

Table SI. The target genes of *Fructus arctii* active ingredients and keloid formation.

<i>Fructus arctii</i> screening targets	Keloid targets	Target intersection
KCNC2	TKCR	PTGS2
SCN5A	TKC	PTGS1
F10	PDGFRB	PIK3CG
PTGS2	H19	ADRA1A
VEGFC	ASAHI	ADRA1B
PTPN22	FLNA	BAX
ADRB2	TGFB1	CASP9
HSP90AB1	DDR2	JUN
NCOA7	MAP3K7	CASP3
MUC4	SMAD3	CASP8
PAQR6	NEDD4	TGFB1
PNRC2	CD36	NOS2
PTGS1	SERPINH1	PTEN
PIK3CG	BMP6	DPP4
PRKACA	EP300	F2R
DRD1	CREBBP	AKT1
CHRM3	TP53	MAP3K7
CHRM1	EP300-AS1	XDH
GABRA2	LOC126863158	MMP1
CHRM4	HOXA11-AS	CYP3A4
PDE3A	SMAD2	AKR1C3
HTR2A	OCRL	SLPI
GABRA5	NOTCH3	MMP2
ADRA1A	ENSG00000277966	CAV1
GABRA3	ENSG00000278592	CTNNB1
CHRM2	ENSG00000273961	MYC
ADRA1B	ENSG00000276496	GJA1
CHRNA2	ENSG00000278020	MMP10
SLC6A4	ENSG00000278334	ADRA1D
OPRM1	COL17A1	
GABRA1	MIR21	
CHRNA7	STAT3	
FGFR4	FGF2	
Bcl2	SERPINE1	
BAX	CACNA1G-AS1	
CASP9	IL6	
JUN	TGFBR2	
CASP3	SMAD7	
CASP8	BANF1	
C3	VEGFA	
TGFB1	TGFB2	
PON2	MMP1	
MAP4	TGFBR1	
NOS2	GALK1	
AR	TGFB3	
PPARG	SMAD4	
DPP4	MMP2	
PRSS1	AGPAT5	
F2R	FAS	

NOS3	APC	
ACHE	ATP7A	
PTEN	COL7A1	
SLC6A2	LEMD3	
TOP2A	HIF1A	
F7	ELN	
CALML5	POSTN	
RELA	HLA-DRB1	
IKBKB	CCN2	
AKT1	TIMP2	
TNF	IFNG	
AHSA1	MAPK14	
MAP3K7	MAPK8	
XDH	MAPK1	
MMP1	FOXL2	
STAT4	TIMP1	
CDK1	MIR29A	
HMOX1	STK11	
CYP3A4	ITGB4	
CYP1A2	LAMC2	
CYP1A1	LAMB3	
ICAM2	LAMA3	
SELE	AEBP1	
VCAM1	LOC107988032	
NR1I2	DEL16P13.3	
CYP1B1	EGR1	
ALOX5	ITGB1	
HAS2	CTNNB1	
GSTP1	FBLN5	
AHR	DLEU2	
PSMD11	TNC	
SLC2A2	RUNX3	
INSR	TNFAIP6	
DIO1	FBN1	
PPP3CA	PCNA	
GSTM2	TIMP3	
AKR1C3	DCN	
SLPI	RUNX2	
MMP2	PIK3CG	
CYP2B6	SP1	
ALB	TMSB4X	
CAV1	MMP9	
CTNNB1	JUN	
MYC	VDR	
CASP7	AKT1	
F3	HTRA1	
GJA1	HYAL1	
MMP10	DUSP10	
SLC6A3	FOXL2NB	
ADRA1D	GAB1	
	ANXA2	

	CCND1	
	MMP13	
	NR3C1	
	HLA-A	
	HLA-B	
	HLA-C	
	TGFBR3	
	LSS	
	RAB3GAP2	
	FBXW2	
	CHORDC1	
	KRT2	
	CASP6	
	HLA-DQA1	
	HLA-DQB1	
	MIR203A	
	PTGS2	
	PTGS1	
	PTEN	
	CDK11B	
	MIR196B	
	LINC00312	
	CXCL12	
	MIAT	
	COL1A1	
	THBS1	
	EIF3A	
	MIR141	
	TNFRSF1B	
	MYH9	
	IL17A	
	SMAD5	
	EMSLR	
	FOS	
	MIR152	
	SMAD6	
	FOXM1	
	IGFBP5	
	GDF9	
	HDAC2	
	TERT	
	IL10	
	CCDC65	
	BCL2L1	
	HNF1A-AS1	
	MTOR	
	VCAN	
	MDFI	
	CD44	
	AKR1B10	
	ADAM17	

	SFRP2	
	BCL2	
	CCL2	
	COL6A2	
	PAX5	
	CMA1	
	FBXL6	
	FN1	
	HSPA9	
	MET	
	HMGB1	
	CYCS	
	APAF1	
	CASP9	
	EGFR	
	HSPB6	
	MMP14	
	CKLF	
	SOD2-OT1	
	GZMB	
	DDR1	
	COL3A1	
	FASLG	
	RAF1	
	KDR	
	JAK3	
	MIR199A1	
	MMP8	
	UNC5C	
	HOXD3	
	MIR125A	
	MIR193A	
	IGF1R	
	CASP3	
	IFNA2	
	MYC	
	FAP	
	TAGLN	
	POMC	
	TP63	
	LEPR	
	PHGDH	
	MAPK10	
	NME2	
	IL11RA	
	FXR1	
	SFRP1	
	SHC1	
	DYNLL1	
	CBR3	
	RRP1	

	MIR503	
	CXCR2	
	STAT6	
	COL5A1	
	COMP	
	ATF3	
	NOX4	
	PTBP1	
	IL13RA2	
	MIR10B	
	MIR155	
	MIR20A	
	MIR31	
	MIR877	
	MIR372	
	MIR941-1	
	MIR941-2	
	MIR941-4	
	MIR941-3	
	MIR941-5	
	LGALS3	
	PTPN1	
	WNT2	
	HSPA4	
	USP37	
	NEAT1	
	ZNF252P-AS1	
	MIR15A	
	LINC02605	
	CCL15-CCL14	
	S100A15A	
	ENSG00000285090	
	PDGFB	
	IL6R	
	DPP4	
	NR2F2	
	SPARC	
	CYP3A4	
	FOXP3	
	MMP19	
	CASP14	
	TGIF1	
	ADAM12	
	ADIPOQ	
	MYH10	
	PEPD	
	SPHK1	
	WNT10A	
	CXCL8	
	SPHK2	
	USP10	

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	COL14A1	
	CTHRC1	
	HOXA11	
	LUM	
	IL37	
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	MIR769	
	COL6A3	
	LTBP2	
	AKR1C3	
	PLAUR	
	CPOX	
	DKK3	
	HLA-E	
	KLRC1	
	PTGES	
	PTN	
	DLEU1	
	DANCR	
	MIR145	
	MIR148B	
	MIR31HG	
	MIR1224	
	CCND2-AS1	
	LINC00937	
	PWAR1	
	LINC02126	
	ENTPD3-AS1	
	ERBB2	
	CASP8	
	PLAU	
	BAX	
	NFKBIA	
	NRG1	
	COL1A2	
	YAP1	
	CXCR1	
	DGKQ	
	FOXF1	
	PHLPP2	
	CYGB	
	LARP6	
	FAM215A	
	MIR205	
	MIR335	
	MIR181A1	
	NR2F1-AS1	
	LINC01116	
	MIR124-3	
	ADIRF-AS1	

	LINC01655	
	LINC01725	
	LINC02257	
	PWAR6	
	VSIG10L-AS1	
	JAK1	
	HSPB1	
	TLR4	
	IL6ST	
	MYD88	
	PIK3CB	
	PLK4	
	IRF5	
	SOX9	
	UBE2L3	
	RAPGEF3	
	RSPO2	
	KLF10	
	HDGF	
	ZNF217	
	MIR196A2	
	MIR200C	
	MIR196A1	
	MIR133A2	
	LINC-ROR	
	MIR133A1	
	MIR637	
	TMEM92-AS1	
	RF00873	
	G6PD	
	ATF2	
	ZEB2	
	ADRA1A	
	ADRA1B	
	DDIT3	
	ADRA1D	
	APOL1	
	ILK	
	H6PD	
	LTA	
	TM4SF1	
	TMEM88	
	MIR214	
	BDNF-AS	
	MIR2392	
	MIR1587	
	FGFR1	
	PDGFRA	
	MME	
	CAV1	
	MC1R	

	ITGA2	
	S100A4	
	TRAF3IP2	
	IRF3	
	IGFBP2	
	IGFBP4	
	PDGFA	
	SERPINB2	
	FOSB	
	LGALS1	
	ACKR1	
	FERMT2	
	P4HTM	
	DPT	
	GADD45GIP1	
	SNORD95	
	ASPN	
	MECP2	
	IGF1	
	WNT3A	
	HABP2	
	SPP1	
	MT2A	
	MT1X	
	MT1A	
	MT1F	
	SKOR1	
	MT1G	
	MIR661	
	ADAM3A	
	NFKB1	
	SDHA	
	FGF1	
	MIF	
	AGER	
	CD34	
	SATB1	
	HLA-DRB5	
	NLRC5	
	RPL32	
	MIR34A	
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	MIR140	
	MIR320A	
	MIR19A	
	GAPDH	
	THY1	
	MYH8	
	MIR188	
	MYHAS	

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	MIR7-2	
	MIR7-1	
	MIR493HG	
	ENSG00000276919	
	LOX	
	MIR3141	
	PRKN	
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	ITGB1-DT	
	LINC01615	
	COL1A2-AS1	
	ENSG00000228073	
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	TLR7	
	TLR6	
	TGFB1I1	
	TNFSF12	
	TRD-GTC9-1	
	PGR-AS1	
	SNORD15A	
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	HYAL2	
	MRPS22	
	XK	
	TNNI1	
	HHIPL2	
	HYAL3	
	ARMC8	
	PHLDA3	
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	PRR23C	
	PRR23A	
	BPESC1	
	LINC01705	
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	ENSG00000236230	
	RNU6-403P	
	QRSL1P2	
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	HSALNG0009652	
	HSALNG0009654	
	lnc-CSR1-2	
	CM034951-547	
	CM034953-264	

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	HSALNG0010830-002	
	piR-36393-365	
	piR-44198-015	
	LOC124904518	
	piR-50308-462	
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	SLC44A1	
	TBR1	
	FSCN2	
	PELI2	
	NDUFAF6	
	CDKN1B	
	SKP2	
	TAB2	
	IL13	
	JAG1	
	CD19	
	CD4	
	CR2	
	CYP11B1	
	CD2	
	ERAL1	
	TOR1B	
	CD1E	
	LAMTOR5	
	FOLH1	
	BMX	
	NOTCH1	
	NOTCH2	
	PIKFYVE	
	INPPL1	
	LRP2	
	NOTCH4	
	CRYAA	
	CUBN	
	PI4KB	
	SYNJ1	
	APPL1	
	CLCN5	
	RAB5A	
	NAGLU	
	ARHGAP1	
	HEY1	
	INPP5K	
	ATP6V1H	
	CDKN3	
	INPP4A	
	INPP5B	
	INPP5E	
	INPP5J	

	PIP4K2B	
	PHF6	
	PLEK	
	SNX9	
	EOGT	
	INPP5A	
	RAB35	
	RAB8A	
	SACMIL	
	SYNJ2	
	HEY2	
	HEYL	
	HYDIN	
	TAF3	
	HES7	
	MESP2	
	PHETA1	
	CFAP47	
	SNORD108	
	S100A7	
	S100A14	
	CTSK	
	EDN1	
	ACTC1	
	TPSAB1	
	DNM3	
	F13A1	
	KRT14	
	KRT5	
	PIK3CA	
	FOXO1	
	NOS2	
	PLOD1	
	TP73	
	SNAI1	
	GNAI1	
	XDH	
	GNAI2	
	GNAI3	
	NR4A3	
	S100A1	
	RPS6KA3	
	HDAC4	
	DBH	
	SMARCA4	
	CREB1	
	HDAC1	
	KAT5	
	LMNA	
	SMARCA2	
	KAT2A	

	PMS2	
	CP	
	HDAC8	
	KDM6A	
	ATP7B	
	FLNB	
	KAT2B	
	KMT2A	
	SMC1A	
	SMC3	
	ALDH18A1	
	AVPR2	
	CHD7	
	EHMT1	
	KAT6A	
	KDM5C	
	LBR	
	LMNB1	
	EMD	
	FLNC	
	KAT6B	
	PPM1A	
	RAD21	
	ADCY9	
	ARID1B	
	ATP6V0A2	
	EFEMP2	
	MADD	
	NSD1	
	PDE4A	
	SMAD1	
	KMT2D	
	NCOA1	
	NIPBL	
	PAM	
	TAB1	
	ADGRV1	
	FANCE	
	KDM4C	
	LMNB2	
	LTBP4	
	RHBDF2	
	SVIL	
	TRIT1	
	AH11	
	ATOX1	
	CHD8	
	PRRT2	
	RBCK1	
	RIN2	
	SRCAP	

	SYNE1	
	KRT3	
	AP1S1	
	EVL	
	LRRK1	
	MIA2	
	OMD	
	RPL14	
	SNRNP70	
	SYNE2	
	ANKRD11	
	DCBLD2	
	DR1	
	H2BC21	
	H4C3	
	LY86	
	SLC4A8	
	DCTPP1	
	DUSP14	
	GORAB	
	H2AC20	
	PTBP3	
	FHL5	
	H4C11	
	H4C16	
	H4C9	
	NEUROD4	
	RAB40B	
	COX17	
	FAHD2A	
	H4C1	
	H4C2	
	H4C5	
	H4C8	
	FAM53B	
	H4C12	
	H4C4	
	CCDC85C	
	GLYATL1	
	H4C6	
	TAF1L	
	H4C13	
	SLC35E3	
	CLRN2	
	DTD2	
	H4C14	
	H2AC18	
	RFLNB	
	H4C15	
	OR10G2	
	KRTAP10-5	

	STPG3	
	H3-7	
	MIR3187	
	MIR1972-1	
	hsa-miR-1273d-001	
	CYBB	
	AXIN2	
	F2R	
	PLOD3	
	COL6A1	
	PLOD2	
	F2RL1	
	FGF7	
	HBEGF	
	MEP1A	
	MEP1B	
	CAMP	
	FSTL3	
	S100A12	
	FOXF2	
	CDKN2A	
	VIM	
	GJA1	
	BMP1	
	WNT1	
	DES	
	GLUL	
	ABCC9	
	ESR2	
	MUC1	
	MMP7	
	KCNA2	
	MAPKAPK2	
	SFN	
	S100B	
	HOXA5	
	MX1	
	PIK3AP1	
	BRAF	
	KIT	
	NTRK2	
	NT5E	
	PTPRC	
	COL2A1	
	IL2RA	
	GATA4	
	GLI1	
	MMP3	
	NTRK1	
	ENG	
	CFI	

	ERN1	
	BECN1	
	KITLG	
	CDKN1C	
	SOX10	
	MB	
	MKI67	
	MMP10	
	COL11A1	
	SERPINB5	
	EDA	
	MMP24	
	PECAM1	
	MFAP2	
	PRG2	
	SLPI	
	CCL3	
	CALB2	
	CEMIP	
	CEMIP2	
	MIR155HG	
	MIR146B	
	MIR200B	
	MIR98	
	MIR506	
	SLX1A-SULT1A3	
	LOC125146381	
	LOC125146382	

Table SII. Protein-protein interaction network for common genes was initially constructed using the STRING database.

