Figure S1 - Bar-plots shows number of OCRs within 5 different categories, that were analysis across traits (A) and across cell types (B).

A

trait	Total OCRs by ATAC-seq	OCRs at promoters	putative cREs	cREs ±500 bases	OCRs not cREs
GD	23	40	34	23	9
ALG	22	12	28	33	11
CEL	22	7	22	23	11
CRO	22	2	22	23	10
IBD	22		22	24	14
RA	21	17	26	28	14
MS	21	8	24	24	3
UC	21		22	23	8
VIT	20	11	17	22	13
T1D	19	2	20	21	2
HT	18	4	22	24	5
SLE	12		13	23	
ECZ	6		19	37	
PSO	5		3	2	2
AS	1		2		2
JIA			1	3	

B

Cell type	Total OCRs by ATAC-seq	OCRs at promoters	putative cREs	cREs ¬±500 bases	OCRs not cREs	system
Treg	13	5	13	14	8	immune
Th17	13	5	13	13	8	
Treg_act	13	5	12	13	6	
Th1	13	4	13	13	7	
GCB	13	2	12	13	3	
TFH	12	8	13	13	9	
naiveT_8h	12	7	15	15		
naiveT_24h	12	5	13	14	2	
Th1_act	12	5	13	13	6	
Th2	12	4	13	13	3	
Tr1	12	4	11	13	8	
Tr1_act	12	3	11	13	9	
naiveB	12	2	9	13	6	
Th17_act	11	5	13	13	9	
naiveT (tonsil)	11	5	12	13	7	
Th2_act	11	5	12	13	5	
NK	11	3	12	13	1	
PGF	11	3	11	11	2	
naiveT_unstim	11	1	14	13	3	
pDC	10	1	13	13		
cDC_CD1c	8	1	10	13		
Monocytes	5	1	7	10		
Enteroid	1	1	2	4		metabolic
Hepatocytes	1	1	1	3	1	
Myotubes	1		1	4		
HEPG2		2	3	3		
Osteo_hMSC		1	2	1		
MiaPaCa		1	2			
Adipo_hMSC		1	1	3		
Panc1		1	1			
Hepato_iPSC		1				
Panc_Acir		1				
Adipocytes			3	3		
PreAdipo_SGBS			2	2		
PreAdipocytes			1	3		
Panc_Alpha(sc)				3		
Adipo_SGBS				2		
EndoC_BH1				1		
Microglia		1	1	1		neural
Microglia_act		1	1	1		
NPC_hESC		1	1	1		
HNs_hESC		1	1			
NPC_iPSC			1	1		
Astrocytes				2		
hESC	1	1	2	5	1	other
NCIH716	1	1	1			
Melano_YRI		1	1			
hMSC			1	2		
NTERA2			1			
hTM				1		

Figure S2 - **A**. Upset-plot showing intersections of V2G SNPs implicated across 16 immune traits. **B**. Box-plot depicting numbers of genes contacted by variants for each trait in each cell type category.

