

THE SUPPLEMENTARY TABLES & FIGURES

Supplementary Table S1

Supplementary Table S1. The top 273 genes for the MetaCore analysis extracted from TCGA

No.	Correlated Gene	Spearman's Correlation	p-Value
1	APRT	0.669646244	8.73E-65
2	SLC25A10	0.585874288	2.61E-46
3	ACY1	0.574263342	3.70E-44
4	SLC25A39	0.561980496	5.66E-42
5	PPP1R14B	0.558187831	2.56E-41
6	PYCR1	0.542233971	1.20E-38
7	POLD2	0.5406823	2.14E-38
8	SIGMAR1	0.53733003	7.44E-38
9	CGREF1	0.536231365	1.11E-37
10	PPIA	0.535028926	1.73E-37
11	RAC3	0.530840369	7.94E-37
12	SPATA33	0.525009456	6.39E-36
13	MRPL12	0.518974919	5.30E-35
14	CTU2	0.515248621	1.92E-34
15	PAFAH1B3	0.508719413	1.76E-33
16	SAMD10	0.506656538	3.50E-33
17	KATNB1	0.504363889	7.49E-33
18	HMG20B	0.503243849	1.08E-32
19	GAS8	0.502603921	1.34E-32
20	POLDIP2	0.50159287	1.86E-32
21	BSG	0.500848058	2.38E-32
22	PPM1G	0.497974698	6.06E-32
23	ALG3	0.496320092	1.03E-31
24	GGCT	0.496293452	1.04E-31
25	MFSD12	0.493107633	2.89E-31
26	HMBS	0.492358394	3.67E-31
27	SRM	0.489118262	1.02E-30
28	RITA1	0.487664596	1.61E-30
29	DDX49	0.487434033	1.73E-30
30	GNB2	0.486549719	2.29E-30
31	NMRAL1	0.485659739	3.02E-30
32	NALF2	0.484133276	4.84E-30
33	PGLS	0.483082213	6.70E-30
34	TIMM13	0.482939472	7.00E-30
35	NME1	0.478780589	2.50E-29

36	ACOT8	0.477897217	3.27E-29
37	SRD5A1	0.477878941	3.29E-29
38	SLC4A5	0.477257598	3.97E-29
39	FARSA	0.475614375	6.51E-29
40	NPRL2	0.475219222	7.33E-29
41	DDX41	0.473027842	1.41E-28
42	HSD17B10	0.473027635	1.41E-28
43	ASPHD1	0.472892716	1.47E-28
44	AP1M2	0.472646343	1.58E-28
45	UQCC3	0.472373948	1.72E-28
46	ZNF524	0.472325016	1.74E-28
47	SLC27A5	0.471544684	2.20E-28
48	NUTF2	0.471470556	2.25E-28
49	PKP3	0.471282099	2.37E-28
50	SAPCD2	0.47083272	2.71E-28
51	STK32C	0.47046729	3.02E-28
52	DNPH1	0.469302643	4.26E-28
53	DTYMK	0.468654724	5.16E-28
54	C19ORF54	0.468553686	5.31E-28
55	FIBP	0.466609183	9.39E-28
56	RABGGTA	0.466551334	9.55E-28
57	SLC19A1	0.466114243	1.09E-27
58	B3GAT3	0.46521435	1.41E-27
59	CHMP1A	0.464441154	1.76E-27
60	CENPX	0.464351526	1.81E-27
61	TKFC	0.46416015	1.91E-27
62	SSC4D	0.463745505	2.16E-27
63	DHPS	0.463473548	2.34E-27
64	MAZ	0.462664704	2.95E-27
65	CENPBD1P	0.462362468	3.22E-27
66	POP7	0.461627478	3.98E-27
67	ZP3	0.461409707	4.23E-27
68	AP1S1	0.461281679	4.39E-27
69	KARS1	0.460913346	4.88E-27
70	YIF1A	0.460313171	5.79E-27
71	RUVBL2	0.459960171	6.41E-27
72	PRR19	0.459667435	6.97E-27
73	CENPM	0.459271647	7.80E-27
74	MCRIP2	0.458891658	8.69E-27
75	HYAL3	0.457926196	1.14E-26
76	PRELID1	0.457920012	1.15E-26
77	MLST8	0.457192754	1.41E-26

