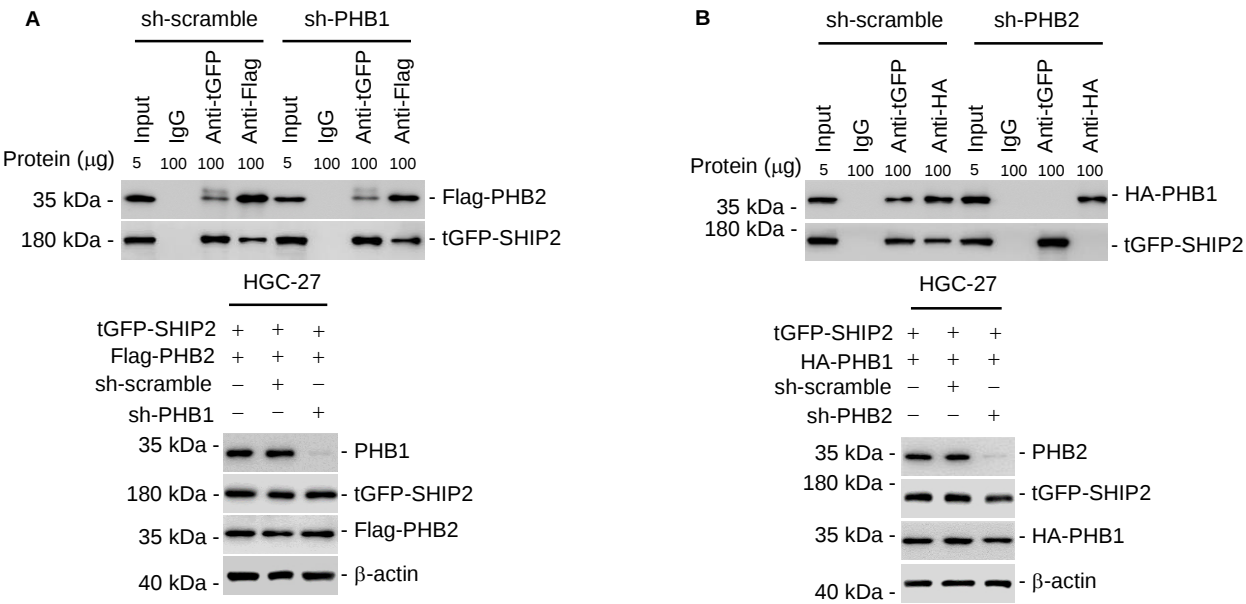


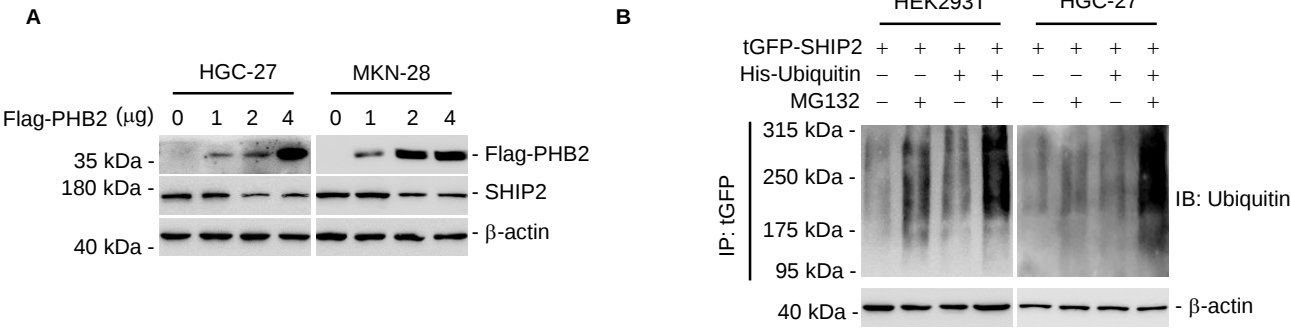
Supplementary Figure 1



Supplementary Figure 1. SHIP2 directly interacts with PHB2.

A, PHB1 silencing didn't affect the interaction between SHIP2 and PHB2. **B**, PHB2 silencing inhibited the interaction between SHIP2 and PHB1. Data are representatives of three independent experiments.

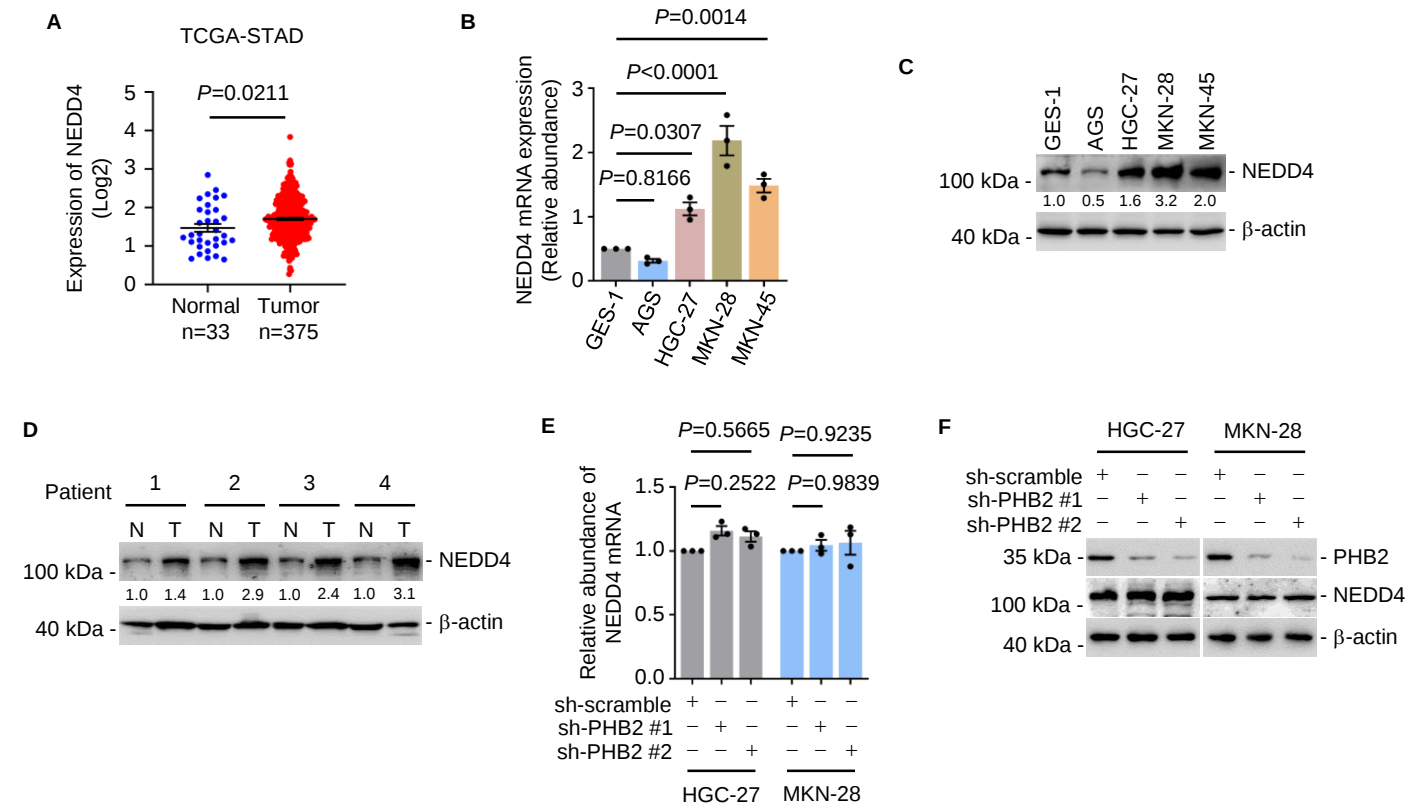
Supplementary Figure 2



Supplementary Figure 2. PHB2 regulates the protein expression of SHIP2 through ubiquitination.

