

Figure 1

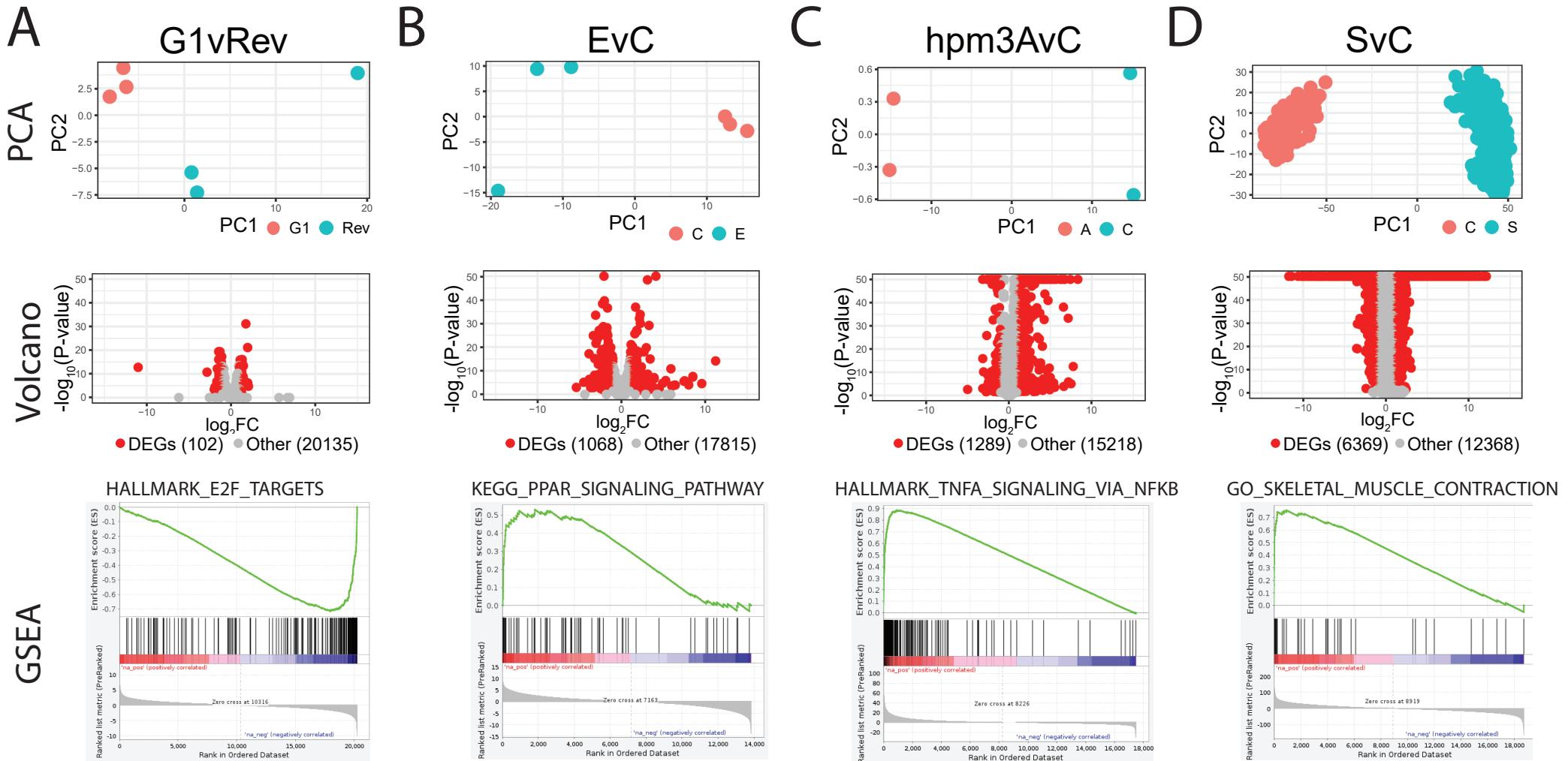
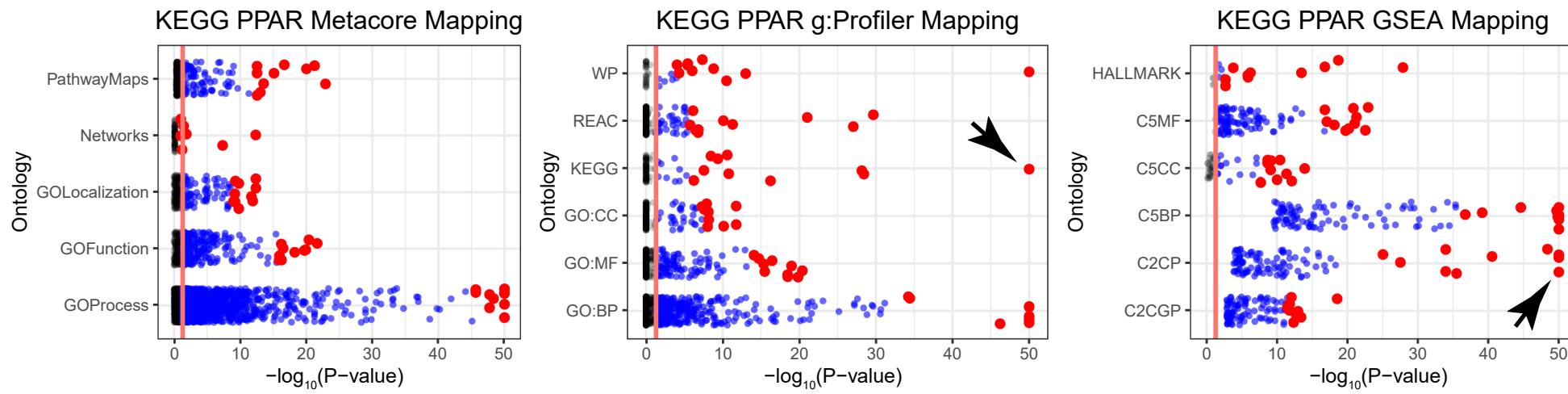


