

Supplemental information

Assessment of circulating proteins in thyroid

cancer: Proteome-wide Mendelian

randomization and colocalization analysis

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SUPPLEMENTAL INFORMATION

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Table S1: Detailed colocalization analysis results, related to Figure 1

Proteins	Nsnps	PP.H0.abf	PP.H1.abf	PP.H2.abf	PP.H3.abf	PP.H4.abf
ADAM23	2125	7.80E-299	1.69E-299	0.81	0.18	0.01
BMP1	2394	1.46E-11	2.36E-12	0.4	0.06	0.53
COL15A1	1239	1.07E-122	1.20E-123	0.75	0.08	0.16
COL18A1	2968	3.72E-95	7.93E-96	0.77	0.16	0.06
EIF2B1	2268	1.45E-08	3.17E-09	0.65	0.14	0.21
FAM20B	2008	3.28E-20	4.14E-21	0.85	0.11	0.05
GSTA1	2686	1.23E-303	3.64E-304	0.56	0.16	0.28
GUSB	1327	1.61E-62	3.49E-63	0.68	0.15	0.17
HINT1	2009	1.64E-18	3.28E-19	0.72	0.14	0.14
IL5RA	1722	1.23E-295	1.49E-296	0.86	0.1	0.04
INHBA	2461	5.98E-19	1.10E-19	0.76	0.14	0.1
KYNU	2092	1.37E-250	2.24E-251	0.67	0.11	0.22
LGMN	1394	3.34E-197	3.56E-198	0.22	0.02	0.76
LHB	2728	4.14E-298	1.25E-298	0.68	0.2	0.12
MSR1	1600	2.89E-188	4.63E-189	0.71	0.11	0.18
MTHFD1	2112	2.24E-32	3.51E-33	0.82	0.13	0.05
NANS	2296	3.85E-93	1.49E-48	2.58E-45	1	0
NPTX1	2650	2.82E-291	9.22E-291	0.06	0.21	0.73
OMD	1211	4.85E-13	3.82E-14	0.83	0.07	0.1
PDCD6IP	1997	2.79E-30	7.68E-31	0.72	0.2	0.08
PLEKHA7	2091	3.42E-251	1.85E-251	0.19	0.1	0.71
SEMA4A	1674	3.81E-75	8.40E-76	0.7	0.15	0.14
SPOCK2	2174	1.28E-110	1.87E-111	0.81	0.12	0.07
TNFAIP3	2394	2.91E-49	8.80E-50	0.3	0.09	0.61
VCAM1	1016	9.99E-26	1.96E-26	0.15	0.03	0.82
VPS26A	2521	1.18E-78	2.18E-79	0.78	0.14	0.07

Table S2: Genome-wide association meta-analysis of TCs with lambda values, linkage disequilibrium regression scores and genetic contribution details for each cohort, related to STAR Methods

Cohort	Mean chisq	Lambda	Ldsc	se (Ldsc)	Ratio	se (Ratio)	h ²	se (h ²)	Z (h ²)	pval (h ²)
Aleksandra et al.,GWAS	1.268	1.198	1.248	0.01	0.926	0.039	0.897	0.53	1.691	0.091
UKBB	1.024	1.023	1.017	0.007	0.698	0.307	0.072	0.103	0.699	0.485
FinnGen R9	1.079	1.057	1.019	0.01	0.236	0.124	0.009	0.003	3.361	1.00E-03
Meta GWAS	1.109	1.075	1.035	0.009	0.325	0.085	0.011	0.003	4.124	3.72E-05

Notes: Mean chisq:the average of the Chi-square values of each SNP, Lambda:Genetic structure bias in GWAS, Ldsc:Estimates of genetic correlation, se: standard error, Ratio: The proportion of the contribution of genetic variation to complex traits relative to the underlying risk (confounding factor), h²: genetic contribution, Z: Genetic correlation Z score =h² observed/h² observed se, pval: The P-value of genetic correlation

