



Supplementary Figure S1

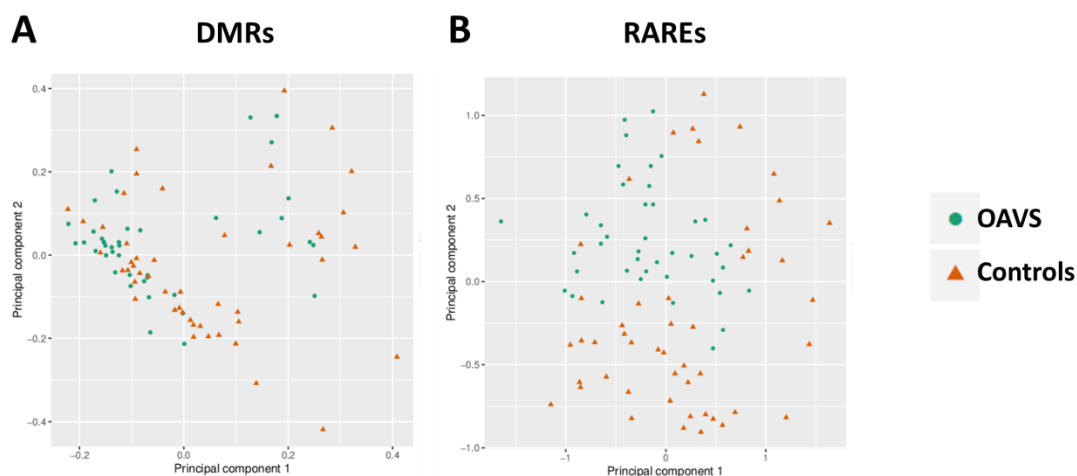
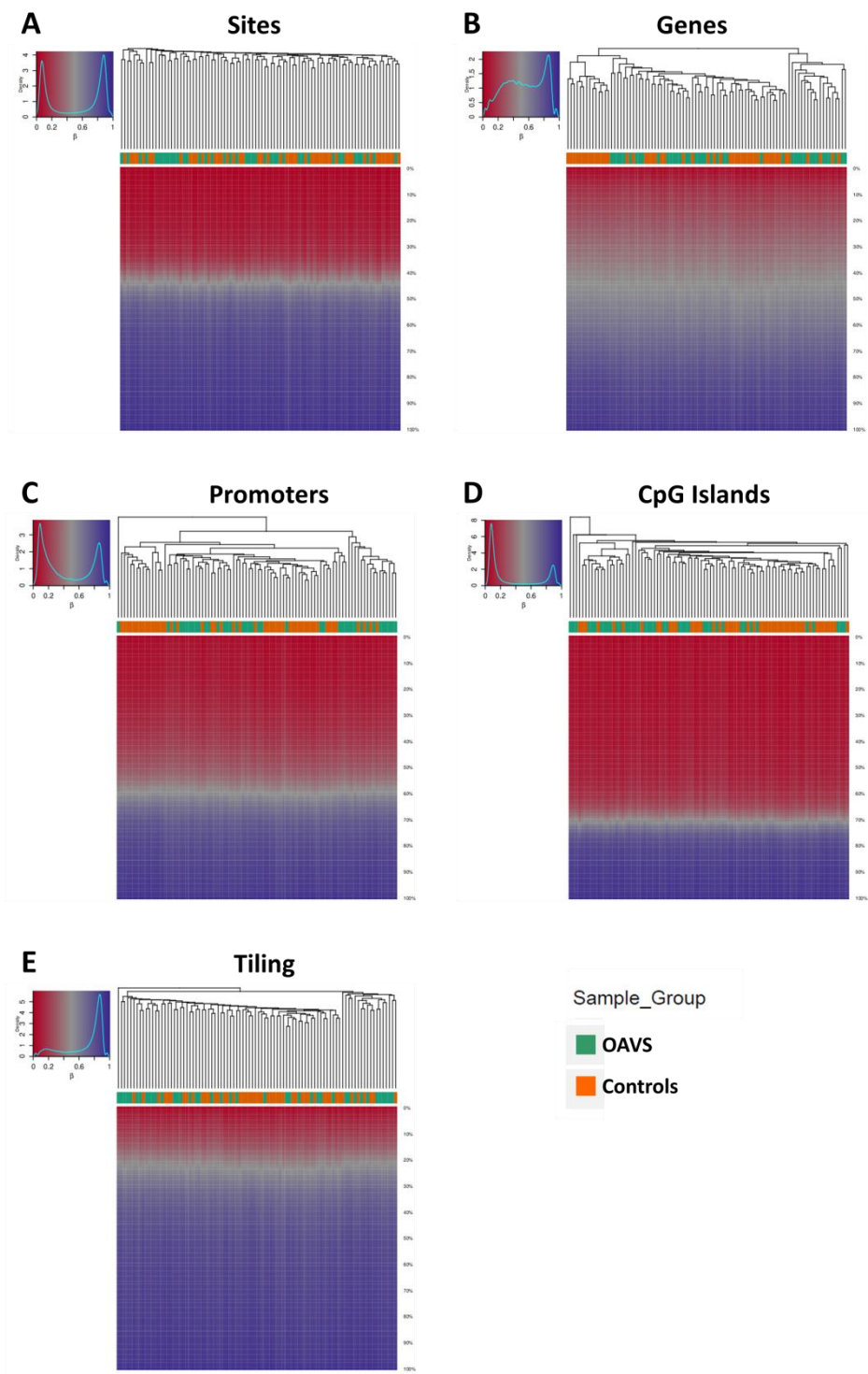