78	MRTO4	0.456809679	1.57E-26
79	DEAF1	0.455771925	2.10E-26
80	PGAP2	0.455697785	2.15E-26
81	HGH1	0.455097857	2.54E-26
82	NHP2	0.454806153	2.76E-26
83	TOMM40	0.454505529	3.00E-26
84	SLC2A4RG	0.454244533	3.23E-26
85	IDH3G	0.453905124	3.55E-26
86	NELFCD	0.453834082	3.62E-26
87	DUS1L	0.453796393	3.66E-26
88	MPST	0.452852202	4.77E-26
89	PYCR3	0.452768253	4.88E-26
90	TRAPPC2L	0.452392974	5.42E-26
91	SPDEF	0.451988346	6.07E-26
92	ECE2	0.451731039	6.51E-26
93	AKT1	0.451627356	6.71E-26
94	PLEKHJ1	0.451275659	7.39E-26
95	ECHS1	0.451047729	7.88E-26
96	LRFN1	0.451013281	7.95E-26
97	ELMO3	0.450743468	8.57E-26
98	NCLN	0.450368085	9.51E-26
99	EIF3B	0.449416563	1.24E-25
100	MRPS2	0.449175312	1.32E-25
101	MON1A	0.448254033	1.70E-25
102	ZNF511	0.448126085	1.76E-25
103	AKT1S1	0.448010332	1.82E-25
104	PRMT7	0.4478445	1.91E-25
105	EXOSC5	0.447732465	1.97E-25
106	ATP6V1F	0.447617189	2.03E-25
107	EEF2KMT	0.447370156	2.17E-25
108	RUVBL1	0.447095478	2.34E-25
109	CDT1	0.447025664	2.39E-25
110	PRR7	0.447015648	2.39E-25
111	PODXL2	0.446003732	3.15E-25
112	CPNE7	0.445528332	3.59E-25
113	DPM2	0.444798596	4.38E-25
114	MCAT	0.444672323	4.53E-25
115	MRPS24	0.444597966	4.62E-25
116	ESRP2	0.444147555	5.23E-25
117	RPUSD1	0.442613245	7.91E-25
118	SYNGR2	0.441233305	1.15E-24
119	LSM4	0.440830289	1.28E-24

120	BDH1	0.440436165	1.42E-24
121	TCF25	0.440254832	1.49E-24
122	BCS1L	0.440127206	1.54E-24
123	MRPS15	0.439359792	1.89E-24
124	TRUB2	0.43923485	1.96E-24
125	NR2F6	0.438713873	2.25E-24
126	MOSPD3	0.438459796	2.41E-24
127	FMC1	0.438054715	2.68E-24
128	PCBD1	0.437084193	3.47E-24
129	DPCD	0.436926725	3.62E-24
130	MRPL48	0.435359991	5.47E-24
131	LAGE3	0.435180942	5.73E-24
132	BPHL	0.435048772	5.93E-24
133	MARCHF9	0.434954704	6.08E-24
134	RFXANK	0.434876538	6.21E-24
135	MRPL15	0.434644322	6.60E-24
136	PAM16	0.434567693	6.73E-24
137	YIF1B	0.434314412	7.20E-24
138	METTL26	0.434140618	7.53E-24
139	TBRG4	0.433835812	8.16E-24
140	RPL13	0.43382248	8.19E-24
141	RRP9	0.433321782	9.33E-24
142	MRPS34	0.432700582	1.10E-23
143	COA4	0.432617253	1.12E-23
144	BTBD2	0.432487768	1.16E-23
145	RAD23A	0.431947419	1.34E-23
146	CORO1B	0.430542697	1.92E-23
147	FAAP100	0.430408255	1.99E-23
148	POLR2H	0.429964039	2.24E-23
149	ZMYND19	0.429813283	2.32E-23
150	DANCR	0.429764648	2.35E-23
151	EIPR1	0.429512079	2.51E-23
152	CLPP	0.427471466	4.25E-23
153	IFI27L1	0.427463153	4.26E-23
154	CDK16	0.427359254	4.37E-23
155	CBS	0.427065072	4.71E-23
156	NDUFA7	0.426957477	4.85E-23
157	PDZD11	0.426525881	5.41E-23
158	CACFD1	0.42589455	6.36E-23
159	AP2S1	0.42558901	6.87E-23
160	TPRN	0.425064655	7.86E-23
161	YBEY	0.424738566	8.54E-23

162	EMC10	0.424729067	8.56E-23
163	NAA10	0.424649248	8.73E-23
164	SPATA2L	0.424328189	9.47E-23
165	MARVELD3	0.423927681	1.05E-22
166	TALDO1	0.42375111	1.10E-22
167	ATAD3A	0.423545627	1.16E-22
168	SNRPA	0.422887254	1.36E-22
169	COX5A	0.422812764	1.39E-22
170	KRT18	0.422755394	1.41E-22
171	PEBP1	0.422175353	1.63E-22
172	MTX1	0.420919054	2.24E-22
173	CINP	0.420715326	2.36E-22
174	CDK10	0.420677533	2.38E-22
175	NDUFAF3	0.420509739	2.48E-22
176	RNASEH2A	0.420437624	2.53E-22
177	SYNE4	0.420295995	2.62E-22
178	CAMK2B	0.419009917	3.61E-22
179	TIMM50	0.418319638	4.29E-22
180	GTF3A	0.418026654	4.61E-22
181	MFSD3	0.41796918	4.68E-22
182	NCBP2AS2	0.416980382	5.98E-22
183	LBHD1	0.416779442	6.28E-22
184	NOP16	0.41676323	6.31E-22
185	DHODH	0.416725448	6.37E-22
186	SMARCD2	0.416077494	7.47E-22
187	CLN6	0.416073983	7.48E-22
188	KDF1	0.41598198	7.65E-22
189	MRPL41	0.415901852	7.80E-22
190	MRPS33	0.415875274	7.86E-22
191	RPP25L	0.415787401	8.03E-22
192	P4HTM	0.415733615	8.14E-22
193	NME2	0.415649283	8.31E-22
194	ATP5MC1	0.415574421	8.46E-22
195	SGTA	0.415560791	8.49E-22
196	KCTD13	0.415316906	9.02E-22
197	MRPS12	0.414827763	1.02E-21
198	CFAP65	0.414392633	1.13E-21
199	TMEM161A	0.414333054	1.15E-21
200	NKIRAS2	0.414169596	1.20E-21
201	ALKBH2	0.414103408	1.21E-21
202	MRPL57	0.414090976	1.22E-21
203	NDUFB10	0.41394151	1.26E-21