A, Overexpression of flag tagged PHB2 inhibited endogenous SHIP2 expression in a dose dependent manner. **B**, Co-transfection of tGFP-SHIP2 and His-Ubiquitin confirmed the presence of ubiquitinated tGFP-SHIP2 in GC cells. MG132: 10 μM. Data are representatives of three independent experiments.

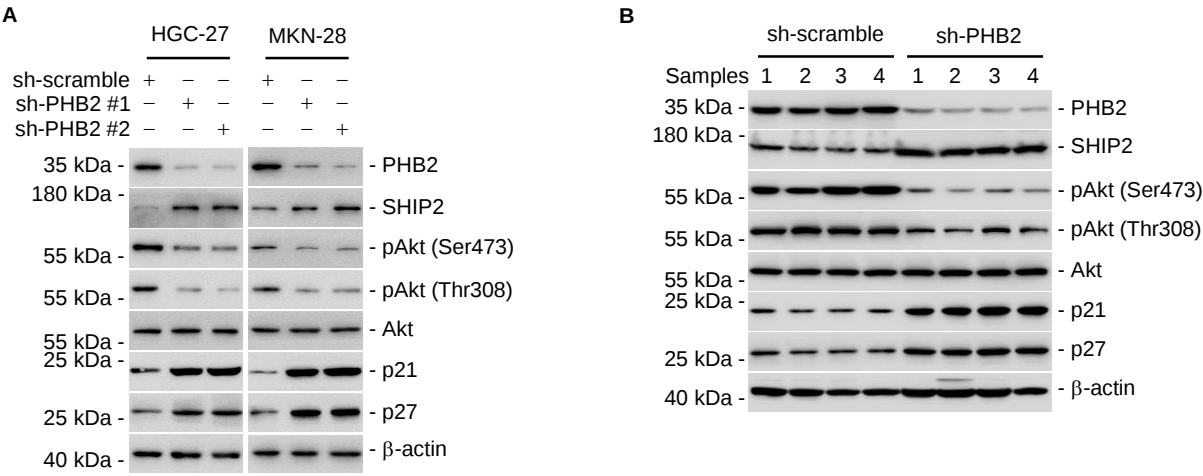
Supplementary Figure 3



Supplementary Figure 3. PHB2 induces the ubiquitination degradation of SHIP2 by enhancing the interaction between NEDD4 and SHIP2.

A, NEDD4 mRNA expression levels in GC compared with normal gastric tissues in STAD dataset derived from TCGA. Data are mean $\pm$ SEM; two-tailed Student's t-test. **B**, **C**, qRT-PCR (**B**) and Western blotting (**C**) analysis of NEDD4 expression in a panel of GC cell lines and normal gastric epithelial cell line GES-1. Data are representatives or mean $\pm$ SEM; n =3 independent experiments, one-way ANOVA followed by Tukey's multiple comparison. **D**, Western blotting analysis of NEDD4 expression in GC tumor (T) compared with corresponding paired adjacent normal (N) tissues. Data are representatives of three independent experiments. **E**, **F**, qRT-PCR (**E**) and Western blotting (**F**) analysis of NEDD4 expression after PHB2 knockdown. Data are representatives or mean $\pm$ SEM; n =3 independent experiments, one-way ANOVA followed by Tukey's multiple comparison.

Supplementary Figure 4



Supplementary Figure 4. PHB2 destabilizes the protein expression of SHIP2, which in turn activates Akt.

A, B, Silencing of PHB2 increased SHIP2 expression and diminished Akt activation in HGC-27 and MKN-28 cells (A) and in MKN-28.sh-PHB2 xenografts (B). Data are representatives of three independent experiments.

Supplementary Table 1. List of primers

Gene	Primer sequences
PHB2-FL	F: GACAAGCTTGCGGCCGC GAATTCG ATGCCCCAGAACTGAAGGA
	R: TTGTTCCGATCCTCTAGA GTCGACTCATTTCTTACCCTTGATGAGGC
PHB2-del N	F: GACAAGCTTGCGGCCGC GAATTCG ATGCTTCACTTCAGGATCCC
	R: TTGTTCCGATCCTCTAGA GTCGAC TCATTCTTACCCTTGATGAGGGC
PHB2-del PHB	F1: GACAAGCTTGCGGCCGC GAATTCG ATGCCCCAGAACTGAAGGA
	R1: GCAGCTGTGTACTCTCGGCT GCCCTCGGCCAGGATAGT
	F2: AGCCGAGAGTACACAGCTGC
	R2: TTGTTCCGATCCTCTAGA GTCGACTCATTTCTTACCCTTGATGAGGC
PHB2-del C	F: GACAAGCTTGCGGCCGC GAATTCG ATGCCCCAGAACTGAAGGA
	R: TTGTTCCGATCCTCTAGA GTCGAC TCATGTGATGGCCACATCAT
PHB2-N	F: GACAAGCTTGCGGCCGC GAATTCG ATGCCCCAGAACTGAAGGA
	R: TTGTTCCGATCCTCTAGA GTCGAC TCAGCCCTCGGCCAGGATAG
PHB2-PHB	F: GACAAGCTTGCGGCCGC GAATTCG ATGCGCGAATCTGTGTTTAC
	R: TTGTTCCGATCCTCTAGA GTCGAC TCAAAAGCTCAGCTCTGTGA
PHB2-C	F: GACAAGCTTGCGGCCGC GAATTCG ATGGAGCTGAGCTTTAGCCG
	R: TTGTTCCGATCCTCTAGA GTCGAC TCATTCTTACCCTTGATGAGGC
PHB1-FL	F: CTTATGGCCATGGAGGCCC GAATTC GC ATGGCTGCCAAAGTGTTTGA
	R: GGTACCTCGAGAGATCTCG GTCGAC TCACTGGGGCAGCTGGAGGA
GST-PHB1	F: GGTCTGTGGGATCCCCAGGAATTCTATGGCTGCCAAAGTGTTTGA
	R: ACGATGCGGCCGCTCGAGTCGACTCATTTCTTACCCTTGATGA
GST-PHB2	F: GGTCTGTGGGATCCCCAGGAATTCTATGGCCCAGAACTGAAGGA
	R: TTGTTCCGATCCTCTAGA GTCGACTCATTTCTTACCCTTGATGAGGGC

Supplementary Table 2. shRNA and siRNA sequences

NEDD4 siRNA#1 (1597)	5'-CCAAUGAUCUAGGGCCUUUTT-3'
	5'-AAAGGCCCCUAGAUCAUUGGTT-3'
NEDD4 siRNA#2 (2804)	5'-GGACUUGCCACCUUAUGAATT-3'
	5'-UUCAUAAGGUGGCAAGUCCTT-3'
PHB2 shRNA#1 (82672-1)	ccgggcTGAGCTTTAGCCGAGAGTActcgagTACTCTCGGCTAAAGCTCAgctttttg
PHB2 shRNA#2 (82673-1)	ccggGAGCAAGAACCCTGGCTACATctcgagATGTAGCCAGGGTTCTTGCTCtttttg
PHB1 shRNA#1 (84139-1)	ccgggcTGCCGTCCATCACAACTGActcgagTCAGTTGTGATGGACGGCAgctttttg
PHB1 shRNA#2 (84141-1)	ccggTGCCGTTCTCGACCACGTAATctcgagATTACGTGGTCGAGAACGGCAtttttg
SHIP2 shRNA#1 (34900-1)	ccggccGGATTCTGTGGAAATCCTActcgagTAGGATTCCACAGAATCCggtttttg
SHIP2 shRNA#2 (34901-1)	ccggccTGAAC TACATCAGCAGGAActcgagTTCCTGCTGATGTAGTTCAggtttttg

Supplementary Table 3. Gastric cancer tissue array (90 cases/180 cores)