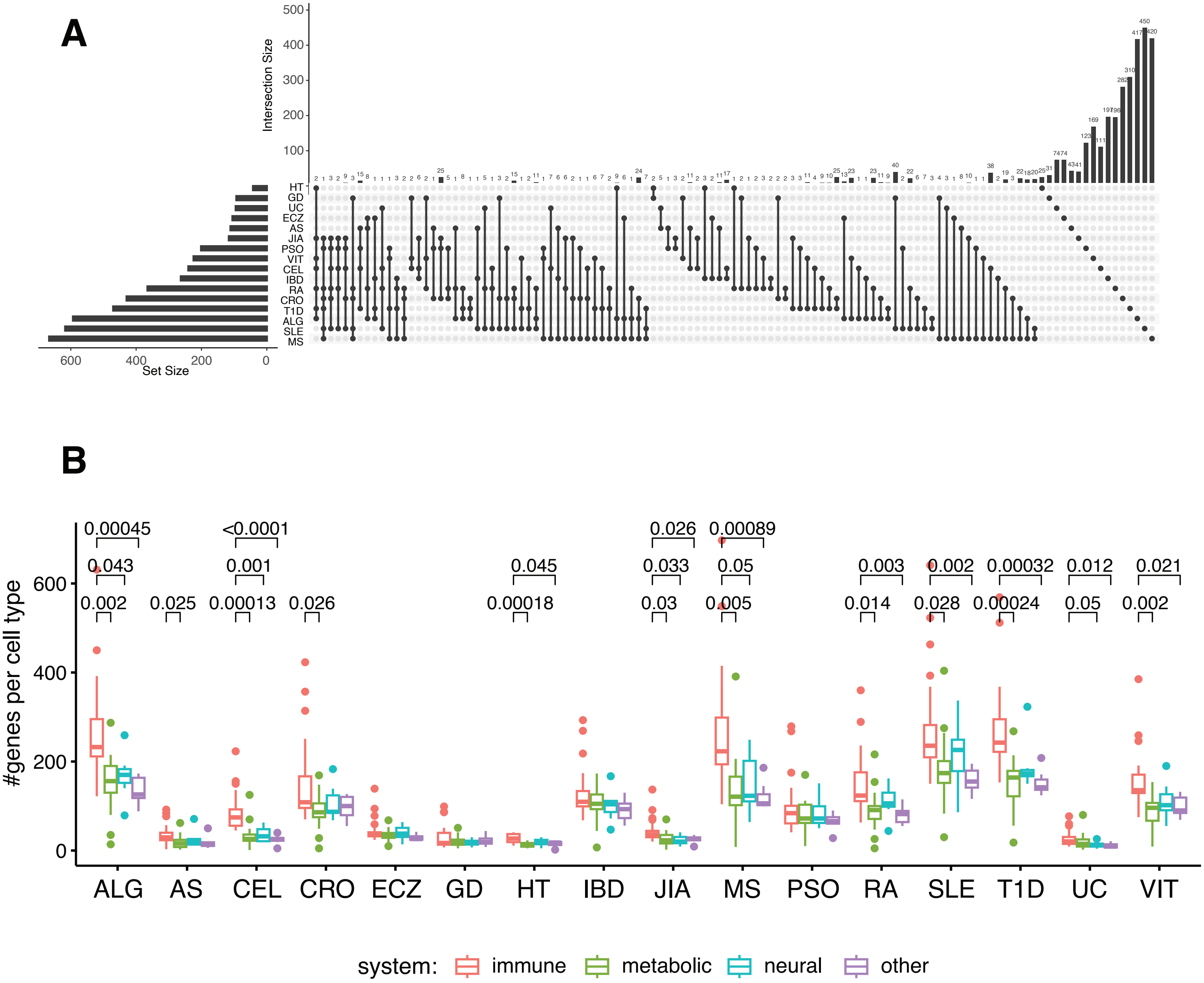

Figure S3 - **A**. Upset-plot showing intersections of V2G genes implicated in any cell type across 16 immune traits. **B**. Upset-plot depicting intersections of V2G genes for any trait across the cell types listed.