204	CDKN2AIPNL	0.413867567	1.29E-21
205	FAM174C	0.41358051	1.38E-21
206	FAM89B	0.413466822	1.42E-21
207	DHRS11	0.413278501	1.49E-21
208	ERAL1	0.413059377	1.57E-21
209	TUFM	0.412887721	1.64E-21
210	EIF3I	0.412558628	1.77E-21
211	TIMM17B	0.412301319	1.89E-21
212	GLOD5	0.412076619	1.99E-21
213	THEM6	0.411609212	2.23E-21
214	HSPBP1	0.411580723	2.25E-21
215	SNRNP25	0.411414054	2.34E-21
216	MRPL37	0.411318953	2.40E-21
217	PRELID1P6	0.411055129	2.56E-21
218	DESI1	0.411023388	2.58E-21
219	TTLL1	0.410748763	2.75E-21
220	NFS1	0.410324269	3.05E-21
221	CSKMT	0.410229272	3.12E-21
222	SLC29A2	0.410181392	3.16E-21
223	UBE2M	0.410070255	3.25E-21
224	ATPAF2	0.410038049	3.27E-21
225	TRPT1	0.409882945	3.40E-21
226	COPE	0.409674127	3.57E-21
227	EPN1	0.409334449	3.88E-21
228	ADM2	0.409247185	3.96E-21
229	RNF187	0.409240691	3.97E-21
230	TMEM208	0.408320445	4.95E-21
231	DVL1	0.408219056	5.07E-21
232	DCXR	0.407801636	5.61E-21
233	RALY	0.407792147	5.62E-21
234	ANAPC11	0.407767726	5.65E-21
235	TREX1	0.407720206	5.72E-21
236	GPS1	0.407452872	6.10E-21
237	NDOR1	0.406824857	7.09E-21
238	SLIRP	0.406740815	7.23E-21
239	BOLA3	0.406421118	7.80E-21
240	TAF10	0.406071445	8.48E-21
241	TTLL12	0.406018825	8.59E-21
242	TXN	0.405945408	8.74E-21
243	TRPM4	0.405902247	8.83E-21
244	PDF	0.405870237	8.90E-21
245	PDXP	0.40584563	8.95E-21

246	OXLD1	0.405813548	9.02E-21
247	TUBB4A	0.405673737	9.33E-21
248	GATD3	0.405582973	9.53E-21
249	OAZ1	0.405548072	9.61E-21
250	GARIN5A	0.405338355	1.01E-20
251	NOP10	0.404771365	1.16E-20
252	BOLA2	0.404765996	1.16E-20
253	ASPSCR1	0.404573213	1.21E-20
254	ITPA	0.404334377	1.28E-20
255	C2CD2L	0.404017995	1.38E-20
256	H2AC17	0.402944277	1.78E-20
257	ELL3	0.402862641	1.82E-20
258	CDK5	0.402722933	1.88E-20
259	MYL5	0.402705689	1.89E-20
260	ZNF821	0.402424828	2.02E-20
261	FKBP4	0.402336253	2.06E-20
262	C19ORF73	0.40228068	2.09E-20
263	RAB1B	0.402043496	2.20E-20
264	USE1	0.402025426	2.21E-20
265	RANGAP1	0.40185536	2.30E-20
266	PDCD2L	0.401407334	2.56E-20
267	PRDX4	0.401057795	2.78E-20
268	SOX12	0.400517725	3.16E-20
269	MICOS13	0.400486366	3.18E-20
270	MRPS17	0.400332718	3.29E-20
271	PPP1CA	0.400136734	3.45E-20
272	GLRX5	0.400067758	3.51E-20
273	WBP1	0.400021808	3.54E-20