Node1	Node2	Node1 String id	Node2 String id	Phylogenetic cooccurrence	Homology	Coexpression	Experimentally determined interaction	Database annotated	Automated textmining	Combined score
ADRA1 A	ADRA1 B	9606.ENSP00 000369960	9606.ENSP00000 306662	0.063	0.935	0.08	0.541	0.9	0.1	0.957
ADRA1 A	ADRA1 D	9606.ENSP00 000369960	9606.ENSP00000 368766	0	0.929	0.078	0	0.9	0.093	0.909
ADRA1 B	ADRA1 D	9606.ENSP00 000306662	9606.ENSP00000 368766	0	0.93	0.099	0.292	0.9	0.301	0.949
ADRA1 B	ADRA1 A	9606.ENSP00 000306662	9606.ENSP00000 369960	0.063	0.935	0.08	0.541	0.9	0.1	0.957
ADRA1 D	ADRA1 B	9606.ENSP00 000368766	9606.ENSP00000 306662	0	0.93	0.099	0.292	0.9	0.301	0.949
ADRA1 D	ADRA1 A	9606.ENSP00 000368766	9606.ENSP00000 369960	0	0.929	0.078	0	0.9	0.093	0.909
AKR1C3	PTGS1	9606.ENSP00 000369927	9606.ENSP00000 354612	0	0	0.059	0	0	0.432	0.442
AKR1C3	PTGS2	9606.ENSP00 000369927	9606.ENSP00000 356438	0	0	0.047	0	0	0.513	0.516
AKR1C3	CYP3A 4	9606.ENSP00 000369927	9606.ENSP00000 498939	0	0	0.063	0	0.9	0.363	0.935
AKT1	MMP2	9606.ENSP00 000451828	9606.ENSP00000 219070	0	0	0.055	0	0	0.844	0.846
AKT1	TGFB1	9606.ENSP00 000451828	9606.ENSP00000 221930	0	0	0.104	0.126	0	0.845	0.868

AKT1	GJA1	9606.ENSP00 000451828	9606.ENSP00000 282561	0	0	0	0.304	0	0.575	0.692
AKT1	BAX	9606.ENSP00 000451828	9606.ENSP00000 293288	0	0	0.16	0.292	0	0.631	0.761
AKT1	CASP3	9606.ENSP00 000451828	9606.ENSP00000 311032	0	0	0.044	0.311	0	0.923	0.945
AKT1	F2R	9606.ENSP00 000451828	9606.ENSP00000 321326	0	0	0	0.084	0	0.446	0.47
AKT1	MMP1	9606.ENSP00 000451828	9606.ENSP00000 322788	0	0	0.055	0	0	0.571	0.578
AKT1	NOS2	9606.ENSP00 000451828	9606.ENSP00000 327251	0	0	0	0.045	0.9	0.775	0.976
AKT1	CASP9	9606.ENSP00 000451828	9606.ENSP00000 330237	0	0	0.085	0.067	0.9	0.887	0.989
AKT1	CAV1	9606.ENSP00 000451828	9606.ENSP00000 339191	0	0	0.074	0.046	0.5	0.875	0.937
AKT1	CASP8	9606.ENSP00 000451828	9606.ENSP00000 351273	0	0	0.059	0.067	0	0.78	0.79
AKT1	DPP4	9606.ENSP00 000451828	9606.ENSP00000 353731	0	0	0	0	0	0.527	0.527
AKT1	PTGS1	9606.ENSP00 000451828	9606.ENSP00000 354612	0	0	0.061	0	0	0.403	0.415
AKT1	PTGS2	9606.ENSP00 000451828	9606.ENSP00000 356438	0	0	0.078	0	0	0.767	0.775

AKT1	MAP3K 7	9606.ENSP00 000451828	9606.ENSP00000 358335	0	0.595	0	0	0	0.488	0.487
AKT1	JUN	9606.ENSP00 000451828	9606.ENSP00000 360266	0	0	0.049	0.085	0.9	0.915	0.991
AKT1	PTEN	9606.ENSP00 000451828	9606.ENSP00000 361021	0	0	0	0.648	0	0.967	0.988
AKT1	XDH	9606.ENSP00 000451828	9606.ENSP00000 368727	0	0	0	0	0	0.546	0.546
AKT1	PIK3C G	9606.ENSP00 000451828	9606.ENSP00000 419260	0	0	0	0.098	0.9	0.947	0.994
AKT1	CYP3A 4	9606.ENSP00 000451828	9606.ENSP00000 498939	0	0	0.062	0.051	0	0.435	0.453
AKT1	MYC	9606.ENSP00 000451828	9606.ENSP00000 478887	0	0	0	0.169	0	0.918	0.928
AKT1	CTNNB 1	9606.ENSP00 000451828	9606.ENSP00000 495360	0	0	0.074	0.539	0.4	0.93	0.979
BAX	TGFB1	9606.ENSP00 000293288	9606.ENSP00000 221930	0	0	0.109	0	0	0.397	0.44
BAX	CTNNB 1	9606.ENSP00 000293288	9606.ENSP00000 495360	0	0	0.063	0	0	0.397	0.411
BAX	MYC	9606.ENSP00 000293288	9606.ENSP00000 478887	0	0	0.065	0	0	0.4	0.415
BAX	PTEN	9606.ENSP00 000293288	9606.ENSP00000 361021	0	0	0	0.057	0	0.432	0.442

BAX	JUN	9606.ENSP00 000293288	9606.ENSP00000 360266	0	0	0	0	0	0.56	0.56
BAX	PTGS2	9606.ENSP00 000293288	9606.ENSP00000 356438	0	0	0	0	0	0.664	0.664
BAX	AKT1	9606.ENSP00 000293288	9606.ENSP00000 451828	0	0	0.16	0.292	0	0.631	0.761
BAX	CASP8	9606.ENSP00 000293288	9606.ENSP00000 351273	0	0	0.049	0.349	0	0.782	0.853
BAX	CASP9	9606.ENSP00 000293288	9606.ENSP00000 330237	0	0	0.108	0.349	0	0.773	0.856
BAX	CASP3	9606.ENSP00 000293288	9606.ENSP00000 311032	0	0	0.049	0.349	0	0.828	0.884
CASP3	MMP2	9606.ENSP00 000311032	9606.ENSP00000 219070	0	0	0.09	0	0	0.698	0.713
CASP3	TGFB1	9606.ENSP00 000311032	9606.ENSP00000 221930	0	0	0.042	0	0	0.706	0.706
CASP3	GJA1	9606.ENSP00 000311032	9606.ENSP00000 282561	0	0	0	0	0	0.513	0.513
CASP3	BAX	9606.ENSP00 000311032	9606.ENSP00000 293288	0	0	0.049	0.349	0	0.828	0.884
CASP3	MAP3K 7	9606.ENSP00 000311032	9606.ENSP00000 358335	0	0	0.077	0.067	0	0.377	0.417
CASP3	DPP4	9606.ENSP00 000311032	9606.ENSP00000 353731	0	0	0.086	0	0	0.42	0.447

CASP3	CAV1	9606.ENSP00 000311032	9606.ENSP00000 339191	0	0	0.045	0	0	0.484	0.486
CASP3	MMP1	9606.ENSP00 000311032	9606.ENSP00000 322788	0	0	0.114	0	0	0.45	0.492
CASP3	NOS2	9606.ENSP00 000311032	9606.ENSP00000 327251	0	0	0	0	0	0.537	0.537
CASP3	XDH	9606.ENSP00 000311032	9606.ENSP00000 368727	0	0	0.048	0	0	0.54	0.544
CASP3	PTGS1	9606.ENSP00 000311032	9606.ENSP00000 354612	0	0	0.055	0	0	0.54	0.547
CASP3	F2R	9606.ENSP00 000311032	9606.ENSP00000 321326	0	0	0.054	0.071	0	0.525	0.547
CASP3	CYP3A 4	9606.ENSP00 000311032	9606.ENSP00000 498939	0	0	0	0	0	0.565	0.565
CASP3	PTEN	9606.ENSP00 000311032	9606.ENSP00000 361021	0	0	0.044	0	0	0.748	0.748
CASP3	JUN	9606.ENSP00 000311032	9606.ENSP00000 360266	0	0	0	0.046	0	0.808	0.809
CASP3	PTGS2	9606.ENSP00 000311032	9606.ENSP00000 356438	0	0	0.055	0	0	0.863	0.865
CASP3	MYC	9606.ENSP00 000311032	9606.ENSP00000 478887	0	0	0	0	0	0.881	0.881
CASP3	AKT1	9606.ENSP00 000311032	9606.ENSP00000 451828	0	0	0.044	0.311	0	0.923	0.945

CASP3	CTNNB1	9606.ENSP0000311032	9606.ENSP0000495360	0	0	0.088	0.395	0.75	0.782	0.965
CASP3	CASP8	9606.ENSP0000311032	9606.ENSP0000351273	0.088	0.828	0.105	0.786	0.9	0.983	0.999
CASP3	CASP9	9606.ENSP0000311032	9606.ENSP0000330237	0	0.827	0.049	0.846	0.9	0.957	0.999
CASP8	MMP2	9606.ENSP0000351273	9606.ENSP0000219070	0	0	0.063	0	0	0.478	0.49
CASP8	TGFB1	9606.ENSP0000351273	9606.ENSP0000221930	0	0	0.08	0	0	0.48	0.501
CASP8	BAX	9606.ENSP0000351273	9606.ENSP0000293288	0	0	0.049	0.349	0	0.782	0.853
CASP8	CASP3	9606.ENSP0000351273	9606.ENSP0000311032	0.088	0.828	0.105	0.786	0.9	0.983	0.999
CASP8	CASP9	9606.ENSP0000351273	9606.ENSP0000330237	0	0.7	0.104	0.628	0.54	0.678	0.944
CASP8	PTGS1	9606.ENSP0000351273	9606.ENSP0000354612	0	0	0.083	0	0	0.411	0.436
CASP8	PTGS2	9606.ENSP0000351273	9606.ENSP0000356438	0	0	0.098	0	0	0.681	0.7
CASP8	MAP3K7	9606.ENSP0000351273	9606.ENSP0000358335	0	0	0.076	0.067	0	0.73	0.747
CASP8	CTNNB1	9606.ENSP0000351273	9606.ENSP0000495360	0	0	0.094	0	0	0.755	0.768

CASP8	PTEN	9606.ENSP00 000351273	9606.ENSP00000 361021	0	0	0.049	0.174	0	0.744	0.781
CASP8	JUN	9606.ENSP00 000351273	9606.ENSP00000 360266	0	0	0	0	0	0.782	0.782
CASP8	MYC	9606.ENSP00 000351273	9606.ENSP00000 478887	0	0	0.067	0.124	0	0.763	0.79
CASP8	AKT1	9606.ENSP00 000351273	9606.ENSP00000 451828	0	0	0.059	0.067	0	0.78	0.79
CASP9	MMP2	9606.ENSP00 000330237	9606.ENSP00000 219070	0	0	0.074	0	0	0.574	0.589
CASP9	TGFB1	9606.ENSP00 000330237	9606.ENSP00000 221930	0	0	0.06	0	0	0.48	0.49
CASP9	BAX	9606.ENSP00 000330237	9606.ENSP00000 293288	0	0	0.108	0.349	0	0.773	0.856
CASP9	CASP3	9606.ENSP00 000330237	9606.ENSP00000 311032	0	0.827	0.049	0.846	0.9	0.957	0.999
CASP9	PIK3C G	9606.ENSP00 000330237	9606.ENSP00000 419260	0	0	0	0.062	0	0.458	0.47
CASP9	CTNNB 1	9606.ENSP00 000330237	9606.ENSP00000 495360	0	0	0.067	0.045	0	0.609	0.621
CASP9	PTEN	9606.ENSP00 000330237	9606.ENSP00000 361021	0	0	0.059	0	0	0.635	0.642
CASP9	MYC	9606.ENSP00 000330237	9606.ENSP00000 478887	0	0	0	0	0	0.717	0.717

CASP9	PTGS2	9606.ENSP00 000330237	9606.ENSP00000 356438	0	0	0.055	0	0	0.722	0.726
CASP9	JUN	9606.ENSP00 000330237	9606.ENSP00000 360266	0	0	0	0.301	0	0.685	0.77
CASP9	CASP8	9606.ENSP00 000330237	9606.ENSP00000 351273	0	0.7	0.104	0.628	0.54	0.678	0.944
CASP9	AKT1	9606.ENSP00 000330237	9606.ENSP00000 451828	0	0	0.085	0.067	0.9	0.887	0.989
CAV1	MMP2	9606.ENSP00 000339191	9606.ENSP00000 219070	0	0	0.188	0	0	0.635	0.69
CAV1	TGFB1	9606.ENSP00 000339191	9606.ENSP00000 221930	0	0	0.054	0	0	0.688	0.692
CAV1	GJA1	9606.ENSP00 000339191	9606.ENSP00000 282561	0	0	0.165	0.329	0.4	0.908	0.965
CAV1	CASP3	9606.ENSP00 000339191	9606.ENSP00000 311032	0	0	0.045	0	0	0.484	0.486
CAV1	F2R	9606.ENSP00 000339191	9606.ENSP00000 321326	0	0	0.086	0.51	0	0.302	0.66
CAV1	NOS2	9606.ENSP00 000339191	9606.ENSP00000 327251	0	0	0	0.294	0	0.257	0.453
CAV1	JUN	9606.ENSP00 000339191	9606.ENSP00000 360266	0	0	0.045	0	0	0.448	0.451
CAV1	MYC	9606.ENSP00 000339191	9606.ENSP00000 478887	0	0	0.072	0.161	0	0.479	0.558

CAV1	PTGS2	9606.ENSP00 000339191	9606.ENSP00000 356438	0	0	0.061	0.625	0	0.547	0.826
CAV1	PTEN	9606.ENSP00 000339191	9606.ENSP00000 361021	0	0	0	0.345	0	0.872	0.912
CAV1	AKT1	9606.ENSP00 000339191	9606.ENSP00000 451828	0	0	0.074	0.046	0.5	0.875	0.937
CAV1	CTNNB 1	9606.ENSP00 000339191	9606.ENSP00000 495360	0	0	0.043	0.514	0	0.886	0.942
CAV1	DPP4	9606.ENSP00 000339191	9606.ENSP00000 353731	0	0	0.058	0	0	0.991	0.991
CTNNB 1	MMP2	9606.ENSP00 000495360	9606.ENSP00000 219070	0	0	0.056	0.049	0	0.798	0.803
CTNNB 1	TGFB1	9606.ENSP00 000495360	9606.ENSP00000 221930	0	0	0.048	0.051	0	0.785	0.789
CTNNB 1	GJA1	9606.ENSP00 000495360	9606.ENSP00000 282561	0	0	0.062	0.126	0	0.855	0.87
CTNNB 1	BAX	9606.ENSP00 000495360	9606.ENSP00000 293288	0	0	0.063	0	0	0.397	0.411
CTNNB 1	CASP3	9606.ENSP00 000495360	9606.ENSP00000 311032	0	0	0.088	0.395	0.75	0.782	0.965
CTNNB 1	MMP1	9606.ENSP00 000495360	9606.ENSP00000 322788	0	0	0.051	0.049	0	0.477	0.486
CTNNB 1	CASP9	9606.ENSP00 000495360	9606.ENSP00000 330237	0	0	0.067	0.045	0	0.609	0.621