Characteristic	No. (%)
Gender, n(%)	
Male	61(67.78)
Female	29(32.22)
Age (years)	
Mean(range)	64.30(31-83)
Stage, n(%)	
1	6(6.67)
2	32(35.56)
3	51(56.67)
4	1(1.11)
Paired gastric cancer and corresponding normal tissues, n(%)	66/90 (73.33)

Supplementary Table 4. Relationship between PHB2 expression and clinicopathologic characteristics of gastric cancer

Clinicopathologic characteristics	PHB2 expression			<i>P</i>
	Total	Low(number)	High(number)	
Gender				0.83
Male	61	16	45	
Female	29	7	22	
Age				1
≤55	19	5	14	
>55	71	18	53	
Tumor size (cm)				0.11
≤ 5	42	14	28	
> 5	48	9	39	
Pathology grade				0.83
I -II	15	3	12	
III-IV	75	20	55	
T stage				0.7
T1-T2	8	3	5	
T3-T4	82	20	62	
N stage				0.98
N0-N1	35	9	26	
N2-N3	55	14	41	
TNM stage				0.79
1-2	37	10	27	
3-4	53	13	40	

Supplementary Table 5. PHB2-interacting protein candidates identified by immunoprecipitation plus mass spectrometry analysis in HGC-27 cells.

Accession	Description	Gene name	Peptides	PSM
J3KPX7	Prohibitin	PHB2	15	96
P23396	40S ribosomal protein S3	RPS3	10	19
O15357	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	INPPL1	7	13
P12236	ADP/ATP translocase 3	SLC25A6	8	10
P05387	60S acidic ribosomal protein P2	RPLP2	3	5
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	PCMT1	4	5
P60866	40S ribosomal protein S20	RPS20	2	5
B3KUD7	DNA replication licensing factor MCM7	MCM7	4	4
Q8NI62	Ribosomal protein S2	OK/KNS-cl.6	2	3
P16403	Histone H1.2	H1-2	3	3
B4DUR8	T-complex protein 1 subunit gamma	CCT3	3	3
Q9Y678	Coatomer subunit gamma-1	COPG1	3	3
P62857	40S ribosomal protein S28	RPS28	2	2
E5RH77	40S ribosomal protein S14	RPS14	2	2
J3KT73	60S ribosomal protein L38	RPL38	2	2
Q06830	Peroxiredoxin-1	PRDX1	2	2
M0QZC5	40S ribosomal protein S11	RPS11	2	2
Q9NS69	Mitochondrial import receptor subunit TOM22 homolog	TOMM22	2	2
P62753	40S ribosomal protein S6	RPS6	2	2
F8W7C6	60S ribosomal protein L10	RPL10	2	2
B3KS35	Endoplasmic reticulum class 1/2 Ca(2+) ATPase	B3KS35	1	2
P43490	Nicotinamide phosphoribosyltransferase	NAMPT	2	2
Q8N7L7	HEAT repeat-containing protein 1	Q8N7L7	2	2
P49207	60S ribosomal protein L34	RPL34	1	1
Q8N5F4	IGL@ protein	IGL@	1	1
C9JYQ9	60S ribosomal protein L22-like 1	RPL22L1	1	1
H0YLA2	Signal recognition particle 14 kDa protein	SRP14	1	1
C9JXB8	60S ribosomal protein L24	RPL24	1	1
P26373	60S ribosomal protein L13	RPL13	1	1
E9PKH2	Collagen-binding protein	SERPINH1	1	1
H0YLP6	60S ribosomal protein L28	RPL28	1	1
O00570	Transcription factor SOX-1	SOX1	1	1
Q9NZ23	Drug-sensitive protein 1	YA61	1	1
P14174	Macrophage migration inhibitory factor	MIF	1	1
Q5T8U5	Surfeit locus protein 4	SURF4	1	1
I3L3H2	RNA helicase	EIF4A3	1	1
H3BM89	60S ribosomal protein L4	RPL4	1	1
P62277	40S ribosomal protein S13	RPS13	1	1
F8VVM2	Phosphate carrier protein, mitochondrial	SLC25A3	1	1
A0A2R8YCS7	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	SAMHD1	1	1
B7ZAY8	E3 UFM1-protein ligase 1	B7ZAY8	1	1
Q86YZ3	Hornerin	HRNR	1	1
P61619	Protein transport protein Sec61 subunit alpha isoform 1	SEC61A1	1	1
Q8IZX4	Transcription initiation factor TFIID subunit 1-like	TAF1L	1	1
P23258	Tubulin gamma-1 chain	TUBG1	1	1
Q08J23	RNA cytosine C(5)-methyltransferase NSUN2	NSUN2	1	1

Supplementary Table 6. SHIP2-interacting protein candidates identified by immunoprecipitation plus mass spectrometry analysis in HGC-27 cells.

ProteinID	Gene_name	Description
O15357	SHIP2	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2
A0A384NYT8	A0A384NYT8	Tubulin beta chain (Fragment)
B3KT06	B3KT06	Tubulin alpha chain
P05141	ADT2	ADP/ATP translocase 2
P68371	TBB4B	Tubulin beta-4B chain
Q02878	RL6	60S ribosomal protein L6
B4DI39	B4DI39	cDNA FLJ54328, highly similar to Heat shock 70 kDa protein 1
P02768	ALBU	Albumin
P19338	NUCL	Nucleolin
V9HW22	V9HW22	Epididymis luminal protein 33
Q9BV28	Q9BV28	Tubulin beta chain (Fragment)
V9HW84	V9HW84	75 kDa glucose-regulated protein
Q9UQ35	SRRM2	Serine/arginine repetitive matrix protein 2
P18124	RL7	60S ribosomal protein L7
P46777	RL5	60S ribosomal protein L5
A0A024R2Q4	A0A024R2Q4	Ribosomal protein L15
A0A4D5RAC7	A0A4D5RAC7	Tr-type G domain-containing protein
F8VWS0	F8VWS0	60S acidic ribosomal protein P0
G5E9G0	G5E9G0	60S ribosomal protein L3
P22061	PIMT	Protein-L-isoaspartate(D-aspartate) O-methyltransferase
X5D2T3	X5D2T3	Ribosomal protein L10 isoform A (Fragment)
Q7Z3M3	Q7Z3M3	Tubulin alpha chain (Fragment)
A0A024QZD1	A0A024QZD1	Ribosomal protein L18, isoform CRA_c
A8K4W0	A8K4W0	40S ribosomal protein S3a
B4DVF9	B4DVF9	cDNA FLJ54388, highly similar to Tax1-binding protein 1
Q5T8U3	Q5T8U3	60S ribosomal protein L7a (Fragment)
Q8J014	Q8J014	40S ribosomal protein S2
A0A024R9D3	A0A024R9D3	60S ribosomal protein L30
A0A024RCJ9	A0A024RCJ9	Histone H2B
A0A0S2Z4G7	A0A0S2Z4G7	Nucleophosmin (Fragment)
A3KPC7	A3KPC7	Histone H2A
A8K7N0	A8K7N0	60S ribosomal protein L14
H0YKD8	H0YKD8	60S ribosomal protein L28
Q53H34	Q53H34	60S ribosomal protein L13a (Fragment)
A0A5C2GTX6	A0A5C2GTX6	IG c1329_heavy_IGHV3-21_IGHD7-27_IGHJ3 (Fragment)
A0A5C2G1L4	A0A5C2G1L4	IGL c3161_light_IGKV2-30_IGKJ1 (Fragment)
A0A5C2G1Z7	A0A5C2G1Z7	IGL c2570_light_IGKV2D-29_IGKJ4 (Fragment)
A2J423	A2J423	Anti-Mpl scFv (Fragment)
A0A0J9YX35	HV64D	Immunoglobulin heavy variable 3-64D
A0A5C2G6D8	A0A5C2G6D8	IGL c3926_light_IGKV2-24_IGKJ1 (Fragment)
A0A5C2GG88	A0A5C2GG88	IG c54_heavy_IGHV3-23_IGHD3-22_IGHJ4 (Fragment)
A0A5C2GHB9	A0A5C2GHB9	IG c974_light_IGKV4-1_IGKJ5 (Fragment)
A0A5C2GUY6	A0A5C2GUY6	IG c583_light_IGKV1-5_IGKJ4 (Fragment)
S6BAN6	S6BAN6	IgG L chain
A5A3E0	POTEF	POTE ankyrin domain family member F
P02766	TTHY	Transthyretin
P18077	RL35A	60S ribosomal protein L35a
P26373	RL13	60S ribosomal protein L13
P46778	RL21	60S ribosomal protein L21
P49207	RL34	60S ribosomal protein L34
P52272	HNRPM	Heterogeneous nuclear ribonucleoprotein M
P61353	RL27	60S ribosomal protein L27
P62906	RL10A	60S ribosomal protein L10a
P62917	RL8	60S ribosomal protein L8
P63173	RL38	60S ribosomal protein L38
Q00839	HNRPU	Heterogeneous nuclear ribonucleoprotein U