Figure S1. RnBeads scatter plot locating samples in the first two principal components at sites encompassing A) imprinted-associated Differentially Methylated Regions (DMR) (variance explained: PC1=27.44%, PC2=23.20%) and B) Retinoic Acid Response Elements (RAREs) (± 10 Kb) (variance explained: PC1=24.21%, PC2=15.77%).

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Supplementary Figure S2



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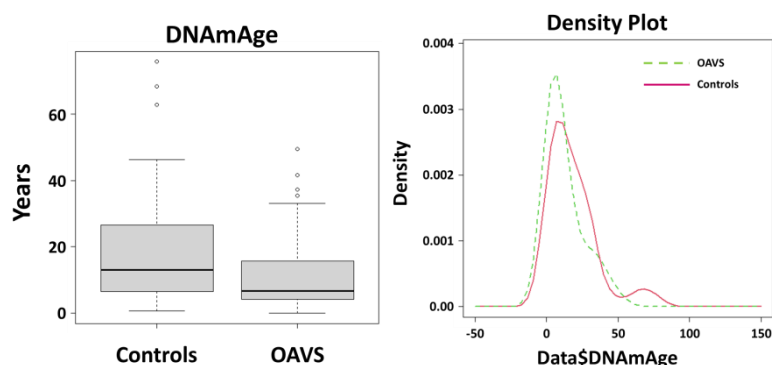
25 **Figure S2.** Hierarchical clustering of samples based on 1000 most variable loci. The heatmap displays
26 methylation percentiles per sample (based on beta-values). (A) sites, (B) genes, (C) promoters, (D)
27 CpG island, and (E) tiling regions. OAVS samples are depicted as orange bars while controls as
28 green.

