

Supplementary Table S3- KEGG Pathway associations for Core and NS4B extended PPI networks**KEGG Pathway associations- Core extended PPI network**

Gene ID	Symbol	KEGG Pathway	KEGG Pathway description	p -value	Adjusted p -value (BH)
5682	PSMA1	hsa03050	Proteasome	1.47E-09	1.13E-07
5683	PSMA2	hsa03050	Proteasome	1.47E-09	1.13E-07
5684	PSMA3	hsa03050	Proteasome	1.47E-09	1.13E-07
5685	PSMA4	hsa03050	Proteasome	1.47E-09	1.13E-07
5686	PSMA5	hsa03050	Proteasome	1.47E-09	1.13E-07
5687	PSMA6	hsa03050	Proteasome	1.47E-09	1.13E-07
5688	PSMA7	hsa03050	Proteasome	1.47E-09	1.13E-07
5695	PSMB7	hsa03050	Proteasome	1.47E-09	1.13E-07
5710	PSMD4	hsa03050	Proteasome	1.47E-09	1.13E-07
5717	PSMD11	hsa03050	Proteasome	1.47E-09	1.13E-07
5719	PSMD13	hsa03050	Proteasome	1.47E-09	1.13E-07
4214	MAP3K1	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
4790	NFKB1	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
4792	NFKBIA	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
5970	RELA	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
6885	MAP3K7	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
7186	TRAF2	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
7189	TRAF6	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
8517	IKBKG	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
8717	TRADD	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
8737	RIPK1	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
9474	ATG5	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
9641	IKBKE	hsa04622	RIG-I-like receptor signaling pathway	1.04E-08	4.01E-07
4790	NFKB1	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
4792	NFKBIA	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
5562	PRKAA1	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
5564	PRKAB1	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
5970	RELA	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
7132	TNFRSF1A	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
7133	TNFRSF1B	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
7186	TRAF2	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
8517	IKBKG	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
8717	TRADD	hsa04920	Adipocytokine signaling pathway	6.38E-07	1.64E-05
1956	EGFR	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	6.70E-06	0.000128879
4790	NFKB1	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	6.70E-06	0.000128879
4792	NFKBIA	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	6.70E-06	0.000128879
523	ATP6V1A	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	6.70E-06	0.000128879
526	ATP6V1B2	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	6.70E-06	0.000128879
5970	RELA	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	6.70E-06	0.000128879
8517	IKBKG	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	6.70E-06	0.000128879
9114	ATP6V0D1	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	6.70E-06	0.000128879
998	CDC42	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	6.70E-06	0.000128879

4790	NFKB1	hsa04210	Apoptosis	0.0003347	0.00257719
4792	NFKBIA	hsa04210	Apoptosis	0.0003347	0.00257719
596	BCL2	hsa04210	Apoptosis	0.0003347	0.00257719
5970	RELA	hsa04210	Apoptosis	0.0003347	0.00257719
7132	TNFRSF1A	hsa04210	Apoptosis	0.0003347	0.00257719
7186	TRAF2	hsa04210	Apoptosis	0.0003347	0.00257719
8517	IKBKG	hsa04210	Apoptosis	0.0003347	0.00257719
8717	TRADD	hsa04210	Apoptosis	0.0003347	0.00257719
8737	RIPK1	hsa04210	Apoptosis	0.0003347	0.00257719
10912	GADD45G	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
1647	GADD45A	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
1956	EGFR	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
2885	GRB2	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
4214	MAP3K1	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
4609	MYC	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
4790	NFKB1	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
5970	RELA	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
6885	MAP3K7	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
7132	TNFRSF1A	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
7186	TRAF2	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
7189	TRAF6	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
7786	MAP3K12	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
8517	IKBKG	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
998	CDC42	hsa04010	MAPK signaling pathway	0.0003017	0.00258121
4609	MYC	hsa05222	Small cell lung cancer	0.0002425	0.0026675
4790	NFKB1	hsa05222	Small cell lung cancer	0.0002425	0.0026675
4792	NFKBIA	hsa05222	Small cell lung cancer	0.0002425	0.0026675
596	BCL2	hsa05222	Small cell lung cancer	0.0002425	0.0026675
5970	RELA	hsa05222	Small cell lung cancer	0.0002425	0.0026675
7185	TRAF1	hsa05222	Small cell lung cancer	0.0002425	0.0026675
7186	TRAF2	hsa05222	Small cell lung cancer	0.0002425	0.0026675
7189	TRAF6	hsa05222	Small cell lung cancer	0.0002425	0.0026675
8517	IKBKG	hsa05222	Small cell lung cancer	0.0002425	0.0026675
4790	NFKB1	hsa04621	NOD-like receptor signaling pathway	0.0002084	0.00267447
4792	NFKBIA	hsa04621	NOD-like receptor signaling pathway	0.0002084	0.00267447
5970	RELA	hsa04621	NOD-like receptor signaling pathway	0.0002084	0.00267447
6885	MAP3K7	hsa04621	NOD-like receptor signaling pathway	0.0002084	0.00267447
7189	TRAF6	hsa04621	NOD-like receptor signaling pathway	0.0002084	0.00267447
8517	IKBKG	hsa04621	NOD-like receptor signaling pathway	0.0002084	0.00267447
8767	RIPK2	hsa04621	NOD-like receptor signaling pathway	0.0002084	0.00267447
292	SLC25A5	hsa05012	Parkinson's disease	0.0002893	0.00278451
293	SLC25A6	hsa05012	Parkinson's disease	0.0002893	0.00278451
4704	NDUFA9	hsa05012	Parkinson's disease	0.0002893	0.00278451
4720	NDUFS2	hsa05012	Parkinson's disease	0.0002893	0.00278451
4722	NDUFS3	hsa05012	Parkinson's disease	0.0002893	0.00278451
4729	NDUFV2	hsa05012	Parkinson's disease	0.0002893	0.00278451
498	ATP5A1	hsa05012	Parkinson's disease	0.0002893	0.00278451

506	ATP5B	hsa05012	Parkinson's disease	0.0002893	0.00278451
5071	PARK2	hsa05012	Parkinson's disease	0.0002893	0.00278451
7416	VDAC1	hsa05012	Parkinson's disease	0.0002893	0.00278451
2885	GRB2	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
4214	MAP3K1	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
4790	NFKB1	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
4792	NFKBIA	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
596	BCL2	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
5970	RELA	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
7189	TRAF6	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
7532	YWHAG	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
7534	YWHAZ	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
8767	RIPK2	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
998	CDC42	hsa04722	Neurotrophin signaling pathway	0.0001856	0.00285824
4790	NFKB1	hsa04620	Toll-like receptor signaling pathway	0.0008493	0.00544968
4792	NFKBIA	hsa04620	Toll-like receptor signaling pathway	0.0008493	0.00544968
5970	RELA	hsa04620	Toll-like receptor signaling pathway	0.0008493	0.00544968
6885	MAP3K7	hsa04620	Toll-like receptor signaling pathway	0.0008493	0.00544968
7189	TRAF6	hsa04620	Toll-like receptor signaling pathway	0.0008493	0.00544968
8517	IKBKG	hsa04620	Toll-like receptor signaling pathway	0.0008493	0.00544968
8737	RIPK1	hsa04620	Toll-like receptor signaling pathway	0.0008493	0.00544968
9641	IKBKE	hsa04620	Toll-like receptor signaling pathway	0.0008493	0.00544968
4790	NFKB1	hsa04623	Cytosolic DNA-sensing pathway	0.0007994	0.0055958
4792	NFKBIA	hsa04623	Cytosolic DNA-sensing pathway	0.0007994	0.0055958
5970	RELA	hsa04623	Cytosolic DNA-sensing pathway	0.0007994	0.0055958
8517	IKBKG	hsa04623	Cytosolic DNA-sensing pathway	0.0007994	0.0055958
8737	RIPK1	hsa04623	Cytosolic DNA-sensing pathway	0.0007994	0.0055958
9641	IKBKE	hsa04623	Cytosolic DNA-sensing pathway	0.0007994	0.0055958
10381	TUBB3	hsa05130	Pathogenic Escherichia coli infection	0.001057	0.00626069
10382	TUBB4	hsa05130	Pathogenic Escherichia coli infection	0.001057	0.00626069
60	ACTB	hsa05130	Pathogenic Escherichia coli infection	0.001057	0.00626069
7534	YWHAZ	hsa05130	Pathogenic Escherichia coli infection	0.001057	0.00626069
8440	NCK2	hsa05130	Pathogenic Escherichia coli infection	0.001057	0.00626069
998	CDC42	hsa05130	Pathogenic Escherichia coli infection	0.001057	0.00626069
4704	NDUFA9	hsa00190	Oxidative phosphorylation	0.001397	0.00717127
4720	NDUFS2	hsa00190	Oxidative phosphorylation	0.001397	0.00717127
4722	NDUFS3	hsa00190	Oxidative phosphorylation	0.001397	0.00717127
4729	NDUFV2	hsa00190	Oxidative phosphorylation	0.001397	0.00717127
498	ATP5A1	hsa00190	Oxidative phosphorylation	0.001397	0.00717127
506	ATP5B	hsa00190	Oxidative phosphorylation	0.001397	0.00717127
523	ATP6V1A	hsa00190	Oxidative phosphorylation	0.001397	0.00717127
526	ATP6V1B2	hsa00190	Oxidative phosphorylation	0.001397	0.00717127
9114	ATP6V0D1	hsa00190	Oxidative phosphorylation	0.001397	0.00717127
2885	GRB2	hsa04660	T cell receptor signaling pathway	0.001318	0.007249
4790	NFKB1	hsa04660	T cell receptor signaling pathway	0.001318	0.007249
4792	NFKBIA	hsa04660	T cell receptor signaling pathway	0.001318	0.007249
5970	RELA	hsa04660	T cell receptor signaling pathway	0.001318	0.007249