Supplementary Table S2

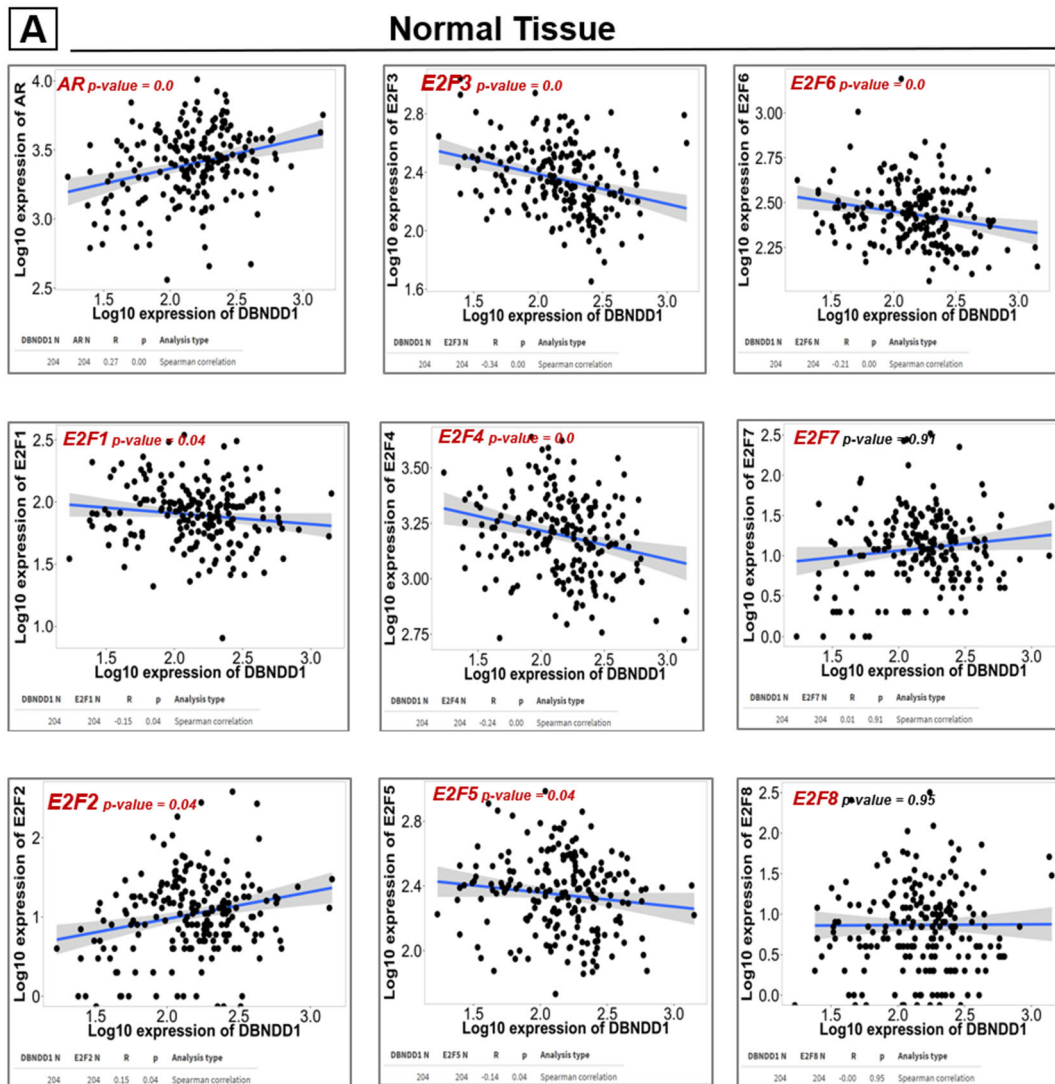
Supplementary Table S2. Pathway maps and network objects in the MetaCore analysis.