Q02543	RL18A	60S ribosomal protein L18a
Q9C0B2	CFA74	Cilia- and flagella-associated protein 74
Q9H1K1	ISCU	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial
A0A087WXM6	A0A087WXM6	60S ribosomal protein L17 (Fragment)
A0A5E4	A0A5E4	Uncharacterized protein
B0YJC4	B0YJC4	Vimentin
B7Z732	B7Z732	40S ribosomal protein S9
H7C5R8	H7C5R8	Protein mono-ADP-ribosyltransferase PARP14 (Fragment)
J3QQQ9	J3QQQ9	KOW domain-containing protein
K7EJV9	K7EJV9	60S ribosomal protein L23a (Fragment)
Q53G74	Q53G74	60S ribosomal protein L4 (Fragment)
Q53HV1	Q53HV1	Ribosomal protein S4, X-linked X isoform variant (Fragment)
Q59FI9	Q59FI9	60S ribosomal protein L12 (Fragment)
Q5CZ94	Q5CZ94	Uncharacterized protein DKFZp781M0386
Q8NB80	Q8NB80	cDNA FLJ34106 fis, clone FCBBF3008073, highly similar to SPL
V9HWB4	V9HWB4	78 kDa glucose-regulated protein
Q9P2N5	RBM27	RNA-binding protein 27
J3QLS5	J3QLS5	Nucleolar protein 3 (Fragment)
A8MVJ9	HPF1L	Putative histone PARylation factor 1-like
A0A0B6CEA2	A0A0B6CEA2	Cytochrome c oxidase subunit 1
P08183	MDR1	ATP-dependent translocase ABCB1
Q8N387	MUC15	Mucin-15
Q59EX2	Q59EX2	Farnesyltransferase, CAAX box, alpha variant (Fragment)
Q6AW86	Z324B	Zinc finger protein 324B
Q7Z7L7	ZER1	Protein zer-1 homolog
Q9HAY2	MAGF1	Melanoma-associated antigen F1
Q9UNE2	RPH3L	Rab effector Noc2
A8K321	A8K321	Dolichyl-phosphate-mannose--protein mannosyltransferase
B0I1R8	B0I1R8	DNAH6 variant protein (Fragment)
C3W8I1	C3W8I1	NAD(P)(+)--arginine ADP-ribosyltransferase (Fragment)
E9PN42	E9PN42	Unconventional myosin-XVIIIa (Fragment)
R4GNF4	R4GNF4	Catechol O-methyltransferase domain-containing protein 1 (I
A6H8Y1	BDP1	Transcription factor TFIIIB component B homolog
P05387	RLA2	60S acidic ribosomal protein P2
Q15198	PGFRL	Platelet-derived growth factor receptor-like protein
Q8N1K5	THMS1	Protein THEMIS
Q99536	VAT1	Synaptic vesicle membrane protein VAT-1 homolog
A0A024R1I5	A0A024R1I5	SEC14-like 2 (S. cerevisiae), isoform CRA_b
A0A075B6Z2	A0A075B6Z2	T cell receptor alpha joining 56 (Fragment)
A0A2X0U2Q1	A0A2X0U2Q1	VAV3 (Fragment)
A0A4P2STK4	A0A4P2STK4	MHC class II antigen (Fragment)
F2Z2Z6	F2Z2Z6	Prostaglandin F2-alpha receptor
H0YDJ2	H0YDJ2	Liprin-beta-2 (Fragment)
H7BYN4	H7BYN4	Kinesin-like protein
L0R5A1	L0R5A1	Alternative protein CSF2RB
L8E885	L8E885	Alternative protein FAM169A
Q53G41	Q53G41	Tripartite motif protein TRIM29 isoform alpha variant (Fragme
Q68D69	Q68D69	Uncharacterized protein DKFZp779G1236
A0A1B0GUC4	MYCOS	Myocilin opposite strand protein
A8MTL3	R212B	RING finger protein 212B
O00522	KRIT1	Krev interaction trapped protein 1
O43320	FGF16	Fibroblast growth factor 16
O43345	ZN208	Zinc finger protein 208
O60437	PEPL	Periplakin
O75344	FKBP6	Inactive peptidyl-prolyl cis-trans isomerase FKBP6
P01024	CO3	Complement C3
P02649	APOE	Apolipoprotein E
P05109	S10A8	Protein S100-A8

P05556	ITB1	Integrin beta-1
P11229	ACM1	Muscarinic acetylcholine receptor M1
P13682	ZNF35	Zinc finger protein 35
P15924	DESP	Desmoplakin
P19838	NFKB1	Nuclear factor NF-kappa-B p105 subunit
P25398	RS12	40S ribosomal protein S12
P26447	S10A4	Protein S100-A4
P29322	EPHA8	Ephrin type-A receptor 8
P29374	ARI4A	AT-rich interactive domain-containing protein 4A
P43351	RAD52	DNA repair protein RAD52 homolog
P47914	RL29	60S ribosomal protein L29
P62249	RS16	40S ribosomal protein S16
P62266	RS23	40S ribosomal protein S23
P62805	H4	Histone H4
P62857	RS28	40S ribosomal protein S28
P62910	RL32	60S ribosomal protein L32
P81605	DCD	Dermcidin
P83731	RL24	60S ribosomal protein L24
Q02224	CENPE	Centromere-associated protein E
Q03721	KCNC4	Potassium voltage-gated channel subfamily C member 4
Q04656	ATP7A	Copper-transporting ATPase 1
Q12788	TBL3	Transducin beta-like protein 3
Q14674	ESPL1	Separin
Q14781	CBX2	Chromobox protein homolog 2
Q15691	MARE1	Microtubule-associated protein RP/EB family member 1
Q16850	CP51A	Lanosterol 14-alpha demethylase
Q2M2D7	TBC28	TBC1 domain family member 28
Q2M389	WASC4	WASH complex subunit 4
Q3SY69	AL1L2	Mitochondrial 10-formyltetrahydrofolate dehydrogenase
Q3ZM63	ETDA	Embryonic testis differentiation protein homolog A
Q4AC94	C2CD3	C2 domain-containing protein 3
Q5T3J3	LRIF1	Ligand-dependent nuclear receptor-interacting factor 1
Q5T6F0	DCA12	DDB1- and CUL4-associated factor 12
Q68D51	DEN2C	DENN domain-containing protein 2C
Q6AWC2	WWC2	Protein WWC2
Q6NV74	CRCDL	CRACD-like protein
Q6UXN9	WDR82	WD repeat-containing protein 82
Q6Y288	B3GLT	Beta-1,3-glucosyltransferase
Q70CQ4	UBP31	Ubiquitin carboxyl-terminal hydrolase 31
Q7KZ85	SPT6H	Transcription elongation factor SPT6
Q8IV76	PASD1	Circadian clock protein PASD1
Q8IVF2	AHNAK2	Protein AHNAK2
Q8IXT5	RB12B	RNA-binding protein 12B
Q8N3K9	CMYA5	Cardiomyopathy-associated protein 5
Q8NFC6	BD1L1	Biorientation of chromosomes in cell division protein 1-like 1
Q8TDF5	NETO1	Neuropilin and tolloid-like protein 1
Q92993	KAT5	Histone acetyltransferase KAT5
Q96BN2	TADA1	Transcriptional adapter 1
Q96I45	TM141	Transmembrane protein 141
Q99619	SPSB2	SPRY domain-containing SOCS box protein 2
Q9BYE9	CDHR2	Cadherin-related family member 2
Q9BZF9	UACA	Uveal autoantigen with coiled-coil domains and ankyrin repeats
Q9BZG2	PPAT	Testicular acid phosphatase
Q9H361	PABP3	Polyadenylate-binding protein 3
Q9HCM2	PLXA4	Plexin-A4
Q9NR48	ASH1L	Histone-lysine N-methyltransferase ASH1L
Q9NZQ7	PD1L1	Programmed cell death 1 ligand 1
Q9P2B4	CT2NL	CTTNBP2 N-terminal-like protein