6885	MAP3K7	hsa04660	T cell receptor signaling pathway	0.001318	0.007249
8440	NCK2	hsa04660	T cell receptor signaling pathway	0.001318	0.007249
8517	IKBKKG	hsa04660	T cell receptor signaling pathway	0.001318	0.007249
998	CDC42	hsa04660	T cell receptor signaling pathway	0.001318	0.007249
1200	TPP1	hsa04142	Lysosome	0.002202	0.0105971
1511	CTSG	hsa04142	Lysosome	0.002202	0.0105971
2629	GBA	hsa04142	Lysosome	0.002202	0.0105971
2720	GLB1	hsa04142	Lysosome	0.002202	0.0105971
2990	GUSB	hsa04142	Lysosome	0.002202	0.0105971
427	ASAH1	hsa04142	Lysosome	0.002202	0.0105971
9114	ATP6V0D1	hsa04142	Lysosome	0.002202	0.0105971
950	SCARB2	hsa04142	Lysosome	0.002202	0.0105971
2885	GRB2	hsa05220	Chronic myeloid leukemia	0.003651	0.0165369
4609	MYC	hsa05220	Chronic myeloid leukemia	0.003651	0.0165369
4790	NFKB1	hsa05220	Chronic myeloid leukemia	0.003651	0.0165369
4792	NFKBIA	hsa05220	Chronic myeloid leukemia	0.003651	0.0165369
5970	RELA	hsa05220	Chronic myeloid leukemia	0.003651	0.0165369
8517	IKBKKG	hsa05220	Chronic myeloid leukemia	0.003651	0.0165369
375	ARF1	hsa05110	Vibrio cholerae infection	0.004941	0.0211365
523	ATP6V1A	hsa05110	Vibrio cholerae infection	0.004941	0.0211365
526	ATP6V1B2	hsa05110	Vibrio cholerae infection	0.004941	0.0211365
60	ACTB	hsa05110	Vibrio cholerae infection	0.004941	0.0211365
9114	ATP6V0D1	hsa05110	Vibrio cholerae infection	0.004941	0.0211365
2885	GRB2	hsa05221	Acute myeloid leukemia	0.006634	0.0255409
4609	MYC	hsa05221	Acute myeloid leukemia	0.006634	0.0255409
4790	NFKB1	hsa05221	Acute myeloid leukemia	0.006634	0.0255409
5970	RELA	hsa05221	Acute myeloid leukemia	0.006634	0.0255409
8517	IKBKKG	hsa05221	Acute myeloid leukemia	0.006634	0.0255409
2597	GAPDH	hsa05010	Alzheimer's disease	0.00636	0.0257747
4035	LRP1	hsa05010	Alzheimer's disease	0.00636	0.0257747
4704	NDUFA9	hsa05010	Alzheimer's disease	0.00636	0.0257747
4720	NDUFS2	hsa05010	Alzheimer's disease	0.00636	0.0257747
4722	NDUFS3	hsa05010	Alzheimer's disease	0.00636	0.0257747
4729	NDUFV2	hsa05010	Alzheimer's disease	0.00636	0.0257747
498	ATP5A1	hsa05010	Alzheimer's disease	0.00636	0.0257747
506	ATP5B	hsa05010	Alzheimer's disease	0.00636	0.0257747
7132	TNFRSF1A	hsa05010	Alzheimer's disease	0.00636	0.0257747
1356	CP	hsa00860	Porphyrin and chlorophyll metabolism	0.00866	0.03031
2495	FTH1	hsa00860	Porphyrin and chlorophyll metabolism	0.00866	0.03031
2990	GUSB	hsa00860	Porphyrin and chlorophyll metabolism	0.00866	0.03031
3163	HMOX2	hsa00860	Porphyrin and chlorophyll metabolism	0.00866	0.03031
1956	EGFR	hsa05215	Prostate cancer	0.008418	0.030866
2885	GRB2	hsa05215	Prostate cancer	0.008418	0.030866
354	KLK3	hsa05215	Prostate cancer	0.008418	0.030866
4790	NFKB1	hsa05215	Prostate cancer	0.008418	0.030866
4792	NFKBIA	hsa05215	Prostate cancer	0.008418	0.030866
596	BCL2	hsa05215	Prostate cancer	0.008418	0.030866

5970	RELA	hsa05215	Prostate cancer	0.008418	0.030866
8517	IKBKKG	hsa05215	Prostate cancer	0.008418	0.030866
292	SLC25A5	hsa05016	Huntington's disease	0.01124	0.0376296
293	SLC25A6	hsa05016	Huntington's disease	0.01124	0.0376296
4704	NDUFA9	hsa05016	Huntington's disease	0.01124	0.0376296
4720	NDUFS2	hsa05016	Huntington's disease	0.01124	0.0376296
4722	NDUFS3	hsa05016	Huntington's disease	0.01124	0.0376296
4729	NDUFV2	hsa05016	Huntington's disease	0.01124	0.0376296
498	ATP5A1	hsa05016	Huntington's disease	0.01124	0.0376296
506	ATP5B	hsa05016	Huntington's disease	0.01124	0.0376296
7350	UCP1	hsa05016	Huntington's disease	0.01124	0.0376296
7416	VDAC1	hsa05016	Huntington's disease	0.01124	0.0376296
9001	HAP1	hsa05016	Huntington's disease	0.01124	0.0376296
1956	EGFR	hsa05212	Pancreatic cancer	0.01408	0.0451733
4790	NFKB1	hsa05212	Pancreatic cancer	0.01408	0.0451733
5970	RELA	hsa05212	Pancreatic cancer	0.01408	0.0451733
8517	IKBKKG	hsa05212	Pancreatic cancer	0.01408	0.0451733
998	CDC42	hsa05212	Pancreatic cancer	0.01408	0.0451733
2885	GRB2	hsa04662	B cell receptor signaling pathway	0.01658	0.0510664
4790	NFKB1	hsa04662	B cell receptor signaling pathway	0.01658	0.0510664
4792	NFKBIA	hsa04662	B cell receptor signaling pathway	0.01658	0.0510664
5970	RELA	hsa04662	B cell receptor signaling pathway	0.01658	0.0510664
8517	IKBKKG	hsa04662	B cell receptor signaling pathway	0.01658	0.0510664
1956	EGFR	hsa04520	Adherens junction	0.01839	0.0544627
60	ACTB	hsa04520	Adherens junction	0.01839	0.0544627
6885	MAP3K7	hsa04520	Adherens junction	0.01839	0.0544627
7414	VCL	hsa04520	Adherens junction	0.01839	0.0544627
998	CDC42	hsa04520	Adherens junction	0.01839	0.0544627
1956	EGFR	hsa05200	Pathways in cancer	0.02213	0.0631115
2885	GRB2	hsa05200	Pathways in cancer	0.02213	0.0631115
3091	HIF1A	hsa05200	Pathways in cancer	0.02213	0.0631115
354	KLK3	hsa05200	Pathways in cancer	0.02213	0.0631115
4609	MYC	hsa05200	Pathways in cancer	0.02213	0.0631115
4790	NFKB1	hsa05200	Pathways in cancer	0.02213	0.0631115
4792	NFKBIA	hsa05200	Pathways in cancer	0.02213	0.0631115
596	BCL2	hsa05200	Pathways in cancer	0.02213	0.0631115
5970	RELA	hsa05200	Pathways in cancer	0.02213	0.0631115
7185	TRAF1	hsa05200	Pathways in cancer	0.02213	0.0631115
7186	TRAF2	hsa05200	Pathways in cancer	0.02213	0.0631115
7189	TRAF6	hsa05200	Pathways in cancer	0.02213	0.0631115
7428	VHL	hsa05200	Pathways in cancer	0.02213	0.0631115
8517	IKBKKG	hsa05200	Pathways in cancer	0.02213	0.0631115
998	CDC42	hsa05200	Pathways in cancer	0.02213	0.0631115
11345	GABARAPL	hsa04140	Regulation of autophagy	0.03199	0.0879725
5562	PRKAA1	hsa04140	Regulation of autophagy	0.03199	0.0879725
9474	ATG5	hsa04140	Regulation of autophagy	0.03199	0.0879725
2629	GBA	hsa00511	Other glycan degradation	0.03959	0.105118