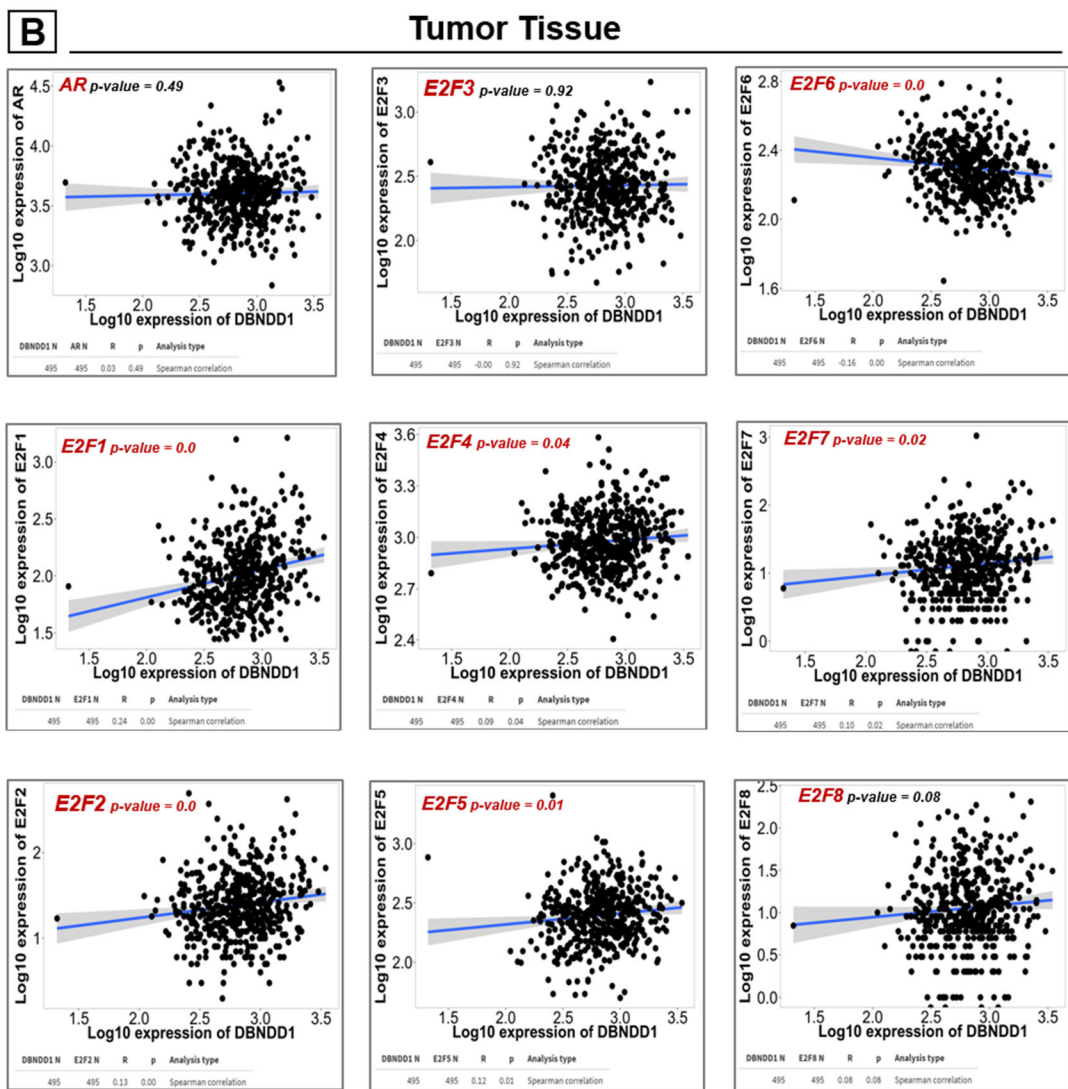
No.	Enrichment of pathway maps	p-Value	Network Objects from Active Data
1	Regulation of GSK3 beta in bipolar disorder	3.640E-05	AKT1, DVL-1, AKT(PKB), Dsh, PP1-cat
2	ATP/ITP metabolism	6.907E-05	ITPA, APRT, NDPK A, NDPK B, RPB8, NDPK complex, RRP46
3	GTP-XTP metabolism	9.711E-05	ITPA, NDPK A, NDPK B, RPB8, NDPK complex, RRP46
4	TTP metabolism	2.397E-04	NDPK A, NDPK B, NDPK complex, Thymidylate kinase, POLD reg (p50)
5	CTP/UTP metabolism	2.518E-04	ITPA, NDPK A, NDPK B, RPB8, NDPK complex, RRP46
6	Role of activation of WNT signaling in the progression of lung cancer	4.285E-04	DVL-1, ARD1, CD147, Dsh, RUVBL1
7	Inhibition of remyelination in multiple sclerosis: regulation of cytoskeleton proteins	4.607E-04	Tubulin beta, CDK5, MRLC, Tubulin beta 4
8	GTP metabolism	1.008E-03	ITPA, NDPK A, NDPK B, NDPK complex
9	dATP/dITP metabolism	1.066E-03	ITPA, NDPK A, NDPK B, NDPK complex, POLD reg (p50)
10	Development_Regulation of cytoskeleton proteins in oligodendrocyte differentiation and myelination	1.405E-03	Tubulin beta, CDK5, MRLC, Tubulin beta 4
11	Neuroprotective action of lithium	1.793E-03	CDK5, Thioredoxin, Dsh, PP1-cat
12	dGTP metabolism	1.901E-03	NDPK A, NDPK B, NDPK complex, POLD reg (p50)
13	Deregulation of canonical WNT signaling in major depressive disorder	2.073E-03	AKT1, DVL-1, Dsh
14	G-protein signaling_Rac1 inhibition	2.073E-03	CDK5, AKT1, NDPK A
15	N-Glycan biosynthesis p1	2.927E-03	DPM2 (reg), ALG10-A, ALG3, OST48
16	Signal transduction_mTORC1 upstream signaling	3.233E-03	PRAS40, GBL, AKT(PKB), Dsh
17	dCTP/dUTP metabolism	3.233E-03	NDPK A, NDPK B, NDPK complex, POLD reg (p50)
18	Translation_Regulation of EIF2 activity	3.731E-03	PP1-cat alpha, AKT(PKB), PP1-cat
19	Butanoic acid metabolism	4.018E-03	ECHS1, PTE1, HCD2
20	CHDI_DEGs from Replication data_Causal network	4.473E-03	CDK5, AKT(PKB), Dsh, PP1-cat
21	Apoptosis and survival_BAD phosphorylation	4.958E-03	PP1-cat alpha, PP2C, AKT(PKB)