Q9P2D8	UNC79	Protein unc-79 homolog
Q9P2K8	E2AK4	eIF-2-alpha kinase GCN2
Q9P2M7	CING	Cingulin
Q9UL45	BL1S6	Biogenesis of lysosome-related organelles complex 1 subunit
Q9UM07	PADI4	Protein-arginine deiminase type-4
Q9UQ26	RIMS2	Regulating synaptic membrane exocytosis protein 2
Q9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3
Q9Y6Q3	ZFP37	Zinc finger protein 37 homolog
A0A024R0G5	A0A024R0G5	Zinc finger protein 607, isoform CRA_b
A0A024R0X7	A0A024R0X7	Solute carrier family 38, member 4, isoform CRA_c
A0A024R2L1	A0A024R2L1	USP1-associated factor 1
A0A024R301	A0A024R301	Choline dehydrogenase, isoform CRA_a
A0A024R4X1	A0A024R4X1	Protein kinase C and casein kinase substrate in neurons 2, isoform CRA_b
A0A024R599	A0A024R599	Solute carrier family 3 (Activators of dibasic and neutral amines)
A0A024R6H1	A0A024R6H1	Serine palmitoyltransferase, long chain base subunit 2, isoform CRA_a
A0A024R9F1	A0A024R9F1	HCG2044510, isoform CRA_a
A0A024RBK8	A0A024RBK8	RAS protein activator like 1 (GAP1 like), isoform CRA_b
A0A024RDB9	A0A024RDB9	NAD(P)(+)-L-arginine ADP-ribosyltransferase
A0A075B6G6	A0A075B6G6	Filamin A interacting protein 1, isoform CRA_c
A0A087WSW7	A0A087WSW7	Helicase, lymphoid-specific, isoform CRA_d
A0A087WU46	A0A087WU46	DNA-binding protein Ikaros
A0A087WZF2	A0A087WZF2	Empty spiracles homolog 1 (Drosophila), isoform CRA_a
A0A087X1N7	A0A087X1N7	Nebulin
A0A087X2D0	A0A087X2D0	Serine/arginine-rich-splicing factor 3
A0A0A6YYJ0	A0A0A6YYJ0	Protein MSANTD3-TMEFF1
A0A0C4DGW6	A0A0C4DGW6	UPF0600 protein C5orf51
A0A0U1RQT6	A0A0U1RQT6	Dedicator of cytokinesis protein 7 (Fragment)
A0A0U1RR27	A0A0U1RR27	C-myc promoter-binding protein
A0A140VJU4	A0A140VJU4	Testicular tissue protein Li 171
A0A140VKH5	A0A140VKH5	Testis tissue sperm-binding protein Li 92mP
A0A182DWH7	A0A182DWH7	Selenoprotein P (Fragment)
A0A1B0GTQ8	A0A1B0GTQ8	Protein FAM47E
A0A1B0GU21	A0A1B0GU21	Glutamine--tRNA ligase (Fragment)
A0A1D5RMT4	A0A1D5RMT4	Ras-related protein Rab-2A (Fragment)
A0A286YFA2	A0A286YFA2	D-3-phosphoglycerate dehydrogenase
A0A286YFF2	A0A286YFF2	RNA-binding protein fox-1 homolog 1
A0A2R8Y702	A0A2R8Y702	Gamma-crystallin N
A0A2R8Y8A0	A0A2R8Y8A0	40S ribosomal protein S24 (Fragment)
A0A2R8YHI4	A0A2R8YHI4	Amino acid transporter (Fragment)
A0A3B3IRL3	A0A3B3IRL3	cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase
A0A494C0A7	A0A494C0A7	Zinc finger matrix-type protein 1
A0A494C0S9	A0A494C0S9	C3 and PZP-like alpha-2-macroglobulin domain-containing protein
A0A5C2FV28	A0A5C2FV28	IGL c622_light_IGKV3-15_IGKJ2 (Fragment)
A0A5C2FWU2	A0A5C2FWU2	IGL c656_light_IGKV1-27_IGKJ4 (Fragment)
A0A5C2FX73	A0A5C2FX73	IGL c195_light_IGLV1-40_IGLJ2 (Fragment)
A0A5C2G3P0	A0A5C2G3P0	IGL c3908_light_IGKV3-15_IGKJ2 (Fragment)
A0A5C2G4T0	A0A5C2G4T0	IGL c2925_light_IGLV3-1_IGLJ3 (Fragment)
A0A5C2G5G0	A0A5C2G5G0	IGH c236_heavy_IGHV2-5_IGHD3-16_IGHJ3 (Fragment)
A0A5C2G860	A0A5C2G860	IGH c124_heavy_IGHV1-46_IGHD3-10_IGHJ5 (Fragment)
A0A5C2GDG0	A0A5C2GDG0	IG c1087_heavy_IGHV1-69_IGHD4-23_IGHJ6 (Fragment)
A0A5C2GDI3	A0A5C2GDI3	IG c661_heavy_IGHV1-69_IGHD5-12_IGHJ5 (Fragment)
A0A5C2GDM1	A0A5C2GDM1	IGH + IGL c97_heavy_IGHV4-34_IGHD4-17_IGHJ4 (Fragment)
A0A5C2GDW9	A0A5C2GDW9	IG c1179_heavy_IGHV3-15_IGHD2-15_IGHJ4 (Fragment)
A0A5C2GDX6	A0A5C2GDX6	IGH c191_heavy_IGHV1-46_IGHD1-14_IGHJ4 (Fragment)
A0A5C2GR64	A0A5C2GR64	IG c1403_heavy_IGHV3-15_IGHD3-16_IGHJ4 (Fragment)
A0A5C2GU23	A0A5C2GU23	IG c253_light_IGLV1-47_IGLJ2 (Fragment)
A0A5C2GXM0	A0A5C2GXM0	IG c388_light_IGKV4-1_IGKJ3 (Fragment)
A2A3R7	A2A3R7	40S ribosomal protein S6