Figure 2

A



Lorem ipsum

B

termID	termName
GO:0022402	cell cycle process
GO:0000278	mitotic cell cycle
GO:1903047	mitotic cell cycle process*
GO:0007049	cell cycle
GO:0006259	DNA metabolic process
GO:0051276	chromosome organization
GO:0006260	DNA replication
GO:0044770	cell cycle phase transition
GO:0044772	mitotic cell cycle phase transition*
GO:0006974	cellular response to DNA damage stimulus
GO:0006281	DNA repair
GO:0090304	nucleic acid metabolic process*
GO:0007067	mitotic nuclear division*
GO:0051301	cell division
GO:0006139	nucleobase-containing compound metabolic process*
GO:0051726	regulation of cell cycle
GO:0000722	telomere maintenance via recombination
GO:0007062	sister chromatid cohesion
GO:0006297	nucleotide-excision repair, DNA gap filling
GO:0006270	DNA replication initiation
GO:1901796	regulation of signal transduction by p53 class mediator
GO:0000082	G1/S transition of mitotic cell cycle*

SetSize	DAVID DIRECT	DAVID ALL	GSEA	g:profiler	Metacore
1422		1	1	1	3
1053		2	3	4	2
880		3		2	4
1881	50	4	2	3	1
943	43	5	5	5	6
1253		6	4	6	5
273	1	7	7	7	8
647		8	6	8	11
432		9		9	14
865	17	12	8	10	7
563	7	15	9	11	16
2955		17		24	10
217	6	18			45
603	3	19	12	17	32
3616		20		20	9
1226		23	10	16	17
13	4	30		327	372
63	5	35	73	84	113
23	9	61	61	68	111
39	8	66	57	73	96
180	10	71	71	104	102
221	2			30	47