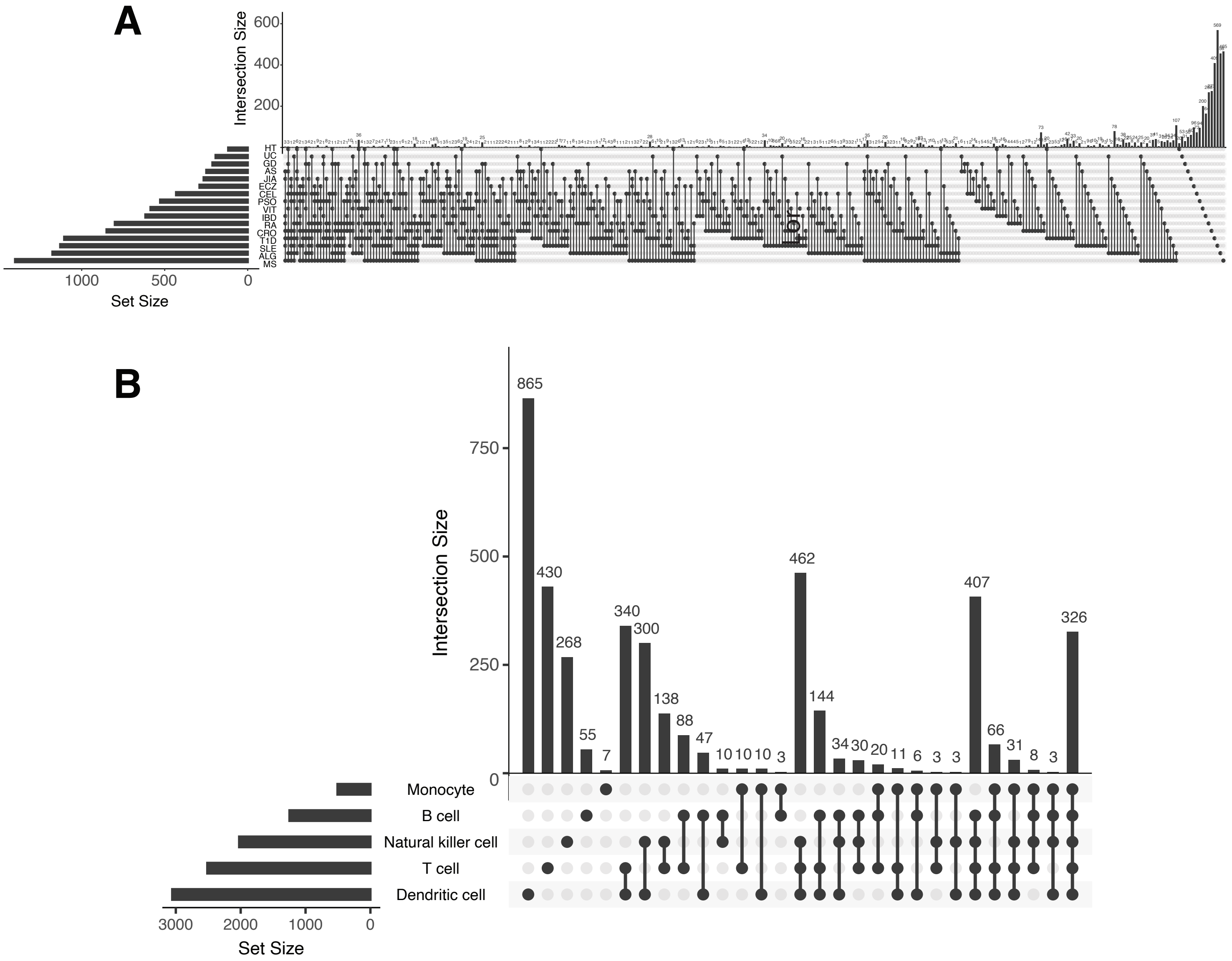

Figure S4 - Degree of overlap of implicated variants (**A**) and target genes (**B**) across cell types.