A2RUF6	A2RUF6	DENN/MADD domain containing 2A
A3R0T7	A3R0T7	Liver histone H1e
A4D1H4	A4D1H4	Protein-serine/threonine kinase
A5PKX5	A5PKX5	Alpha-mannosidase
A8K0S7	A8K0S7	cDNA FLJ78551, highly similar to Homo sapiens solute carrier
A8K8F3	A8K8F3	cDNA FLJ76680, highly similar to Homo sapiens chromodoma
A9XA89	A9XA89	Alpha-helical coiled-coil rod protein (Fragment)
B2RD09	B2RD09	cDNA, FLJ96406, highly similar to Homo sapiens NOL1/NOP2.
B3KN57	B3KN57	Sorting nexin-2
B3KTW0	B3KTW0	cDNA FLJ38844 fis, clone MESAN2003662, highly similar to Cu
B3KU66	B3KU66	cDNA FLJ39263 fis, clone OCBBF2009571, highly similar to AT
B3KVA9	B3KVA9	cDNA FLJ16319 fis, clone SPLEN2036076, highly similar to Hoi
B4DGL0	B4DGL0	cDNA FLJ53619, highly similar to Heat shock protein HSP 90-I
B4DH14	B4DH14	cDNA FLJ60515, highly similar to Period circadian protein 2
B4DP44	B4DP44	cDNA FLJ60751, highly similar to Protein arginine N-methyltra
B4DQ75	B4DQ75	Death-associated protein 1
B4DQQ8	B4DQQ8	cDNA FLJ60806, highly similar to RalBP1-associated Eps doma
B4DR60	B4DR60	cDNA FLJ56882, highly similar to Activating signal cointegratc
B4DRA9	B4DRA9	cDNA FLJ61347, highly similar to General transcription factor I
B4DW39	B4DW39	cDNA FLJ60915, highly similar to Fc receptor-like protein 5
B4E1C0	B4E1C0	cDNA FLJ54225, moderately similar to Bifunctional coenzyme
B4E1M5	B4E1M5	60S ribosomal protein L9
B5MDV5	B5MDV5	KIAA1244
B6RFS7	B6RFS7	Toll-like receptor
B7Z313	B7Z313	ABPP
B7Z4E3	B7Z4E3	60S ribosomal protein L31
B7Z4S3	B7Z4S3	cDNA FLJ58678, highly similar to Formin-2
B7Z5S1	B7Z5S1	cDNA FLJ61699, highly similar to Homo sapiens androgen-inc
B7Z633	B7Z633	cDNA FLJ54145, highly similar to Limb region 1 protein homo
B7Z786	B7Z786	cDNA FLJ53106, highly similar to Cytochrome P450 39A1
B7Z7M0	B7Z7M0	cDNA FLJ59069, weakly similar to Golgin subfamily A member
B7Z8B9	B7Z8B9	cDNA FLJ52576
B7Z915	B7Z915	cDNA FLJ52394, highly similar to Ral guanine nucleotide dissc
B7ZA42	B7ZA42	cDNA, FLJ79056 (Fragment)
B7ZB80	B7ZB80	cDNA, FLJ79444, highly similar to 2-oxoisovalerate dehydroge
D6R9G8	D6R9G8	Synphilin-1 (Fragment)
D6RB73	D6RB73	Solute carrier family 35 member B1 (Fragment)
D6REZ7	D6REZ7	Nuclear receptor subfamily 1 group I member 3
D6RHE6	D6RHE6	Protocadherin Fat 1
D7R528	D7R528	Mitogen-activated protein kinase 9
E5KQF6	E5KQF6	Glucocorticoid receptor
E5RJU6	E5RJU6	Protein SFI1 homolog
E9M4D4	E9M4D4	Hemoglobin alpha-1 globin chain (Fragment)
E9PJD9	E9PJD9	60S ribosomal protein L27a
E9PL09	E9PL09	40S ribosomal protein S3
F2WF76	F2WF76	Cytochrome b
F2Z388	F2Z388	60S ribosomal protein L35
F2Z3N8	F2Z3N8	Protein Jade-3 (Fragment)
F8VRU3	F8VRU3	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondri
F8VV56	F8VV56	CD63 antigen
H0Y3U8	H0Y3U8	Chitinase-3-like protein 1 (Fragment)
H0Y3Z4	H0Y3Z4	Nicastrin (Fragment)
H0Y5F5	H0Y5F5	Polyadenylate-binding protein (Fragment)
P46934	NEDD4	HECT-type E3 ubiquitin transferase (Fragment)
H0YC82	H0YC82	Dystonin (Fragment)
H0YD93	H0YD93	RUN and FYVE domain-containing protein 2 (Fragment)
H0YGD6	H0YGD6	Protein quaking (Fragment)
H0YJJ4	H0YJJ4	Dolichyl-phosphate-mannose--protein mannosyltransferase

H0YN04	H0YN04	Ceramide synthase 4
H3BM70	H3BM70	Probable D-lactate dehydrogenase, mitochondrial
H3BVC7	H3BVC7	40S ribosomal protein S15a (Fragment)
H3BVI4	H3BVI4	Lipase maturation factor
H7BXE0	H7BXE0	Rho GTPase-activating protein 40 (Fragment)
H7BZC1	H7BZC1	Hippocalcin-like protein 1 (Fragment)
H7BZG0	H7BZG0	UDP-glucose:glycoprotein glucosyltransferase 1 (Fragment)
H7C071	H7C071	Calcium/calmodulin-dependent protein kinase type 1 (Fragment)
H7C1A2	H7C1A2	CDP-diacylglycerol synthase (Fragment)
H7C2W0	H7C2W0	Cystathionine beta-synthase (Fragment)
H7C3H4	H7C3H4	Histone-lysine N-methyltransferase SETD2 (Fragment)
H7C3J1	H7C3J1	Testis-specific serine/threonine-protein kinase 4
H7C4U7	H7C4U7	Membrane-associated guanylate kinase, WW and PDZ domain containing
I3L504	I3L504	Eukaryotic translation initiation factor 5A-1
J3JS69	J3JS69	40S ribosomal protein S18
J3KTA4	J3KTA4	DEAD box protein 5
J3QR09	J3QR09	Ribosomal protein L19
J3QRG3	J3QRG3	Src kinase-associated phosphoprotein 1 (Fragment)
J3QRT1	J3QRT1	Beta-crystallin A3 (Fragment)
K7EJT1	K7EJT1	Ubinuclein-1 (Fragment)
K7EL56	K7EL56	RNA helicase (Fragment)
K7EQN2	K7EQN2	DNA-directed RNA polymerases I, II, and III subunit RPABC1
K7ES89	K7ES89	Dual specificity protein phosphatase (Fragment)
M0QZQ0	M0QZQ0	Uncharacterized protein
P78409	P78409	Butyrophilin
Q15559	Q15559	(clone tec14) (Fragment)
Q1L838	Q1L838	GTBP-ALT
Q4FD37	Q4FD37	ZBP-89 delta-Nter isoform
Q53TR0	Q53TR0	Uncharacterized protein CRIM1 (Fragment)
Q53YE2	Q53YE2	Syntaxin 3A
Q59GV2	Q59GV2	RNA binding motif protein 14 variant (Fragment)
Q5CAQ4	Q5CAQ4	TNF receptor-associated protein 1
Q5FBW8	Q5FBW8	Postmeiotic segregation increased 2 nirs variant 5
Q5HYD9	Q5HYD9	Uncharacterized protein DKFZp686M0619 (Fragment)
Q5JC45	Q5JC45	Transformation-related protein 2
Q5JR94	Q5JR94	40S ribosomal protein S8
Q5JVX6	Q5JVX6	Uncharacterized protein C1orf141 (Fragment)
Q5VVD0	Q5VVD0	60S ribosomal protein L11
Q6I9S2	Q6I9S2	SNW1 protein
Q6KAV0	Q6KAV0	T-cell receptor T3 zeta chain
Q6PIN8	Q6PIN8	TAOK2 protein (Fragment)
Q6PJR2	Q6PJR2	eIF4ENIF1 protein (Fragment)
Q71RE3	Q71RE3	PP10513
Q75MH1	Q75MH1	40S ribosomal protein S26
Q86XC3	Q86XC3	C16orf55 protein (Fragment)
Q86XG0	Q86XG0	CIDEC protein
Q86YB2	Q86YB2	RNA helicase
Q8N220	Q8N220	Splicing factor, arginine/serine-rich 2, isoform CRA_f
Q8TEL7	Q8TEL7	FLJ00176 protein (Fragment)
Q8TEZ9	Q8TEZ9	SR rich protein (Fragment)
Q8WUM5	Q8WUM5	Gem (Nuclear organelle) associated protein 4
Q96GA5	Q96GA5	PCTK1 protein (Fragment)
Q9BUS0	Q9BUS0	ZYX protein (Fragment)
Q9NPS2	Q9NPS2	Uncharacterized protein (Fragment)
S4R3B4	S4R3B4	Sterol regulatory element-binding protein 1 (Fragment)