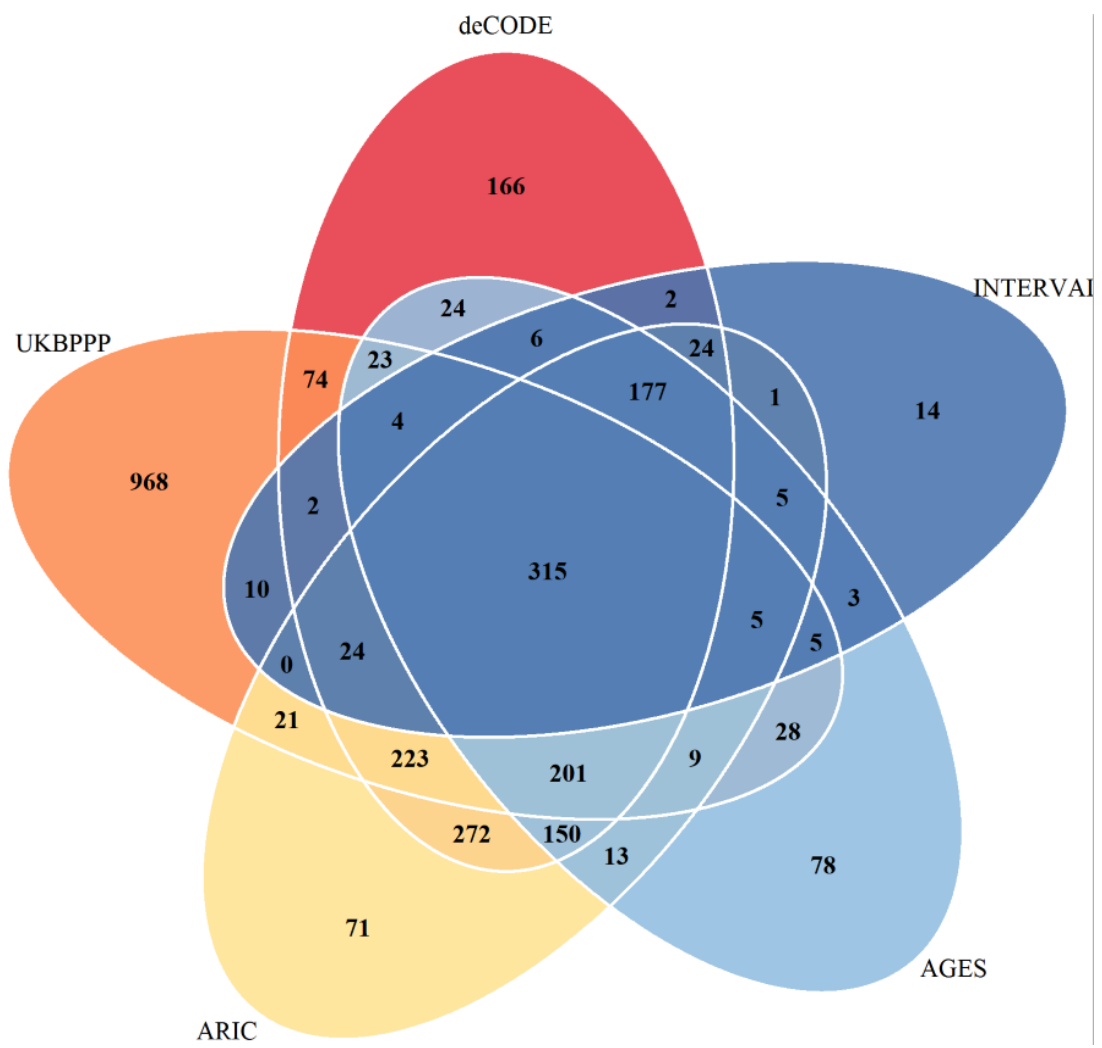


Figure S1: Common Protein Details Across Five Cohorts, related to STAR Methods

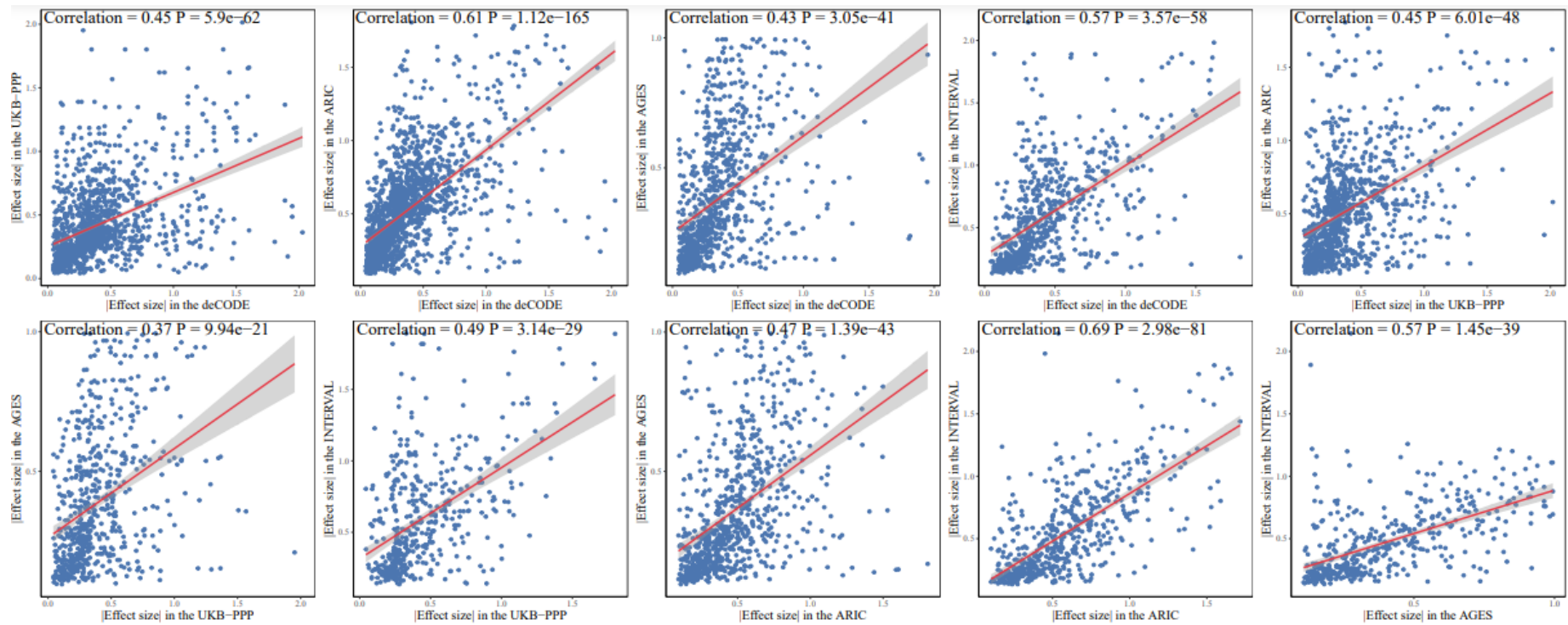


