

A

	sNkIK	IN	EN	Oligo	Clio	astro	Immune	
0.04	0.05	-0.01	-0.01	-0.02	0.14	0.16	CDR	Correlation 
0.06	0.08	0.12	-0.09	0.01	0.14	0.26	Braak	
0.09	0.10	0.15	-0.03	0.07	0.10	0.30	β amyloid density	

B

	CDR	Braak	β amyloid density		
-1.93	-6.53	-8.36	-0.36	M406 (86 genes)	 Signed log ₂ p-value
-8.05	-12.74	-11.98	-0.83	M824 (62 genes)	
-2.26	-8.02	-12.56	-0.84	M947 (52 genes)	
				sNkIK	Immune

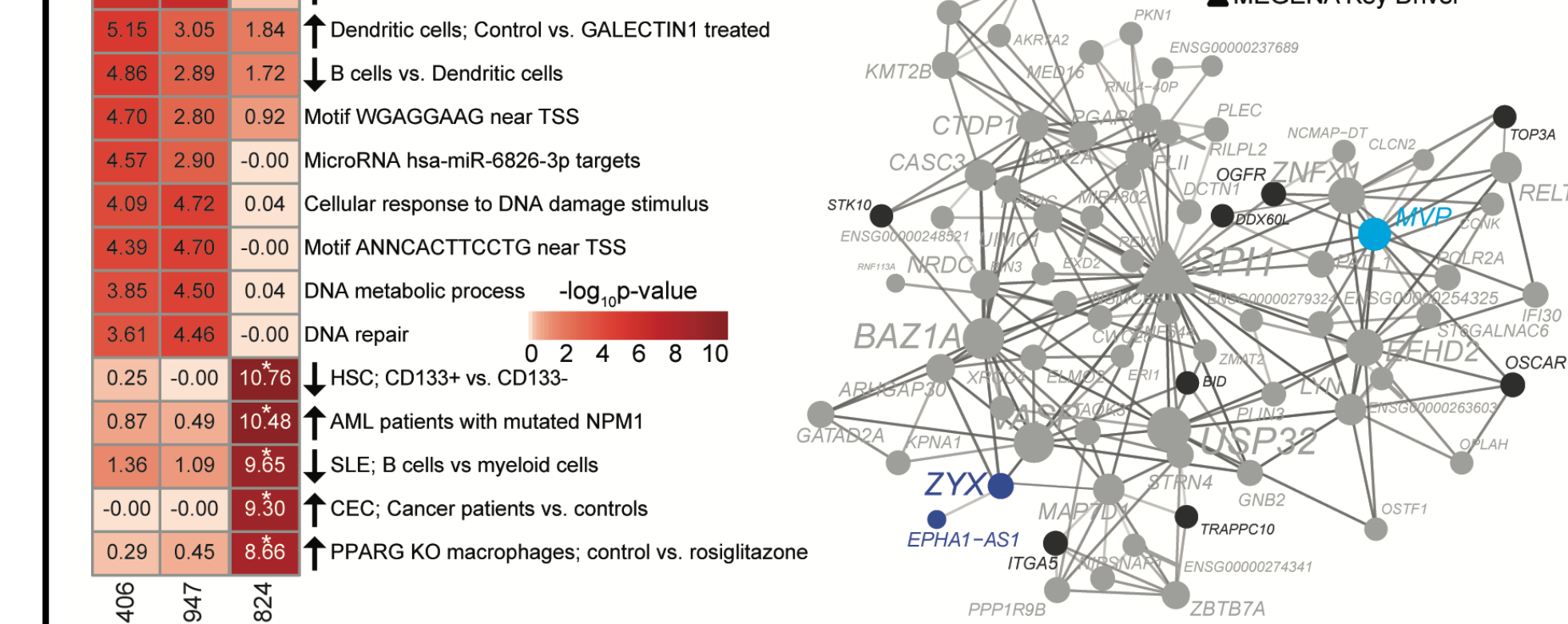
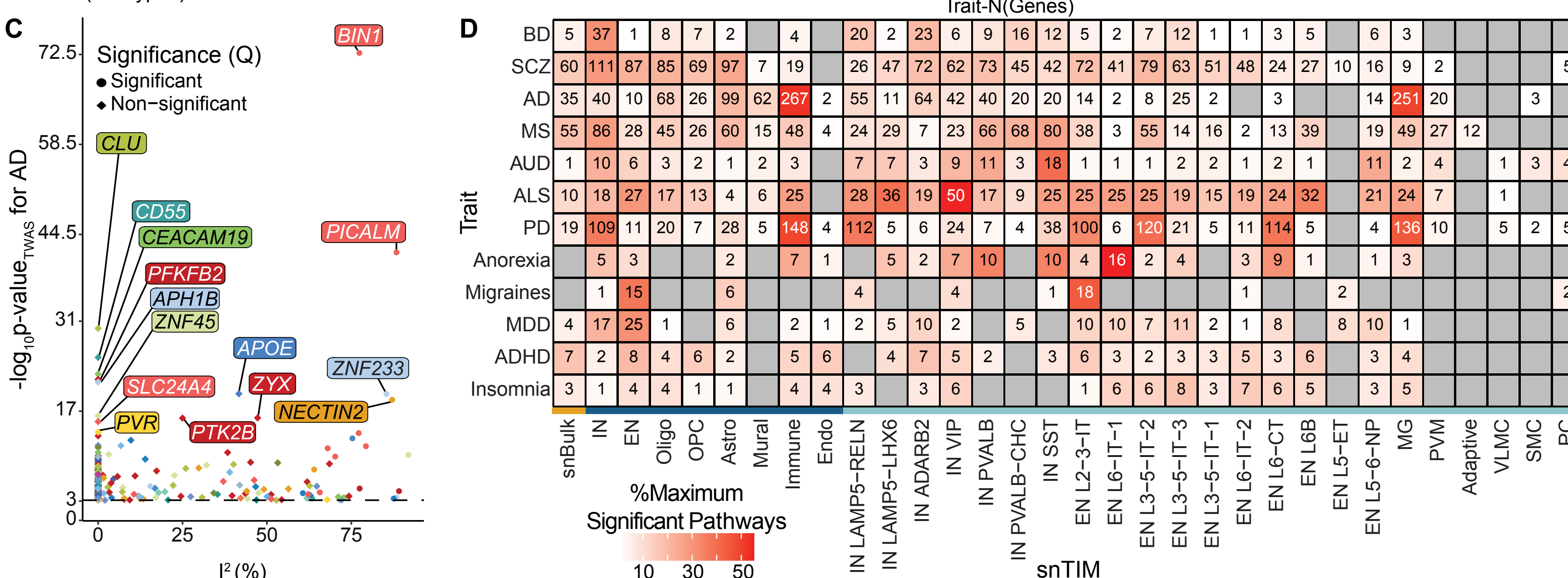
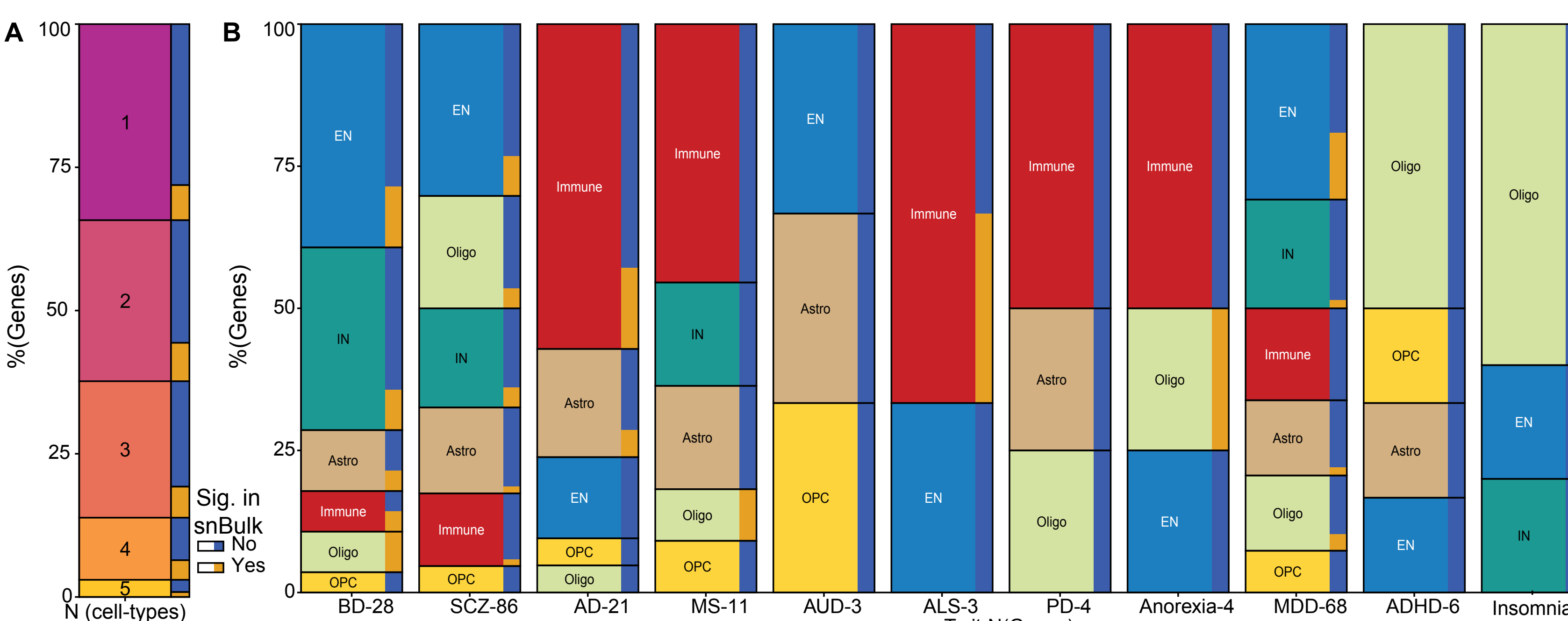
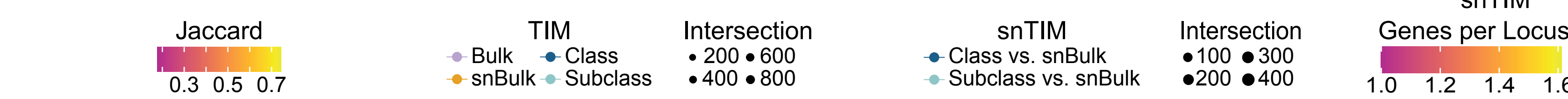
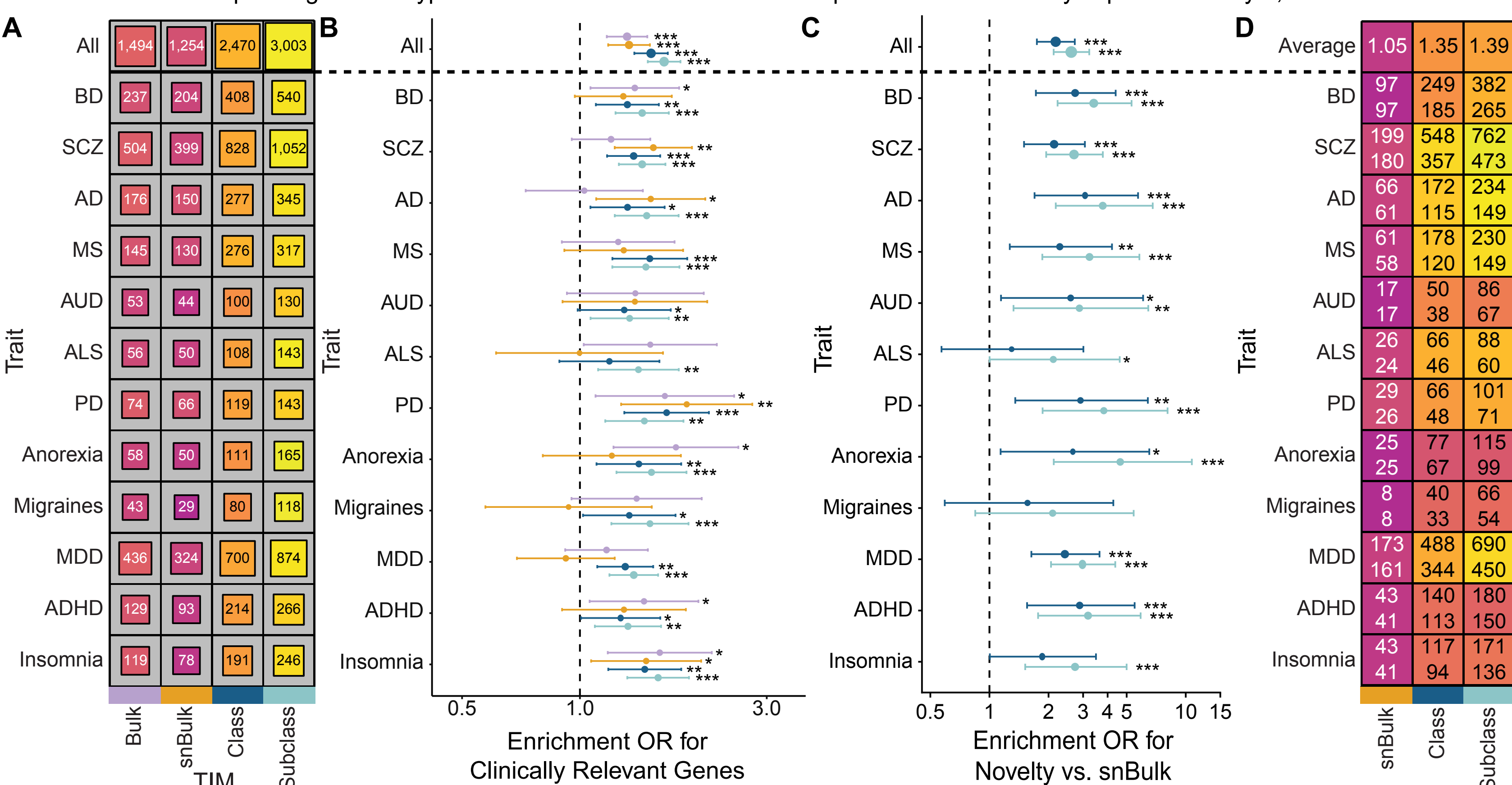
C