PepCount Sequence	UniquePepCount MH+	CoverPercent Diff(MH+)	MW Charge	PI Rank	
79	52	52.38%	138597.16	6.1	
14	11	35.07%	49468.01	4.8	
11	10	28.85%	46340.8	5	
10	10	33.89%	32851.84	9.71	
11	9	28.76%	49830.48	4.79	
10	9	30.90%	32727.51	10.59	
9	9	14.72%	67530.52	5.36	
16	8	10.67%	69365.97	5.92	
8	8	11.97%	76613.47	4.6	
8	8	14.55%	70897.24	5.37	
9	7	23.15%	45621.9	4.9	
8	7	9.57%	73778.79	5.97	
7	7	2.36%	299611.6	12.05	
6	6	18.95%	29225.43	10.66	
6	6	16.16%	34362.24	9.73	
6	6	24.02%	24145.77	11.62	
6	6	11.76%	46209.96	9.12	
6	6	16.37%	30455.74	5.9	
6	6	10.83%	40266.63	10.02	
5	5	26.87%	24636.11	6.7	
5	5	19.16%	24576.61	10.11	
5	4	11.27%	53968.56	9.21	
4	4	21.28%	21634.23	11.73	
4	4	13.64%	29954.63	9.75	
4	4	4.30%	80598.65	5.27	
4	4	24.08%	21544.51	11.02	
4	4	13.30%	25604.91	9.88	
3	3	20.87%	12783.92	9.65	
3	3	26.19%	13921.97	10.31	
3	3	8.68%	29464.3	4.47	
3	3	27.34%	13906.08	10.88	
3	3	12.39%	23645.79	10.85	
3	3	15.88%	19071.79	11.46	
3	3	9.36%	23557.9	10.86	
5	2	19.67%	13264.67	8.65	
4	2	17.86%	12485.88	8.66	
4	2	17.70%	12338.86	6.76	
4	2	4.18%	25261.86	8.84	
3	2	13.68%	12822.43	7.68	
3	2	10.71%	12390.91	8.7	
3	2	19.35%	13750.22	8.6	
3	2	11.50%	12747.17	8.62	
3	2	10.28%	11663.97	8.66	
3	2	8.33%	22919.41	8.56	
2	2	2.05%	121443.31	5.82	
2	2	8.16%	15886.83	5.52	
2	2	14.55%	12537.52	11.07	
2	2	7.58%	24261.18	11.65	
2	2	11.25%	18564.62	10.49	
2	2	15.38%	13292.81	11.48	
2	2	2.05%	77514.87	8.84	
2	2	13.97%	15797.53	10.56	
2	2	9.68%	24831.02	9.94	
2	2	5.84%	28024.32	11.04	
2	2	28.57%	8217.79	10.1	
2	2	1.58%	90583.42	5.76	

2	2	9.66%	20762.13	10.72
2	2	1.96%	178586.68	6.01
2	2	7.19%	17998.79	9.54
2	2	7.69%	19585.55	10.05
2	2	7.66%	24746.44	5.66
2	2	3.71%	49652.81	5.19
2	2	9.55%	18563.87	10.81
2	2	0.79%	171145.16	7.33
2	2	16.82%	12691.67	10.78
2	2	8.24%	19254.71	10.47
2	2	4.92%	47717.83	11.01
2	2	4.56%	29578.33	10.11
2	2	7.11%	21482.58	10.12
2	2	7.69%	25001.87	6.88
2	2	14.60%	15861.68	9.96
2	2	2.29%	72332.07	5.07
22	1	1.23%	118716.52	9.24
9	1	11.32%	11527.88	11.55
5	1	4.03%	39721.21	8.28
5	1	0.97%	56969.65	6.19
4	1	0.47%	141476.79	9.06
4	1	2.40%	36293.98	4.93
4	1	17.39%	8081.27	8.83
3	1	1.10%	60600.96	9.78
3	1	1.96%	88168.53	5.43
3	1	2.28%	35221.15	9.71
3	1	1.59%	34463.62	9.23
3	1	1.67%	102027.26	9
3	1	0.27%	257457.08	5.59
3	1	2.97%	27478.1	8.9
3	1	51.85%	2967.51	8.9
3	1	4.23%	27746.88	9.06
2	1	0.23%	293881.79	5.06
2	1	16.52%	11664.8	4.42
2	1	1.33%	41860.4	8.75
2	1	2.34%	73451.49	5.62
2	1	3.56%	41919.78	5.88
2	1	2.98%	46144.7	7.95
2	1	38.10%	2110.41	10.29
2	1	1.41%	98193.13	6.65
2	1	7.87%	10886.9	5.43
2	1	2.02%	33544.4	9.18
2	1	2.22%	24128.63	6.83
2	1	0.84%	109128.57	8.81
2	1	7.41%	11645.44	11.3
2	1	28.30%	6159.45	9.25
2	1	1.02%	65815.91	6.57
2	1	0.89%	113382.86	9.3
1	1	6.48%	12045.53	9
1	1	2.33%	33569.55	9.78
1	1	1.63%	84347.09	8.63
1	1	5.31%	23758.52	9.22
1	1	0.63%	147485.55	9.2
1	1	0.57%	204744.31	5.47
1	1	3.67%	37213.36	6.48
1	1	0.42%	187145.88	6.02
1	1	3.47%	36153.66	5.65
1	1	5.38%	10834.38	6.51

1	1	1.38%	88414.5	5.27
1	1	1.52%	51420.37	9.45
1	1	1.14%	59088.51	8.44
1	1	0.28%	331770.08	6.44
1	1	0.62%	105354.77	5.2
1	1	6.06%	14514.8	6.81
1	1	5.94%	11728.41	5.85
1	1	0.60%	111001.43	8.42
1	1	0.56%	142750.06	5.02
1	1	2.63%	46168.14	8.49
1	1	5.03%	17751.86	11.66
1	1	6.85%	16445.12	10.21
1	1	7.69%	15807.36	10.5
1	1	11.65%	11367.2	11.36
1	1	13.04%	7840.94	10.7
1	1	7.41%	15859.62	11.32
1	1	5.45%	11283.74	6.09
1	1	5.10%	17778.75	11.26
1	1	0.48%	316411.56	5.51
1	1	2.05%	69766	6.56
1	1	0.40%	163370.95	5.92
1	1	0.74%	89033.66	6.44
1	1	0.38%	233172.78	7.65
1	1	2.63%	56080.01	10.02
1	1	1.87%	29998.72	5.02
1	1	2.19%	56805.12	8.72
1	1	5.71%	24071.65	9.69
1	1	0.77%	136401.82	7.1
1	1	2.49%	101744.53	6.13
1	1	11.86%	6991.11	10.43
1	1	0.38%	260385.7	6.7
1	1	0.78%	84567.09	9.72
1	1	1.55%	50516.67	9.23
1	1	1.62%	106864.15	8.75
1	1	0.84%	133889.72	5.4
1	1	1.14%	102156.03	8.14
1	1	1.92%	35078.65	7.59
1	1	1.41%	56563.18	7.23
1	1	0.74%	146649.84	9.35
1	1	0.35%	199070.42	4.81
1	1	0.91%	87427.35	4.96
1	1	0.24%	616622.3	5.2
1	1	1.10%	118101.34	6.34
1	1	0.25%	449205.58	4.73
1	1	0.16%	330462.7	5
1	1	2.25%	60190.77	6.61
1	1	1.36%	58581.36	8.75
1	1	3.58%	37381.13	6.92
1	1	7.41%	11874.58	8.69
1	1	2.28%	28630.07	8.32
1	1	0.46%	141541.07	4.31
1	1	0.35%	162503.5	6.6
1	1	1.41%	46089	8.45
1	1	1.11%	70030.14	9.68
1	1	0.26%	212452.68	6.42
1	1	0.44%	332786.41	9.46
1	1	2.76%	33274.97	6.76
1	1	0.94%	70157.18	8.22