CTNNB1	CAV1	9606.ENSP0000495360	9606.ENSP0000339191	0	0	0.043	0.514	0	0.886	0.942
CTNNB1	CASP8	9606.ENSP0000495360	9606.ENSP0000351273	0	0	0.094	0	0	0.755	0.768
CTNNB1	PTGS2	9606.ENSP0000495360	9606.ENSP0000356438	0	0	0.104	0.292	0	0.664	0.768
CTNNB1	MAP3K7	9606.ENSP0000495360	9606.ENSP0000358335	0	0	0.056	0.098	0	0.369	0.416
CTNNB1	JUN	9606.ENSP0000495360	9606.ENSP0000360266	0	0	0.045	0.095	0	0.891	0.898
CTNNB1	PTEN	9606.ENSP0000495360	9606.ENSP0000361021	0	0	0.069	0.527	0	0.881	0.943
CTNNB1	PIK3CG	9606.ENSP0000495360	9606.ENSP0000419260	0	0	0	0	0	0.4	0.4
CTNNB1	AKT1	9606.ENSP0000495360	9606.ENSP0000451828	0	0	0.074	0.539	0.4	0.93	0.979
CTNNB1	MYC	9606.ENSP0000495360	9606.ENSP0000478887	0	0	0.058	0.567	0.5	0.937	0.985
CYP3A4	CASP3	9606.ENSP0000498939	9606.ENSP0000311032	0	0	0	0	0	0.565	0.565
CYP3A4	NOS2	9606.ENSP0000498939	9606.ENSP0000327251	0	0	0.045	0.045	0	0.194	0.416
CYP3A4	DPP4	9606.ENSP0000498939	9606.ENSP0000353731	0	0	0.056	0	0	0.451	0.46

CYP3A4	PTGS2	9606.ENSP00 000498939	9606.ENSP00000 356438	0	0	0.056	0	0	0.396	0.406
CYP3A4	XDH	9606.ENSP00 000498939	9606.ENSP00000 368727	0	0	0.097	0	0.116	0.37	0.453
CYP3A4	AKRIC 3	9606.ENSP00 000498939	9606.ENSP00000 369927	0	0	0.063	0	0.9	0.363	0.935
CYP3A4	AKT1	9606.ENSP00 000498939	9606.ENSP00000 451828	0	0	0.062	0.051	0	0.435	0.453
DPP4	TGFB1	9606.ENSP00 000353731	9606.ENSP00000 221930	0	0	0.042	0	0	0.475	0.475
DPP4	MMP10	9606.ENSP00 000353731	9606.ENSP00000 279441	0	0	0.074	0	0	0.446	0.465
DPP4	CASP3	9606.ENSP00 000353731	9606.ENSP00000 311032	0	0	0.086	0	0	0.42	0.447
DPP4	MMP1	9606.ENSP00 000353731	9606.ENSP00000 322788	0	0	0.097	0	0	0.508	0.536
DPP4	CAV1	9606.ENSP00 000353731	9606.ENSP00000 339191	0	0	0.058	0	0	0.991	0.991
DPP4	CYP3A 4	9606.ENSP00 000353731	9606.ENSP00000 498939	0	0	0.056	0	0	0.451	0.46
DPP4	AKT1	9606.ENSP00 000353731	9606.ENSP00000 451828	0	0	0	0	0	0.527	0.527
F2R	MMP2	9606.ENSP00 000321326	9606.ENSP00000 219070	0	0	0.093	0.05	0	0.375	0.415

F2R	CASP3	9606.ENSP00 000321326	9606.ENSP00000 311032	0	0	0.054	0.071	0	0.525	0.547
F2R	PTGS1	9606.ENSP00 000321326	9606.ENSP00000 354612	0	0	0.063	0.046	0	0.448	0.464
F2R	AKT1	9606.ENSP00 000321326	9606.ENSP00000 451828	0	0	0	0.084	0	0.446	0.47
F2R	CAV1	9606.ENSP00 000321326	9606.ENSP00000 339191	0	0	0.086	0.51	0	0.302	0.66
F2R	PIK3C G	9606.ENSP00 000321326	9606.ENSP00000 419260	0	0	0.05	0	0.65	0.212	0.715
F2R	MMP1	9606.ENSP00 000321326	9606.ENSP00000 322788	0	0	0.083	0.398	0	0.828	0.897
GJA1	MMP2	9606.ENSP00 000282561	9606.ENSP00000 219070	0	0	0.172	0	0	0.418	0.498
GJA1	TGFB1	9606.ENSP00 000282561	9606.ENSP00000 221930	0	0	0	0	0	0.52	0.52
GJA1	JUN	9606.ENSP00 000282561	9606.ENSP00000 360266	0	0	0.044	0	0	0.419	0.42
GJA1	PTGS2	9606.ENSP00 000282561	9606.ENSP00000 356438	0	0	0.06	0	0	0.459	0.47
GJA1	CASP3	9606.ENSP00 000282561	9606.ENSP00000 311032	0	0	0	0	0	0.513	0.513
GJA1	AKT1	9606.ENSP00 000282561	9606.ENSP00000 451828	0	0	0	0.304	0	0.575	0.692

GJA1	CTNNB1	9606.ENSP0000282561	9606.ENSP0000495360	0	0	0.062	0.126	0	0.855	0.87
GJA1	CAV1	9606.ENSP0000282561	9606.ENSP0000339191	0	0	0.165	0.329	0.4	0.908	0.965
JUN	MMP2	9606.ENSP0000360266	9606.ENSP0000219070	0	0	0	0	0	0.633	0.633
JUN	TGFB1	9606.ENSP0000360266	9606.ENSP0000221930	0	0	0.103	0	0	0.703	0.722
JUN	GJA1	9606.ENSP0000360266	9606.ENSP0000282561	0	0	0.044	0	0	0.419	0.42
JUN	BAX	9606.ENSP0000360266	9606.ENSP0000293288	0	0	0	0	0	0.56	0.56
JUN	CASP3	9606.ENSP0000360266	9606.ENSP0000311032	0	0	0	0.046	0	0.808	0.809
JUN	MMP1	9606.ENSP0000360266	9606.ENSP0000322788	0	0	0	0.608	0	0.614	0.842
JUN	NOS2	9606.ENSP0000360266	9606.ENSP0000327251	0	0	0	0	0	0.534	0.534
JUN	CASP9	9606.ENSP0000360266	9606.ENSP0000330237	0	0	0	0.301	0	0.685	0.77
JUN	CAV1	9606.ENSP0000360266	9606.ENSP0000339191	0	0	0.045	0	0	0.448	0.451
JUN	CASP8	9606.ENSP0000360266	9606.ENSP0000351273	0	0	0	0	0	0.782	0.782

JUN	PTGS2	9606.ENSP00 000360266	9606.ENSP00000 356438	0	0	0.166	0	0	0.846	0.866
JUN	MAP3K 7	9606.ENSP00 000360266	9606.ENSP00000 358335	0	0	0	0.085	0	0.741	0.753
JUN	XDH	9606.ENSP00 000360266	9606.ENSP00000 368727	0	0	0	0	0	0.466	0.466
JUN	PIK3C G	9606.ENSP00 000360266	9606.ENSP00000 419260	0	0	0	0	0	0.596	0.596
JUN	PTEN	9606.ENSP00 000360266	9606.ENSP00000 361021	0	0	0	0.077	0	0.766	0.775
JUN	CTNNB 1	9606.ENSP00 000360266	9606.ENSP00000 495360	0	0	0.045	0.095	0	0.891	0.898
JUN	MYC	9606.ENSP00 000360266	9606.ENSP00000 478887	0	0	0.079	0.626	0	0.922	0.97
JUN	AKT1	9606.ENSP00 000360266	9606.ENSP00000 451828	0	0	0.049	0.085	0.9	0.915	0.991
MAP3K 7	TGFB1	9606.ENSP00 000358335	9606.ENSP00000 221930	0	0	0.048	0.126	0	0.452	0.504
MAP3K 7	CASP3	9606.ENSP00 000358335	9606.ENSP00000 311032	0	0	0.077	0.067	0	0.377	0.417
MAP3K 7	CASP8	9606.ENSP00 000358335	9606.ENSP00000 351273	0	0	0.076	0.067	0	0.73	0.747
MAP3K 7	CTNNB 1	9606.ENSP00 000358335	9606.ENSP00000 495360	0	0	0.056	0.098	0	0.369	0.416

MAP3K 7	MYC	9606.ENSP00 000358335	9606.ENSP00000 478887	0	0	0.051	0.132	0	0.352	0.421
MAP3K 7	PTEN	9606.ENSP00 000358335	9606.ENSP00000 361021	0	0	0.061	0.092	0	0.395	0.439
MAP3K 7	AKT1	9606.ENSP00 000358335	9606.ENSP00000 451828	0	0.595	0	0	0	0.488	0.487
MAP3K 7	JUN	9606.ENSP00 000358335	9606.ENSP00000 360266	0	0	0	0.085	0	0.741	0.753
MMP1	MMP2	9606.ENSP00 000322788	9606.ENSP00000 219070	0	0.864	0.181	0	0.9	0.215	0.93
MMP1	TGFB1	9606.ENSP00 000322788	9606.ENSP00000 221930	0	0	0.072	0	0.4	0.691	0.812
MMP1	MMP10	9606.ENSP00 000322788	9606.ENSP00000 279441	0.067	0.946	0.562	0	0.5	0.09	0.789
MMP1	CASP3	9606.ENSP00 000322788	9606.ENSP00000 311032	0	0	0.114	0	0	0.45	0.492
MMP1	F2R	9606.ENSP00 000322788	9606.ENSP00000 321326	0	0	0.083	0.398	0	0.828	0.897
MMP1	MYC	9606.ENSP00 000322788	9606.ENSP00000 478887	0	0	0.069	0	0	0.417	0.434
MMP1	CTNNB 1	9606.ENSP00 000322788	9606.ENSP00000 495360	0	0	0.051	0.049	0	0.477	0.486
MMP1	DPP4	9606.ENSP00 000322788	9606.ENSP00000 353731	0	0	0.097	0	0	0.508	0.536

MMP1	AKT1	9606.ENSP00 000322788	9606.ENSP00000 451828	0	0	0.055	0	0	0.571	0.578
MMP1	PTGS2	9606.ENSP00 000322788	9606.ENSP00000 356438	0	0	0.143	0	0	0.728	0.757
MMP1	JUN	9606.ENSP00 000322788	9606.ENSP00000 360266	0	0	0	0.608	0	0.614	0.842
MMP10	MMP2	9606.ENSP00 000279441	9606.ENSP00000 219070	0.062	0.869	0.068	0	0.5	0.438	0.721
MMP10	TGFB1	9606.ENSP00 000279441	9606.ENSP00000 221930	0	0	0	0	0	0.419	0.418
MMP10	PTGS2	9606.ENSP00 000279441	9606.ENSP00000 356438	0	0	0.164	0	0	0.36	0.442
MMP10	DPP4	9606.ENSP00 000279441	9606.ENSP00000 353731	0	0	0.074	0	0	0.446	0.465
MMP10	MMP1	9606.ENSP00 000279441	9606.ENSP00000 322788	0.067	0.946	0.562	0	0.5	0.09	0.789
MMP2	F2R	9606.ENSP00 000219070	9606.ENSP00000 321326	0	0	0.093	0.05	0	0.375	0.415
MMP2	CASP8	9606.ENSP00 000219070	9606.ENSP00000 351273	0	0	0.063	0	0	0.478	0.49
MMP2	GJA1	9606.ENSP00 000219070	9606.ENSP00000 282561	0	0	0.172	0	0	0.418	0.498
MMP2	CASP9	9606.ENSP00 000219070	9606.ENSP00000 330237	0	0	0.074	0	0	0.574	0.589

MMP2	JUN	9606.ENSP00 000219070	9606.ENSP00000 360266	0	0	0	0	0	0.633	0.633
MMP2	MYC	9606.ENSP00 000219070	9606.ENSP00000 478887	0	0	0.074	0	0	0.621	0.634
MMP2	CAV1	9606.ENSP00 000219070	9606.ENSP00000 339191	0	0	0.188	0	0	0.635	0.69
MMP2	CASP3	9606.ENSP00 000219070	9606.ENSP00000 311032	0	0	0.09	0	0	0.698	0.713
MMP2	MMP10	9606.ENSP00 000219070	9606.ENSP00000 279441	0.062	0.869	0.068	0	0.5	0.438	0.721
MMP2	PTEN	9606.ENSP00 000219070	9606.ENSP00000 361021	0	0	0	0	0	0.745	0.745
MMP2	PTGS2	9606.ENSP00 000219070	9606.ENSP00000 356438	0	0	0.079	0	0	0.755	0.764
MMP2	CTNNB 1	9606.ENSP00 000219070	9606.ENSP00000 495360	0	0	0.056	0.049	0	0.798	0.803
MMP2	AKT1	9606.ENSP00 000219070	9606.ENSP00000 451828	0	0	0.055	0	0	0.844	0.846
MMP2	MMP1	9606.ENSP00 000219070	9606.ENSP00000 322788	0	0.864	0.181	0	0.9	0.215	0.93
MMP2	TGFB1	9606.ENSP00 000219070	9606.ENSP00000 221930	0	0	0.07	0.6	0.4	0.85	0.962
MYC	MMP2	9606.ENSP00 000478887	9606.ENSP00000 219070	0	0	0.074	0	0	0.621	0.634

MYC	TGFB1	9606.ENSP00 000478887	9606.ENSP00000 221930	0	0	0.072	0.048	0	0.787	0.796
MYC	BAX	9606.ENSP00 000478887	9606.ENSP00000 293288	0	0	0.065	0	0	0.4	0.415
MYC	CASP3	9606.ENSP00 000478887	9606.ENSP00000 311032	0	0	0	0	0	0.881	0.881
MYC	MMP1	9606.ENSP00 000478887	9606.ENSP00000 322788	0	0	0.069	0	0	0.417	0.434
MYC	CASP9	9606.ENSP00 000478887	9606.ENSP00000 330237	0	0	0	0	0	0.717	0.717
MYC	CAV1	9606.ENSP00 000478887	9606.ENSP00000 339191	0	0	0.072	0.161	0	0.479	0.558
MYC	CASP8	9606.ENSP00 000478887	9606.ENSP00000 351273	0	0	0.067	0.124	0	0.763	0.79
MYC	PTGS2	9606.ENSP00 000478887	9606.ENSP00000 356438	0	0	0.091	0	0	0.699	0.715
MYC	MAP3K 7	9606.ENSP00 000478887	9606.ENSP00000 358335	0	0	0.051	0.132	0	0.352	0.421
MYC	JUN	9606.ENSP00 000478887	9606.ENSP00000 360266	0	0	0.079	0.626	0	0.922	0.97
MYC	PTEN	9606.ENSP00 000478887	9606.ENSP00000 361021	0	0	0.044	0.317	0	0.87	0.908
MYC	PIK3C G	9606.ENSP00 000478887	9606.ENSP00000 419260	0	0	0	0	0	0.419	0.419

MYC	AKT1	9606.ENSP00 000478887	9606.ENSP00000 451828	0	0	0	0.169	0	0.918	0.928
MYC	CTNNB 1	9606.ENSP00 000478887	9606.ENSP00000 495360	0	0	0.058	0.567	0.5	0.937	0.985
NOS2	TGFB1	9606.ENSP00 000327251	9606.ENSP00000 221930	0	0	0.054	0	0	0.488	0.495
NOS2	CASP3	9606.ENSP00 000327251	9606.ENSP00000 311032	0	0	0	0	0	0.537	0.537
NOS2	CYP3A 4	9606.ENSP00 000327251	9606.ENSP00000 498939	0	0	0.045	0.045	0	0.194	0.416
NOS2	CAV1	9606.ENSP00 000327251	9606.ENSP00000 339191	0	0	0	0.294	0	0.257	0.453
NOS2	XDH	9606.ENSP00 000327251	9606.ENSP00000 368727	0	0	0.055	0	0	0.486	0.493
NOS2	JUN	9606.ENSP00 000327251	9606.ENSP00000 360266	0	0	0	0	0	0.534	0.534
NOS2	PTGS2	9606.ENSP00 000327251	9606.ENSP00000 356438	0	0	0	0.095	0	0.902	0.908
NOS2	AKT1	9606.ENSP00 000327251	9606.ENSP00000 451828	0	0	0	0.045	0.9	0.775	0.976
PIK3CG	F2R	9606.ENSP00 000419260	9606.ENSP00000 321326	0	0	0.05	0	0.65	0.212	0.715
PIK3CG	CASP9	9606.ENSP00 000419260	9606.ENSP00000 330237	0	0	0	0.062	0	0.458	0.47