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Supplementary Figure S3

A)



B)

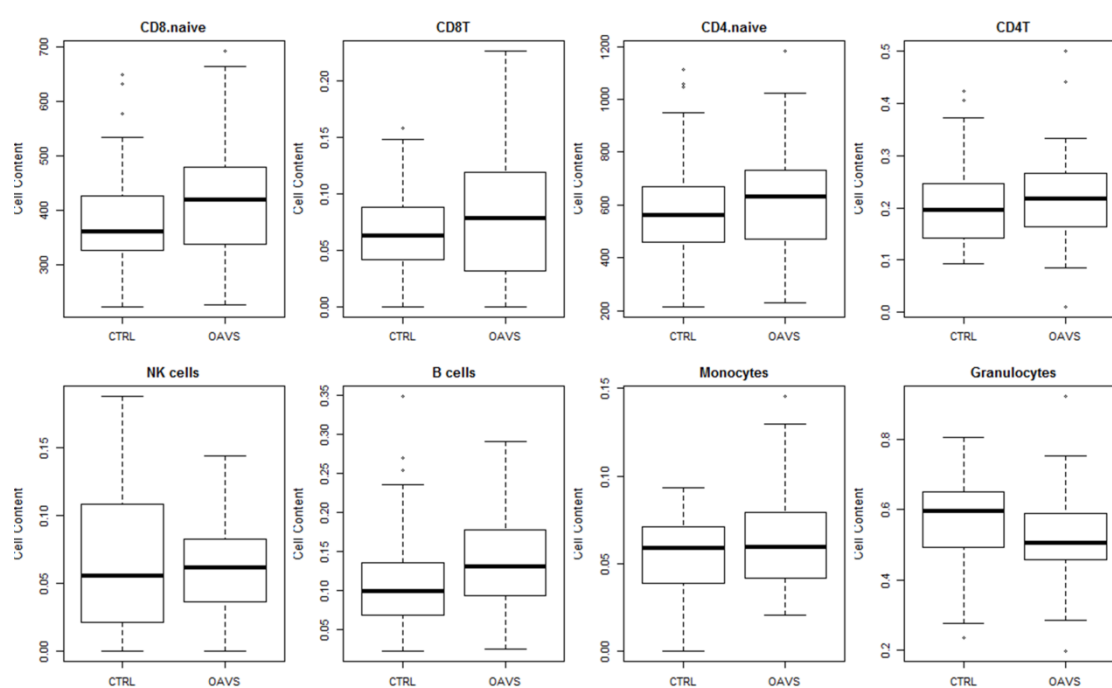
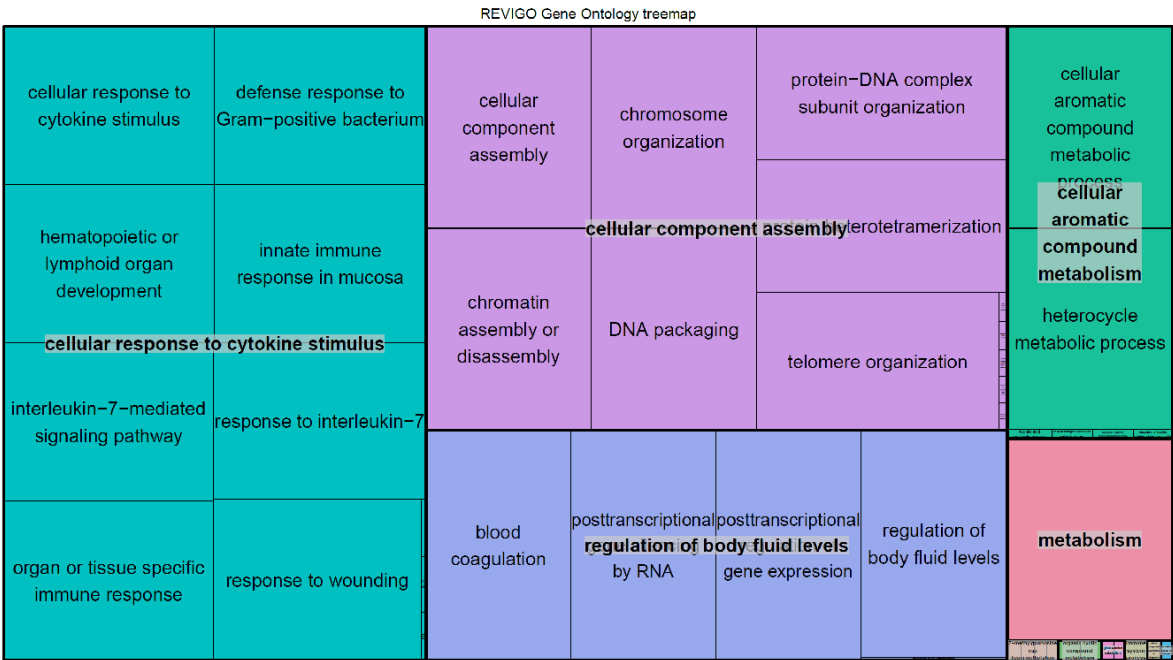