Figure S2: Correlation Between Different Protein Cohorts, related to result

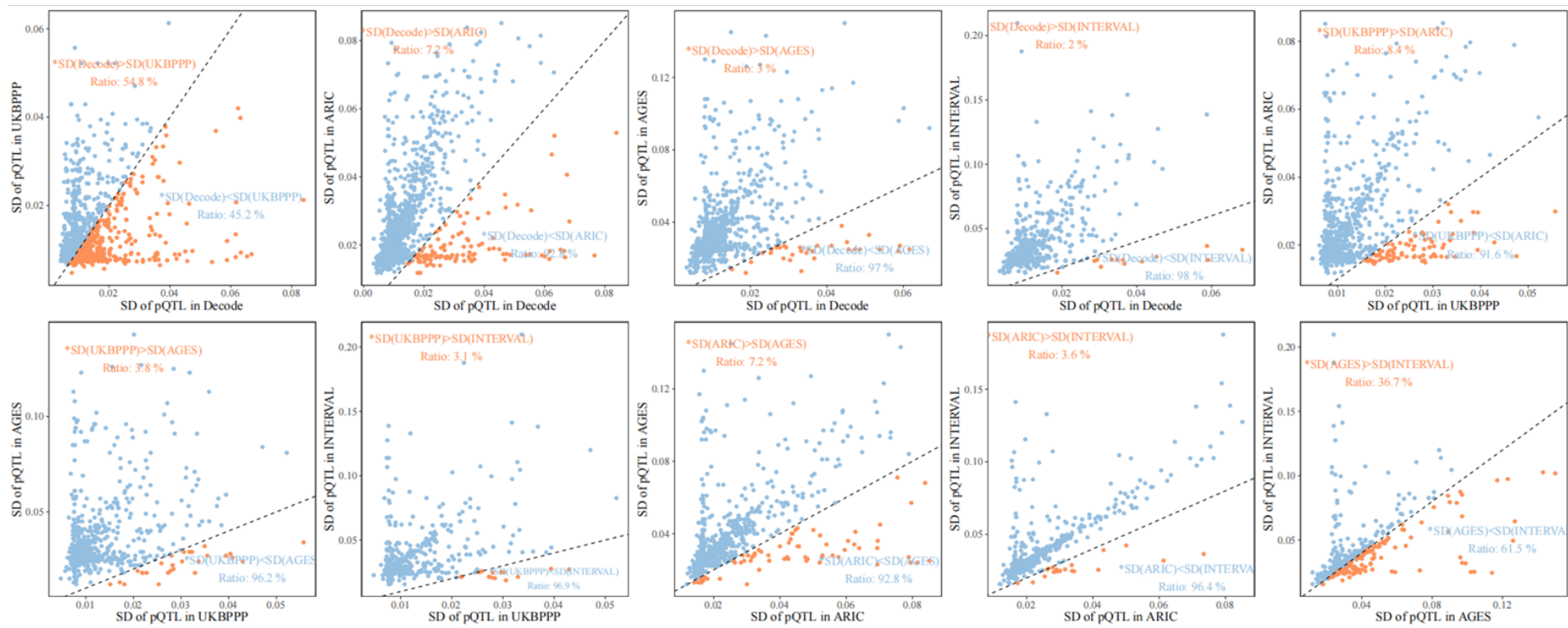


Figure S3: Variability Among Different Protein Cohorts, related to result