22	Development_Role of CDK5 in the nervous system	5.764E-03	Tubulin beta, CDK5, PCTK1, AKT(PKB)
23	Neurophysiological process_HTR2A signaling in the nervous system	7.633E-03	SFK, AKT(PKB), SRD5A1
24	Development_NOTCH signaling inhibition	8.429E-03	Presenilin 2, AKT1, RITA1, AKT(PKB)
25	LRRK2 in neuronal apoptosis in Parkinson's disease	8.454E-03	AKT1, Thioredoxin
26	Transport_RAN regulation pathway	9.460E-03	NTF2, RanGAP1
27	ATP metabolism	1.036E-02	ITPA, NDPK A, NDPK B, NDPK complex
28	Aberrant B-Raf signaling in melanoma progression	1.049E-02	AKT1, RKIP, AKT(PKB)
29	Cytoskeleton remodeling_Alpha-1A adrenergic receptor-dependent inhibition of PI3K	1.052E-02	MRLC, AKT(PKB)
30	Cell adhesion_Desmosomes	1.052E-02	Plakophilin 3, Keratin 18
31	Cytoskeleton remodeling_Regulation of actin cytoskeleton organization by the kinase effectors of Rho GTPases	1.212E-02	Rac3, MRLC, Rac1-related
32	Development_H3K9 demethylases in pluripotency maintenance of stem cells	1.398E-02	AKT1, AKT(PKB)
33	Inhibition of GSK3 beta by lithium in major depressive disorder	1.398E-02	AKT(PKB), PP1-cat
34	Stem cells_Aberrant Wnt signaling in medulloblastoma stem cells	1.523E-02	AKT(PKB), Dsh
35	Canonical WNT signaling pathway in colorectal cancer	1.714E-02	AKT1, DVL-1, Dsh
36	Development_ErbB4 signaling	1.784E-02	CDK5, SFK, AKT(PKB)
37	Ligand-independent activation of Androgen receptor in Prostate Cancer	1.784E-02	NCOA3 (pCIP/SRC3), AKT(PKB), SRD5A1
38	Apoptosis and survival_Role of nuclear PI3K in NGF/ TrkA signaling	1.787E-02	AKT1, AKT(PKB)
39	Signal transduction_mTORC2 downstream signaling	1.856E-02	AKT1, PRAS40, AKT(PKB)
40	Nicotine / nAChR alpha-3/nAChR beta-2 signaling in NSCLC	1.925E-02	AKT1, AKT(PKB)
41	Transcription_Negative regulation of HIF1A function	1.929E-02	PRDX4, ARD1, RUVBL2
42	Signal transduction_Ephrin reverse signaling	2.216E-02	MRLC, SFK
43	CHDI_Correlations from Discovery data_Causal network	2.236E-02	CDK5, AKT(PKB), Dsh
44	Development_Positive regulation of WNT/Beta-catenin signaling in the cytoplasm	2.483E-02	AKT(PKB), Dsh, PP1-cat
45	DNA damage_Intra S-phase checkpoint	2.483E-02	Cdt1, PP1-cat alpha, PP1-cat
46	Apoptosis and survival_NGF/ TrkA PI3K-mediated signaling	2.569E-02	AKT1, MRLC, AKT(PKB)

47	Role of inhibition of WNT signaling in the progression of lung cancer	2.683E-02	Keratin 18, Dsh
48	Immune response_IL-23 signaling pathway	2.683E-02	AKT1, AKT(PKB)
49	NETosis in SLE	2.683E-02	Histone H2, Histone H2A
50	Development_Androgen receptor in non-reproductive systems development	2.835E-02	NCOA3 (pCIP/SRC3), AKT(PKB), SRD5A1