	0.55	0.40	0.37	
Monocytes; Anti-TREM1 vs. Anti-TREM1 and LPS				

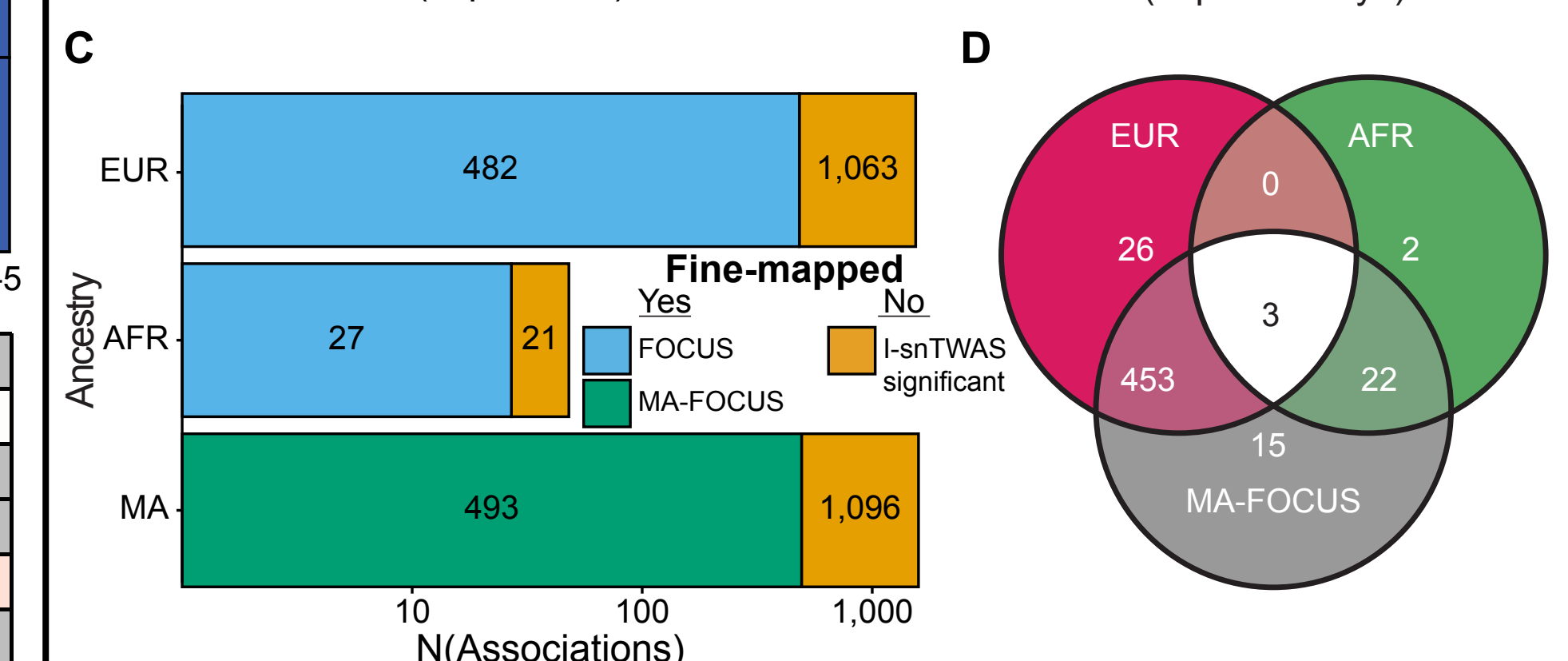
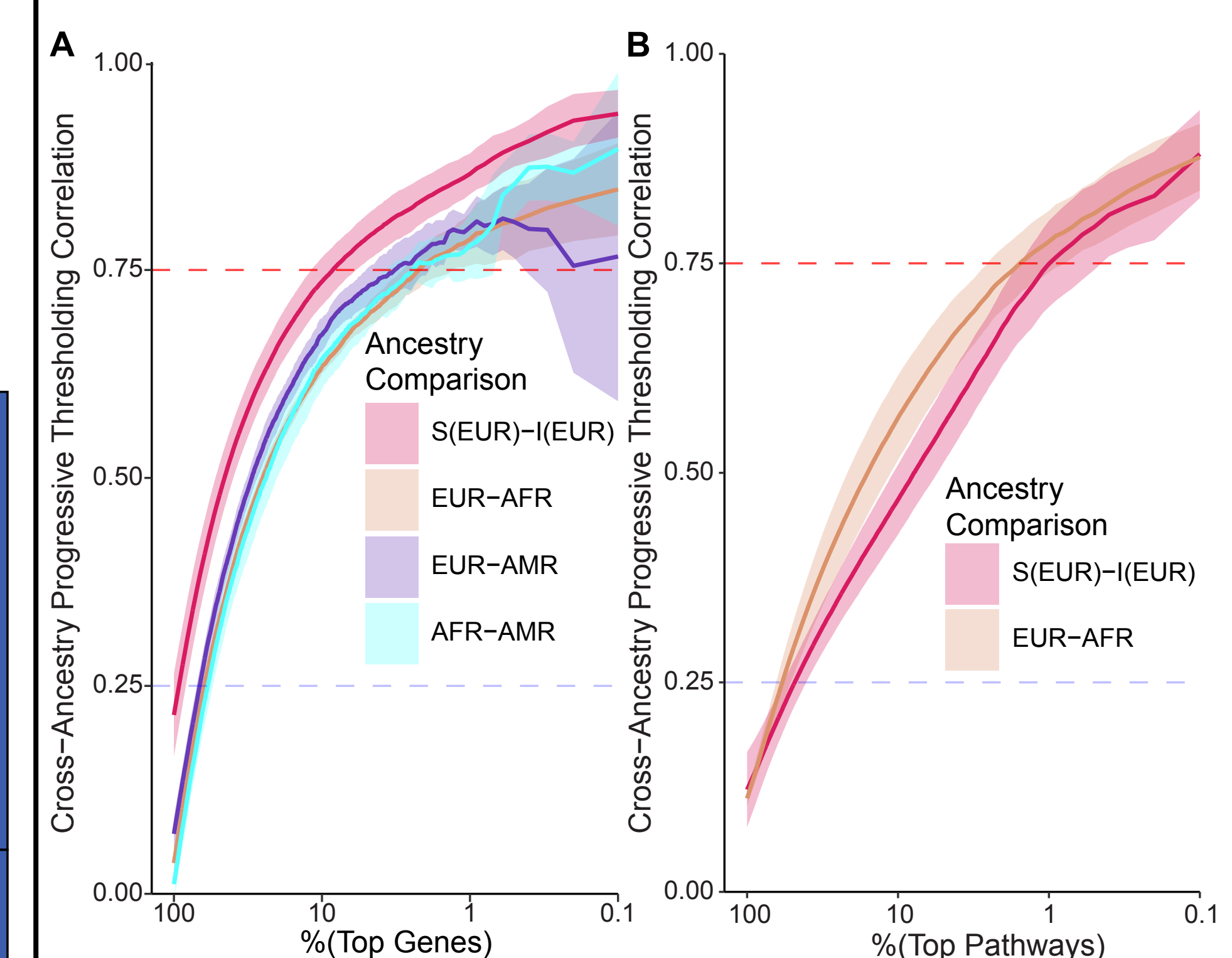
D

SETD9 M947

● Down regulated (FDR < 0.05)
● Down normal (FDR > 0.05)
● Not significant (p > 0.05)
● Not included in TWAS
● MGC-NK cell



Ancestry-specific snTWAS uncovers shared biology and aids in fine-mapping of risk genes



Discussion

- Across 12 traits, we found the greatest number of FDR significantly associated genes in the subclass level (4,953), followed by Class (4,183) and snBulk (2,472), demonstrating that increased cell-type resolution contributes more significant GTAs
- Between ancestries, we report strong correlation and concordance among the top ranked GTAs for both snTWAS and GREx-PheWAS. In addition, non-EUR snTWAS uncover ancestry-specific GTAs and aid in the multi-ancestry fine-mapping of GTAs.

Future Directions

- We are performing follow-up analyses on specific curated phenotypes
- We will utilize snTIMs to perform computational drug repurposing
- We are combining snTWAS results with other analyses, and performing in vivo analyses of high priority gene targets
- We are using snTIMs to perform AD patient clustering in the MVP