C

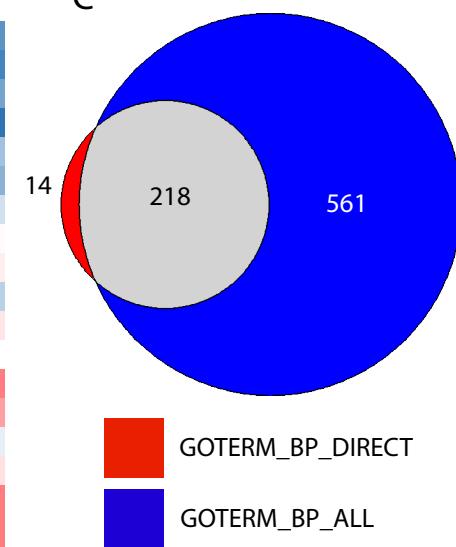


Figure 3

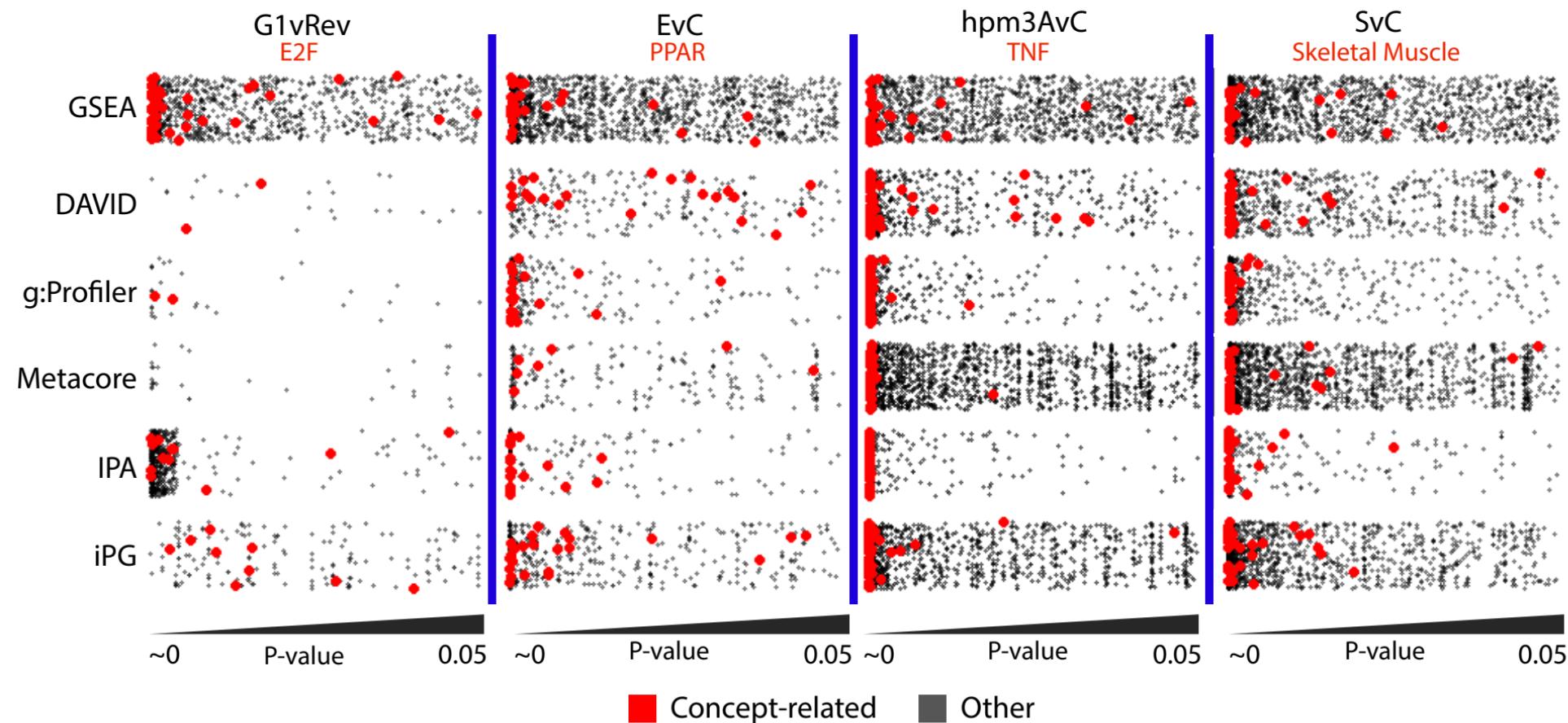


Figure 4

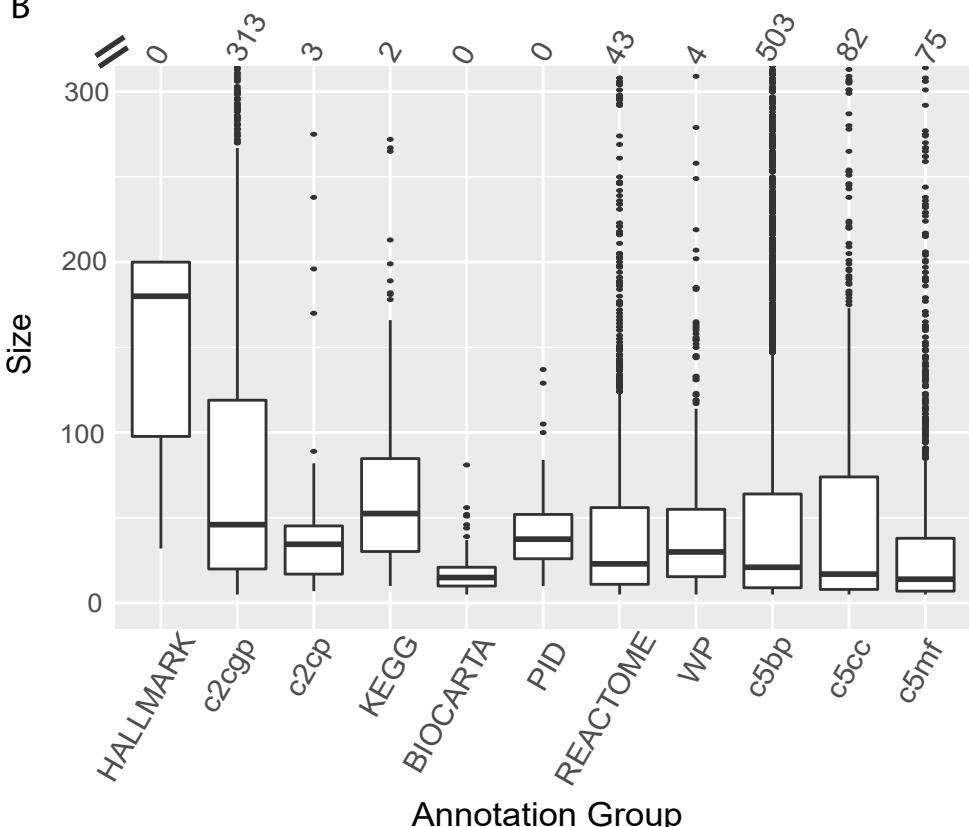
A

a # DEGs in Set	c # non-DEGs in Set
b # DEGs not in Set	d # Genes

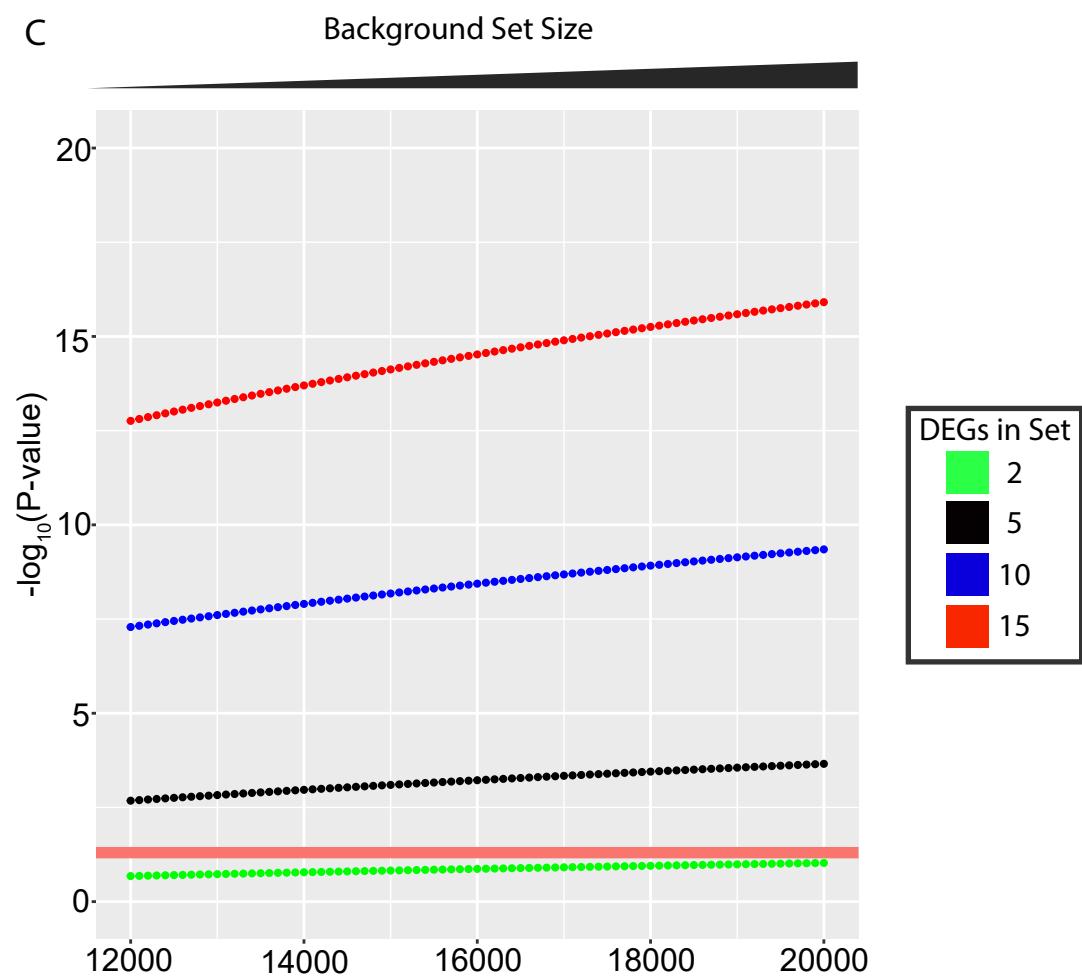
Input
Values

DEGs
Set (Pathway)
Genes (Background)