2720	GLB1	hsa00511	Other glycan degradation	0.03959	0.105118
2629	GBA	hsa00600	Sphingolipid metabolism	0.04498	0.115449
2720	GLB1	hsa00600	Sphingolipid metabolism	0.04498	0.115449
427	ASAH1	hsa00600	Sphingolipid metabolism	0.04498	0.115449
2885	GRB2	hsa05211	Renal cell carcinoma	0.05065	0.125808
3091	HIF1A	hsa05211	Renal cell carcinoma	0.05065	0.125808
7428	VHL	hsa05211	Renal cell carcinoma	0.05065	0.125808
998	CDC42	hsa05211	Renal cell carcinoma	0.05065	0.125808
10563	CXCL13	hsa04062	Chemokine signaling pathway	0.05561	0.133812
2885	GRB2	hsa04062	Chemokine signaling pathway	0.05561	0.133812
4790	NFKB1	hsa04062	Chemokine signaling pathway	0.05561	0.133812
4792	NFKBIA	hsa04062	Chemokine signaling pathway	0.05561	0.133812
5829	PXN	hsa04062	Chemokine signaling pathway	0.05561	0.133812
5970	RELA	hsa04062	Chemokine signaling pathway	0.05561	0.133812
8517	IKBKG	hsa04062	Chemokine signaling pathway	0.05561	0.133812
998	CDC42	hsa04062	Chemokine signaling pathway	0.05561	0.133812
2720	GLB1	hsa00531	Glycosaminoglycan degradation	0.06498	0.15162
2990	GUSB	hsa00531	Glycosaminoglycan degradation	0.06498	0.15162
1956	EGFR	hsa05213	Endometrial cancer	0.08494	0.192364
2885	GRB2	hsa05213	Endometrial cancer	0.08494	0.192364
4609	MYC	hsa05213	Endometrial cancer	0.08494	0.192364
1956	EGFR	hsa04320	Dorso-ventral axis formation	0.08822	0.194084
2885	GRB2	hsa04320	Dorso-ventral axis formation	0.08822	0.194084
1583	CYP11A1	hsa00140	Steroid hormone biosynthesis	0.09669	0.20122
1588	CYP19A1	hsa00140	Steroid hormone biosynthesis	0.09669	0.20122
412	STS	hsa00140	Steroid hormone biosynthesis	0.09669	0.20122
1956	EGFR	hsa04012	ErbB signaling pathway	0.09556	0.204392
2885	GRB2	hsa04012	ErbB signaling pathway	0.09556	0.204392
4609	MYC	hsa04012	ErbB signaling pathway	0.09556	0.204392
8440	NCK2	hsa04012	ErbB signaling pathway	0.09556	0.204392
10381	TUBB3	hsa04540	Gap junction	0.105	0.212763
10382	TUBB4	hsa04540	Gap junction	0.105	0.212763
1956	EGFR	hsa04540	Gap junction	0.105	0.212763
2885	GRB2	hsa04540	Gap junction	0.105	0.212763
10912	GADD45G	hsa04110	Cell cycle	0.1124	0.221918
1647	GADD45A	hsa04110	Cell cycle	0.1124	0.221918
4609	MYC	hsa04110	Cell cycle	0.1124	0.221918
5347	PLK1	hsa04110	Cell cycle	0.1124	0.221918
7532	YWHAG	hsa04110	Cell cycle	0.1124	0.221918
7534	YWHAZ	hsa04110	Cell cycle	0.1124	0.221918
1956	EGFR	hsa04912	GnRH signaling pathway	0.1428	0.27489
2885	GRB2	hsa04912	GnRH signaling pathway	0.1428	0.27489
4214	MAP3K1	hsa04912	GnRH signaling pathway	0.1428	0.27489
998	CDC42	hsa04912	GnRH signaling pathway	0.1428	0.27489
10912	GADD45G	hsa04115	p53 signaling pathway	0.159	0.29861
1647	GADD45A	hsa04115	p53 signaling pathway	0.159	0.29861
9540	TP53I3	hsa04115	p53 signaling pathway	0.159	0.29861

1956	EGFR	hsa05219	Bladder cancer	0.2047	0.375283
4609	MYC	hsa05219	Bladder cancer	0.2047	0.375283
3106	HLA-B	hsa04940	Type I diabetes mellitus	0.2194	0.392879
3329	HSPD1	hsa04940	Type I diabetes mellitus	0.2194	0.392879
1956	EGFR	hsa05210	Colorectal cancer	0.2411	0.421925
2885	GRB2	hsa05210	Colorectal cancer	0.2411	0.421925
4609	MYC	hsa05210	Colorectal cancer	0.2411	0.421925
596	BCL2	hsa05210	Colorectal cancer	0.2411	0.421925
5829	PXN	hsa04670	Leukocyte transendothelial migration	0.2997	0.435413
60	ACTB	hsa04670	Leukocyte transendothelial migration	0.2997	0.435413
7414	VCL	hsa04670	Leukocyte transendothelial migration	0.2997	0.435413
998	CDC42	hsa04670	Leukocyte transendothelial migration	0.2997	0.435413
5562	PRKAA1	hsa05410	Hypertrophic cardiomyopathy (HCM)	0.2627	0.439737
5564	PRKAB1	hsa05410	Hypertrophic cardiomyopathy (HCM)	0.2627	0.439737
60	ACTB	hsa05410	Hypertrophic cardiomyopathy (HCM)	0.2627	0.439737
3106	HLA-B	hsa04612	Antigen processing and presentation	0.2627	0.439737
3309	HSPA5	hsa04612	Antigen processing and presentation	0.2627	0.439737
821	CANX	hsa04612	Antigen processing and presentation	0.2627	0.439737
1956	EGFR	hsa04510	Focal adhesion	0.297	0.439788
2885	GRB2	hsa04510	Focal adhesion	0.297	0.439788
5829	PXN	hsa04510	Focal adhesion	0.297	0.439788
596	BCL2	hsa04510	Focal adhesion	0.297	0.439788
60	ACTB	hsa04510	Focal adhesion	0.297	0.439788
7414	VCL	hsa04510	Focal adhesion	0.297	0.439788
998	CDC42	hsa04510	Focal adhesion	0.297	0.439788
4128	MAOA	hsa00330	Arginine and proline metabolism	0.2939	0.443731
5009	OTC	hsa00330	Arginine and proline metabolism	0.2939	0.443731
6303	SAT1	hsa00330	Arginine and proline metabolism	0.2939	0.443731
1956	EGFR	hsa05223	Non-small cell lung cancer	0.2939	0.443731
2885	GRB2	hsa05223	Non-small cell lung cancer	0.2939	0.443731
596	BCL2	hsa05014	Amyotrophic lateral sclerosis (ALS)	0.2864	0.450057
7132	TNFRSF1A	hsa05014	Amyotrophic lateral sclerosis (ALS)	0.2864	0.450057
7133	TNFRSF1B	hsa05014	Amyotrophic lateral sclerosis (ALS)	0.2864	0.450057
3091	HIF1A	hsa04150	mTOR signaling pathway	0.279	0.457085
5562	PRKAA1	hsa04150	mTOR signaling pathway	0.279	0.457085
1511	CTSG	hsa04080	Neuroactive ligand-receptor interaction	0.286	0.458792
4543	MTNR1A	hsa04080	Neuroactive ligand-receptor interaction	0.286	0.458792
5340	PLG	hsa04080	Neuroactive ligand-receptor interaction	0.286	0.458792
5646	PRSS3	hsa04080	Neuroactive ligand-receptor interaction	0.286	0.458792
2023	ENO1	hsa03018	RNA degradation	0.3309	0.471839
3329	HSPD1	hsa03018	RNA degradation	0.3309	0.471839
4214	MAP3K1	hsa04120	Ubiquitin mediated proteolysis	0.357	0.4998
5071	PARK2	hsa04120	Ubiquitin mediated proteolysis	0.357	0.4998
7189	TRAF6	hsa04120	Ubiquitin mediated proteolysis	0.357	0.4998
7428	VHL	hsa04120	Ubiquitin mediated proteolysis	0.357	0.4998
1956	EGFR	hsa05214	Glioma	0.3747	0.515212
2885	GRB2	hsa05214	Glioma	0.3747	0.515212

