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Supplemental Information

Germline Features Associated with Immune Infiltration in Solid Tumors

Sahar Shahamatdar, Meng Xiao He, Matthew A. Reyna, Alexander Gusev, Saud H. AlDubayan, Eliezer M. Van Allen, and Sohini Ramachandran

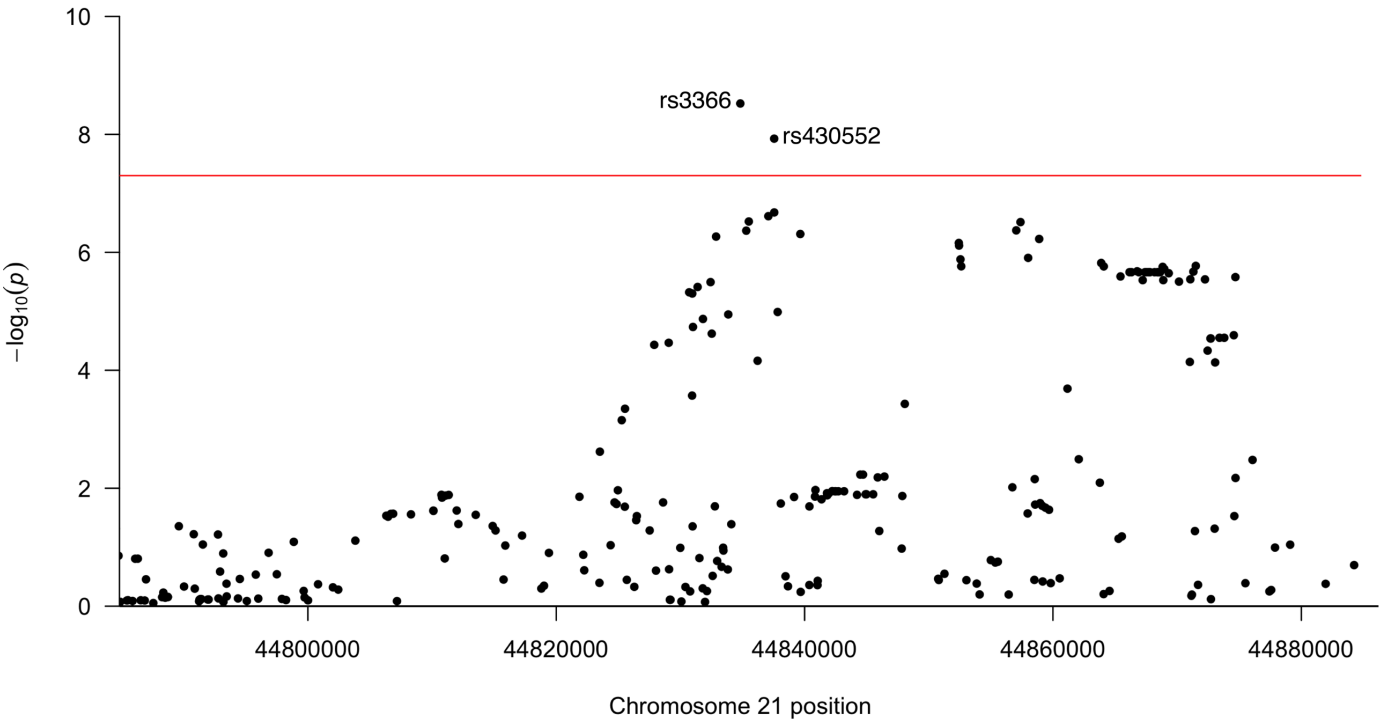

Figure S1. Zoomed-in Manhattan plot for GWAS meta-analysis for the follicular helper T cell phenotype. Related to Figure 1B. Positions along chromosome 21 are on the x-axis, and $-\log_{10}$-transformed p-values are on the y-axis. The red line indicates genome-wide significance ($p < 5 \times 10^{-8}$). Two significant SNPs are annotated with ids.

Table S3. Final number of SNPs included in the calculation of PRS for each of the five diseases at nine p-value thresholds. Related to Figure 4. Summary statistics from the five studies were downloaded. SNPs were excluded based on the following criteria: absence from our genotyped data; missing odds ratios, risk alleles, or p-values; and ambiguous or mismatched variants. SNPs were further filtered via LD-clumping, with a 250kb window and an r^2 threshold of 0.1.

p-value threshold	Rheumatoid arthritis	Ulcerative colitis	Celiac disease	Systemic lupus erythematosus	Multiple sclerosis
1.00E+00	206221	112262	87547	236909	85271
1.00E-01	44291	33294	21999	63842	20171
1.00E-02	6860	7313	3824	12430	3499
1.00E-03	1480	1829	659	2401	760
1.00E-04	564	607	158	616	266
1.00E-05	386	322	59	277	159
1.00E-06	310	212	29	173	116
1.00E-07	260	152	16	132	82
5.00E-08	251	143	13	119	88