Figure S3. A) Boxplot and density plot showing the distribution of estimated values of epigenetic ages in Control and OAVS cohorts. Boxplots and density plots were created by using “Graphics” and “sm” packages, respectively. B) Boxplot of selected cellular components of OAVS patients and controls. For each panel, the thick horizontal line represents the median of the distribution while the box represents the interquartile range. Whiskers are set as the default option for the boxplot function and extend to the most extreme data point which is no more than 1.5 times the interquartile range from the box. Open circles represent single values exceeding 1.5 interquartile ranges.

Supplementary Figure S4

A)



B)

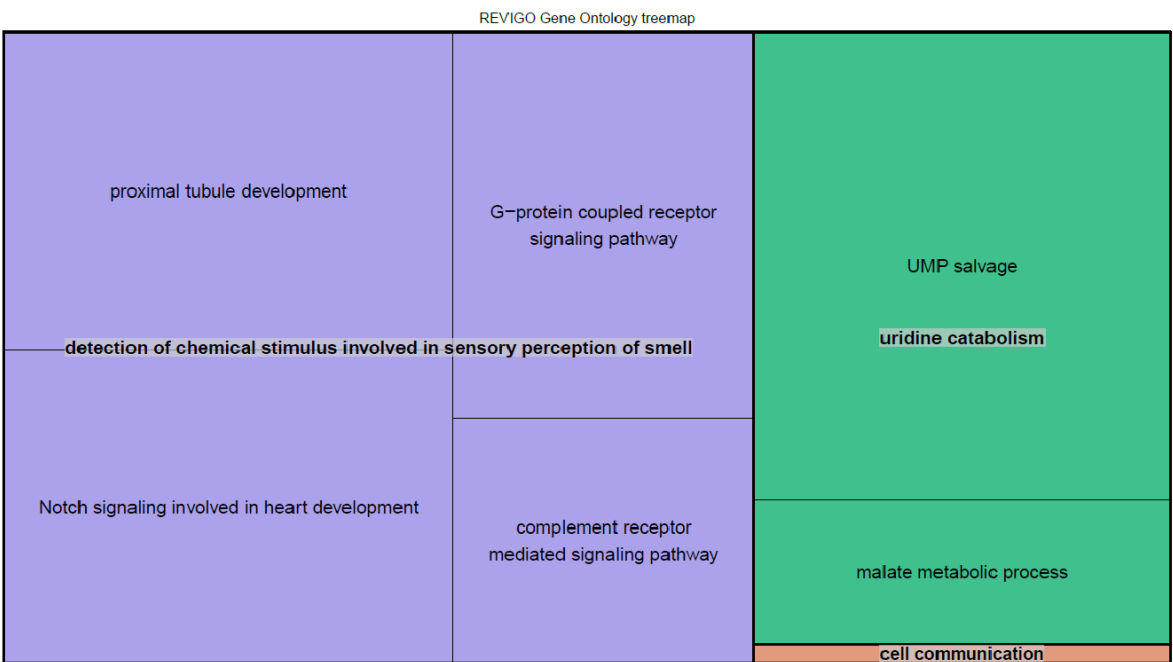


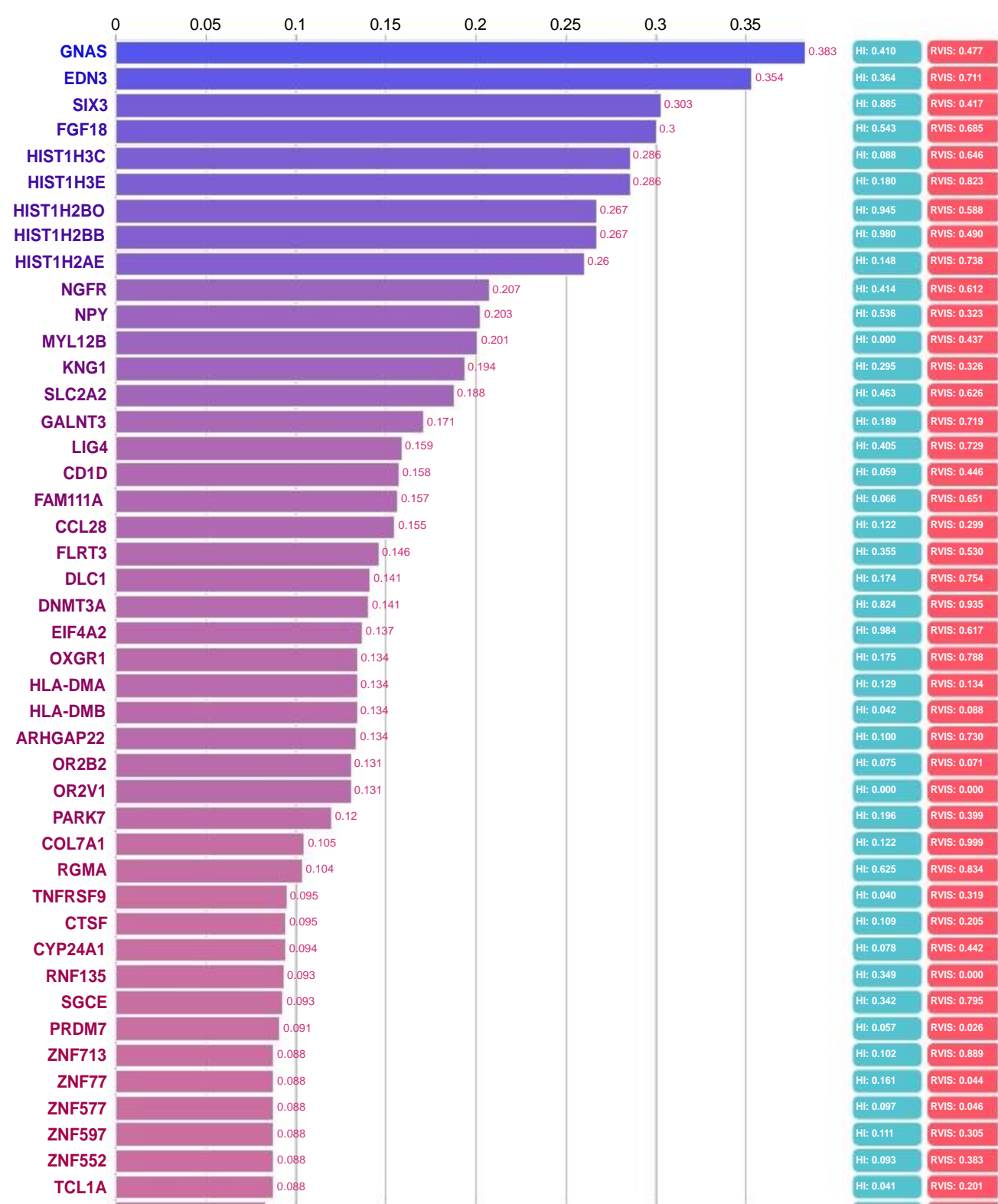
Figure S4. REVIGO treemaps of Gene Ontology (GO) biological processes enriched in hyper- (top panel A) and hypomethylated (bottom panel B) gene regions. For each panel, not all enriched terms are reported due to space constraints.