2	A2M	hsa04610	Complement and coagulation cascades	0.4032	0.535283
3827	KN1G1	hsa04610	Complement and coagulation cascades	0.4032	0.535283
5265	SERPINA1	hsa04610	Complement and coagulation cascades	0.4032	0.535283
5340	PLG	hsa04610	Complement and coagulation cascades	0.4032	0.535283
335	APOA1	hsa03320	PPAR signaling pathway	0.4032	0.535283
34	ACADM	hsa03320	PPAR signaling pathway	0.4032	0.535283
7350	UCP1	hsa03320	PPAR signaling pathway	0.4032	0.535283
3035	HARS	hsa00970	Aminoacyl-tRNA biosynthesis	0.5645	0.73672
3735	KARS	hsa00970	Aminoacyl-tRNA biosynthesis	0.5645	0.73672
51520	LARS	hsa00970	Aminoacyl-tRNA biosynthesis	0.5645	0.73672
7407	VARS	hsa00970	Aminoacyl-tRNA biosynthesis	0.5645	0.73672
833	CARS	hsa00970	Aminoacyl-tRNA biosynthesis	0.5645	0.73672
5829	PXN	hsa04370	VEGF signaling pathway	0.6647	0.787414
998	CDC42	hsa04370	VEGF signaling pathway	0.6647	0.787414
10563	CXCL13	hsa04060	Cytokine-cytokine receptor interaction	0.66	0.794063
1956	EGFR	hsa04060	Cytokine-cytokine receptor interaction	0.66	0.794063
7132	TNFRSF1A	hsa04060	Cytokine-cytokine receptor interaction	0.66	0.794063
7133	TNFRSF1B	hsa04060	Cytokine-cytokine receptor interaction	0.66	0.794063
1583	CYP11A1	hsa01100	Metabolic pathways	0.6298	0.794993
1588	CYP19A1	hsa01100	Metabolic pathways	0.6298	0.794993
2023	ENO1	hsa01100	Metabolic pathways	0.6298	0.794993
251	ALPPL2	hsa01100	Metabolic pathways	0.6298	0.794993
2597	GAPDH	hsa01100	Metabolic pathways	0.6298	0.794993
2629	GBA	hsa01100	Metabolic pathways	0.6298	0.794993
2720	GLB1	hsa01100	Metabolic pathways	0.6298	0.794993
2990	GUSB	hsa01100	Metabolic pathways	0.6298	0.794993
34	ACADM	hsa01100	Metabolic pathways	0.6298	0.794993
4128	MAOA	hsa01100	Metabolic pathways	0.6298	0.794993
427	ASAH1	hsa01100	Metabolic pathways	0.6298	0.794993
4597	MVD	hsa01100	Metabolic pathways	0.6298	0.794993
4704	NDUFA9	hsa01100	Metabolic pathways	0.6298	0.794993
4720	NDUFS2	hsa01100	Metabolic pathways	0.6298	0.794993
4722	NDUFS3	hsa01100	Metabolic pathways	0.6298	0.794993
4729	NDUFV2	hsa01100	Metabolic pathways	0.6298	0.794993
4790	NFKB1	hsa01100	Metabolic pathways	0.6298	0.794993
4831	NME2	hsa01100	Metabolic pathways	0.6298	0.794993
498	ATP5A1	hsa01100	Metabolic pathways	0.6298	0.794993
5009	OTC	hsa01100	Metabolic pathways	0.6298	0.794993
506	ATP5B	hsa01100	Metabolic pathways	0.6298	0.794993
523	ATP6V1A	hsa01100	Metabolic pathways	0.6298	0.794993
526	ATP6V1B2	hsa01100	Metabolic pathways	0.6298	0.794993
6303	SAT1	hsa01100	Metabolic pathways	0.6298	0.794993
65220	NADK	hsa01100	Metabolic pathways	0.6298	0.794993
9114	ATP6V0D1	hsa01100	Metabolic pathways	0.6298	0.794993
1956	EGFR	hsa04810	Regulation of actin cytoskeleton	0.6212	0.797207
5829	PXN	hsa04810	Regulation of actin cytoskeleton	0.6212	0.797207
60	ACTB	hsa04810	Regulation of actin cytoskeleton	0.6212	0.797207

7414	VCL	hsa04810	Regulation of actin cytoskeleton	0.6212	0.797207
998	CDC42	hsa04810	Regulation of actin cytoskeleton	0.6212	0.797207
6124	RPL4	hsa03010	Ribosome	0.6958	0.799651
6234	RPS28	hsa03010	Ribosome	0.6958	0.799651
3106	HLA-B	hsa05416	Viral myocarditis	0.6578	0.803978
60	ACTB	hsa05416	Viral myocarditis	0.6578	0.803978
4093	SMAD9	hsa04350	TGF-beta signaling pathway	0.693	0.8085
4609	MYC	hsa04350	TGF-beta signaling pathway	0.693	0.8085
4128	MAOA	hsa00982	Drug metabolism - cytochrome P450	0.6555	0.814089
9446	GSTO1	hsa00982	Drug metabolism - cytochrome P450	0.6555	0.814089
1956	EGFR	hsa04144	Endocytosis	0.789	0.820986
3106	HLA-B	hsa04144	Endocytosis	0.789	0.820986
7189	TRAF6	hsa04144	Endocytosis	0.789	0.820986
998	CDC42	hsa04144	Endocytosis	0.789	0.820986
2885	GRB2	hsa04630	Jak-STAT signaling pathway	0.7709	0.824435
4609	MYC	hsa04630	Jak-STAT signaling pathway	0.7709	0.824435
1956	EGFR	hsa04020	Calcium signaling pathway	0.7817	0.824533
292	SLC25A5	hsa04020	Calcium signaling pathway	0.7817	0.824533
293	SLC25A6	hsa04020	Calcium signaling pathway	0.7817	0.824533
7416	VDAC1	hsa04020	Calcium signaling pathway	0.7817	0.824533
2885	GRB2	hsa04910	Insulin signaling pathway	0.7546	0.83006
5562	PRKAA1	hsa04910	Insulin signaling pathway	0.7546	0.83006
5564	PRKAB1	hsa04910	Insulin signaling pathway	0.7546	0.83006
4609	MYC	hsa04310	Wnt signaling pathway	0.7704	0.835504
6885	MAP3K7	hsa04310	Wnt signaling pathway	0.7704	0.835504
2035	EPB41	hsa04530	Tight junction	0.7505	0.837514
60	ACTB	hsa04530	Tight junction	0.7505	0.837514
998	CDC42	hsa04530	Tight junction	0.7505	0.837514
1942	EFNA1	hsa04360	Axon guidance	0.7441	0.842584
8440	NCK2	hsa04360	Axon guidance	0.7441	0.842584
998	CDC42	hsa04360	Axon guidance	0.7441	0.842584
5347	PLK1	hsa04114	Oocyte meiosis	1	1
7532	YWHAG	hsa04114	Oocyte meiosis	1	1
7534	YWHAZ	hsa04114	Oocyte meiosis	1	1
1511	CTSG	hsa05322	Systemic lupus erythematosus	1	1
1991	ELANE	hsa05322	Systemic lupus erythematosus	1	1
2885	GRB2	hsa04650	Natural killer cell mediated cytotoxicity	1	1
3106	HLA-B	hsa04650	Natural killer cell mediated cytotoxicity	1	1