B



C



D

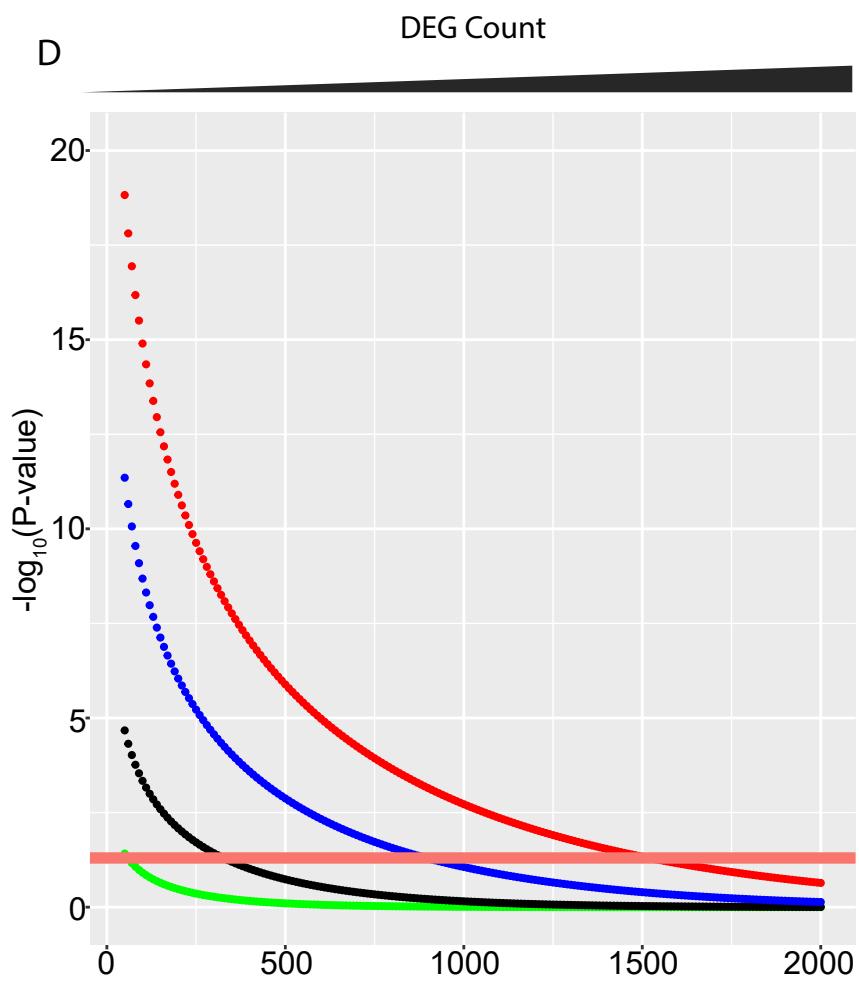


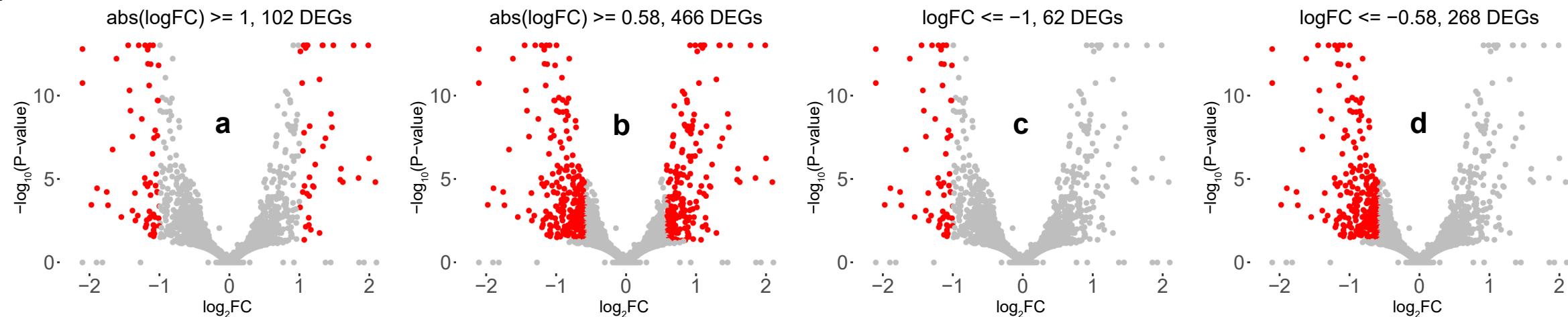
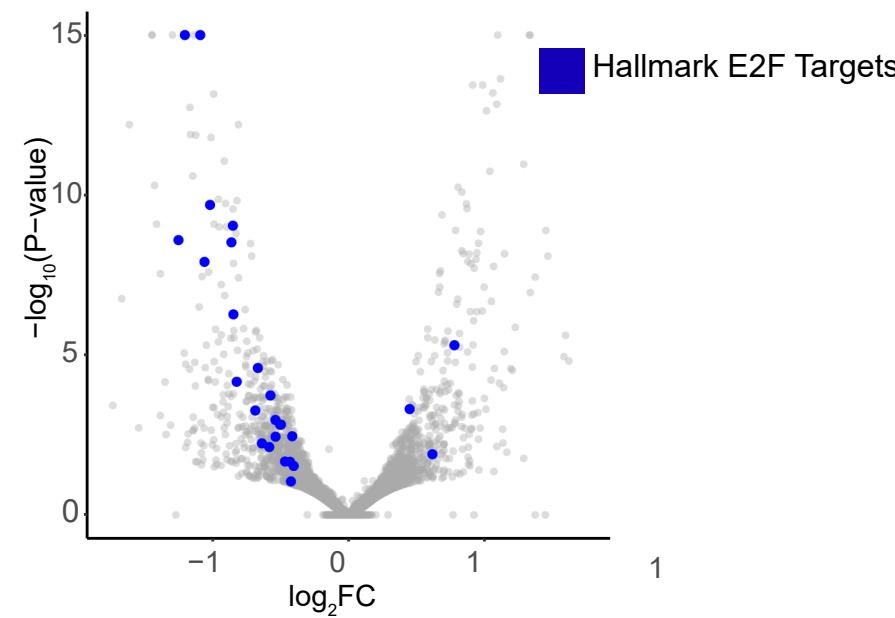