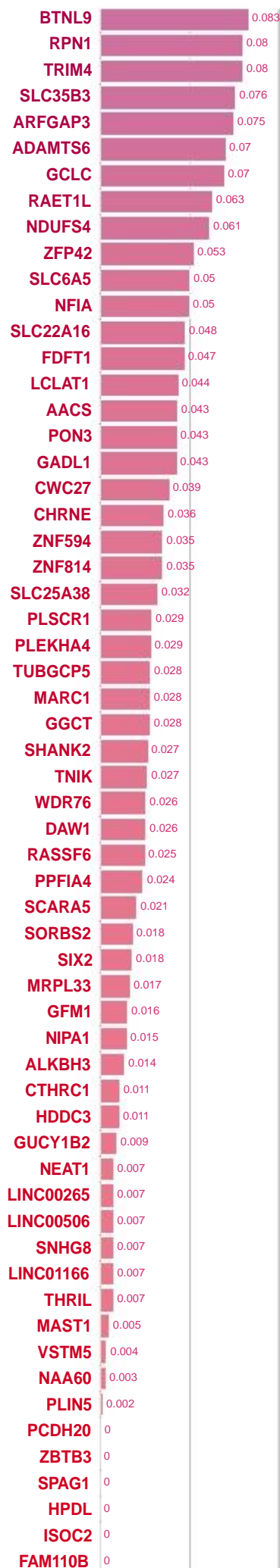
Supplementary Figure S5

Summary Network **Barplot** Details

Barplot

View source data (http://phenolyzer.wglab.org/done/38799/-tgXxHlvOQYJ7usU/index.htmlout.final_gene_list)





HI: 0.109	RVIS: 0.561
HI: 0.188	RVIS: 0.479
HI: 0.110	RVIS: 0.286
HI: 0.150	RVIS: 0.612
HI: 0.106	RVIS: 0.083
HI: 0.351	RVIS: 0.811
HI: 0.598	RVIS: 0.766
HI: 0.077	RVIS: 0.009
HI: 0.333	RVIS: 0.823
HI: 0.194	RVIS: 0.342
HI: 0.236	RVIS: 0.127
HI: 0.318	RVIS: 0.797
HI: 0.101	RVIS: 0.212
HI: 0.157	RVIS: 0.935
HI: 0.000	RVIS: 0.547
HI: 0.159	RVIS: 0.940
HI: 0.091	RVIS: 0.160
HI: 0.118	RVIS: 0.184
HI: 0.000	RVIS: 0.668
HI: 0.424	RVIS: 0.900
HI: 0.053	RVIS: 0.072
HI: 0.000	RVIS: 0.671
HI: 0.185	RVIS: 0.463
HI: 0.192	RVIS: 0.240
HI: 0.073	RVIS: 0.442
HI: 0.000	RVIS: 0.868
HI: 0.000	RVIS: 0.381
HI: 0.000	RVIS: 0.387
HI: 0.292	RVIS: 0.000
HI: 0.806	RVIS: 0.960
HI: 0.650	RVIS: 0.427
HI: 0.000	RVIS: 0.000
HI: 0.074	RVIS: 0.058
HI: 0.145	RVIS: 0.755
HI: 0.150	RVIS: 0.166
HI: 0.387	RVIS: 0.790
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HI: 0.064	RVIS: 0.471
HI: 0.086	RVIS: 0.165
HI: 0.346	RVIS: 0.685
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HI: 0.000	RVIS: 0.000
HI: 0.000	RVIS: 0.000
HI: 0.000	RVIS: 0.000
HI: 0.437	RVIS: 0.981
HI: 0.000	RVIS: 0.061
HI: 0.000	RVIS: 0.629
HI: 0.000	RVIS: 0.000
HI: 0.268	RVIS: 0.907
HI: 0.450	RVIS: 0.316
HI: 0.051	RVIS: 0.123
HI: 0.051	RVIS: 0.517
HI: 0.151	RVIS: 0.517
HI: 0.136	RVIS: 0.657

Supplementary Figure S6