1	1	0.49%	295323.24	5.9
1	1	0.36%	186908.33	5.88
1	1	1.00%	136384.3	5.46
1	1	6.98%	19743.38	6.01
1	1	1.21%	74078.4	6.15
1	1	0.35%	160401.07	9.17
1	1	2.12%	30658.3	8.84
1	1	1.43%	71208.71	9.26
1	1	1.44%	80418.68	8.93
1	1	1.65%	60763.52	6.02
1	1	1.18%	76209.61	6.59
1	1	1.52%	65400.75	8.67
1	1	3.68%	50020.19	6.04
1	1	3.02%	43518.25	5.33
1	1	1.42%	62923.59	7.89
1	1	0.57%	98096.36	5.76
1	1	1.12%	90125.31	5.99
1	1	2.91%	42741.37	5.71
1	1	1.26%	127204.27	8.22
1	1	1.43%	81034.72	8.29
1	1	3.57%	37743.83	5.98
1	1	3.35%	22156.51	11.53
1	1	0.21%	990835.86	9.06
1	1	9.47%	10320.49	4.99
1	1	2.05%	37756.86	5.49
1	1	5.92%	16961.11	4.5
1	1	3.47%	19810.93	9.9
1	1	0.37%	214763.56	6.7
1	1	1.15%	97344.42	9.07
1	1	2.65%	62846.78	9.06
1	1	2.90%	35115.57	7.61
1	1	6.98%	15257.45	9.17
1	1	13.64%	4897.63	10.69
1	1	60.00%	1146.4	8.35
1	1	1.80%	47603.45	5.63
1	1	7.46%	21948.02	5.2
1	1	3.85%	21172.33	5.72
1	1	16.67%	10247.95	10.76
1	1	6.45%	17015.9	5.05
1	1	10.00%	6947.78	9.38
1	1	1.01%	79595.6	8.73
1	1	0.31%	211282.69	6.16
1	1	6.48%	11553.69	6.85
1	1	16.82%	11472.74	8.62
1	1	6.25%	11807.96	7.98
1	1	14.81%	11876.14	8.7
1	1	9.35%	11466.52	4.69
1	1	5.43%	14062.89	6.91
1	1	8.94%	13632.33	9.69
1	1	8.80%	13576.17	8.62
1	1	5.69%	13507	7.95
1	1	8.26%	13148.55	7.96
1	1	9.45%	13756.4	7.95
1	1	9.48%	12696.15	8.6
1	1	5.38%	14290.81	4.64
1	1	12.73%	11640.67	8.68
1	1	6.19%	12459.89	8.93
1	1	16.48%	10414.9	5.4

1	1	1.19%	113891.53	9.11
1	1	5.02%	21878.97	11.03
1	1	1.46%	46468.7	6.19
1	1	0.87%	131035.9	7.24
1	1	3.04%	46272.47	8.85
1	1	1.26%	61992.18	9.39
1	1	8.62%	13062.54	4.96
1	1	1.72%	50394.38	9.24
1	1	2.89%	58451.37	5.07
1	1	0.99%	69884.74	6.67
1	1	1.28%	59946.99	9.53
1	1	1.95%	84639.68	5.65
1	1	0.98%	82169	4.98
1	1	1.13%	134142.6	6.37
1	1	1.54%	51589.77	5.91
1	1	3.43%	23223.27	9.61
1	1	1.31%	51073.73	6.3
1	1	2.11%	119064.48	6.47
1	1	3.02%	59619.71	9.12
1	1	0.98%	67633.85	6.85
1	1	9.14%	19037.81	11.39
1	1	4.76%	16943.66	10.7
1	1	0.28%	232814.69	5.45
1	1	0.63%	91916.78	6.83
1	1	5.76%	31449.25	5.31
1	1	7.50%	13955.18	10.66
1	1	4.03%	28388.2	6.15
1	1	0.54%	148738.2	8.26
1	1	1.93%	45714.28	5.3
1	1	1.34%	51832.3	8.72
1	1	3.48%	22453.86	9.05
1	1	2.05%	32934.69	9.19
1	1	1.22%	83538.78	6.07
1	1	0.95%	77241.56	8.95
1	1	4.04%	35507.44	5.24
1	1	1.17%	93857.52	6.12
1	1	3.94%	28291.24	9.33
1	1	5.49%	31371.33	7.77
1	1	21.15%	5953.93	9.52
1	1	9.68%	13720.94	9.33
1	1	1.03%	85814.57	6.1
1	1	1.54%	46723.67	10.53
1	1	7.00%	10783.13	8.08
1	1	12.09%	10126.88	10.23
1	1	3.90%	25370.51	9.73
1	1	1.58%	42597.05	7.83
1	1	13.54%	10644.63	10.3
1	1	4.30%	21366.91	5.25
1	1	9.09%	13079.71	5.55
1	1	4.14%	16020.52	8.11
1	1	7.89%	16713.57	5.9
1	1	2.22%	35366.38	4.91
1	1	1.09%	60132.93	9.45
1	1	0.45%	149112.74	6.15
1	1	2.90%	50372.6	5.24
1	1	1.13%	71322.89	5.72
1	1	7.57%	19741.99	9.69
1	1	9.84%	21600.91	9.92

1	1	7.52%	35729.63	9.11
1	1	17.14%	4049.68	10.02
1	1	10.34%	6668.87	9.03
1	1	1.71%	40146.99	9.44
1	1	1.69%	65039.36	9.13
1	1	6.80%	11474.14	6.47
1	1	9.16%	15495.83	8.93
1	1	5.38%	28517.12	6.1
1	1	20.00%	6206.11	8.11
1	1	5.03%	16871.39	8.52
1	1	0.42%	189559.1	5.44
1	1	5.93%	15387.62	8.93
1	1	1.06%	123109.54	5.45
1	1	4.30%	20503.5	5.09
1	1	9.76%	9767.19	11.42
1	1	1.47%	69086.33	9.01
1	1	2.59%	23134.28	11.48
1	1	5.05%	11282.17	4.29
1	1	10.67%	8346.27	6.43
1	1	4.17%	33036.96	9.58
1	1	14.81%	11940.36	4.39
1	1	13.73%	6101.88	10.74
1	1	6.82%	14245.87	9.4
1	1	7.84%	16372.62	8.77
1	1	1.92%	80181.15	8.4
1	1	4.90%	11658.72	10.94
1	1	1.12%	121087.03	8.5
1	1	1.65%	74523.19	7.92
1	1	7.45%	18546	6.18
1	1	4.84%	33154.65	5.31
1	1	1.45%	55629.4	9.51
1	1	1.21%	57233.19	7.21
1	1	2.12%	84697.37	8.29
1	1	5.61%	11872.89	4.72
1	1	1.37%	48685.07	5.26
1	1	5.77%	24204.9	10.32
1	1	5.23%	33213.64	9.49
1	1	7.87%	20252.15	9.64
1	1	1.12%	61448.61	9.49
1	1	3.11%	34925.93	10.36
1	1	1.96%	64356.38	9.77
1	1	1.83%	49380.71	8.1
1	1	7.92%	10947.5	10.45
1	1	7.83%	12985.28	10.98
1	1	9.26%	11413.69	10.11
1	1	11.48%	6983.14	10.18
1	1	0.98%	139313.01	8.6
1	1	4.30%	20450.19	9.88
1	1	2.23%	42607.44	8.49
1	1	2.20%	57036.04	5
1	1	1.61%	120039.92	5.74
1	1	4.05%	45213.5	8.21
1	1	1.72%	62449.86	7.39
1	1	5.05%	21446.09	12.22
1	1	8.85%	11484.5	5.42