KEGG Pathway associations- NS4B extended PPI network

Gene ID	Symbol	KEGG Pathway	KEGG Pathway description	<i>p</i> -value	Adjusted <i>p</i> -value (BH)
10747	MASP2	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
1361	CPB2	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
2147	F2	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
2149	F2R	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
2153	F5	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14

2160	F11	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
2165	F13B	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
2243	FGA	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
2244	FGB	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
2266	FGG	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
3053	SERPIND1	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
4179	CD46	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
462	SERPINC1	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
5054	SERPINE1	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
5265	SERPINA1	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
5327	PLAT	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
5648	MASP1	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
7056	THBD	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
710	SERPING1	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
712	C1QA	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
714	C1QC	hsa04610	Complement and coagulation cascades	2.20E-16	2.49E-14
1514	CTSL1	hsa04612	Antigen processing and presentation	0.0004116	0.0155036
3106	HLA-B	hsa04612	Antigen processing and presentation	0.0004116	0.0155036
3109	HLA-DMB	hsa04612	Antigen processing and presentation	0.0004116	0.0155036
3112	HLA-DOB	hsa04612	Antigen processing and presentation	0.0004116	0.0155036
3122	HLA-DRA	hsa04612	Antigen processing and presentation	0.0004116	0.0155036
3312	HSPA8	hsa04612	Antigen processing and presentation	0.0004116	0.0155036
811	CALR	hsa04612	Antigen processing and presentation	0.0004116	0.0155036
821	CANX	hsa04612	Antigen processing and presentation	0.0004116	0.0155036
920	CD4	hsa04612	Antigen processing and presentation	0.0004116	0.0155036
1791	DNTT	hsa04640	Hematopoietic cell lineage	0.0003781	0.0213626
2811	GP1BA	hsa04640	Hematopoietic cell lineage	0.0003781	0.0213626
3122	HLA-DRA	hsa04640	Hematopoietic cell lineage	0.0003781	0.0213626
3674	ITGA2B	hsa04640	Hematopoietic cell lineage	0.0003781	0.0213626
3690	ITGB3	hsa04640	Hematopoietic cell lineage	0.0003781	0.0213626
3815	KIT	hsa04640	Hematopoietic cell lineage	0.0003781	0.0213626
920	CD4	hsa04640	Hematopoietic cell lineage	0.0003781	0.0213626
928	CD9	hsa04640	Hematopoietic cell lineage	0.0003781	0.0213626
930	CD19	hsa04640	Hematopoietic cell lineage	0.0003781	0.0213626
10477	UBE2E3	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
51465	UBE2J1	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
672	BRCA1	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
7189	TRAF6	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
7322	UBE2D2	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
7323	UBE2D3	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
7324	UBE2E1	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
7328	UBE2H	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
7428	VHL	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
90293	KLHL13	hsa04120	Ubiquitin mediated proteolysis	0.002683	0.0505298
3106	HLA-B	hsa05330	Allograft rejection	0.002621	0.0592346
3109	HLA-DMB	hsa05330	Allograft rejection	0.002621	0.0592346
3112	HLA-DOB	hsa05330	Allograft rejection	0.002621	0.0592346

3122	HLA-DRA	hsa05330	Allograft rejection	0.002621	0.0592346
959	CD40LG	hsa05330	Allograft rejection	0.002621	0.0592346
3106	HLA-B	hsa05416	Viral myocarditis	0.002489	0.0703142
3109	HLA-DMB	hsa05416	Viral myocarditis	0.002489	0.0703142
3112	HLA-DOB	hsa05416	Viral myocarditis	0.002489	0.0703142
3122	HLA-DRA	hsa05416	Viral myocarditis	0.002489	0.0703142
3683	ITGAL	hsa05416	Viral myocarditis	0.002489	0.0703142
54205	CYCS	hsa05416	Viral myocarditis	0.002489	0.0703142
959	CD40LG	hsa05416	Viral myocarditis	0.002489	0.0703142
3106	HLA-B	hsa04514	Cell adhesion molecules (CAMs)	0.007148	0.100965
3109	HLA-DMB	hsa04514	Cell adhesion molecules (CAMs)	0.007148	0.100965
3112	HLA-DOB	hsa04514	Cell adhesion molecules (CAMs)	0.007148	0.100965
3122	HLA-DRA	hsa04514	Cell adhesion molecules (CAMs)	0.007148	0.100965
3683	ITGAL	hsa04514	Cell adhesion molecules (CAMs)	0.007148	0.100965
3688	ITGB1	hsa04514	Cell adhesion molecules (CAMs)	0.007148	0.100965
4267	CD99	hsa04514	Cell adhesion molecules (CAMs)	0.007148	0.100965
920	CD4	hsa04514	Cell adhesion molecules (CAMs)	0.007148	0.100965
959	CD40LG	hsa04514	Cell adhesion molecules (CAMs)	0.007148	0.100965
3109	HLA-DMB	hsa05310	Asthma	0.006763	0.109174
3112	HLA-DOB	hsa05310	Asthma	0.006763	0.109174
3122	HLA-DRA	hsa05310	Asthma	0.006763	0.109174
959	CD40LG	hsa05310	Asthma	0.006763	0.109174
3106	HLA-B	hsa05320	Autoimmune thyroid disease	0.01104	0.138613
3109	HLA-DMB	hsa05320	Autoimmune thyroid disease	0.01104	0.138613
3112	HLA-DOB	hsa05320	Autoimmune thyroid disease	0.01104	0.138613
3122	HLA-DRA	hsa05320	Autoimmune thyroid disease	0.01104	0.138613
959	CD40LG	hsa05320	Autoimmune thyroid disease	0.01104	0.138613
3106	HLA-B	hsa05332	Graft-versus-host disease	0.02182	0.189666
3109	HLA-DMB	hsa05332	Graft-versus-host disease	0.02182	0.189666
3112	HLA-DOB	hsa05332	Graft-versus-host disease	0.02182	0.189666
3122	HLA-DRA	hsa05332	Graft-versus-host disease	0.02182	0.189666
1327	COX4I1	hsa05012	Parkinson's disease	0.02035	0.191629
4513	COX2	hsa05012	Parkinson's disease	0.02035	0.191629
4538	ND4	hsa05012	Parkinson's disease	0.02035	0.191629
4712	NDUFB6	hsa05012	Parkinson's disease	0.02035	0.191629
51465	UBE2J1	hsa05012	Parkinson's disease	0.02035	0.191629
517	ATP5G2	hsa05012	Parkinson's disease	0.02035	0.191629
54205	CYCS	hsa05012	Parkinson's disease	0.02035	0.191629
9377	COX5A	hsa05012	Parkinson's disease	0.02035	0.191629
1601	DAB2	hsa04144	Endocytosis	0.02832	0.20001
1785	DNM2	hsa04144	Endocytosis	0.02832	0.20001
1956	EGFR	hsa04144	Endocytosis	0.02832	0.20001
2065	ERBB3	hsa04144	Endocytosis	0.02832	0.20001
2149	F2R	hsa04144	Endocytosis	0.02832	0.20001
3106	HLA-B	hsa04144	Endocytosis	0.02832	0.20001
3312	HSPA8	hsa04144	Endocytosis	0.02832	0.20001
3815	KIT	hsa04144	Endocytosis	0.02832	0.20001