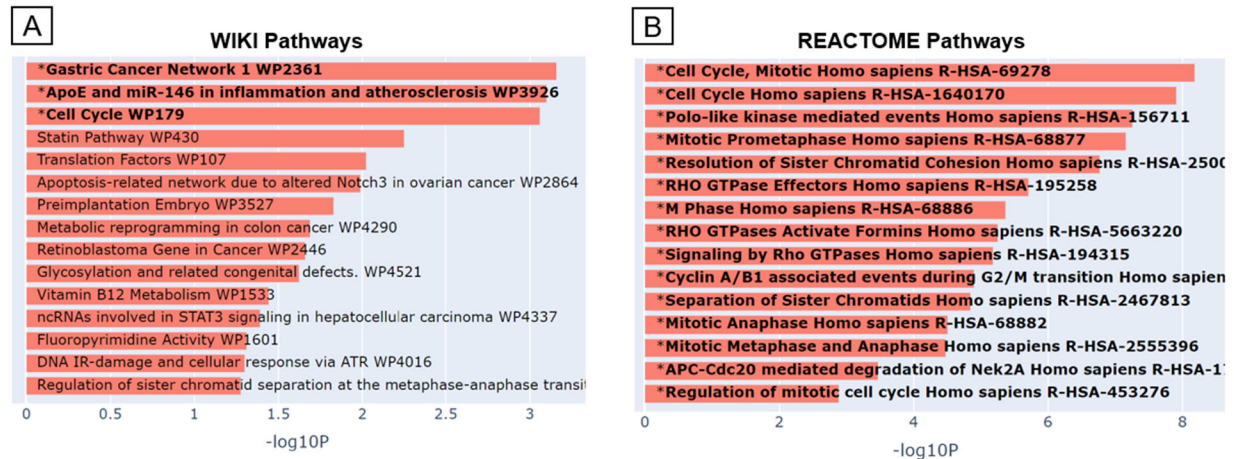
Supplementary Figure S1





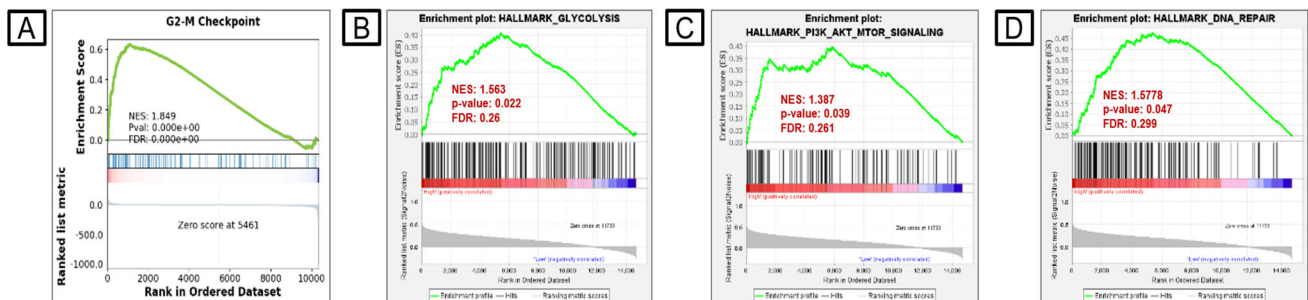
Supplementary Figure S1. Interactions of DBNDD1 expression with the androgen receptor (AR) and E2Fs in prostate cancer using RNA-seq data. The correlations between the genes were described using Spearman correlations ($p < 0.05$ was considered statistically significant).

Supplementary Figure S2



Supplementary Figure S2. Gene ontology (GO) enrichment results for primary tumor tissues vs. solid normal tissues in TCGA prostate cancer differential gene expression analysis. Results of an enrichment analysis including WIKI pathways (A), and Reactome pathways (B). Important phrases are emphasized in boldface font.