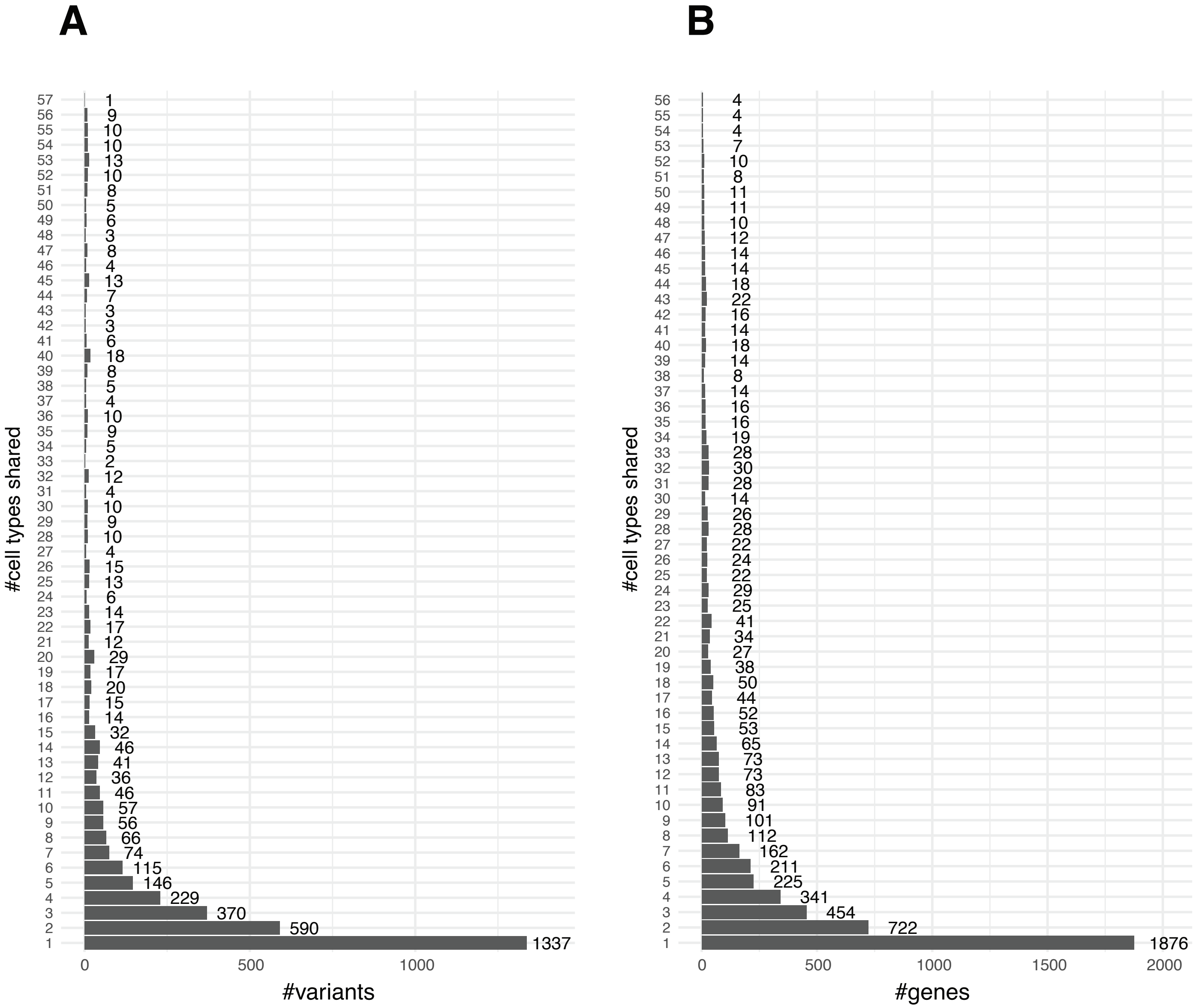

Figure S5 - Cytokine/receptor gene enrichment across trait and cell type (**A**) and in KEGG pathway (**B**).

