

Supplementary material

Integrative Proteomics and Genomics Identify Novel Biomarkers and Therapeutic Targets in Vitiligo via Mendelian Randomization

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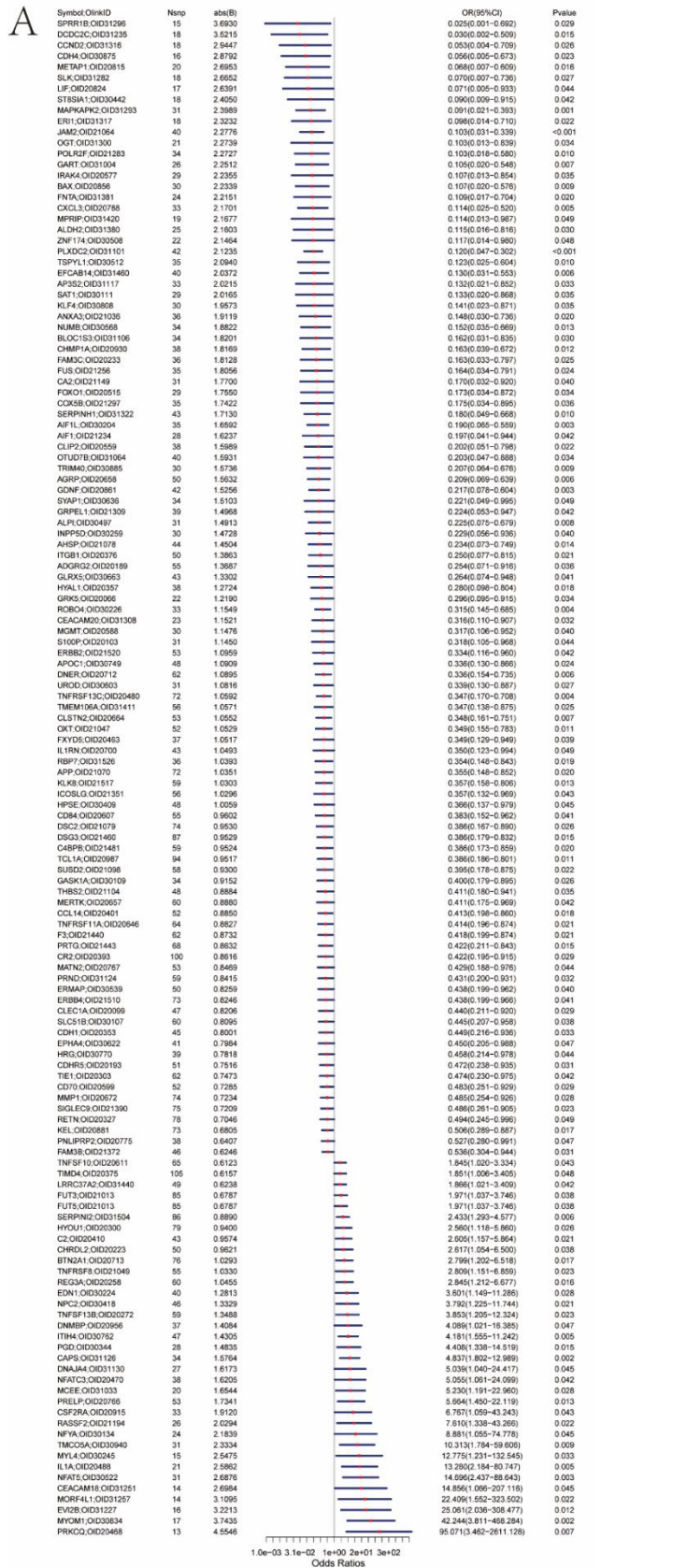


Fig.S1. Forest plots revealed 140 pairs of protein level associated with pQTLs positive outcomes of causal relationships ($P<0.05$).