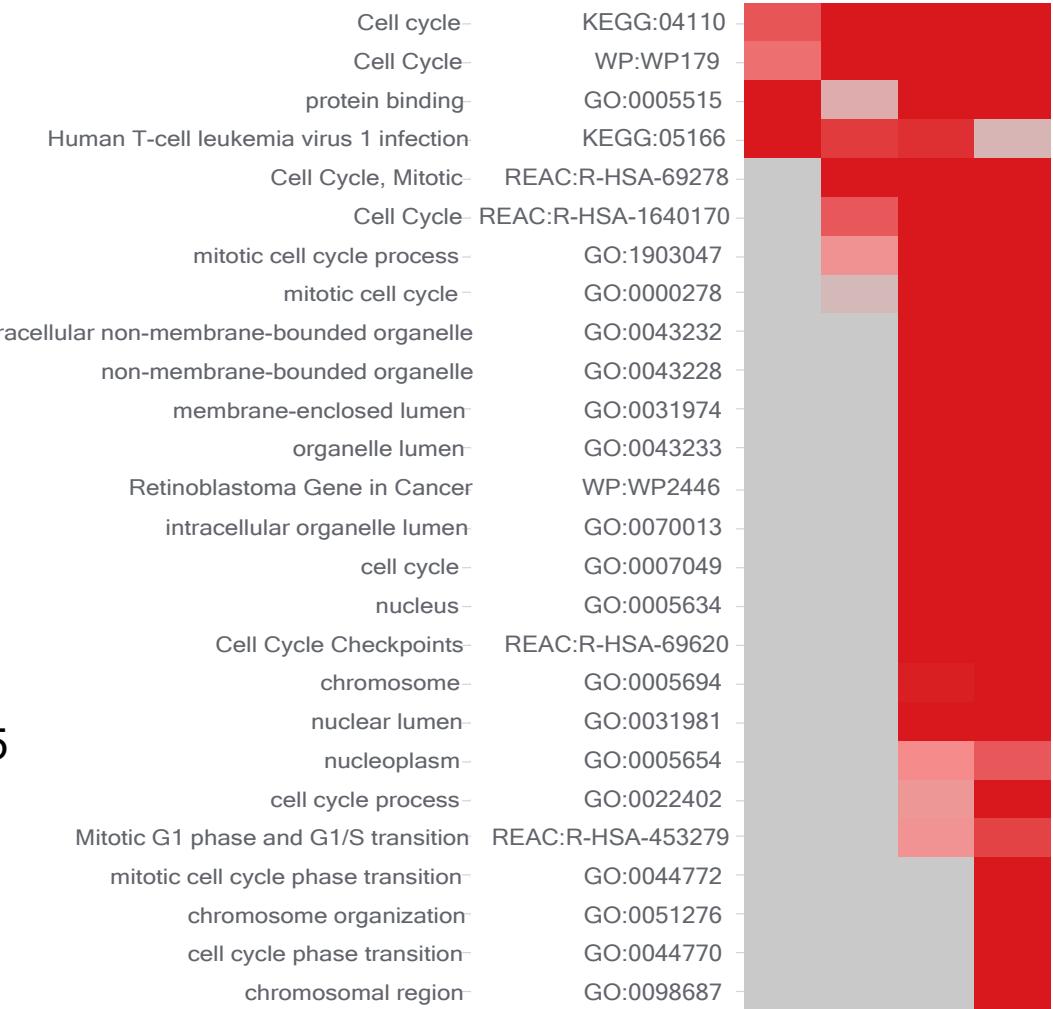
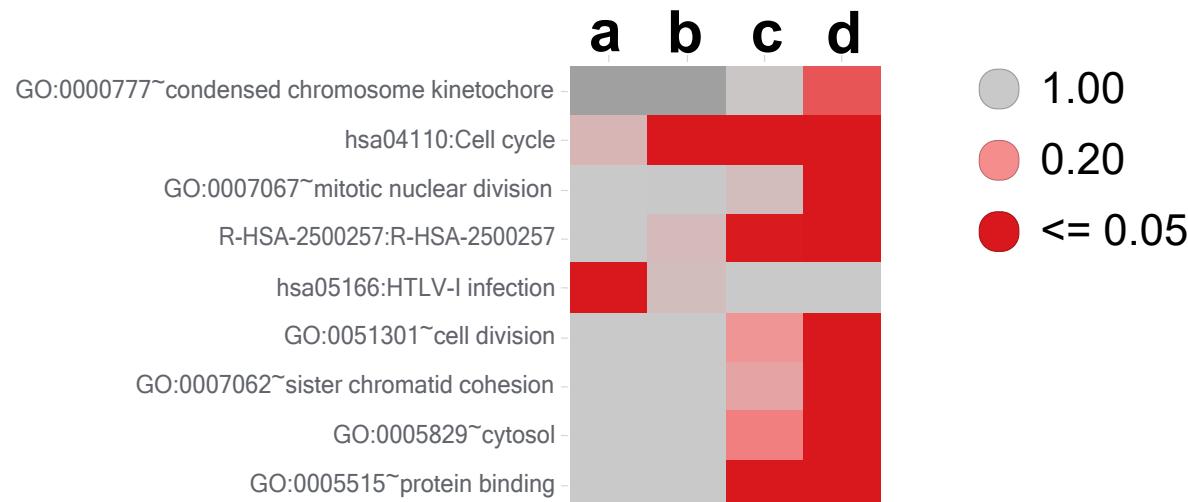
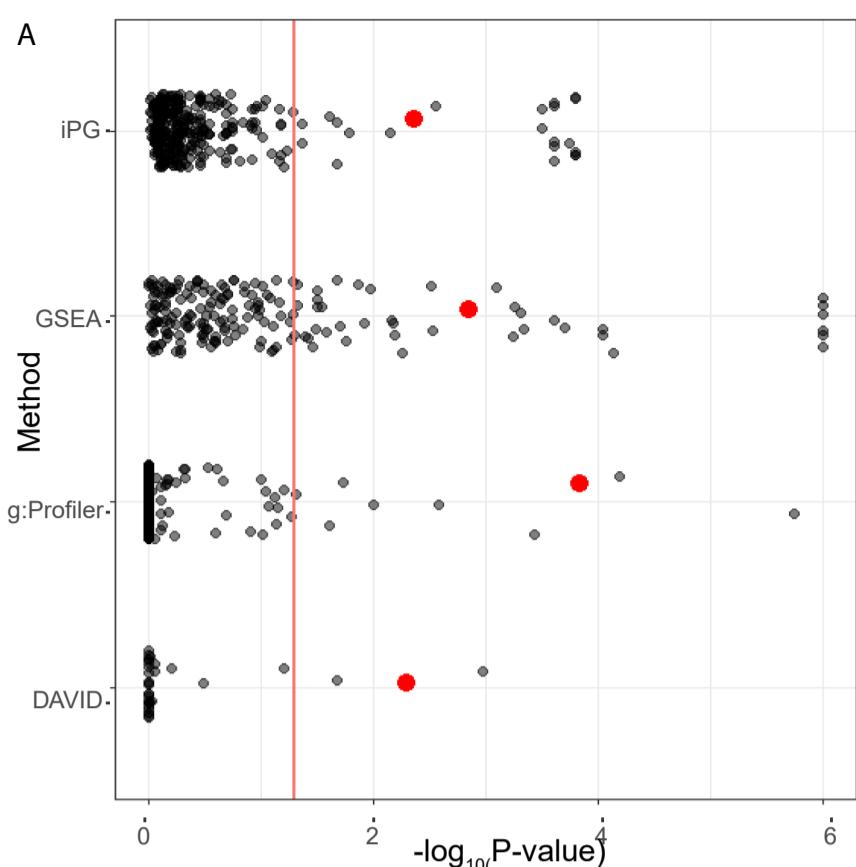
Figure 5**A****B****C****D**