PIK3CG	PTGS1	9606.ENSP00 000419260	9606.ENSP00000 354612	0	0	0.08	0	0	0.4	0.424
PIK3CG	PTGS2	9606.ENSP00 000419260	9606.ENSP00000 356438	0	0	0.059	0	0	0.549	0.557
PIK3CG	JUN	9606.ENSP00 000419260	9606.ENSP00000 360266	0	0	0	0	0	0.596	0.596
PIK3CG	PTEN	9606.ENSP00 000419260	9606.ENSP00000 361021	0	0	0.043	0.134	0	0.818	0.836
PIK3CG	CTNNB 1	9606.ENSP00 000419260	9606.ENSP00000 495360	0	0	0	0	0	0.4	0.4
PIK3CG	MYC	9606.ENSP00 000419260	9606.ENSP00000 478887	0	0	0	0	0	0.419	0.419
PIK3CG	AKT1	9606.ENSP00 000419260	9606.ENSP00000 451828	0	0	0	0.098	0.9	0.947	0.994
PTEN	MMP2	9606.ENSP00 000361021	9606.ENSP00000 219070	0	0	0	0	0	0.745	0.745
PTEN	TGFB1	9606.ENSP00 000361021	9606.ENSP00000 221930	0	0	0.103	0.045	0	0.639	0.664
PTEN	BAX	9606.ENSP00 000361021	9606.ENSP00000 293288	0	0	0	0.057	0	0.432	0.442
PTEN	CASP3	9606.ENSP00 000361021	9606.ENSP00000 311032	0	0	0.044	0	0	0.748	0.748
PTEN	CASP9	9606.ENSP00 000361021	9606.ENSP00000 330237	0	0	0.059	0	0	0.635	0.642

PTEN	CAV1	9606.ENSP00 000361021	9606.ENSP00000 339191	0	0	0	0.345	0	0.872	0.912
PTEN	CASP8	9606.ENSP00 000361021	9606.ENSP00000 351273	0	0	0.049	0.174	0	0.744	0.781
PTEN	PTGS2	9606.ENSP00 000361021	9606.ENSP00000 356438	0	0	0.049	0.057	0	0.674	0.682
PTEN	MAP3K 7	9606.ENSP00 000361021	9606.ENSP00000 358335	0	0	0.061	0.092	0	0.395	0.439
PTEN	JUN	9606.ENSP00 000361021	9606.ENSP00000 360266	0	0	0	0.077	0	0.766	0.775
PTEN	PIK3C G	9606.ENSP00 000361021	9606.ENSP00000 419260	0	0	0.043	0.134	0	0.818	0.836
PTEN	MYC	9606.ENSP00 000361021	9606.ENSP00000 478887	0	0	0.044	0.317	0	0.87	0.908
PTEN	CTNNB 1	9606.ENSP00 000361021	9606.ENSP00000 495360	0	0	0.069	0.527	0	0.881	0.943
PTEN	AKT1	9606.ENSP00 000361021	9606.ENSP00000 451828	0	0	0	0.648	0	0.967	0.988
PTGS1	CASP3	9606.ENSP00 000354612	9606.ENSP00000 311032	0	0	0.055	0	0	0.54	0.547
PTGS1	F2R	9606.ENSP00 000354612	9606.ENSP00000 321326	0	0	0.063	0.046	0	0.448	0.464
PTGS1	CASP8	9606.ENSP00 000354612	9606.ENSP00000 351273	0	0	0.083	0	0	0.411	0.436

PTGS1	AKT1	9606.ENSP00 000354612	9606.ENSP00000 451828	0	0	0.061	0	0	0.403	0.415
PTGS1	PIK3C G	9606.ENSP00 000354612	9606.ENSP00000 419260	0	0	0.08	0	0	0.4	0.424
PTGS1	AKR1C 3	9606.ENSP00 000354612	9606.ENSP00000 369927	0	0	0.059	0	0	0.432	0.442
PTGS1	PTGS2	9606.ENSP00 000354612	9606.ENSP00000 356438	0.057	0.966	0.157	0.292	0.9	0.192	0.946
PTGS2	MMP2	9606.ENSP00 000356438	9606.ENSP00000 219070	0	0	0.079	0	0	0.755	0.764
PTGS2	TGFB1	9606.ENSP00 000356438	9606.ENSP00000 221930	0	0	0.084	0	0	0.673	0.688
PTGS2	MMP10	9606.ENSP00 000356438	9606.ENSP00000 279441	0	0	0.164	0	0	0.36	0.442
PTGS2	GJA1	9606.ENSP00 000356438	9606.ENSP00000 282561	0	0	0.06	0	0	0.459	0.47
PTGS2	BAX	9606.ENSP00 000356438	9606.ENSP00000 293288	0	0	0	0	0	0.664	0.664
PTGS2	CASP3	9606.ENSP00 000356438	9606.ENSP00000 311032	0	0	0.055	0	0	0.863	0.865
PTGS2	MMP1	9606.ENSP00 000356438	9606.ENSP00000 322788	0	0	0.143	0	0	0.728	0.757
PTGS2	NOS2	9606.ENSP00 000356438	9606.ENSP00000 327251	0	0	0	0.095	0	0.902	0.908

PTGS2	CASP9	9606.ENSP00 000356438	9606.ENSP00000 330237	0	0	0.055	0	0	0.722	0.726
PTGS2	CAV1	9606.ENSP00 000356438	9606.ENSP00000 339191	0	0	0.061	0.625	0	0.547	0.826
PTGS2	CASP8	9606.ENSP00 000356438	9606.ENSP00000 351273	0	0	0.098	0	0	0.681	0.7
PTGS2	PTGS1	9606.ENSP00 000356438	9606.ENSP00000 354612	0.057	0.966	0.157	0.292	0.9	0.192	0.946
PTGS2	CYP3A 4	9606.ENSP00 000356438	9606.ENSP00000 498939	0	0	0.056	0	0	0.396	0.406
PTGS2	AKR1C 3	9606.ENSP00 000356438	9606.ENSP00000 369927	0	0	0.047	0	0	0.513	0.516
PTGS2	PIK3C G	9606.ENSP00 000356438	9606.ENSP00000 419260	0	0	0.059	0	0	0.549	0.557
PTGS2	PTEN	9606.ENSP00 000356438	9606.ENSP00000 361021	0	0	0.049	0.057	0	0.674	0.682
PTGS2	XDH	9606.ENSP00 000356438	9606.ENSP00000 368727	0	0	0.043	0	0	0.704	0.704
PTGS2	MYC	9606.ENSP00 000356438	9606.ENSP00000 478887	0	0	0.091	0	0	0.699	0.715
PTGS2	CTNNB 1	9606.ENSP00 000356438	9606.ENSP00000 495360	0	0	0.104	0.292	0	0.664	0.768
PTGS2	AKT1	9606.ENSP00 000356438	9606.ENSP00000 451828	0	0	0.078	0	0	0.767	0.775

PTGS2	JUN	9606.ENSP00 000356438	9606.ENSP00000 360266	0	0	0.166	0	0	0.846	0.866
TGFB1	MMP2	9606.ENSP00 000221930	9606.ENSP00000 219070	0	0	0.07	0.6	0.4	0.85	0.962
TGFB1	XDH	9606.ENSP00 000221930	9606.ENSP00000 368727	0	0	0	0	0	0.409	0.409
TGFB1	MMP10	9606.ENSP00 000221930	9606.ENSP00000 279441	0	0	0	0	0	0.419	0.418
TGFB1	BAX	9606.ENSP00 000221930	9606.ENSP00000 293288	0	0	0.109	0	0	0.397	0.44
TGFB1	DPP4	9606.ENSP00 000221930	9606.ENSP00000 353731	0	0	0.042	0	0	0.475	0.475
TGFB1	CASP9	9606.ENSP00 000221930	9606.ENSP00000 330237	0	0	0.06	0	0	0.48	0.49
TGFB1	NOS2	9606.ENSP00 000221930	9606.ENSP00000 327251	0	0	0.054	0	0	0.488	0.495
TGFB1	CASP8	9606.ENSP00 000221930	9606.ENSP00000 351273	0	0	0.08	0	0	0.48	0.501
TGFB1	MAP3K 7	9606.ENSP00 000221930	9606.ENSP00000 358335	0	0	0.048	0.126	0	0.452	0.504
TGFB1	GJA1	9606.ENSP00 000221930	9606.ENSP00000 282561	0	0	0	0	0	0.52	0.52
TGFB1	PTEN	9606.ENSP00 000221930	9606.ENSP00000 361021	0	0	0.103	0.045	0	0.639	0.664

TGFB1	PTGS2	9606.ENSP00 000221930	9606.ENSP00000 356438	0	0	0.084	0	0	0.673	0.688
TGFB1	CAV1	9606.ENSP00 000221930	9606.ENSP00000 339191	0	0	0.054	0	0	0.688	0.692
TGFB1	CASP3	9606.ENSP00 000221930	9606.ENSP00000 311032	0	0	0.042	0	0	0.706	0.706
TGFB1	JUN	9606.ENSP00 000221930	9606.ENSP00000 360266	0	0	0.103	0	0	0.703	0.722
TGFB1	CTNNB 1	9606.ENSP00 000221930	9606.ENSP00000 495360	0	0	0.048	0.051	0	0.785	0.789
TGFB1	MYC	9606.ENSP00 000221930	9606.ENSP00000 478887	0	0	0.072	0.048	0	0.787	0.796
TGFB1	MMP1	9606.ENSP00 000221930	9606.ENSP00000 322788	0	0	0.072	0	0.4	0.691	0.812
TGFB1	AKT1	9606.ENSP00 000221930	9606.ENSP00000 451828	0	0	0.104	0.126	0	0.845	0.868
XDH	TGFB1	9606.ENSP00 000368727	9606.ENSP00000 221930	0	0	0	0	0	0.409	0.409
XDH	CASP3	9606.ENSP00 000368727	9606.ENSP00000 311032	0	0	0.048	0	0	0.54	0.544
XDH	NOS2	9606.ENSP00 000368727	9606.ENSP00000 327251	0	0	0.055	0	0	0.486	0.493
XDH	PTGS2	9606.ENSP00 000368727	9606.ENSP00000 356438	0	0	0.043	0	0	0.704	0.704

XDH	JUN	9606.ENSP00 000368727	9606.ENSP00000 360266	0	0	0	0	0	0.466	0.466
XDH	CYP3A 4	9606.ENSP00 000368727	9606.ENSP00000 498939	0	0	0.097	0	0.116	0.37	0.453
XDH	AKT1	9606.ENSP00 000368727	9606.ENSP00000 451828	0	0	0	0	0	0.546	0.546

Table SIII. Outcomes of the Gene Ontology functional enrichment analysis.

Category	Term	Count	%	P-Value	Genes	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:0045907~positive regulation of vasoconstriction	6	20.689655	7.09E-10	CAV1, F2R, ADRA1D, ADRA1B, PTGS2, ADRA1A	31	19414	129.57063	8.00E-07	7.99E-07	7.50E-07
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	7	24.137931	3.11E-09	CASP9, TGFB1, CASP8, MYC, CASP3, CTNNB1, PTGS2	91	19414	51.496021	3.51E-06	1.75E-06	1.65E-06
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	9	31.034483	1.38E-08	CASP9, JUN, TGFB1, CASP8, CASP3, MMP2, BAX, CTNNB1, PTGS2	327	19414	18.425182	1.56E-05	5.18E-06	4.86E-06
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	7	24.137931	4.74E-08	CASP9, CASP8, NOS2, SLPI, CASP3, F2R, PTGS2	143	19414	32.770195	5.35E-05	1.24E-05	1.17E-05
GOTERM_MF_DIRECT	GO:0019899~enzyme binding	9	31.034483	5.33E-08	JUN, TGFB1,	380	18945	15.472323	1.16E-05	1.16E-05	1.09E-05

					SLPI, CAV1, PTEN, CTNNB1, AKT1, CYP3A4, PTGS2						
GOTERM_BP_DIRECT	GO:0009410~response to xenobiotic stimulus	8	27.586207	5.51E-08	JUN, TGFB1, MYC, CASP3, MMP2, CTNNB1, PTGS2, ADRA1A	253	19414	21.168325	6.22E-05	1.24E-05	1.17E-05
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	5	17.241379	1.39E-06	TGFB1, MYC, MMP2, AKT1, PTGS2	58	19414	57.711058	0.00157	2.31E-04	2.16E-04
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	7	24.137931	1.43E-06	JUN, CASP8, MMP2, CAV1, PTEN, PTGS2, PIK3CG	255	19414	18.377011	0.0016147	2.31E-04	2.16E-04
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	8	27.586207	1.91E-06	TGFB1, NOS2, F2R, AKT1, PTGS2, MAP3K7,	428	19414	12.513052	0.002156	2.70E-04	2.53E-04

					PIK3CG, PTGS1						
GOTERM_BP_DIRECT	GO:0000165~MAPK cascade	6	20.689655	2.74E-06	TGFB1, MYC, CAV1, CTNNB1, ADRA1A, MAP3K7	157	19414	25.584011	0.0030932	3.23E-04	3.03E-04
GOTERM_CC_DIRECT	GO:0005901~caveola	5	17.241379	3.09E-06	CAV1, F2R, ADRA1B, PTGS2, ADRA1A	75	20624	47.411494	4.70E-04	4.70E-04	4.27E-04
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	6	20.689655	3.10E-06	DPP4, TGFB1, NOS2, CASP3, MMP2, CAV1	161	19414	24.948383	0.0034989	3.23E-04	3.03E-04
GOTERM_BP_DIRECT	GO:0097190~apoptotic signaling pathway	5	17.241379	3.15E-06	CASP8, CASP3, CAV1, BAX, CTNNB1	71	19414	47.144245	0.003546	3.23E-04	3.03E-04
GOTERM_BP_DIRECT	GO:0010629~negative regulation of gene expression	7	24.137931	4.34E-06	GJA1, TGFB1, NOS2, MYC, CTNNB1, AKT1, XDH	309	19414	15.165495	0.0048918	4.08E-04	3.83E-04
GOTERM_BP_DIRECT	GO:0006919~activation of cysteine-type endopeptidase	5	17.241379	5.33E-06	CASP9, CASP8, F2R,	81	19414	41.323968	0.0060046	4.63E-04	4.34E-04

	activity involved in apoptotic process				BAX, XDH							
GOTERM_MF_DIRECT	GO:0004937~alpha1-adrenergic receptor activity	3	10.344828	6.31E-06	ADRA1D, ADRA1B, ADRA1A	3	18945	653.27586	0.0013691	6.88E-04	6.47E-04	
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	8	27.586207	8.93E-06	DPP4, TGFB1, MYC, F2R, PTEN, AKR1C3, AKT1, ADRA1D	541	19414	9.89942	0.0100353	7.20E-04	6.75E-04	
GOTERM_BP_DIRECT	GO:0007507~heart development	6	20.689655	1.19E-05	GJA1, TGFB1, CASP8, CASP3, MMP2, PTEN	212	19414	18.946649	0.0133043	8.47E-04	7.94E-04	
GOTERM_BP_DIRECT	GO:0001996~positive regulation of heart rate by epinephrine-norepinephrine	3	10.344828	1.20E-05	ADRA1D, ADRA1B, ADRA1A	4	19414	502.08621	0.0134724	8.47E-04	7.94E-04	
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	12	41.37931	1.53E-05	CASP9, DPP4, JUN, TGFB1, CASP8, CAV1, PTEN, BAX, AKT1, ADRA1D, MAP3K7, PIK3CG	1704	18945	4.6005342	0.0033147	0.0011118	0.0010455	