7189	TRAF6	hsa04144	Endocytosis	0.02832	0.20001
9146	HGS	hsa04144	Endocytosis	0.02832	0.20001
1511	CTSG	hsa05322	Systemic lupus erythematosus	0.02673	0.201366
1991	ELANE	hsa05322	Systemic lupus erythematosus	0.02673	0.201366
3109	HLA-DMB	hsa05322	Systemic lupus erythematosus	0.02673	0.201366
3112	HLA-DOB	hsa05322	Systemic lupus erythematosus	0.02673	0.201366
3122	HLA-DRA	hsa05322	Systemic lupus erythematosus	0.02673	0.201366
712	C1QA	hsa05322	Systemic lupus erythematosus	0.02673	0.201366
714	C1QC	hsa05322	Systemic lupus erythematosus	0.02673	0.201366
959	CD40LG	hsa05322	Systemic lupus erythematosus	0.02673	0.201366
3106	HLA-B	hsa04940	Type I diabetes mellitus	0.02545	0.205418
3109	HLA-DMB	hsa04940	Type I diabetes mellitus	0.02545	0.205418
3112	HLA-DOB	hsa04940	Type I diabetes mellitus	0.02545	0.205418
3122	HLA-DRA	hsa04940	Type I diabetes mellitus	0.02545	0.205418
2811	GP1BA	hsa04512	ECM-receptor interaction	0.02021	0.207612
3674	ITGA2B	hsa04512	ECM-receptor interaction	0.02021	0.207612
3674	ITGA2B	hsa05222	Small cell lung cancer	0.02021	0.207612
3688	ITGB1	hsa04512	ECM-receptor interaction	0.02021	0.207612
3688	ITGB1	hsa05222	Small cell lung cancer	0.02021	0.207612
3690	ITGB3	hsa04512	ECM-receptor interaction	0.02021	0.207612
54205	CYCS	hsa05222	Small cell lung cancer	0.02021	0.207612
5743	PTGS2	hsa05222	Small cell lung cancer	0.02021	0.207612
7057	THBS1	hsa04512	ECM-receptor interaction	0.02021	0.207612
7185	TRAF1	hsa05222	Small cell lung cancer	0.02021	0.207612
7189	TRAF6	hsa05222	Small cell lung cancer	0.02021	0.207612
7448	VTN	hsa04512	ECM-receptor interaction	0.02021	0.207612
2810	SFN	hsa04115	p53 signaling pathway	0.03128	0.20792
3732	CD82	hsa04115	p53 signaling pathway	0.03128	0.20792
5054	SERPINE1	hsa04115	p53 signaling pathway	0.03128	0.20792
54205	CYCS	hsa04115	p53 signaling pathway	0.03128	0.20792
7057	THBS1	hsa04115	p53 signaling pathway	0.03128	0.20792
3109	HLA-DMB	hsa04672	Intestinal immune network for IgA production	0.03375	0.211875
3112	HLA-DOB	hsa04672	Intestinal immune network for IgA production	0.03375	0.211875
3122	HLA-DRA	hsa04672	Intestinal immune network for IgA production	0.03375	0.211875
959	CD40LG	hsa04672	Intestinal immune network for IgA production	0.03375	0.211875
1327	COX4I1	hsa05010	Alzheimer's disease	0.04041	0.240333
322	APBB1	hsa05010	Alzheimer's disease	0.04041	0.240333
351	APP	hsa05010	Alzheimer's disease	0.04041	0.240333
4035	LRP1	hsa05010	Alzheimer's disease	0.04041	0.240333
4513	COX2	hsa05010	Alzheimer's disease	0.04041	0.240333
4712	NDUFB6	hsa05010	Alzheimer's disease	0.04041	0.240333
517	ATP5G2	hsa05010	Alzheimer's disease	0.04041	0.240333
54205	CYCS	hsa05010	Alzheimer's disease	0.04041	0.240333
9377	COX5A	hsa05010	Alzheimer's disease	0.04041	0.240333
1080	CFTR	hsa05110	Vibrio cholerae infection	0.05456	0.308264
10952	SEC61B	hsa05110	Vibrio cholerae infection	0.05456	0.308264
29927	SEC61A1	hsa05110	Vibrio cholerae infection	0.05456	0.308264

9601	PDIA4	hsa05110	Vibrio cholerae infection	0.05456	0.308264
920	CD4	hsa05340	Primary immunodeficiency	0.05952	0.320274
930	CD19	hsa05340	Primary immunodeficiency	0.05952	0.320274
959	CD40LG	hsa05340	Primary immunodeficiency	0.05952	0.320274
22861	NLRP1	hsa04621	NOD-like receptor signaling pathway	0.07383	0.379218
7128	TNFAIP3	hsa04621	NOD-like receptor signaling pathway	0.07383	0.379218
7184	HSP90B1	hsa04621	NOD-like receptor signaling pathway	0.07383	0.379218
7189	TRAF6	hsa04621	NOD-like receptor signaling pathway	0.07383	0.379218
1356	CP	hsa00860	Porphyrin and chlorophyll metabolism	0.08692	0.427042
54657	UGT1A4	hsa00860	Porphyrin and chlorophyll metabolism	0.08692	0.427042
54658	UGT1A1	hsa00860	Porphyrin and chlorophyll metabolism	0.08692	0.427042
1956	EGFR	hsa05219	Bladder cancer	0.09192	0.43279
2064	ERBB2	hsa05219	Bladder cancer	0.09192	0.43279
7057	THBS1	hsa05219	Bladder cancer	0.09192	0.43279
1080	CFTR	hsa02010	ABC transporters	0.1023	0.444612
19	ABCA1	hsa02010	ABC transporters	0.1023	0.444612
23460	ABCA6	hsa02010	ABC transporters	0.1023	0.444612
10999	SLC27A4	hsa03320	PPAR signaling pathway	0.1001	0.452452
335	APOA1	hsa03320	PPAR signaling pathway	0.1001	0.452452
345	APOC3	hsa03320	PPAR signaling pathway	0.1001	0.452452
5360	PLTP	hsa03320	PPAR signaling pathway	0.1001	0.452452
10682	EBP	hsa01100	Metabolic pathways	0.1339	0.521748
1327	COX4I1	hsa01100	Metabolic pathways	0.1339	0.521748
1571	CYP2E1	hsa01100	Metabolic pathways	0.1339	0.521748
15	AANAT	hsa01100	Metabolic pathways	0.1339	0.521748
1650	DDOST	hsa01100	Metabolic pathways	0.1339	0.521748
2731	GLDC	hsa01100	Metabolic pathways	0.1339	0.521748
3990	LIPC	hsa01100	Metabolic pathways	0.1339	0.521748
4513	COX2	hsa01100	Metabolic pathways	0.1339	0.521748
4538	ND4	hsa01100	Metabolic pathways	0.1339	0.521748
4712	NDUFB6	hsa01100	Metabolic pathways	0.1339	0.521748
4831	NME2	hsa01100	Metabolic pathways	0.1339	0.521748
517	ATP5G2	hsa01100	Metabolic pathways	0.1339	0.521748
5446	PON3	hsa01100	Metabolic pathways	0.1339	0.521748
54657	UGT1A4	hsa01100	Metabolic pathways	0.1339	0.521748
54658	UGT1A1	hsa01100	Metabolic pathways	0.1339	0.521748
5742	PTGS1	hsa01100	Metabolic pathways	0.1339	0.521748
5860	QDPR	hsa01100	Metabolic pathways	0.1339	0.521748
6185	RPN2	hsa01100	Metabolic pathways	0.1339	0.521748
8708	B3GALT1	hsa01100	Metabolic pathways	0.1339	0.521748
8879	SGPL1	hsa01100	Metabolic pathways	0.1339	0.521748
9377	COX5A	hsa01100	Metabolic pathways	0.1339	0.521748
10952	SEC61B	hsa03060	Protein export	0.1251	0.523567
29927	SEC61A1	hsa03060	Protein export	0.1251	0.523567
54657	UGT1A4	hsa00053	Ascorbate and aldarate metabolism	0.1337	0.539575
54658	UGT1A1	hsa00053	Ascorbate and aldarate metabolism	0.1337	0.539575
1327	COX4I1	hsa00190	Oxidative phosphorylation	0.1609	0.586506