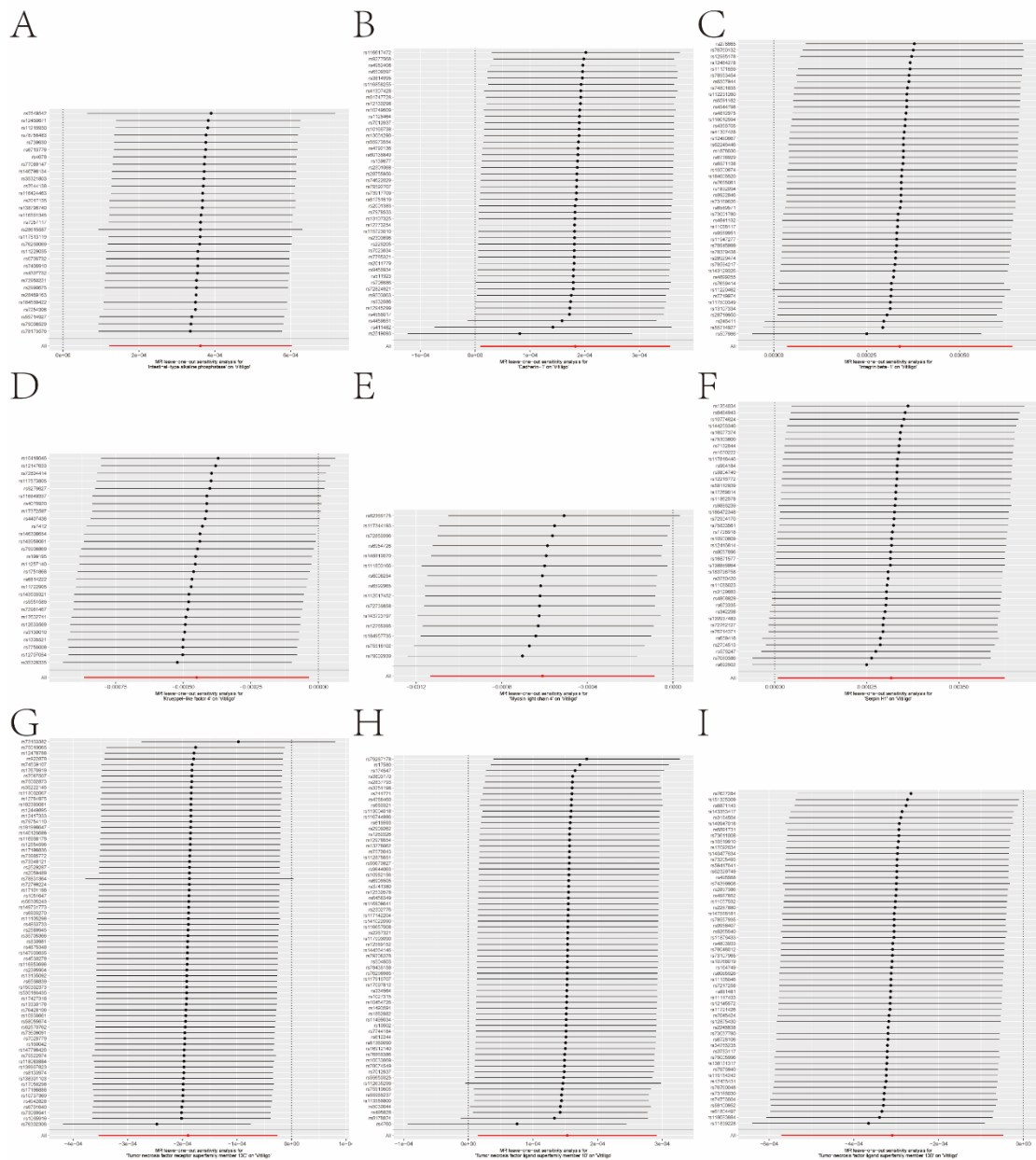


Fig.S2. Leave-one out sensitivity analysis was used to evaluate the effect of 9 SNPs screened from validation set.

Tab.S1 The Results from colocalization for 3 proteome-wide MR-identified proteins

snp	pvalues.df1	MAF.df1	N.df1	V.df1	pvalues.df2	MAF.df2	N.df2	V.df2	SNP.PP.H4	Symbol
rs12633569	1.37E-07	0.484749	32867	6.09E-05	0.263	0.487797	402732	0.033358	0.8359634	KLF4
rs5758504	2.67E-63	0.479119	33084	6.06E-05	0.436	0.481022	402732	0.033386	1	TNFRSF13C
rs304721	7.56E-47	0.478308	34049	5.88E-05	0.182	0.47816	402732	0.033402	0.8317133	TNFSF10

Note: MAF: minor allele frequency, the frequency of the minor allele in the population. df1: number of independent variables in the model. df2: remaining degrees of freedom, reflecting the error term in the model. N: indicates the number of samples. V: variance.

Tab.S2 All the enriched motifs and corresponding transcription factors of the core molecules

Motif	NES	AUC	TF_highconf	Enrichmentgenes
cisbp__M2174	4.03	0.427	BORCS8-MEF2B; MEF2A; MEF2B; MEF2C; MEF2D (inferredBy_Orthology)	KLF4;TNFSF10
cisbp__M0617	3.75	0.4		KLF4;TNFSF10
cisbp__M5570	3.21	0.35	HSFY2 (directAnnotation)	KLF4;TNFSF10
cisbp__M6483	3.2	0.349	SP4 (directAnnotation)	KLF4;TNFRSF13C
cisbp__M2212	3	0.331		KLF4;TNFSF10