GOTERM_BP_DIRECT	GO:0032025~response to cobalt ion	3	10.344828	3.00E-05	CASP9, CASP8, CASP3	6	19414	334.72414	0.0332832	0.0019894	0.0018659
GOTERM_CC_DIRECT	GO:0008303~caspase complex	3	10.344828	3.72E-05	CASP9, CASP8, CASP3	7	20624	304.78818	0.005634	0.0028249	0.0025647
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	7	24.137931	3.99E-05	JUN, TGFB1, F2R, PTEN, CTNNB1, PTGS2, ADRA1A	457	19414	10.254131	0.0440946	0.0025031	0.0023477
GOTERM_BP_DIRECT	GO:0034614~cellular response to reactive oxygen species	4	13.793103	5.03E-05	JUN, MMP2, AKR1C3, AKT1	50	19414	53.555862	0.0552311	0.0029875	0.0028021
GOTERM_BP_DIRECT	GO:0007568~aging	5	17.241379	5.32E-05	CASP9, TGFB1, MMP2, PTGS2, ADRA1A	145	19414	23.084423	0.0582615	0.0029986	0.0028126
GOTERM_BP_DIRECT	GO:0007204~positive regulation of cytosolic calcium ion concentration	5	17.241379	6.55E-05	F2R, ADRA1D, ADRA1B, ADRA1A, PIK3CG	153	19414	21.877395	0.0713175	0.00352	0.0033016
GOTERM_BP_DIRECT	GO:0019371~cyclooxygenase pathway	3	10.344828	7.18E-05	AKR1C3, PTGS2, PTGS1	9	19414	223.14943	0.077828	0.0036595	0.0034324
GOTERM_BP_DIRECT	GO:0043525~positive regulation of neuron apoptotic process	4	13.793103	7.46E-05	CASP9, CASP3, BAX, CTNNB1	57	19414	46.978826	0.0807953	0.0036595	0.0034324

GOTERM_BP_DIRECT	GO:0034644~cellular response to UV	4	13.793103	7.86E-05	CASP9, MYC, BAX, PTGS2	58	19414	46.168847	0.0849313	0.0036916	0.0034625
GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK cascade	5	17.241379	8.18E-05	F2R, CTNNB1, ADRA1D, ADRA1B, ADRA1A	162	19414	20.661984	0.0882366	0.0036916	0.0034625
GOTERM_BP_DIRECT	GO:0044346~fibroblast apoptotic process	3	10.344828	8.96E-05	CASP9, MYC, CASP3	10	19414	200.83448	0.0962386	0.0038883	0.003647
GOTERM_MF_DIRECT	GO:0097153~cysteine-type endopeptidase activity involved in apoptotic process	3	10.344828	9.41E-05	CASP9, CASP8, CASP3	10	18945	195.98276	0.0202135	0.0041027	0.0038581
GOTERM_MF_DIRECT	GO:0097199~cysteine-type endopeptidase activity involved in apoptotic signaling pathway	3	10.344828	9.41E-05	CASP9, CASP8, CASP3	10	18945	195.98276	0.0202135	0.0041027	0.0038581
GOTERM_BP_DIRECT	GO:0007200~phospholipase C-activating G-protein coupled receptor signaling pathway	4	13.793103	1.32E-04	F2R, ADRA1D, ADRA1B, ADRA1A	69	19414	38.808596	0.1385361	0.0055178	0.0051754
GOTERM_MF_DIRECT	GO:0097200~cysteine-type endopeptidase activity involved in execution phase of apoptosis	3	10.344828	1.38E-04	CASP9, CASP8, CASP3	12	18945	163.31897	0.0294536	0.0050053	0.0047068
GOTERM_BP_DIRECT	GO:0032091~negative regulation of protein binding	4	13.793103	1.76E-04	SLPI, CAV1, BAX, AKT1	76	19414	35.23412	0.1802396	0.0068	0.006378
GOTERM_BP_DIRECT	GO:0021854~hypothalamus development	3	10.344828	1.81E-04	MYC, BAX, CTNNB1	14	19414	143.4532	0.1844629	0.0068	0.006378

GOTERM_BP_DIRECT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling	5	17.241379	1.81E-04	GJA1, CASP8, F2R, CTNNB1, MAP3K7	199	19414	16.820308	0.1846997	0.0068	0.006378
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	7	24.137931	2.07E-04	CASP9, JUN, CASP8, CASP3, PTEN, BAX, ADRA1A	616	19414	7.6073668	0.208081	0.0075182	0.0070517
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	18	62.068966	2.43E-04	TGFB1, NOS2, PTEN, AKRIC3, CYP3A4, PTGS2, ADRA1B, ADRA1A, PIK3CG, PTGS1, CASP9, GJA1, CASP8, CASP3, BAX, AKT1, CTNNB1, MAP3K7	5687	20624	2.2509413	0.0362322	0.009665	0.0087748
GOTERM_CC_DIRECT	GO:0032991~macromolecular complex	7	24.137931	2.65E-04	CASP9, CASP8, MYC, CAV1,	685	20624	7.2674553	0.0394498	0.009665	0.0087748

					CTNNB1, AKT1, PTGS2							
GOTERM_BP_DIRECT	GO:0045987~positive regulation of smooth muscle contraction	3	10.344828	2.69E-04	F2R, PTGS2, ADRA1A	17	19414	118.13793	0.2620954	0.0094885	0.0088996	
GOTERM_BP_DIRECT	GO:0070374~positive regulation of ERK1 and ERK2 cascade	5	17.241379	2.89E-04	JUN, TGFB1, F2R, PTEN, ADRA1A	225	19414	14.876628	0.2784829	0.0097013	0.0090993	
GOTERM_BP_DIRECT	GO:0071880~adenylate cyclase-activating adrenergic receptor signaling pathway	3	10.344828	3.03E-04	ADRA1D, ADRA1B, ADRA1A	18	19414	111.57471	0.2893918	0.0097013	0.0090993	
GOTERM_BP_DIRECT	GO:0006508~proteolysis	6	20.689655	3.08E-04	DPP4, CASP8, MMP1, CASP3, MMP2, MMP10	422	19414	9.5182219	0.2939313	0.0097013	0.0090993	
GOTERM_BP_DIRECT	GO:0033138~positive regulation of peptidyl-serine phosphorylation	4	13.793103	3.10E-04	TGFB1, CAV1, AKT1, PTGS2	92	19414	29.106447	0.2950372	0.0097013	0.0090993	
GOTERM_CC_DIRECT	GO:0045121~membrane raft	5	17.241379	3.18E-04	DPP4, GJA1, CASP8, CASP3, CAV1	245	20624	14.513723	0.0471831	0.009665	0.0087748	
GOTERM_BP_DIRECT	GO:1904019~epithelial cell apoptotic process	3	10.344828	3.38E-04	CASP9, CASP3, BAX	19	19414	105.70236	0.3171585	0.0102997	0.0096606	

GOTERM_BP_DIRECT	GO:0097194~execution phase of apoptosis	3	10.344828	4.55E-04	CASP8, CASP3, AKT1	22	19414	91.288401	0.401903	0.0135113	0.0126729
GOTERM_MF_DIRECT	GO:0008233~peptidase activity	4	13.793103	4.90E-04	CASP9, CASP8, MMP1, CASP3	105	18945	24.8867	0.1008904	0.0152592	0.0143492
GOTERM_BP_DIRECT	GO:0006809~nitric oxide biosynthetic process	3	10.344828	4.98E-04	NOS2, CAV1, AKT1	23	19414	87.31934	0.4301972	0.0144058	0.0135118
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	6	20.689655	7.44E-04	GJA1, TGFB1, MYC, CAV1, CTNNB1, AKT1	512	19414	7.845097	0.5684493	0.0209828	0.0196807
GOTERM_BP_DIRECT	GO:0033137~negative regulation of peptidyl-serine phosphorylation	3	10.344828	7.95E-04	CAV1, PTEN, BAX	29	19414	69.25327	0.5925873	0.0218726	0.0205153
GOTERM_BP_DIRECT	GO:0071456~cellular response to hypoxia	4	13.793103	9.28E-04	TGFB1, MYC, PTEN, PTGS2	134	19414	19.983531	0.6495611	0.0249322	0.023385
GOTERM_BP_DIRECT	GO:0048147~negative regulation of fibroblast proliferation	3	10.344828	0.001030231	MYC, CAV1, BAX	33	19414	60.858934	0.6876809	0.0264114	0.0247724
GOTERM_BP_DIRECT	GO:0046677~response to antibiotic	3	10.344828	0.001030231	CASP9, CASP8, CASP3	33	19414	60.858934	0.6876809	0.0264114	0.0247724
GOTERM_BP_DIRECT	GO:0051604~protein maturation	3	10.344828	0.001158893	CASP9, CASP8, CASP3	35	19414	57.381281	0.7299502	0.0290496	0.0272469

GOTERM_BP_DIRECT	GO:0097193~intrinsic apoptotic signaling pathway	3	10.344828	0.00122597	CASP9, CASP3, BAX	36	19414	55.787356	0.7496686	0.0294233	0.0275974
GOTERM_BP_DIRECT	GO:0034612~response to tumor necrosis factor	3	10.344828	0.00122597	CASP8, CASP3, PTGS2	36	19414	55.787356	0.7496686	0.0294233	0.0275974
GOTERM_BP_DIRECT	GO:0071276~cellular response to cadmium ion	3	10.344828	0.001294871	JUN, AKR1C3, AKT1	37	19414	54.27959	0.7684263	0.0304295	0.0285411
GOTERM_BP_DIRECT	GO:0043524~negative regulation of neuron apoptotic process	4	13.793103	0.001386315	JUN, F2R, BAX, CTNNB1	154	19414	17.388267	0.7911702	0.0319135	0.0299331
GOTERM_MF_DIRECT	GO:0020037~heme binding	4	13.793103	0.001458967	NOS2, CYP3A4, PTGS2, PTGS1	153	18945	17.079108	0.2715433	0.0397569	0.037386
GOTERM_BP_DIRECT	GO:0031295~T cell costimulation	3	10.344828	0.001512468	DPP4, CAV1, AKT1	40	19414	50.208621	0.8189295	0.0341213	0.0320038
GOTERM_BP_DIRECT	GO:0030574~collagen catabolic process	3	10.344828	0.001588615	MMP1, MMP2, MMP10	41	19414	48.98402	0.8338679	0.0344607	0.0323222
GOTERM_BP_DIRECT	GO:0001541~ovarian follicle development	3	10.344828	0.001588615	MYC, MMP2, BAX	41	19414	48.98402	0.8338679	0.0344607	0.0323222
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	16	55.172414	0.001611159	JUN, TGFB1, NOS2, MMP2, CAV1, F2R, PTEN, ADRA1D, ADRA1B,	5333	20624	2.1336506	0.2173688	0.040816	0.0370567

					ADRA1A, PIK3CG, DPP4, GJA1, AKT1, CTNNB1, MAP3K7						
GOTERM_MF_DIRECT	GO:0044877~macromolecular complex binding	5	17.241379	0.001775228	TGFB1, CASP8, MYC, CASP3, CAV1	357	18945	9.1495219	0.319935	0.043	0.0404358
GOTERM_BP_DIRECT	GO:0042127~regulation of cell proliferation	4	13.793103	0.001870818	JUN, TGFB1, NOS2, PTGS1	171	19414	15.659609	0.8792619	0.0398166	0.0373458
GOTERM_BP_DIRECT	GO:0022617~extracellular matrix disassembly	3	10.344828	0.001996233	MMP1, MMP2, MMP10	46	19414	43.65967	0.8952312	0.0409409	0.0384003
GOTERM_BP_DIRECT	GO:0014065~phosphatidylinositol 3-kinase signaling	3	10.344828	0.001996233	PTEN, AKT1, PIK3CG	46	19414	43.65967	0.8952312	0.0409409	0.0384003
GOTERM_BP_DIRECT	GO:0007186~G-protein coupled receptor signaling pathway	7	24.137931	0.002135985	F2R, AKR1C3, AKT1, ADRA1D, ADRA1B, ADRA1A, PIK3CG	961	19414	4.8763142	0.9105528	0.0430248	0.0403549
GOTERM_BP_DIRECT	GO:0097191~extrinsic apoptotic signaling pathway	3	10.344828	0.002543868	TGFB1, CASP8, BAX	52	19414	38.622016	0.9436225	0.049656	0.0465745
GOTERM_MF_DIRECT	GO:0004252~serine-type endopeptidase activity	4	13.793103	0.002624566	DPP4, MMP1,	188	18945	13.899486	0.4346326	0.0572155	0.0538036

					MMP2, MMP10							
GOTERM_BP_DIRECT	GO:1902895~positive regulation of pri-miRNA transcription from RNA polymerase II promoter	3	10.344828	0.002641276	JUN, TGFB1, MYC	53	19414	37.893299	0.9495082	0.049656	0.0465745	
GOTERM_BP_DIRECT	GO:0043491~protein kinase B signaling	3	10.344828	0.002641276	TGFB1, PTEN, AKT1	53	19414	37.893299	0.9495082	0.049656	0.0465745	
GOTERM_BP_DIRECT	GO:1904707~positive regulation of vascular smooth muscle cell proliferation	3	10.344828	0.002641276	GJA1, JUN, MMP2	53	19414	37.893299	0.9495082	0.049656	0.0465745	
GOTERM_BP_DIRECT	GO:0031334~positive regulation of protein complex assembly	3	10.344828	0.002740423	TGFB1, MMP1, BAX	54	19414	37.191571	0.954869	0.0506754	0.0475306	
GOTERM_BP_DIRECT	GO:0048146~positive regulation of fibroblast proliferation	3	10.344828	0.002841306	JUN, TGFB1, MYC	55	19414	36.515361	0.9597401	0.0516107	0.0484079	
GOTERM_BP_DIRECT	GO:0071887~leukocyte apoptotic process	2	6.8965517	0.00288251	CASP9, CASP3	2	19414	669.44828	0.9615753	0.0516107	0.0484079	
GOTERM_BP_DIRECT	GO:0042110~T cell activation	3	10.344828	0.002943919	DPP4, CASP8, PIK3CG	56	19414	35.8633	0.9641563	0.0518866	0.0486667	
GOTERM_MF_DIRECT	GO:0004666~prostaglandin-endoperoxide synthase activity	2	6.8965517	0.002953819	PTGS2, PTGS1	2	18945	653.27586	0.4737228	0.0585393	0.0550484	
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	6	20.689655	0.003425765	JUN, TGFB1, MYC, F2R, CTNNB1, AKT1	724	19414	5.5479139	0.9792317	0.0594502	0.0557609	
GOTERM_BP_DIRECT	GO:0007249~I-kappaB kinase/NF-kappaB signaling	3	10.344828	0.00382653	CTNNB1, AKT1, MAP3K7	64	19414	31.380388	0.9868119	0.0653989	0.0613404	

GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	6	20.689655	0.004079633	DPP4, NOS2, BAX, AKT1, PTGS2, XDH	736	18945	5.3256184	0.588148	0.0736	0.069211
GOTERM_BP_DIRECT	GO:0034349~glial cell apoptotic process	2	6.8965517	0.004320759	CASP9, CASP3	3	19414	446.29885	0.9924688	0.0716738	0.067226
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	4	13.793103	0.004320761	GJA1, ADRA1D, ADRA1B, ADRA1A	230	19414	11.642579	0.9924689	0.0716738	0.067226
GOTERM_MF_DIRECT	GO:0097110~scaffold protein binding	3	10.344828	0.004388991	GJA1, CASP8, MAP3K7	67	18945	29.251158	0.6149982	0.0736	0.069211
GOTERM_BP_DIRECT	GO:0009611~response to wounding	3	10.344828	0.004687469	TGFB1, MYC, F2R	71	19414	28.286547	0.9950313	0.0766299	0.0718745
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	4	13.793103	0.005030853	TGFB1, MMP1, MMP2, MMP10	258	20624	11.025929	0.5354191	0.1092414	0.0991797
GOTERM_BP_DIRECT	GO:0042981~regulation of apoptotic process	4	13.793103	0.005035906	CASP9, CASP8, BAX, AKT1	243	19414	11.019725	0.9966537	0.08115	0.0761141
GOTERM_BP_DIRECT	GO:0071260~cellular response to mechanical stimulus	3	10.344828	0.005352138	TGFB1, CASP8, PTGS2	76	19414	26.42559	0.9976628	0.0838502	0.0786467
GOTERM_BP_DIRECT	GO:0030163~protein catabolic process	3	10.344828	0.005352138	CASP3, MMP2, AKT1	76	19414	26.42559	0.9976628	0.0838502	0.0786467

GOTERM_BP_DIRECT	GO:0051402~neuron apoptotic process	3	10.344828	0.005629452	CASP9, CASP3, BAX	78	19414	25.748011	0.998294	0.0869866	0.0815885
GOTERM_BP_DIRECT	GO:0001933~negative regulation of protein phosphorylation	3	10.344828	0.005770544	TGFB1, PTEN, XDH	79	19414	25.422086	0.9985465	0.0879618	0.0825032
GOTERM_CC_DIRECT	GO:0005634~nucleus	16	55.172414	0.005966439	JUN, TGFB1, NOS2, MMP2, PTEN, AKR1C3, ADRA1B, ADRA1A, CASP9, GJA1, MYC, CASP3, BAX, AKT1, CTNNB1, MAP3K7	6033	20624	1.8860863	0.5973208	0.1133623	0.1029211
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	4	13.793103	0.006203429	TGFB1, MMP2, CAV1, F2R	262	19414	10.220584	0.9991111	0.0932996	0.0875097
GOTERM_MF_DIRECT	GO:0005515~protein binding	26	89.655172	0.006234224	PTEN, ADRA1D, ADRA1B, CYP3A4, PTGS2, ADRA1A, PIK3CG, PTGS1,	12648	18945	1.3429137	0.7425838	0.0970758	0.0912869

					CASP9, DPP4, GJA1, CASP8, MYC, CASP3, AKT1, XDH, MAP3K7, JUN, TGFB1, NOS2, MMP2, CAV1, F2R, SLPI, BAX, CTNNB1						
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	5	17.241379	0.006338512	MYC, CASP3, PTEN, CTNNB1, AKT1	522	19414	6.4123398	0.9992375	0.0940769	0.0882388
GOTERM_MF_DIRECT	GO:0019901~protein kinase binding	5	17.241379	0.006901815	CASP9, CAV1, PTEN, CTNNB1, AKT1	522	18945	6.2574316	0.7775129	0.1003064	0.0943248
GOTERM_BP_DIRECT	GO:0016477~cell migration	4	13.793103	0.007088342	TGFB1, MMP2, PTEN, PIK3CG	275	19414	9.7374295	0.9996749	0.1013967	0.0951044
GOTERM_BP_DIRECT	GO:0032310~prostaglandin secretion	2	6.8965517	0.007191258	NOS2, PTGS2	5	19414	267.77931	0.9997108	0.1013967	0.0951044

GOTERM_BP_DIRECT	GO:0002248~connective tissue replacement involved in inflammatory response wound healing	2	6.8965517	0.007191258	TGFB1, F2R	5	19414	267.77931	0.9997108	0.1013967	0.0951044
GOTERM_BP_DIRECT	GO:0010716~negative regulation of extracellular matrix disassembly	2	6.8965517	0.007191258	DPP4, TGFB1	5	19414	267.77931	0.9997108	0.1013967	0.0951044
GOTERM_BP_DIRECT	GO:0007179~transforming growth factor beta receptor signaling pathway	3	10.344828	0.009275495	JUN, TGFB1, MAP3K7	101	19414	19.884602	0.999973	0.1291699	0.121154
GOTERM_CC_DIRECT	GO:0031264~death-inducing signaling complex	2	6.8965517	0.009466243	CASP8, CASP3	7	20624	203.19212	0.7644242	0.1598743	0.1451491
GOTERM_MF_DIRECT	GO:0004197~cysteine-type endopeptidase activity	3	10.344828	0.009535481	CASP9, CASP8, CASP3	100	18945	19.598276	0.8749608	0.1299209	0.1221733
GOTERM_BP_DIRECT	GO:1902512~positive regulation of apoptotic DNA fragmentation	2	6.8965517	0.010053777	CASP3, BAX	7	19414	191.27094	0.9999889	0.1366345	0.1281554
GOTERM_BP_DIRECT	GO:0008635~activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c	2	6.8965517	0.010053777	CASP9, BAX	7	19414	191.27094	0.9999889	0.1366345	0.1281554
GOTERM_MF_DIRECT	GO:0004222~metalloendopeptidase activity	3	10.344828	0.011844467	MMP1, MMP2, MMP10	112	18945	17.498461	0.9246486	0.1518879	0.1428303
GOTERM_CC_DIRECT	GO:0005739~mitochondrion	7	24.137931	0.012088818	CASP9, GJA1, CASP8, MYC, MMP2, BAX, AKT1	1458	20624	3.414408	0.8425579	0.1709582	0.155212
GOTERM_BP_DIRECT	GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity	3	10.344828	0.01248939	PTEN, CTNNB1, AKT1	118	19414	17.019871	0.9999993	0.1677147	0.1573068

GOTERM_BP_DIRECT	GO:0030728~ovulation	2	6.8965517	0.012908336	MYC, PTGS2	9	19414	148.76628	0.9999996	0.1713012	0.1606708
GOTERM_CC_DIRECT	GO:0043005~neuron projection	4	13.793103	0.013265567	CASP8, PTEN, PTGS2, PTGS1	368	20624	7.7301349	0.8686461	0.1709582	0.155212
GOTERM_BP_DIRECT	GO:0006979~response to oxidative stress	3	10.344828	0.013307009	AKT1, PTGS2, PTGS1	122	19414	16.461843	0.9999997	0.1725323	0.1618255
GOTERM_BP_DIRECT	GO:0001764~neuron migration	3	10.344828	0.013307009	GJA1, BAX, CTNNB1	122	19414	16.461843	0.9999997	0.1725323	0.1618255
GOTERM_CC_DIRECT	GO:0005916~fascia adherens	2	6.8965517	0.013496699	GJA1, CTNNB1	10	20624	142.23448	0.8732411	0.1709582	0.155212
GOTERM_BP_DIRECT	GO:0019065~receptor-mediated endocytosis of virus by host cell	2	6.8965517	0.014332637	DPP4, CAV1	10	19414	133.88966	0.9999999	0.1837183	0.1723174
GOTERM_BP_DIRECT	GO:0051897~positive regulation of protein kinase B signaling	3	10.344828	0.014792595	TGFB1, AKR1C3, PIK3CG	129	19414	15.568565	1	0.1874837	0.1758491
GOTERM_CC_DIRECT	GO:0005789~endoplasmic reticulum membrane	6	20.689655	0.015752964	GJA1, CAV1, BAX, CYP3A4, PTGS2, PTGS1	1112	20624	3.8372612	0.9104995	0.1727628	0.1568504
GOTERM_BP_DIRECT	GO:0071492~cellular response to UV-A	2	6.8965517	0.015754956	MMP1, MMP2	11	19414	121.71787	1	0.1974621	0.1852083
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	4	13.793103	0.01591236	DPP4, GJA1, CAV1, PTEN	394	20624	7.2200245	0.9126759	0.1727628	0.1568504
GOTERM_BP_DIRECT	GO:0030193~regulation of blood coagulation	2	6.8965517	0.017175296	CAV1, F2R	12	19414	111.57471	1	0.2083197	0.1953921

GOTERM_BP_DIRECT	GO:0010918~positive regulation of mitochondrial membrane potential	2	6.8965517	0.017175296	MYC, AKT1	12	19414	111.57471	1	0.2083197	0.1953921
GOTERM_BP_DIRECT	GO:0043276~anoikis	2	6.8965517	0.017175296	AKT1, MAP3K7	12	19414	111.57471	1	0.2083197	0.1953921
GOTERM_MF_DIRECT	GO:0046982~protein heterodimerization activity	4	13.793103	0.017349207	CAV1, BAX, ADRA1B, ADRA1A	374	18945	6.9869076	0.9775804	0.2101182	0.1975882
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	4	13.793103	0.019794871	DPP4, GJA1, CAV1, CTNNB1	428	20624	6.6464712	0.9521172	0.200588	0.1821128
GOTERM_BP_DIRECT	GO:0051146~striated muscle cell differentiation	2	6.8965517	0.02001005	CASP3, AKT1	14	19414	95.635468	1	0.2326942	0.2182539
GOTERM_BP_DIRECT	GO:0071498~cellular response to fluid shear stress	2	6.8965517	0.02001005	MMP2, PTGS2	14	19414	95.635468	1	0.2326942	0.2182539
GOTERM_BP_DIRECT	GO:0010524~positive regulation of calcium ion transport into cytosol	2	6.8965517	0.02001005	CAV1, BAX	14	19414	95.635468	1	0.2326942	0.2182539
GOTERM_BP_DIRECT	GO:0007512~adult heart development	2	6.8965517	0.02001005	GJA1, ADRA1A	14	19414	95.635468	1	0.2326942	0.2182539
GOTERM_MF_DIRECT	GO:0016702~oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	2	6.8965517	0.020500835	PTGS2, PTGS1	14	18945	93.325123	0.9888344	0.2352201	0.2211932
GOTERM_BP_DIRECT	GO:0010763~positive regulation of fibroblast migration	2	6.8965517	0.021424468	TGFB1, AKT1	15	19414	89.25977	1	0.2441091	0.2289605
GOTERM_BP_DIRECT	GO:0003376~sphingosine-1-phosphate signaling pathway	2	6.8965517	0.021424468	AKT1, PIK3CG	15	19414	89.25977	1	0.2441091	0.2289605
GOTERM_MF_DIRECT	GO:0005102~receptor binding	4	13.793103	0.021801012	DPP4, GJA1, CAV1, F2R	408	18945	6.4046653	0.9916304	0.237631	0.2234604

GOTERM_CC_DIRECT	GO:0005829~cytosol	14	48.275862	0.022175408	NOS2, PTEN, AKR1C3, ADRA1A, PIK3CG, CASP9, GJA1, CASP8, CASP3, BAX, AKT1, CTNNB1, MAP3K7, XDH	5593	20624	1.7801562	0.9669124	0.2062411	0.1872452
GOTERM_BP_DIRECT	GO:0070848~response to growth factor	2	6.8965517	0.022836918	MYC, AKT1	16	19414	83.681034	1	0.2550499	0.2392224
GOTERM_BP_DIRECT	GO:0060402~calcium ion transport into cytosol	2	6.8965517	0.022836918	BAX, ADRA1A	16	19414	83.681034	1	0.2550499	0.2392224
GOTERM_MF_DIRECT	GO:0005123~death receptor binding	2	6.8965517	0.023396236	CASP8, CASP3	16	18945	81.659483	0.9941266	0.2428752	0.2283918
GOTERM_BP_DIRECT	GO:0051092~positive regulation of NF-kappaB transcription factor activity	3	10.344828	0.023483286	TGFB1, CAV1, MAP3K7	165	19414	12.171787	1	0.2596975	0.2435815
GOTERM_CC_DIRECT	GO:0005576~extracellular region	8	27.586207	0.023768827	DPP4, TGFB1, SLPI, MMP1, MMP2, F2R, PTEN, MMP10	2184	20624	2.6050272	0.974177	0.2062411	0.1872452
GOTERM_BP_DIRECT	GO:0008637~apoptotic mitochondrial changes	2	6.8965517	0.024247402	BAX, AKT1	17	19414	78.758621	1	0.2629911	0.2466707

GOTERM_BP_DIRECT	GO:0032270~positive regulation of cellular protein metabolic process	2	6.8965517	0.024247402	TGFB1, AKT1	17	19414	78.758621	1	0.2629911	0.2466707
GOTERM_CC_DIRECT	GO:0005938~cell cortex	3	10.344828	0.024423287	CAV1, CTNNB1, AKT1	179	20624	11.919091	0.9766796	0.2062411	0.1872452
GOTERM_BP_DIRECT	GO:0019538~protein metabolic process	2	6.8965517	0.025655923	MMP1, MMP2	18	19414	74.383142	1	0.2730177	0.2560752
GOTERM_BP_DIRECT	GO:0033280~response to vitamin D	2	6.8965517	0.025655923	TGFB1, PTGS2	18	19414	74.383142	1	0.2730177	0.2560752
GOTERM_BP_DIRECT	GO:0001516~prostaglandin biosynthetic process	2	6.8965517	0.027062482	PTGS2, PTGS1	19	19414	70.46824	1	0.2852942	0.2675898
GOTERM_CC_DIRECT	GO:0030027~lamellipodium	3	10.344828	0.027808697	DPP4, CTNNB1, AKT1	192	20624	11.112069	0.9862512	0.2224696	0.201979
GOTERM_BP_DIRECT	GO:0019229~regulation of vasoconstriction	2	6.8965517	0.028467084	ADRA1B, ADRA1A	20	19414	66.944828	1	0.291917	0.2738016
GOTERM_BP_DIRECT	GO:0030220~platelet formation	2	6.8965517	0.028467084	CASP9, CASP3	20	19414	66.944828	1	0.291917	0.2738016
GOTERM_BP_DIRECT	GO:0097202~activation of cysteine-type endopeptidase activity	2	6.8965517	0.028467084	CASP9, CASP8	20	19414	66.944828	1	0.291917	0.2738016
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	3	10.344828	0.029314073	MMP1, MMP2, MMP10	186	19414	10.797553	1	0.2978944	0.279408
GOTERM_CC_DIRECT	GO:0045211~postsynaptic membrane	3	10.344828	0.029705955	F2R, CTNNB1, ADRA1A	199	20624	10.721192	0.9897833	0.2257653	0.2049711
GOTERM_BP_DIRECT	GO:0031641~regulation of myelination	2	6.8965517	0.02986973	CTNNB1, AKT1	21	19414	63.756979	1	0.2981686	0.2796653
GOTERM_BP_DIRECT	GO:0044267~cellular protein metabolic process	2	6.8965517	0.02986973	MMP1, MMP2	21	19414	63.756979	1	0.2981686	0.2796653

