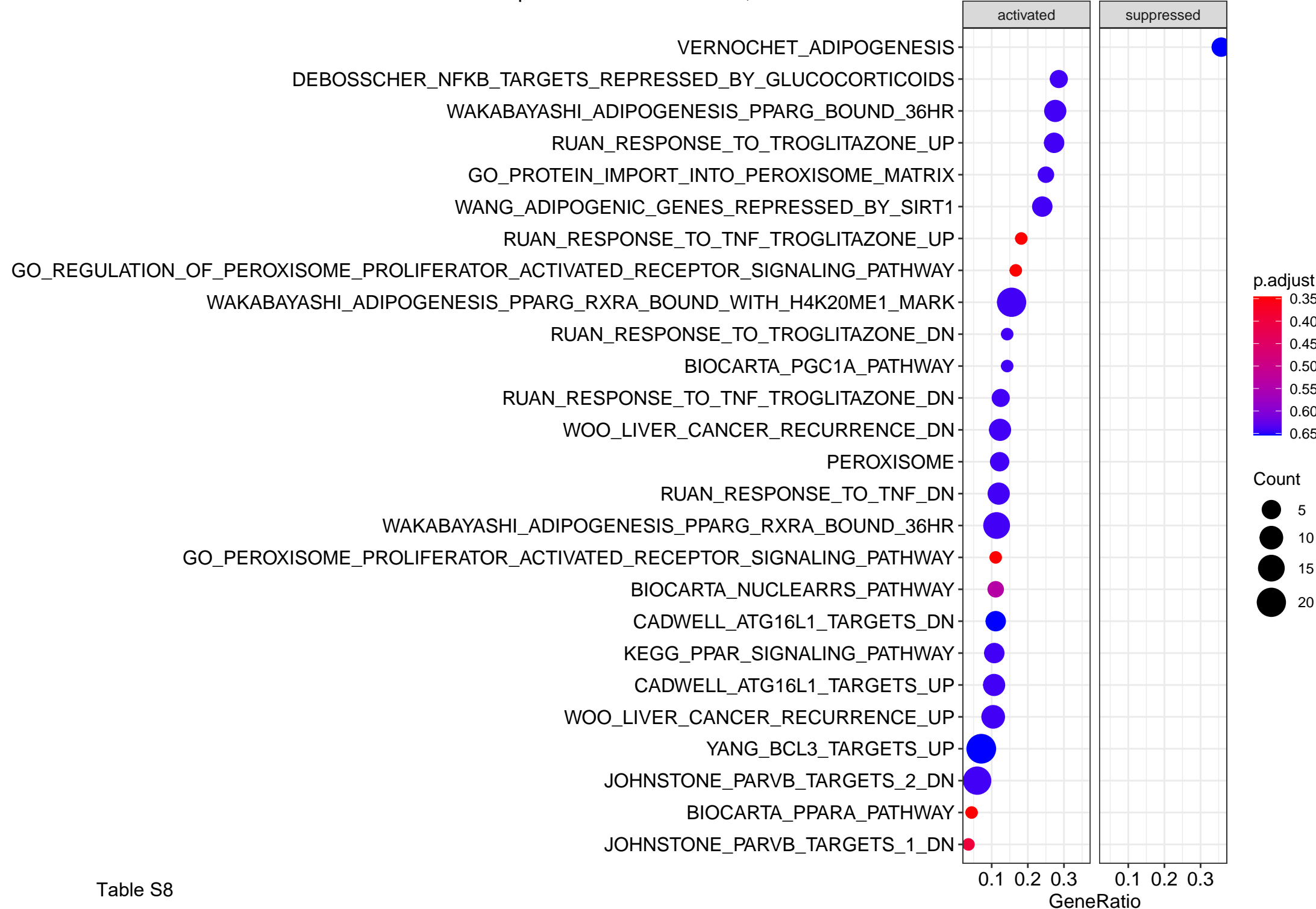


Table S8

GSEA Dotplot for Prostate – PFOS, Prostate



Table S9