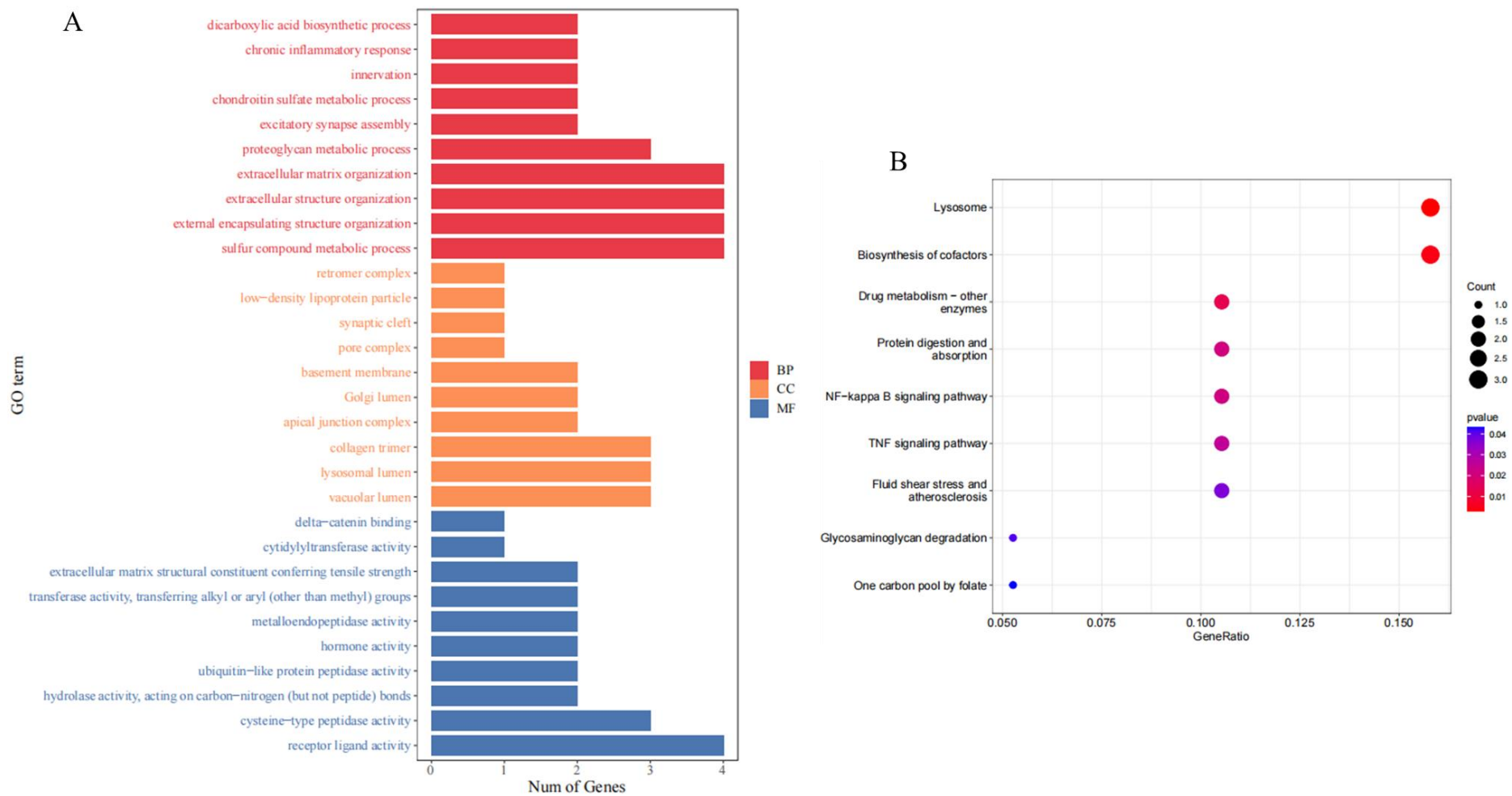


Figure S4: Gene Enrichment Analysis. A: GO Enrichment Analysis; B: KEGG Enrichment Analysis, related to result