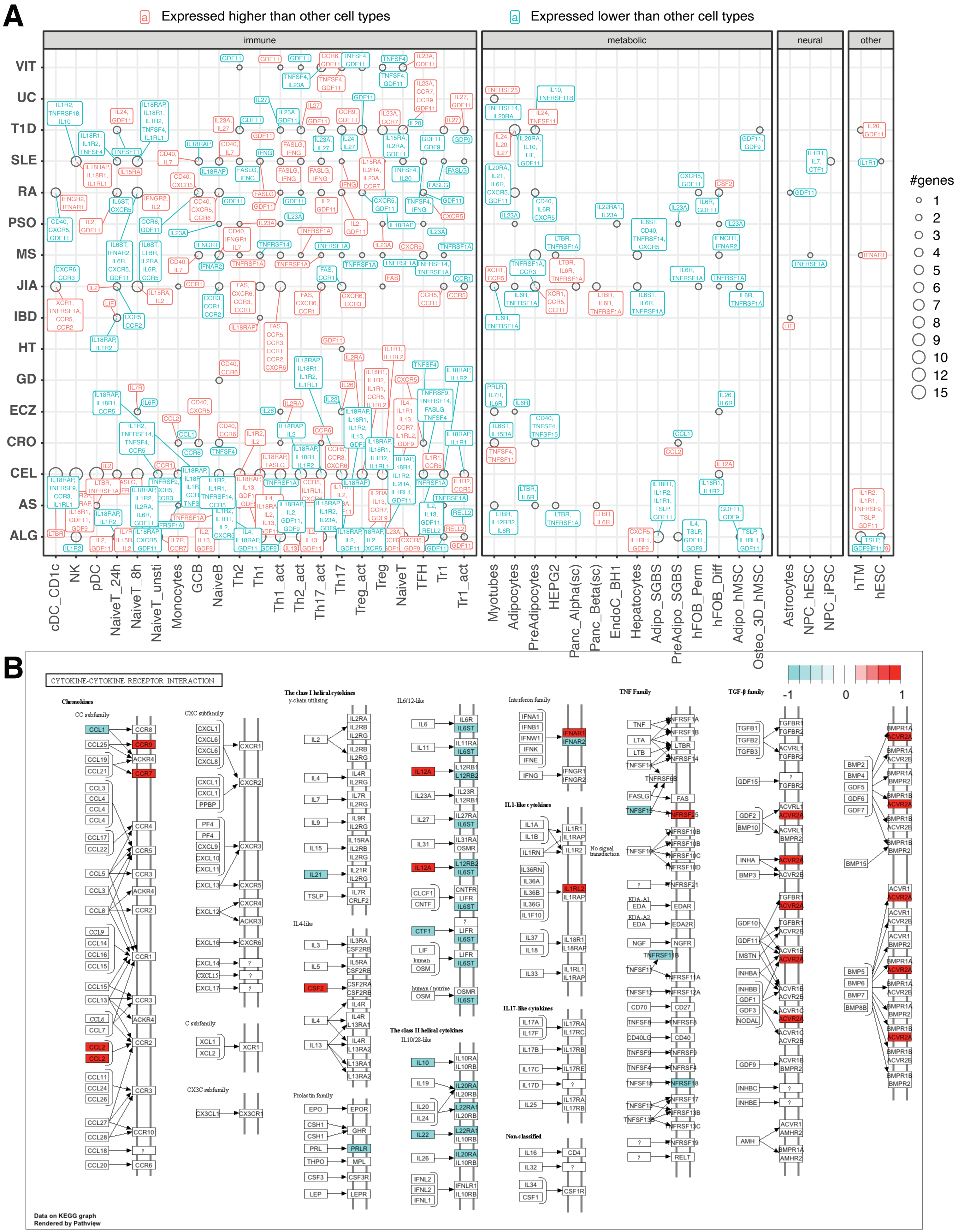

Figure S6 - Salmonella infection gene enrichment across trait and cell type (**A**) and in KEGG pathway (**B**).