GOTERM_BP_DIRECT	GO:0008283~cell proliferation	3	10.344828	0.030484361	JUN, MYC, AKT1	190	19414	10.570236	1	0.3016347	0.2829163
GOTERM_BP_DIRECT	GO:0055117~regulation of cardiac muscle contraction	2	6.8965517	0.031270424	ADRA1B, ADRA1A	22	19414	60.858934	1	0.3040779	0.2852078
GOTERM_BP_DIRECT	GO:0060546~negative regulation of necroptotic process	2	6.8965517	0.031270424	CASP8, CAV1	22	19414	60.858934	1	0.3040779	0.2852078
GOTERM_BP_DIRECT	GO:0002053~positive regulation of mesenchymal cell proliferation	2	6.8965517	0.032669167	MYC, CTNNB1	23	19414	58.212894	1	0.3149643	0.2954186
GOTERM_BP_DIRECT	GO:0051247~positive regulation of protein metabolic process	2	6.8965517	0.034065963	TGFB1, AKT1	24	19414	55.787356	1	0.3256475	0.3054389
GOTERM_BP_DIRECT	GO:0045216~cell-cell junction organization	2	6.8965517	0.035460813	GJA1, TGFB1	25	19414	53.555862	1	0.3361328	0.3152734
GOTERM_BP_DIRECT	GO:0001782~B cell homeostasis	2	6.8965517	0.036853721	CASP3, BAX	26	19414	51.496021	1	0.346425	0.324927
GOTERM_BP_DIRECT	GO:0001701~in utero embryonic development	3	10.344828	0.037886696	GJA1, MYC, CTNNB1	214	19414	9.3847889	1	0.3531917	0.3312738
GOTERM_BP_DIRECT	GO:0046716~muscle cell cellular homeostasis	2	6.8965517	0.03824469	TGFB1, CAV1	27	19414	49.588761	1	0.3536066	0.331663
GOTERM_BP_DIRECT	GO:0032967~positive regulation of collagen biosynthetic process	2	6.8965517	0.039633721	TGFB1, F2R	28	19414	47.817734	1	0.360539	0.3381651
GOTERM_BP_DIRECT	GO:0010332~response to gamma radiation	2	6.8965517	0.039633721	MYC, BAX	28	19414	47.817734	1	0.360539	0.3381651
GOTERM_CC_DIRECT	GO:0030054~cell junction	3	10.344828	0.0408625	DPP4, GJA1, CTNNB1	237	20624	9.0021825	0.9982385	0.2902103	0.2634804
GOTERM_BP_DIRECT	GO:0071549~cellular response to dexamethasone stimulus	2	6.8965517	0.041020818	CASP9, TGFB1	29	19414	46.168847	1	0.3701719	0.3472002
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	6	20.689655	0.04200412	GJA1, CAV1, F2R, ADRA1D,	1438	20624	2.9673397	0.9985301	0.2902103	0.2634804

					ADRA1B, ADRA1A						
GOTERM_BP_DIRECT	GO:0048873~homeostasis of number of cells within a tissue	2	6.8965517	0.042405982	F2R, BAX	30	19414	44.629885	1	0.3737027	0.3505119
GOTERM_BP_DIRECT	GO:0010575~positive regulation of vascular endothelial growth factor production	2	6.8965517	0.042405982	TGFB1, PTGS2	30	19414	44.629885	1	0.3737027	0.3505119
GOTERM_BP_DIRECT	GO:0043085~positive regulation of catalytic activity	2	6.8965517	0.042405982	CAV1, PIK3CG	30	19414	44.629885	1	0.3737027	0.3505119
GOTERM_MF_DIRECT	GO:0016491~oxidoreductase activity	3	10.344828	0.043705223	NOS2, CYP3A4, XDH	226	18945	8.6718035	0.9999386	0.433079	0.4072532
GOTERM_BP_DIRECT	GO:0045736~negative regulation of cyclin-dependent protein serine/threonine kinase activity	2	6.8965517	0.043789218	CASP3, PTEN	31	19414	43.190211	1	0.3770552	0.3536564
GOTERM_BP_DIRECT	GO:0051281~positive regulation of release of sequestered calcium ion into cytosol	2	6.8965517	0.043789218	F2R, BAX	31	19414	43.190211	1	0.3770552	0.3536564
GOTERM_BP_DIRECT	GO:0070269~pyroptosis	2	6.8965517	0.043789218	CASP8, CASP3	31	19414	43.190211	1	0.3770552	0.3536564
GOTERM_BP_DIRECT	GO:0060325~face morphogenesis	2	6.8965517	0.045170526	TGFB1, MMP2	32	19414	41.840517	1	0.3832723	0.3594876
GOTERM_BP_DIRECT	GO:2000379~positive regulation of reactive oxygen species metabolic process	2	6.8965517	0.04654991	AKR1C3, XDH	33	19414	40.572623	1	0.3832723	0.3594876
GOTERM_BP_DIRECT	GO:0032570~response to progesterone	2	6.8965517	0.04654991	TGFB1, CAV1	33	19414	40.572623	1	0.3832723	0.3594876
GOTERM_BP_DIRECT	GO:2001234~negative regulation of apoptotic signaling pathway	2	6.8965517	0.04654991	BAX, CTNNB1	33	19414	40.572623	1	0.3832723	0.3594876
GOTERM_BP_DIRECT	GO:0097421~liver regeneration	2	6.8965517	0.04654991	TGFB1, MYC	33	19414	40.572623	1	0.3832723	0.3594876
GOTERM_BP_DIRECT	GO:0035633~maintenance of permeability of blood-brain barrier	2	6.8965517	0.04654991	GJA1, PTGS2	33	19414	40.572623	1	0.3832723	0.3594876

GOTERM_BP_DIRECT	GO:0051973~positive regulation of telomerase activity	2	6.8965517	0.047927373	MYC, CTNNB1	34	19414	39.37931	1	0.3917542	0.3674432
GOTERM_BP_DIRECT	GO:0043542~endothelial cell migration	2	6.8965517	0.049302917	DPP4, PTEN	35	19414	38.254187	1	0.4000985	0.3752697
GOTERM_BP_DIRECT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	5	17.241379	0.051649677	JUN, TGFB1, MYC, CAV1, CTNNB1	988	19414	3.3878961	1	0.4077113	0.3824101
GOTERM_BP_DIRECT	GO:0010975~regulation of neuron projection development	2	6.8965517	0.052048257	PTEN, AKT1	37	19414	36.186393	1	0.4077113	0.3824101
GOTERM_BP_DIRECT	GO:0045765~regulation of angiogenesis	2	6.8965517	0.052048257	CTNNB1, PIK3CG	37	19414	36.186393	1	0.4077113	0.3824101
GOTERM_BP_DIRECT	GO:2001244~positive regulation of intrinsic apoptotic signaling pathway	2	6.8965517	0.052048257	CAV1, BAX	37	19414	36.186393	1	0.4077113	0.3824101
GOTERM_BP_DIRECT	GO:0043029~T cell homeostasis	2	6.8965517	0.052048257	TGFB1, CASP3	37	19414	36.186393	1	0.4077113	0.3824101
GOTERM_MF_DIRECT	GO:0004601~peroxidase activity	2	6.8965517	0.053303918	PTGS2, PTGS1	37	18945	35.312209	0.9999931	0.4841773	0.4553043
GOTERM_MF_DIRECT	GO:0001221~transcription cofactor binding	2	6.8965517	0.053303918	MYC, CTNNB1	37	18945	35.312209	0.9999931	0.4841773	0.4553043
GOTERM_BP_DIRECT	GO:1900182~positive regulation of protein localization to nucleus	2	6.8965517	0.053418058	TGFB1, AKT1	38	19414	35.23412	1	0.4155557	0.3897676
GOTERM_BP_DIRECT	GO:2000648~positive regulation of stem cell proliferation	2	6.8965517	0.054785951	GJA1, CTNNB1	39	19414	34.330681	1	0.4203983	0.3943098
GOTERM_BP_DIRECT	GO:0001937~negative regulation of endothelial cell proliferation	2	6.8965517	0.054785951	CAV1, XDH	39	19414	34.330681	1	0.4203983	0.3943098
GOTERM_BP_DIRECT	GO:0035094~response to nicotine	2	6.8965517	0.056151938	CASP3, MMP2	40	19414	33.472414	1	0.4237618	0.3974645
GOTERM_BP_DIRECT	GO:0008625~extrinsic apoptotic signaling pathway via death domain receptors	2	6.8965517	0.056151938	CASP8, BAX	40	19414	33.472414	1	0.4237618	0.3974645

GOTERM_BP_DIRECT	GO:0051726~regulation of cell cycle	3	10.344828	0.056351303	JUN, PTEN, BAX	267	19414	7.5218907	1	0.4237618	0.3974645
GOTERM_BP_DIRECT	GO:0009725~response to hormone	2	6.8965517	0.057516021	NOS2, ADRA1A	41	19414	32.656013	1	0.4268294	0.4003418
GOTERM_BP_DIRECT	GO:0007595~lactation	2	6.8965517	0.057516021	CAV1, XDH	41	19414	32.656013	1	0.4268294	0.4003418
GOTERM_BP_DIRECT	GO:0031663~lipopolysaccharide-mediated signaling pathway	2	6.8965517	0.058878203	TGFB1, AKT1	42	19414	31.878489	1	0.430057	0.4033691
GOTERM_BP_DIRECT	GO:0030316~osteoclast differentiation	2	6.8965517	0.060238487	TGFB1, CTNNB1	43	19414	31.137129	1	0.430057	0.4033691
GOTERM_BP_DIRECT	GO:0042542~response to hydrogen peroxide	2	6.8965517	0.060238487	CASP3, MMP2	43	19414	31.137129	1	0.430057	0.4033691
GOTERM_BP_DIRECT	GO:0007566~embryo implantation	2	6.8965517	0.060238487	MMP2, PTGS2	43	19414	31.137129	1	0.430057	0.4033691
GOTERM_BP_DIRECT	GO:0042098~T cell proliferation	2	6.8965517	0.060238487	GJA1, PIK3CG	43	19414	31.137129	1	0.430057	0.4033691
GOTERM_BP_DIRECT	GO:0042307~positive regulation of protein import into nucleus	2	6.8965517	0.060238487	TGFB1, PTGS2	43	19414	31.137129	1	0.430057	0.4033691
GOTERM_BP_DIRECT	GO:0001658~branching involved in ureteric bud morphogenesis	2	6.8965517	0.061596874	MYC, CTNNB1	44	19414	30.429467	1	0.4315607	0.4047795
GOTERM_BP_DIRECT	GO:0071364~cellular response to epidermal growth factor stimulus	2	6.8965517	0.061596874	MYC, AKT1	44	19414	30.429467	1	0.4315607	0.4047795
GOTERM_BP_DIRECT	GO:0007281~germ cell development	2	6.8965517	0.061596874	BAX, AKT1	44	19414	30.429467	1	0.4315607	0.4047795
GOTERM_MF_DIRECT	GO:0004857~enzyme inhibitor activity	2	6.8965517	0.063075408	CASP3, AKT1	44	18945	29.694357	0.9999993	0.5500176	0.5172183
GOTERM_BP_DIRECT	GO:0045429~positive regulation of nitric oxide biosynthetic process	2	6.8965517	0.064307971	AKT1, PTGS2	46	19414	29.106447	1	0.4450269	0.41741
GOTERM_BP_DIRECT	GO:0071407~cellular response to organic cyclic compound	2	6.8965517	0.064307971	TGFB1, CASP8	46	19414	29.106447	1	0.4450269	0.41741

GOTERM_BP_DIRECT	GO:0006974~cellular response to DNA damage stimulus	3	10.344828	0.065962673	CASP9, MYC, CASP3	292	19414	6.8778932	1	0.4536945	0.4255397
GOTERM_CC_DIRECT	GO:0005794~Golgi apparatus	5	17.241379	0.067013221	GJA1, SLPI, CAV1, F2R, PTGS1	1145	20624	3.1055564	0.9999736	0.44287	0.4020793
GOTERM_BP_DIRECT	GO:0043536~positive regulation of blood vessel endothelial cell migration	2	6.8965517	0.06836046	TGFB1, AKT1	49	19414	27.324419	1	0.467337	0.4383356
GOTERM_BP_DIRECT	GO:0043280~positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	2	6.8965517	0.071052711	MYC, F2R	51	19414	26.252874	1	0.4742453	0.4448152
GOTERM_BP_DIRECT	GO:0008630~intrinsic apoptotic signaling pathway in response to DNA damage	2	6.8965517	0.071052711	CASP9, BAX	51	19414	26.252874	1	0.4742453	0.4448152
GOTERM_BP_DIRECT	GO:0001837~epithelial to mesenchymal transition	2	6.8965517	0.071052711	TGFB1, CTNNB1	51	19414	26.252874	1	0.4742453	0.4448152
GOTERM_BP_DIRECT	GO:0007173~epidermal growth factor receptor signaling pathway	2	6.8965517	0.071052711	TGFB1, AKT1	51	19414	26.252874	1	0.4742453	0.4448152
GOTERM_BP_DIRECT	GO:0051209~release of sequestered calcium ion into cytosol	2	6.8965517	0.073737459	F2R, BAX	53	19414	25.262199	1	0.4864085	0.4562236
GOTERM_BP_DIRECT	GO:0008202~steroid metabolic process	2	6.8965517	0.073737459	AKR1C3, CYP3A4	53	19414	25.262199	1	0.4864085	0.4562236
GOTERM_BP_DIRECT	GO:0045786~negative regulation of cell cycle	2	6.8965517	0.075077026	TGFB1, PTGS2	54	19414	24.794381	1	0.4867062	0.4565028
GOTERM_BP_DIRECT	GO:0042572~retinol metabolic process	2	6.8965517	0.075077026	AKR1C3, CYP3A4	54	19414	24.794381	1	0.4867062	0.4565028
GOTERM_BP_DIRECT	GO:0010718~positive regulation of epithelial to mesenchymal transition	2	6.8965517	0.075077026	TGFB1, CTNNB1	54	19414	24.794381	1	0.4867062	0.4565028

GOTERM_MF_DIRECT	GO:0031625~ubiquitin protein ligase binding	3	10.344828	0.077214191	JUN, CASP8, CTNNB1	312	18945	6.2814987	1	0.6474113	0.6088042
GOTERM_BP_DIRECT	GO:0042475~odontogenesis of dentin-containing tooth	2	6.8965517	0.077750557	BAX, CTNNB1	56	19414	23.908867	1	0.4927114	0.4621353
GOTERM_BP_DIRECT	GO:0042733~embryonic digit morphogenesis	2	6.8965517	0.077750557	GJA1, CTNNB1	56	19414	23.908867	1	0.4927114	0.4621353
GOTERM_BP_DIRECT	GO:0043154~negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	2	6.8965517	0.077750557	AKT1, PTGS2	56	19414	23.908867	1	0.4927114	0.4621353
GOTERM_BP_DIRECT	GO:0002062~chondrocyte differentiation	2	6.8965517	0.077750557	TGFB1, CTNNB1	56	19414	23.908867	1	0.4927114	0.4621353
GOTERM_BP_DIRECT	GO:0031397~negative regulation of protein ubiquitination	2	6.8965517	0.079084527	CAV1, AKT1	57	19414	23.489413	1	0.4955964	0.4648413
GOTERM_BP_DIRECT	GO:0051384~response to glucocorticoid	2	6.8965517	0.079084527	CASP3, PTGS2	57	19414	23.489413	1	0.4955964	0.4648413
GOTERM_CC_DIRECT	GO:0000791~euchromatin	2	6.8965517	0.07964266	JUN, CTNNB1	61	20624	23.317128	0.9999967	0.4854747	0.4407599
GOTERM_CC_DIRECT	GO:0005654~nucleoplasm	10	34.482759	0.079847817	GJA1, JUN, CASP8, NOS2, MYC, CASP3, PTEN, CTNNB1, AKT1, ADRA1A	4031	20624	1.764258	0.9999968	0.4854747	0.4407599
GOTERM_BP_DIRECT	GO:0043627~response to estrogen	2	6.8965517	0.081746886	MMP2, CAV1	59	19414	22.693162	1	0.501144	0.4700446
GOTERM_BP_DIRECT	GO:0002931~response to ischemia	2	6.8965517	0.081746886	CASP9, CAV1	59	19414	22.693162	1	0.501144	0.4700446