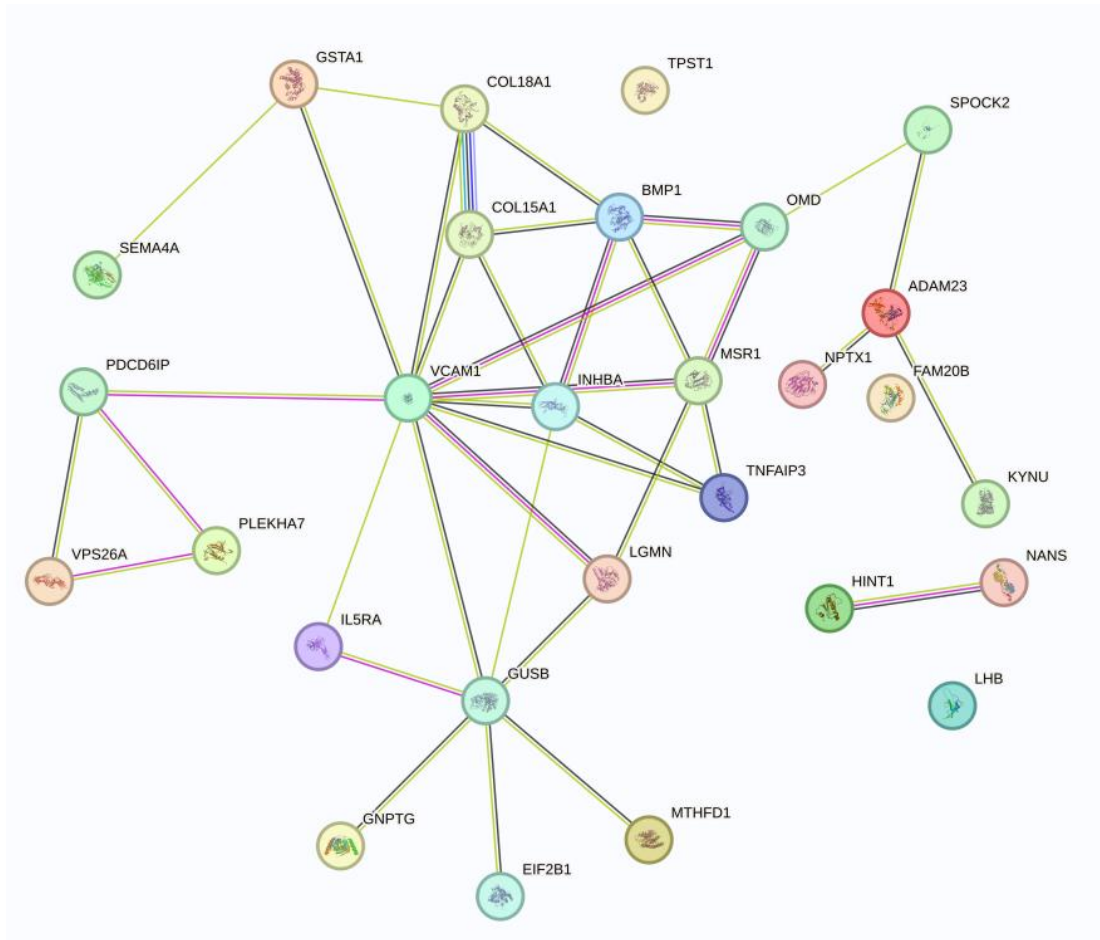


Figure S5: PPI Protein Interaction Network, related to result

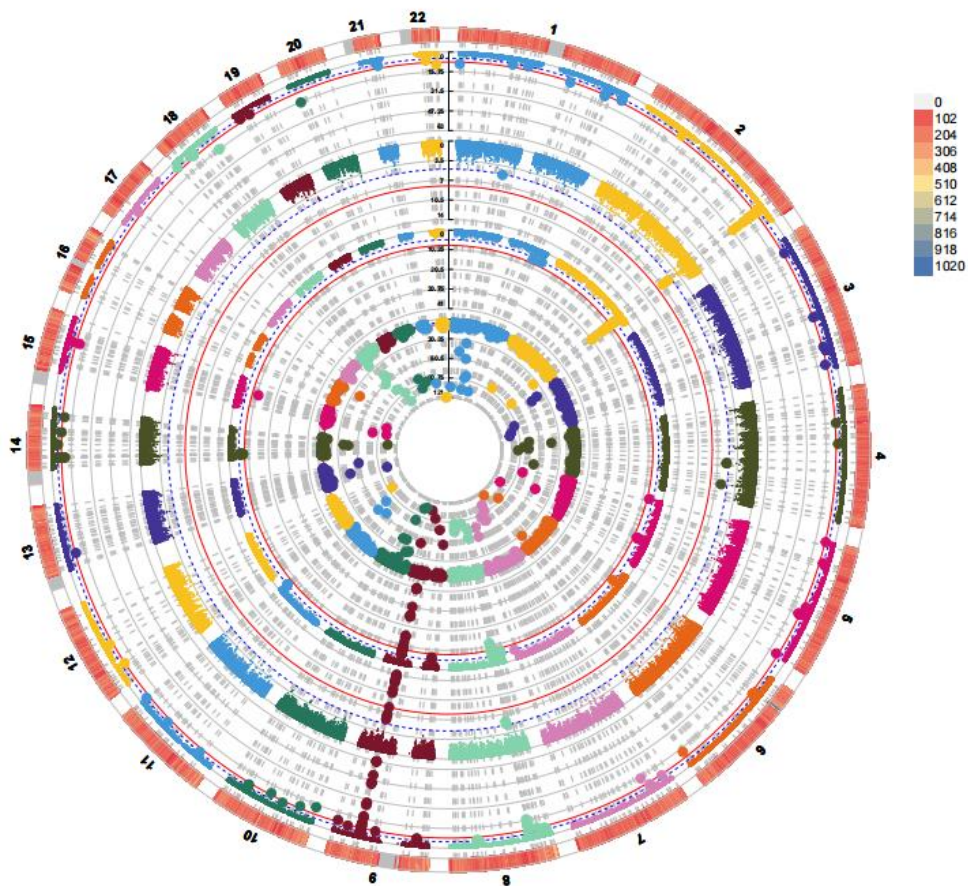


Figure S6: Circular Manhattan Plot of Thyroid Tumor Whole-Genome Association Meta-Analysis, related to STAR Method