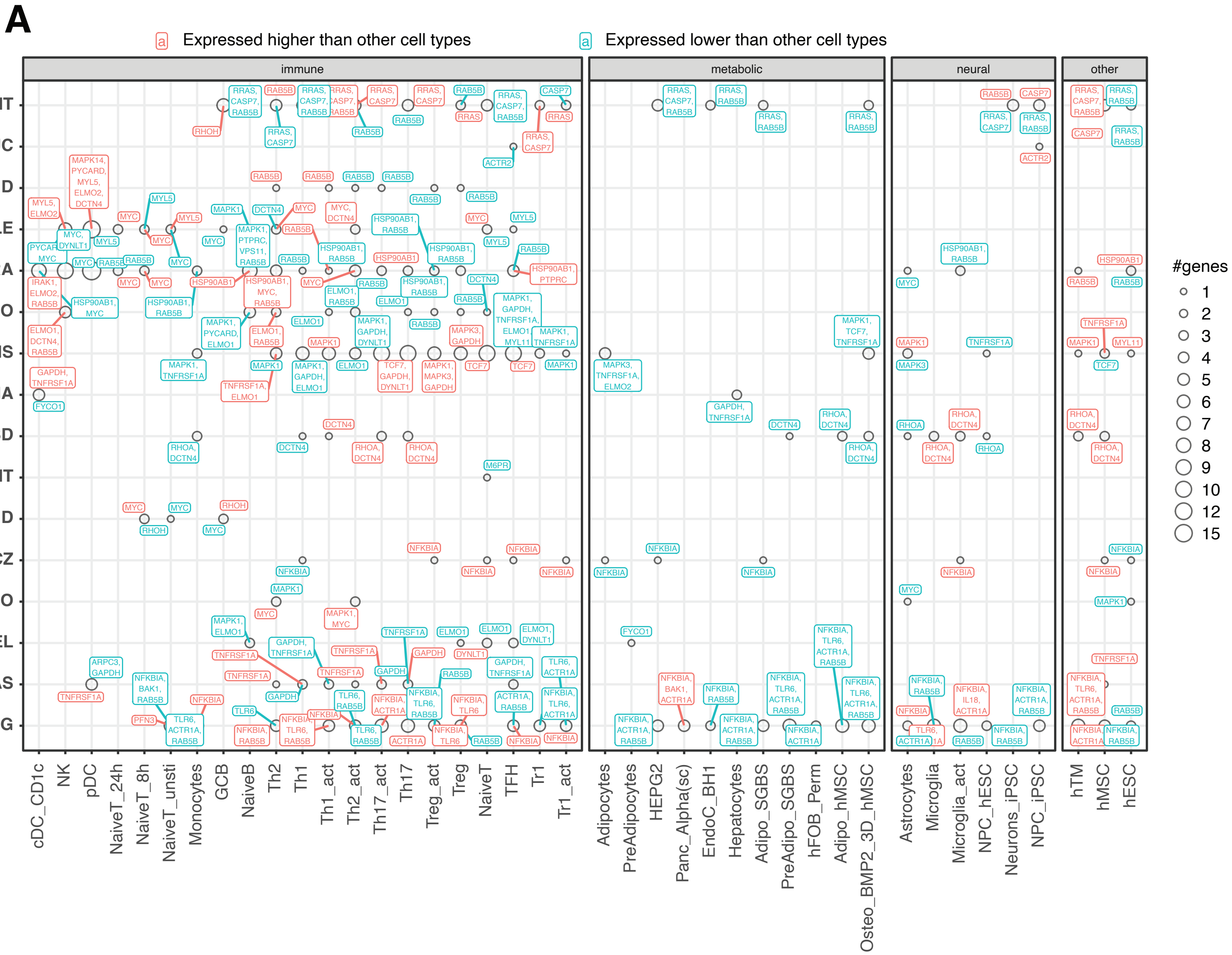

Figure S6 - Salmonella infection gene enrichment across trait and cell type (**A**) and in KEGG pathway (**B**).