4513	COX2	hsa00190	Oxidative phosphorylation	0.1609	0.586506
4538	ND4	hsa00190	Oxidative phosphorylation	0.1609	0.586506
4712	NDUFB6	hsa00190	Oxidative phosphorylation	0.1609	0.586506
517	ATP5G2	hsa00190	Oxidative phosphorylation	0.1609	0.586506
9377	COX5A	hsa00190	Oxidative phosphorylation	0.1609	0.586506
54657	UGT1A4	hsa00040	Pentose and glucuronate interconversions	0.1606	0.604927
54658	UGT1A1	hsa00040	Pentose and glucuronate interconversions	0.1606	0.604927
1956	EGFR	hsa04510	Focal adhesion	0.1751	0.618322
2064	ERBB2	hsa04510	Focal adhesion	0.1751	0.618322
3674	ITGA2B	hsa04510	Focal adhesion	0.1751	0.618322
3688	ITGB1	hsa04510	Focal adhesion	0.1751	0.618322
3690	ITGB3	hsa04510	Focal adhesion	0.1751	0.618322
5829	PXN	hsa04510	Focal adhesion	0.1751	0.618322
7057	THBS1	hsa04510	Focal adhesion	0.1751	0.618322
7448	VTN	hsa04510	Focal adhesion	0.1751	0.618322
81839	VANGL1	hsa04310	Wnt signaling pathway	0.1873	0.622497
1571	CYP2E1	hsa00590	Arachidonic acid metabolism	0.1856	0.635539
5742	PTGS1	hsa00590	Arachidonic acid metabolism	0.1856	0.635539
5743	PTGS2	hsa00590	Arachidonic acid metabolism	0.1856	0.635539
1956	EGFR	hsa05200	Pathways in cancer	0.2057	0.664117
2064	ERBB2	hsa05200	Pathways in cancer	0.2057	0.664117
354	KLK3	hsa05200	Pathways in cancer	0.2057	0.664117
3674	ITGA2B	hsa05200	Pathways in cancer	0.2057	0.664117
3688	ITGB1	hsa05200	Pathways in cancer	0.2057	0.664117
3815	KIT	hsa05200	Pathways in cancer	0.2057	0.664117
54205	CYCS	hsa05200	Pathways in cancer	0.2057	0.664117
5743	PTGS2	hsa05200	Pathways in cancer	0.2057	0.664117
7184	HSP90B1	hsa05200	Pathways in cancer	0.2057	0.664117
7185	TRAF1	hsa05200	Pathways in cancer	0.2057	0.664117
7189	TRAF6	hsa05200	Pathways in cancer	0.2057	0.664117
7428	VHL	hsa05200	Pathways in cancer	0.2057	0.664117
2771	GNAI2	hsa04670	Leukocyte transendothelial migration	0.2302	0.703043
3683	ITGAL	hsa04670	Leukocyte transendothelial migration	0.2302	0.703043
3688	ITGB1	hsa04670	Leukocyte transendothelial migration	0.2302	0.703043
4267	CD99	hsa04670	Leukocyte transendothelial migration	0.2302	0.703043
5829	PXN	hsa04670	Leukocyte transendothelial migration	0.2302	0.703043
712	C1QA	hsa05020	Prion diseases	0.226	0.709389
714	C1QC	hsa05020	Prion diseases	0.226	0.709389
1956	EGFR	hsa04810	Regulation of actin cytoskeleton	0.2681	0.721317
2147	F2	hsa04810	Regulation of actin cytoskeleton	0.2681	0.721317
2149	F2R	hsa04810	Regulation of actin cytoskeleton	0.2681	0.721317
3674	ITGA2B	hsa04810	Regulation of actin cytoskeleton	0.2681	0.721317
3683	ITGAL	hsa04810	Regulation of actin cytoskeleton	0.2681	0.721317
3688	ITGB1	hsa04810	Regulation of actin cytoskeleton	0.2681	0.721317
3690	ITGB3	hsa04810	Regulation of actin cytoskeleton	0.2681	0.721317
5829	PXN	hsa04810	Regulation of actin cytoskeleton	0.2681	0.721317
2771	GNAI2	hsa04530	Tight junction	0.2648	0.729815

1956	EGFR	hsa05215	Prostate cancer	0.2911	0.730984
2064	ERBB2	hsa05215	Prostate cancer	0.2911	0.730984
354	KLK3	hsa05215	Prostate cancer	0.2911	0.730984
3674	ITGA2B	hsa05410	Hypertrophic cardiomyopathy (HCM)	0.2911	0.730984
3688	ITGB1	hsa05410	Hypertrophic cardiomyopathy (HCM)	0.2911	0.730984
3690	ITGB3	hsa05410	Hypertrophic cardiomyopathy (HCM)	0.2911	0.730984
5564	PRKAB1	hsa05410	Hypertrophic cardiomyopathy (HCM)	0.2911	0.730984
7184	HSP90B1	hsa05215	Prostate cancer	0.2911	0.730984
5860	QDPR	hsa00790	Folate biosynthesis	0.2488	0.739853
2810	SFN	hsa04110	Cell cycle	0.2635	0.744387
3312	HSPA8	hsa03040	Spliceosome	0.2635	0.744387
1791	DNTT	hsa03450	Non-homologous end-joining	0.3053	0.749976
1839	HBEGF	hsa04012	ErbB signaling pathway	0.2859	0.751319
1956	EGFR	hsa04012	ErbB signaling pathway	0.2859	0.751319
2064	ERBB2	hsa04012	ErbB signaling pathway	0.2859	0.751319
2065	ERBB3	hsa04012	ErbB signaling pathway	0.2859	0.751319
1327	COX4I1	hsa05016	Huntington's disease	0.3358	0.790529
4513	COX2	hsa05016	Huntington's disease	0.3358	0.790529
4712	NDUFB6	hsa05016	Huntington's disease	0.3358	0.790529
517	ATP5G2	hsa05016	Huntington's disease	0.3358	0.790529
54205	CYCS	hsa05016	Huntington's disease	0.3358	0.790529
6667	SPI1	hsa05016	Huntington's disease	0.3358	0.790529
9377	COX5A	hsa05016	Huntington's disease	0.3358	0.790529
1650	DDOST	hsa00510	N-Glycan biosynthesis	0.3312	0.796289
6185	RPN2	hsa00510	N-Glycan biosynthesis	0.3312	0.796289
10682	EBP	hsa00100	Steroid biosynthesis	0.3575	0.80795
1511	CTSG	hsa04614	Renin-angiotensin system	0.3575	0.80795
1956	EGFR	hsa05213	Endometrial cancer	0.3872	0.810252
2064	ERBB2	hsa05213	Endometrial cancer	0.3872	0.810252
54657	UGT1A4	hsa00500	Starch and sucrose metabolism	0.3872	0.810252
54658	UGT1A1	hsa00500	Starch and sucrose metabolism	0.3872	0.810252
54205	CYCS	hsa05014	Amyotrophic lateral sclerosis (ALS)	0.3963	0.814216
79139	DERL1	hsa05014	Amyotrophic lateral sclerosis (ALS)	0.3963	0.814216
7189	TRAF6	hsa04722	Neurotrophin signaling pathway	0.3816	0.829246
54657	UGT1A4	hsa00983	Drug metabolism - other enzymes	0.378	0.837529
54658	UGT1A1	hsa00983	Drug metabolism - other enzymes	0.378	0.837529
3674	ITGA2B	hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0.4461	0.854395
3688	ITGB1	hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0.4461	0.854395
3690	ITGB3	hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0.4461	0.854395
5617	PRL	hsa04630	Jak-STAT signaling pathway	0.4401	0.857436
6775	STAT4	hsa04630	Jak-STAT signaling pathway	0.4401	0.857436
1571	CYP2E1	hsa00982	Drug metabolism - cytochrome P450	0.4331	0.858602
54657	UGT1A4	hsa00982	Drug metabolism - cytochrome P450	0.4331	0.858602
54658	UGT1A1	hsa00982	Drug metabolism - cytochrome P450	0.4331	0.858602
1571	CYP2E1	hsa00980	Metabolism of xenobiotics by cytochrome P450	0.4273	0.86223
54657	UGT1A4	hsa00980	Metabolism of xenobiotics by cytochrome P450	0.4273	0.86223
54658	UGT1A1	hsa00980	Metabolism of xenobiotics by cytochrome P450	0.4273	0.86223