Figure 6

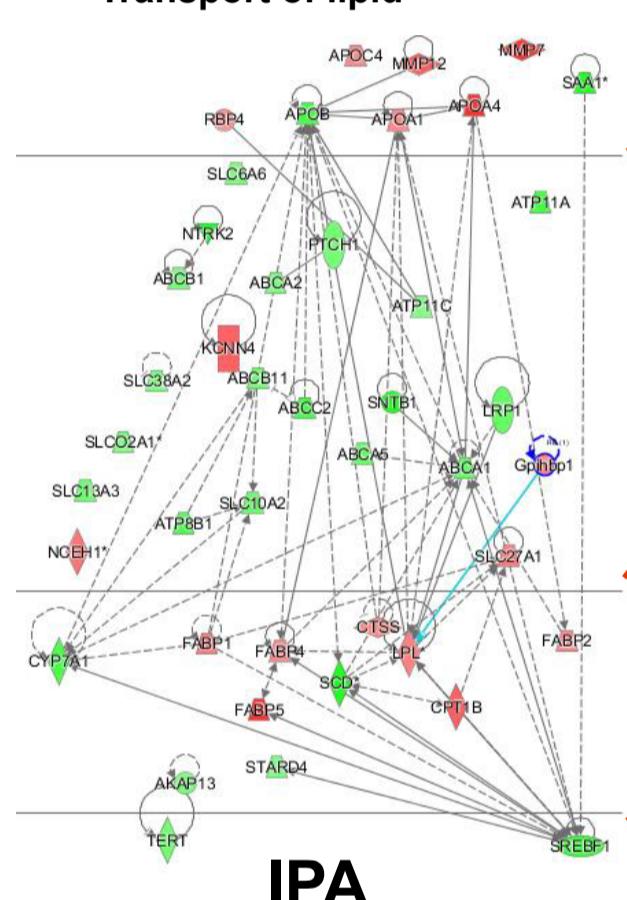


Tool	Result	Ontology	FDR
Metacore	lipid transporter activity	GOFUNCTION	0.000392
Metacore	lipid transport	GOPROCESS	0.000786
Metacore	lipid localization	GOPROCESS	0.001043
Metacore	regulation of lipid metabolic process	GOPROCESS	0.003908
Metacore	Bile acid regulation of lipid metabolism*	Networks	0.006123
IPA	Homeostasis of lipid	DisBio	4.42E-15
IPA	Concentration of triacylglycerol	DisBio	3.61E-14
IPA	Concentration of lipid	DisBio	7.28E-13
IPA	Transport of lipid	DisBio	4.06E-12
IPA	Fatty acid metabolism	DisBio	2.12E-10