B

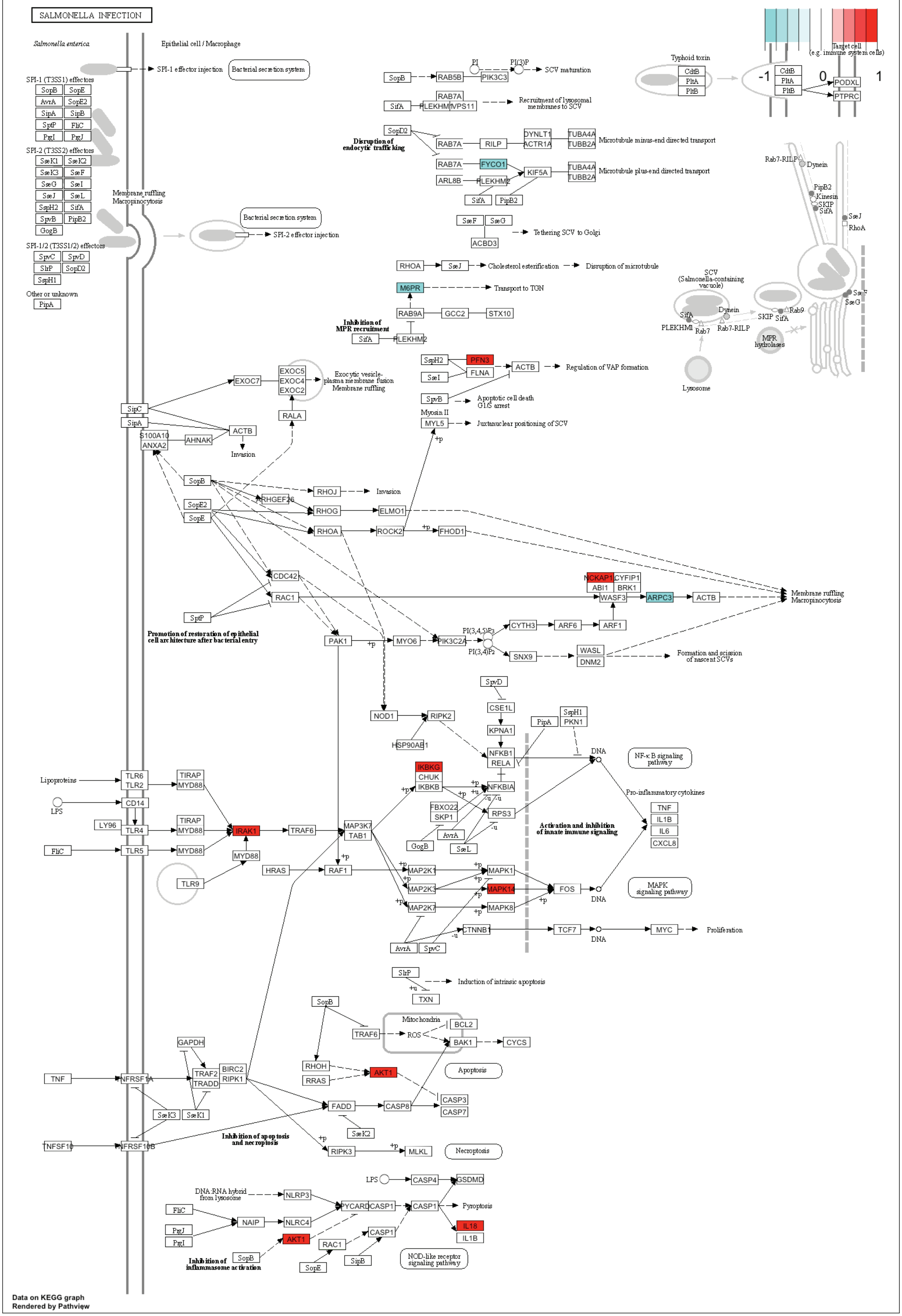

Figure S7 - Sharing of V2G genes in enteroids across UC, CRO, and IBD (**A**). Gene ontology (**B**) and pathway enrichment (**C**) across each trait are shown.

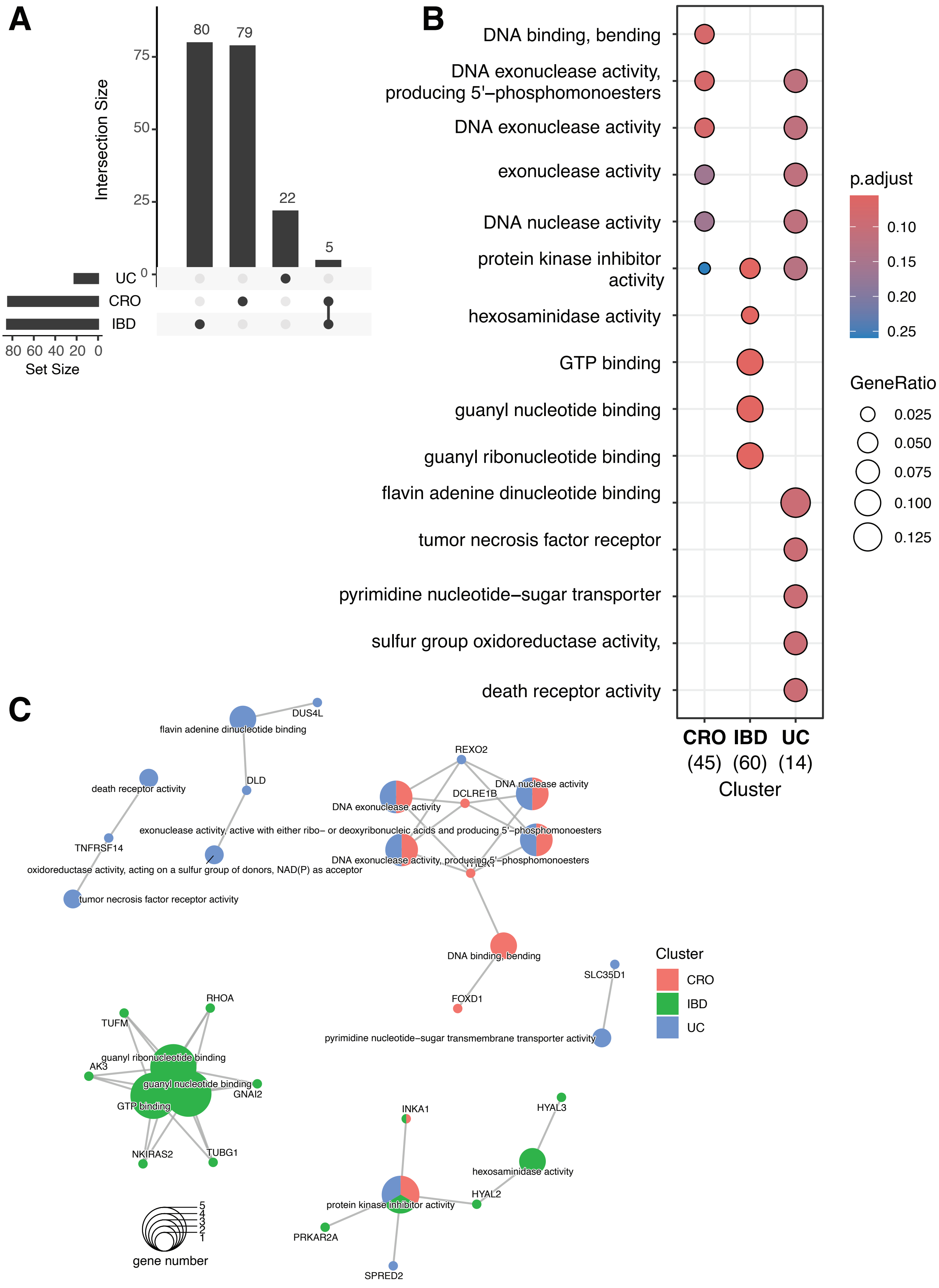

Figure S8 - Gene ontology enrichment of cell type-specific V2G genes across cell type.