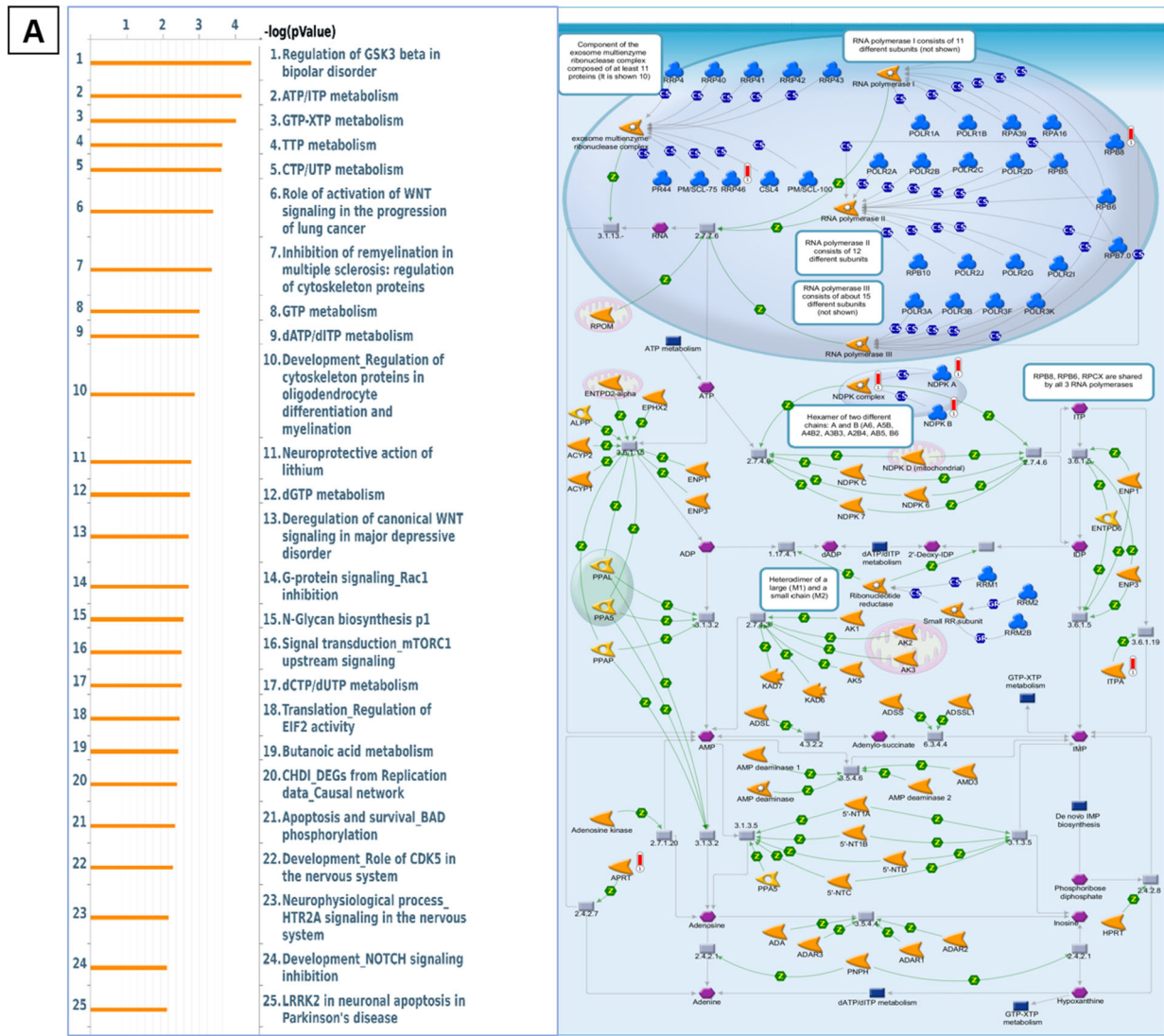
Supplementary Figure S3

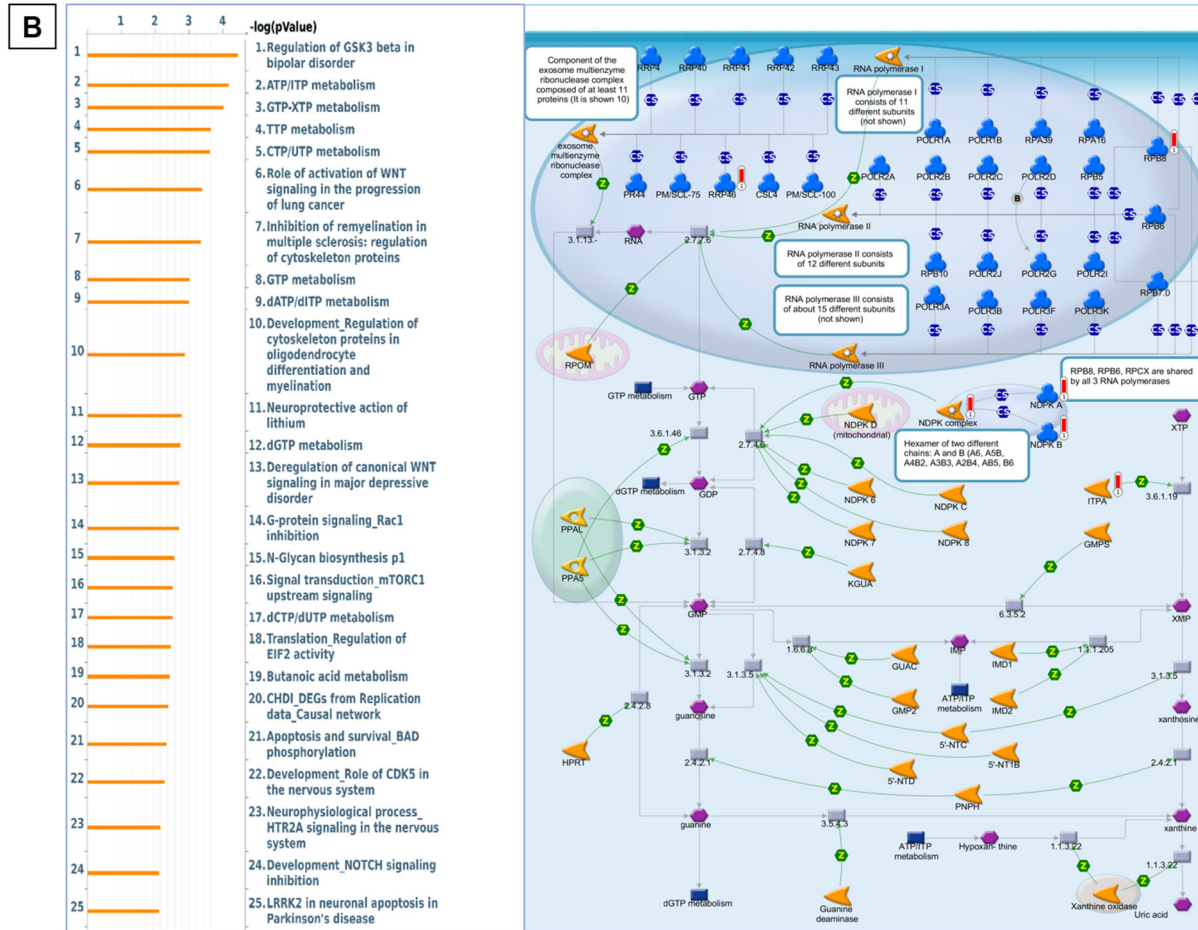


Supplementary Figure S3. Results of a gene set enrichment analysis (GSEA) in prostate cancer patients in TCGA cohort with high *DBNDD1* expression. (A-D) Patients were separated into two groups based on their *DBNDD1* mRNA expression levels in TCGA PRAD dataset; afterward, a gene ranking list was produced and entered into the GSEA. As indicated by the GSEA database, statistical significance was evaluated using a false detection rate (FDR) value of 0.25, a normalized enrichment score (NES) of more than 1.3,

and a nominal p -value of 0.05. Enrichment at the top of the list is indicated by a positive NES value, which suggests the enrichment pathway.

Supplementary Figure S4





Supplementary Figure S4. Expression of the DBNDD1 signaling pathway in PCa (MetaCore). Using the Metacore platform to analyze genes co-expressed with DBNDD1 from the associated TCGA dataset, we found that (A) "ATP/ITP metabolism" and (B) "GTP-XTP metabolism" were linked to prostate cancer progression (with $p < 0.05$ set as the cutoff value).

Supplementary Figure S5



Supplementary Figure S5. Relationships between DBNDD1 expression and immune cell infiltration in prostate cancer (TIMER). Correlation coefficients were calculated using cell type quantification algorithms (xCell, Cibersort, Cibersort abs. mode, EPIC, TIDE, MCP-counter, TIMER, and QUANTISED) and are indicated by colors (blue:

negative correlations; red: positive correlations). Statistical significance was defined by $p < 0.05$ (*), $p < 0.01$ (**), $p < 0.001$ (***). Columns: subtypes of prostate cancer. Rows: immune infiltration levels.