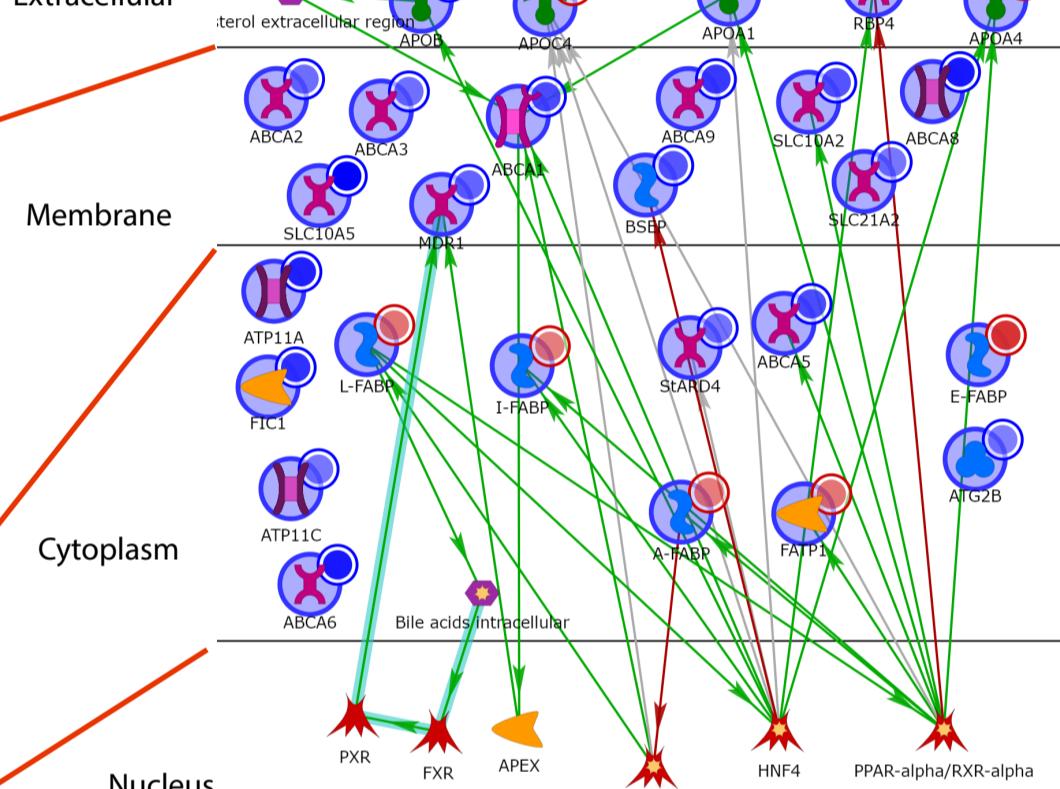
*Regulation of metabolism_Bile acid regulation of lipid metabolism and negative FXR-dependent regulation of bile acids concentration

C

Transport of lipid



Extracellular



Metacore

D

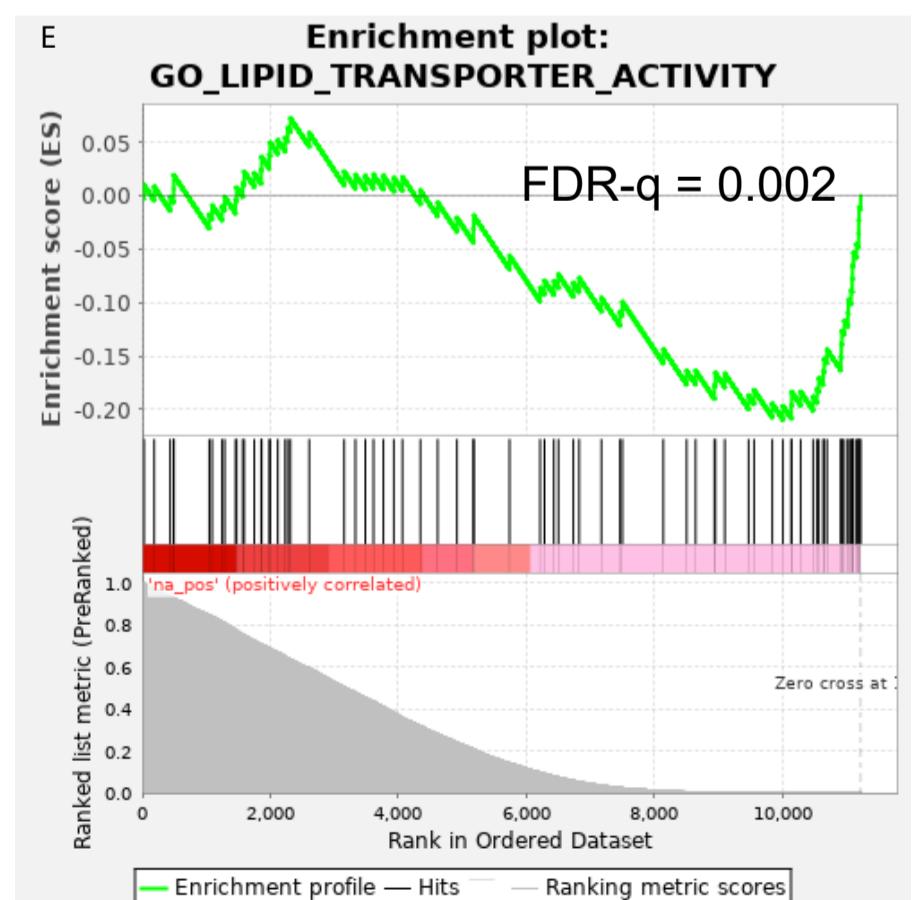
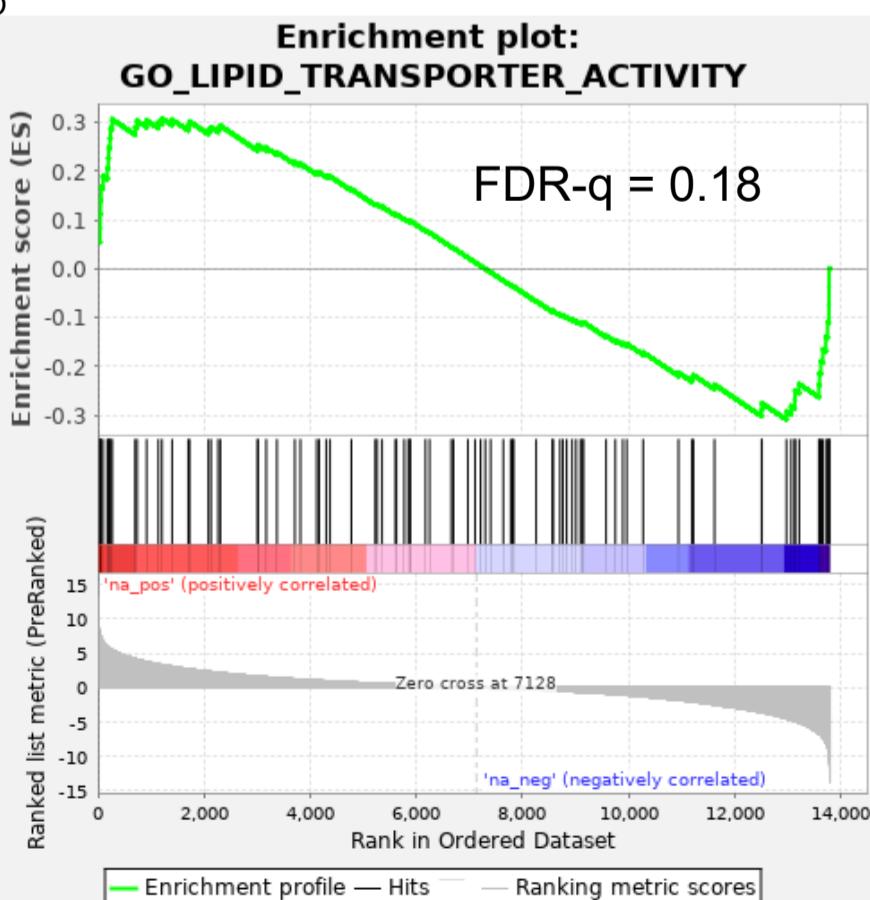
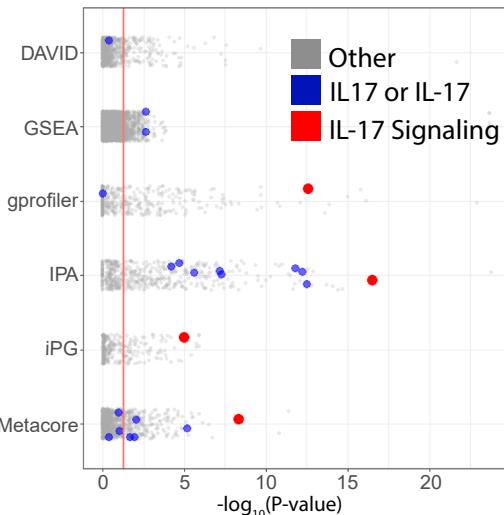