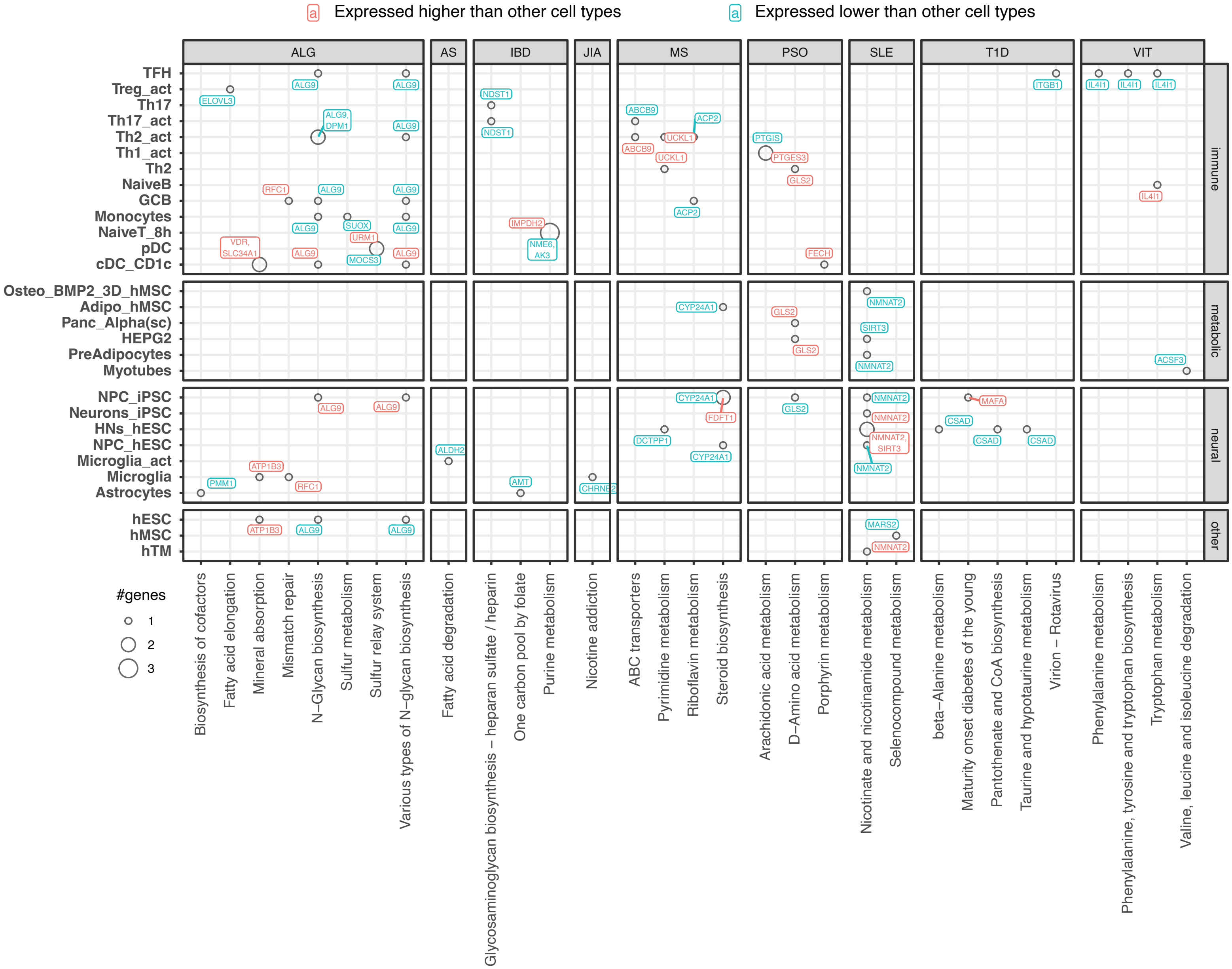

Figure S9 - Expression of *BLK* in sorted immune cells from RA patients, SLE patients, and healthy subjects measured by bulk RNA-seq[66]. Statistically significant differential expression compared to healthy subjects is denoted by p values.