1327	COX4I1	hsa04260	Cardiac muscle contraction	0.4607	0.867652
4513	COX2	hsa04260	Cardiac muscle contraction	0.4607	0.867652
9377	COX5A	hsa04260	Cardiac muscle contraction	0.4607	0.867652
1676	DFFA	hsa04210	Apoptosis	0.4937	0.871689
54205	CYCS	hsa04210	Apoptosis	0.4937	0.871689
8794	TNFRSF10C	hsa04210	Apoptosis	0.4937	0.871689
1956	EGFR	hsa04320	Dorso-ventral axis formation	0.4785	0.872105
2822	GPLD1	hsa00563	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	0.4785	0.872105
4831	NME2	hsa00240	Pyrimidine metabolism	0.5206	0.878027
1571	CYP2E1	hsa00591	Linoleic acid metabolism	0.5303	0.881234
8708	B3GALT1	hsa00601	Glycosphingolipid biosynthesis - lacto and neolacto series	0.492	0.882476
3674	ITGA2B	hsa05414	Dilated cardiomyopathy	0.5114	0.889049
3688	ITGB1	hsa05414	Dilated cardiomyopathy	0.5114	0.889049
3690	ITGB3	hsa05414	Dilated cardiomyopathy	0.5114	0.889049
1785	DNM2	hsa04666	Fc gamma R-mediated phagocytosis	0.5203	0.890817
1956	EGFR	hsa04010	MAPK signaling pathway	0.5562	0.897866
3164	NR4A1	hsa04010	MAPK signaling pathway	0.5562	0.897866
3312	HSPA8	hsa04010	MAPK signaling pathway	0.5562	0.897866
6722	SRF	hsa04010	MAPK signaling pathway	0.5562	0.897866
7189	TRAF6	hsa04010	MAPK signaling pathway	0.5562	0.897866
2731	GLDC	hsa00260	Glycine, serine and threonine metabolism	0.5542	0.907603
1511	CTSG	hsa04080	Neuroactive ligand-receptor interaction	0.5744	0.914186
2147	F2	hsa04080	Neuroactive ligand-receptor interaction	0.5744	0.914186
2149	F2R	hsa04080	Neuroactive ligand-receptor interaction	0.5744	0.914186
2150	F2RL1	hsa04080	Neuroactive ligand-receptor interaction	0.5744	0.914186
4543	MTNR1A	hsa04080	Neuroactive ligand-receptor interaction	0.5744	0.914186
4544	MTNR1B	hsa04080	Neuroactive ligand-receptor interaction	0.5744	0.914186
5617	PRL	hsa04080	Neuroactive ligand-receptor interaction	0.5744	0.914186
5646	PRSS3	hsa04080	Neuroactive ligand-receptor interaction	0.5744	0.914186
799	CALCR	hsa04080	Neuroactive ligand-receptor interaction	0.5744	0.914186
5564	PRKAB1	hsa04910	Insulin signaling pathway	0.5857	0.919224
7248	TSC1	hsa04910	Insulin signaling pathway	0.5857	0.919224
54657	UGT1A4	hsa00140	Steroid hormone biosynthesis	0.6521	0.982497
54658	UGT1A1	hsa00140	Steroid hormone biosynthesis	0.6521	0.982497
1230	CCR1	hsa04062	Chemokine signaling pathway	0.6357	0.984029
2771	GNAI2	hsa04062	Chemokine signaling pathway	0.6357	0.984029
5829	PXN	hsa04062	Chemokine signaling pathway	0.6357	0.984029
1956	EGFR	hsa05223	Non-small cell lung cancer	0.6495	0.991804
2064	ERBB2	hsa05223	Non-small cell lung cancer	0.6495	0.991804
1230	CCR1	hsa04060	Cytokine-cytokine receptor interaction	1	1
1511	CTSG	hsa04142	Lysosome	1	1
1514	CTSL1	hsa04142	Lysosome	1	1
15	AANAT	hsa00380	Tryptophan metabolism	1	1
1839	HBEGF	hsa04912	GnRH signaling pathway	1	1
1956	EGFR	hsa04060	Cytokine-cytokine receptor interaction	1	1
1956	EGFR	hsa04520	Adherens junction	1	1
1956	EGFR	hsa04540	Gap junction	1	1

1956	EGFR	hsa04912	GnRH signaling pathway	1	1
1956	EGFR	hsa05210	Colorectal cancer	1	1
1956	EGFR	hsa05214	Glioma	1	1
1956	EGFR	hsa05218	Melanoma	1	1
2064	ERBB2	hsa04520	Adherens junction	1	1
2771	GNAI2	hsa04360	Axon guidance	1	1
2771	GNAI2	hsa04540	Gap junction	1	1
2771	GNAI2	hsa04730	Long-term depression	1	1
2771	GNAI2	hsa04916	Melanogenesis	1	1
2810	SFN	hsa04960	Aldosterone-regulated sodium reabsorption	1	1
3106	HLA-B	hsa04650	Natural killer cell mediated cytotoxicity	1	1
3683	ITGAL	hsa04650	Natural killer cell mediated cytotoxicity	1	1
3688	ITGB1	hsa04360	Axon guidance	1	1
3688	ITGB1	hsa05130	Pathogenic Escherichia coli infection	1	1
3815	KIT	hsa04060	Cytokine-cytokine receptor interaction	1	1
3815	KIT	hsa04916	Melanogenesis	1	1
3815	KIT	hsa05221	Acute myeloid leukemia	1	1
3931	LCAT	hsa00564	Glycerophospholipid metabolism	1	1
3990	LIPC	hsa00561	Glycerolipid metabolism	1	1
5136	PDE1A	hsa04742	Taste transduction	1	1
54205	CYCS	hsa05210	Colorectal cancer	1	1
5564	PRKAB1	hsa04920	Adipocytokine signaling pathway	1	1
5617	PRL	hsa04060	Cytokine-cytokine receptor interaction	1	1
5693	PSMB5	hsa03050	Proteasome	1	1
64221	ROBO3	hsa04360	Axon guidance	1	1
6667	SP1	hsa04350	TGF-beta signaling pathway	1	1
7057	THBS1	hsa04350	TGF-beta signaling pathway	1	1
7248	TSC1	hsa04150	mTOR signaling pathway	1	1
7428	VHL	hsa05211	Renal cell carcinoma	1	1
8764	TNFRSF14	hsa04060	Cytokine-cytokine receptor interaction	1	1
8794	TNFRSF10C	hsa04060	Cytokine-cytokine receptor interaction	1	1
8794	TNFRSF10C	hsa04650	Natural killer cell mediated cytotoxicity	1	1
8879	SGPL1	hsa00600	Sphingolipid metabolism	1	1
920	CD4	hsa04660	T cell receptor signaling pathway	1	1
930	CD19	hsa04662	B cell receptor signaling pathway	1	1
959	CD40LG	hsa04060	Cytokine-cytokine receptor interaction	1	1
959	CD40LG	hsa04660	T cell receptor signaling pathway	1	1
9641	IKBKE	hsa04623	Cytosolic DNA-sensing pathway	1	1
967	CD63	hsa04142	Lysosome	1	1
6146	RPL22	hsa03010	Ribosome	0.7285	1.00391
54657	UGT1A4	hsa00830	Retinol metabolism	0.6799	1.0109
54658	UGT1A1	hsa00830	Retinol metabolism	0.6799	1.0109
1956	EGFR	hsa05212	Pancreatic cancer	0.7078	1.01242
2064	ERBB2	hsa05212	Pancreatic cancer	0.7078	1.01242
3929	LBP	hsa04620	Toll-like receptor signaling pathway	0.7448	1.014
7189	TRAF6	hsa04620	Toll-like receptor signaling pathway	0.7448	1.014
9641	IKBKE	hsa04620	Toll-like receptor signaling pathway	0.7448	1.014

2771	GNAI2	hsa04914	Progesterone-mediated oocyte maturation	0.727	1.01421
1839	HBEGF	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	0.6937	1.01803
1956	EGFR	hsa05120	Epithelial cell signaling in Helicobacter pylori infection	0.6937	1.01803
5743	PTGS2	hsa04370	VEGF signaling pathway	0.7222	1.02011
5829	PXN	hsa04370	VEGF signaling pathway	0.7222	1.02011
7189	TRAF6	hsa04622	RIG-I-like receptor signaling pathway	0.7043	1.02033
9641	IKBKE	hsa04622	RIG-I-like receptor signaling pathway	0.7043	1.02033
1956	EGFR	hsa04020	Calcium signaling pathway	0.807	1.07284
2064	ERBB2	hsa04020	Calcium signaling pathway	0.807	1.07284
2065	ERBB3	hsa04020	Calcium signaling pathway	0.807	1.07284
2149	F2R	hsa04020	Calcium signaling pathway	0.807	1.07284
5136	PDE1A	hsa04020	Calcium signaling pathway	0.807	1.07284
4831	NME2	hsa00230	Purine metabolism	0.7991	1.07498
5136	PDE1A	hsa00230	Purine metabolism	0.7991	1.07498
5142	PDE4B	hsa00230	Purine metabolism	0.7991	1.07498