Figure 7

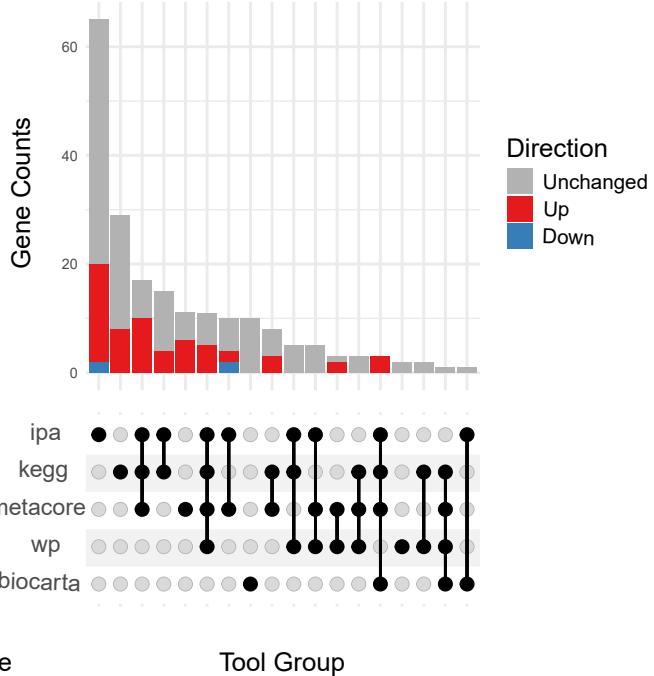
A

Tool	SetName	Ontology	Size	Rank in Ontology	P-value
Metacore	Immune response_IL-17 signaling pathways	PathwayMaps	39	6	5.06E-16
IPA	IL-17 Signaling	Canonical Pathways	132	4	1.26E-18
gProfiler	IL-17 signaling pathway	KEGG	81	4	7.09E-16
iPG	IL-17 signaling pathway	KEGG	81	6	1.92E-06
GSEA	N/A	N/A	N/A	N/A	N/A
DAVID	N/A	N/A	N/A	N/A	N/A

B



C



D

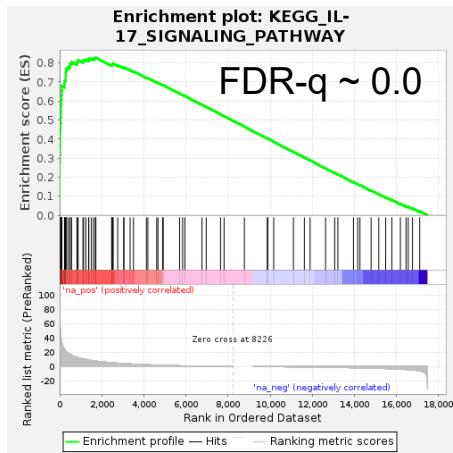


Figure 8