GOTERM_BP_DIRECT	GO:0010507~negative regulation of autophagy	2	6.8965517	0.081746886	AKT1, ADRA1A	59	19414	22.693162	1	0.501144	0.4700446
GOTERM_BP_DIRECT	GO:0007188~adenylate cyclase-modulating G-protein coupled receptor signaling pathway	2	6.8965517	0.081746886	ADRA1D, ADRA1B	59	19414	22.693162	1	0.501144	0.4700446
GOTERM_CC_DIRECT	GO:0071944~cell periphery	2	6.8965517	0.083397391	BAX, CTNNB1	64	20624	22.224138	0.9999982	0.487554	0.4426477
GOTERM_BP_DIRECT	GO:0051898~negative regulation of protein kinase B signaling	2	6.8965517	0.084401823	PTEN, XDH	61	19414	21.949124	1	0.514623	0.4826872
GOTERM_BP_DIRECT	GO:0001570~vasculogenesis	2	6.8965517	0.087049358	TGFB1, CAV1	63	19414	21.252326	1	0.5279122	0.4951517
GOTERM_BP_DIRECT	GO:0006006~glucose metabolic process	2	6.8965517	0.088370355	MYC, AKT1	64	19414	20.920259	1	0.5330575	0.4999777
GOTERM_BP_DIRECT	GO:0060395~SMAD protein signal transduction	2	6.8965517	0.089689509	JUN, TGFB1	65	19414	20.598408	1	0.534049	0.5009076
GOTERM_BP_DIRECT	GO:0032757~positive regulation of interleukin-8 production	2	6.8965517	0.089689509	NOS2, F2R	65	19414	20.598408	1	0.534049	0.5009076
GOTERM_BP_DIRECT	GO:0007611~learning or memory	2	6.8965517	0.091006822	CASP3, PTEN	66	19414	20.286311	1	0.534049	0.5009076
GOTERM_BP_DIRECT	GO:0050680~negative regulation of epithelial cell proliferation	2	6.8965517	0.091006822	TGFB1, PTEN	66	19414	20.286311	1	0.534049	0.5009076
GOTERM_BP_DIRECT	GO:0071560~cellular response to transforming growth factor beta stimulus	2	6.8965517	0.092322297	TGFB1, CAV1	67	19414	19.983531	1	0.534049	0.5009076
GOTERM_BP_DIRECT	GO:0030216~keratinocyte differentiation	2	6.8965517	0.092322297	CASP3, AKR1C3	67	19414	19.983531	1	0.534049	0.5009076
GOTERM_BP_DIRECT	GO:0010595~positive regulation of endothelial cell migration	2	6.8965517	0.092322297	AKT1, PIK3CG	67	19414	19.983531	1	0.534049	0.5009076
GOTERM_BP_DIRECT	GO:0071466~cellular response to xenobiotic stimulus	2	6.8965517	0.092322297	NOS2, MYC	67	19414	19.983531	1	0.534049	0.5009076
GOTERM_BP_DIRECT	GO:0009749~response to glucose	2	6.8965517	0.093635936	TGFB1, CASP3	68	19414	19.689655	1	0.5388844	0.505443

GOTERM_CC_DIRECT	GO:0016328~lateral plasma membrane	2	6.8965517	0.095806782	GJA1, CTNNB1	74	20624	19.220876	0.9999998	0.5393567	0.4896791
GOTERM_MF_DIRECT	GO:0050660~flavin adenine dinucleotide binding	2	6.8965517	0.095844749	NOS2, XDH	68	18945	19.213996	1	0.7738576	0.7277101
GOTERM_BP_DIRECT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	5	17.241379	0.096176854	JUN, TGFB1, MYC, CTNNB1, AKT1	1222	19414	2.7391501	1	0.5506979	0.5165234
GOTERM_BP_DIRECT	GO:0050679~positive regulation of epithelial cell proliferation	2	6.8965517	0.098872184	TGFB1, MYC	72	19414	18.595785	1	0.5632718	0.528317

Table SIV. Pathway enrichment analysis revealed significant enrichment of these 28 core targets in 99 pathways.

Category	Term	Count	%	P-Value	Genes	Populations	Fold Enrichment	Bonferroni	Benjamini	False Discovery Rate
KEGG_PATHWAY	hsa05200:Pathways in cancer	15	51.72413793	5.93E-11	JUN, TGF B1, NOS 2, MMP1, MMP2, F2R, PTE N, PTGS2, CASP9, CASP8, MYC, CASP3, BAX, AKT1, CTN NB1	531	8.856455325	1.10E-08	1.10E-08	5.81E-09
KEGG_PATHWAY	hsa05167:Kaposi sarcoma-associated herpesvirus infection	10	34.48275862	3.23E-09	CASP9, JUN, CASP8, MYC, CASP3, BAX, CTN NB1, AKT1, PTGS2,	194	16.16074838	6.01E-07	3.01E-07	1.58E-07

					PIK3 CG					
KEGG_P ATHWA Y	hsa05161:He patitis B	9	31.034 48276	1.76E- 08	CAS P9, JUN, TGF B1, CAS P8, MYC , CAS P3, BAX , AKT 1, MAP 3K7	1 6 2	17.417 69547	3.28E- 06	6.56E- 07	3.46E- 07
KEGG_P ATHWA Y	hsa05132:Sal monella infection	9	31.034 48276	4.95E- 07	JUN, CAS P8, MYC , CAS P3, BAX , CTN NB1, AKT 1, MAP 3K7, PIK3 CG	2 4 9	11.331 99465	9.20E- 05	1.31E- 05	6.92E- 06
KEGG_P ATHWA Y	hsa05210:Co lorectal cancer	8	27.586 2069	4.91E- 09	CAS P9, JUN, TGF B1, MYC , CAS P3, BAX , CTN NB1, AKT 1	8 6	29.164 51335	9.13E- 07	3.04E- 07	1.60E- 07

KEGG_PATHWAY	hsa05222:Small cell lung cancer	8	27.5862069	7.90E-09	CASP9, NOS2, MYC, CASP3, PTEN, BAX, AKT1, PTGS2	92	27.26247987	1.47E-06	3.68E-07	1.94E-07
KEGG_PATHWAY	hsa05145:Toxoplasmosis	8	27.5862069	3.14E-08	CASP9, TGFBI, CASP8, NOS2, CASP3, AKT1, MAP3K7, PIK3CG	112	22.39417989	5.84E-06	9.74E-07	5.13E-07
KEGG_PATHWAY	hsa05169:Epstein-Barr virus infection	8	27.5862069	1.78E-06	CASP9, JUN, CASP8, MYC, CASP3, BAX, AKT1, MAP3K7	202	12.41657499	3.31E-04	3.67E-05	1.94E-05
KEGG_PATHWAY	hsa05417:Lipid and atherosclerosis	8	27.5862069	2.70E-06	CASP9, JUN, CASP8, MM	215	11.66580534	5.02E-04	5.02E-05	2.64E-05

					P1, CAS P3, BAX , AKT 1, MAP 3K7					
KEGG_P ATHWA Y	hsa05163:Hu man cytomegalovi rus infection	8	27.586 2069	3.65E- 06	CAS P9, CAS P8, MYC , CAS P3, BAX , CTN NB1, AKT 1, PTG S2	2 2 5	11.147 3251	6.79E- 04	5.66E- 05	2.98E- 05
KEGG_P ATHWA Y	hsa05162:Me asles	7	24.137 93103	3.09E- 06	CAS P9, JUN, CAS P8, CAS P3, BAX , AKT 1, MAP 3K7	1 3 9	15.788 70237	5.75E- 04	5.23E- 05	2.75E- 05
KEGG_P ATHWA Y	hsa05160:He patitis C	7	24.137 93103	6.27E- 06	CAS P9, CAS P8, MYC , CAS P3, BAX , CTN NB1, AKT 1	1 5 7	13.978 53267	0.0011 6468	8.96E- 05	4.72E- 05

KEGG_PATHWAY	hsa05152:Tuberculosis	7	24.13793103	1.37E-05	CASP9, TGFBI, CASP8, NOS2, CASP3, BAX, AKT1	180	12.19238683	0.002553317	1.60E-04	8.42E-05
KEGG_PATHWAY	hsa05130:Pathogenic Escherichia coli infection	7	24.13793103	2.30E-05	CASP9, JUN, CASP8, CASP3, F2R, BAX, MAP3K7	197	11.14025193	0.004265228	2.37E-04	1.25E-04
KEGG_PATHWAY	hsa05205:Proteoglycans in cancer	7	24.13793103	2.88E-05	TGFBI, MYC, CASP3, MMP2, CAV1, CTNNB1, AKT1	205	10.70551039	0.005340965	2.82E-04	1.49E-04
KEGG_PATHWAY	hsa05170:Human immunodeficiency virus 1 infection	7	24.13793103	3.48E-05	CASP9, JUN, CASP8, CASP3, BAX, AKT1, MAP3K7	212	10.35202655	0.00645205	3.24E-04	1.71E-04

KEGG_PATHWAY	hsa05165:Human papillomavirus infection	7	24.13793103	4.05E-04	CASP8, CASP3, PTEN, BAX, CTNNB1, AKT1, PTGS2	331	6.630300996	0.072547841	0.002353088	0.001239799
KEGG_PATHWAY	hsa05010:Alzheimer disease	7	24.13793103	8.90E-04	CASP9, CASP8, NOS2, CASP3, CTNNB1, AKT1, PTGS2	384	5.715181327	0.152630654	0.00459847	0.00242285
KEGG_PATHWAY	hsa05022:Pathways of neurodegeneration - multiple diseases	7	24.13793103	0.002687632	CASP9, CASP8, NOS2, CASP3, BAX, CTNNB1, PTGS2	476	4.610566449	0.393816443	0.011361351	0.005986088
KEGG_PATHWAY	hsa05213:Endometrial cancer	6	20.68965517	7.46E-07	CASP9, MYC, PTEN, BAX, CTNNB1,	58	32.43295019	1.39E-04	1.74E-05	9.14E-06

					AKT 1					
KEGG_P ATHWA Y	hsa04657:IL- 17 signaling pathway	6	20.689 65517	8.30E- 06	JUN, CAS P8, MM P1, CAS P3, PTG S2, MAP 3K7	9 4	20.011 82033	0.0015 42242	1.10E- 04	5.81E- 05
KEGG_P ATHWA Y	hsa04933:A GE-RAGE signaling pathway in diabetic complication s	6	20.689 65517	1.12E- 05	JUN, TGF B1, CAS P3, MM P2, BAX , AKT 1	1 0 0	18.811 11111	0.0020 88529	1.39E- 04	7.34E- 05
KEGG_P ATHWA Y	hsa04668:TN F signaling pathway	6	20.689 65517	2.13E- 05	JUN, CAS P8, CAS P3, AKT 1, PTG S2, MAP 3K7	1 1 4	16.500 97466	0.0039 5192	2.33E- 04	1.23E- 04
KEGG_P ATHWA Y	hsa04926:Re laxin signaling pathway	6	20.689 65517	3.87E- 05	JUN, TGF B1, NOS 2, MM P1, MM P2, AKT 1	1 2 9	14.582 25668	0.0071 70094	3.43E- 04	1.81E- 04
KEGG_P ATHWA Y	hsa04210:Ap optosis	6	20.689 65517	4.99E- 05	CAS P9, JUN, CAS P8, CAS P3,	1 3 6	13.831 69935	0.0092 31426	4.22E- 04	2.22E- 04

					BAX , AKT 1					
KEGG_P ATHWA Y	hsa05418:Fluid shear stress and atherosclerosis	6	20.689 65517	5.54E- 05	JUN, MM P2, CAV 1, CTN NB1, AKT 1, MAP 3K7	1 3 9	13.533 17346	0.0102 42846	4.48E- 04	2.36E- 04
KEGG_P ATHWA Y	hsa05224:Breast cancer	6	20.689 65517	7.23E- 05	JUN, MYC , PTE N, BAX , CTN NB1, AKT 1	1 4 7	12.796 67423	0.0133 58483	5.17E- 04	2.73E- 04
KEGG_P ATHWA Y	hsa04932:Non-alcoholic fatty liver disease	6	20.689 65517	9.30E- 05	JUN, TGF B1, CAS P8, CAS P3, BAX , AKT 1	1 5 5	12.136 20072	0.0171 52178	6.18E- 04	3.26E- 04
KEGG_P ATHWA Y	hsa05225:Hepatocellular carcinoma	6	20.689 65517	1.36E- 04	TGF B1, MYC , PTE N, BAX , CTN NB1, AKT 1	1 6 8	11.197 08995	0.0249 9937	8.44E- 04	4.45E- 04
KEGG_P ATHWA Y	hsa05166:Human T-cell leukemia	6	20.689 65517	4.97E- 04	JUN, TGF B1, MYC	2 2 2	8.4734 73473	0.0883 59022	0.0028 02607	0.0014 76642

	virus 1 infection				, PTE N, BAX , AKT 1					
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	6	20.68965517	0.001983576	JUN, TGF B1, MYC , CAS P3, AKT 1, MAP 3K7	302	6.228844739	0.308789995	0.008580121	0.004520709
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	6	20.68965517	0.003956046	CAS P9, MYC , F2R, PTE N, AKT 1, PIK3 CG	354	5.313873195	0.521588428	0.014716491	0.00775385
KEGG_PATHWAY	hsa05168:Herpes simplex virus 1 infection	6	20.68965517	0.018126308	CAS P9, CAS P8, CAS P3, BAX , AKT 1, MAP 3K7	512	3.674045139	0.966707529	0.053515767	0.028196479
KEGG_PATHWAY	hsa01524:Platinum drug resistance	5	17.24137931	6.59E-05	CAS P9, CAS P8, CAS P3, BAX , AKT 1	73	21.47387113	0.012187085	5.11E-04	2.69E-04

KEGG_PATHWAY	hsa04115:p53 signaling pathway	5	17.24137931	6.95E-05	CASP9, CASP8, CASP3, PTEIN, BAX	74	21.18368368	0.012852376	5.17E-04	2.73E-04
KEGG_PATHWAY	hsa05140:Leishmaniasis	5	17.24137931	8.13E-05	JUN, TGFBI, NOS2, PTGS2, MAP3K7	77	20.35834536	0.015005484	5.60E-04	2.95E-04
KEGG_PATHWAY	hsa05142:Chagas disease	5	17.24137931	2.42E-04	JUN, TGFBI, CASP8, NOS2, AKT1	102	15.36855483	0.044070475	0.00145373	7.66E-04
KEGG_PATHWAY	hsa04936:Alcoholic liver disease	5	17.24137931	8.52E-04	CASP8, CASP3, CTNNB1, AKT1, MAP3K7	142	11.03938445	0.146542293	0.00452548	0.002384393
KEGG_PATHWAY	hsa05226:Gastric cancer	5	17.24137931	0.001019415	TGFBI, MYC, BAX, CTNNB1, AKT1	149	10.52075565	0.172799305	0.005124628	0.002700073
KEGG_PATHWAY	hsa04261:Adrenergic signaling in cardiomyocytes	5	17.24137931	0.001152761	AKT1, ADRAID, ADRA1B,	154	10.17917268	0.19308529	0.005642464	0.002972911

					ADR A1A, PIK3 CG					
KEGG_P ATHWA Y	hsa04022:cG MP-PKG signaling pathway	5	17.241 37931	0.0015 56291	AKT 1, ADR A1D, ADR A1B, ADR A1A, PIK3 CG	1 6 7	9.3867 81992	0.2515 08684	0.0070 71164	0.0037 25667
KEGG_P ATHWA Y	hsa05164:Inf luenza A	5	17.241 37931	0.0016 98082	CAS P9, CAS P8, CAS P3, BAX , AKT 1	1 7 1	9.1672 08144	0.2710 21946	0.0075 20076	0.0039 6219
KEGG_P ATHWA Y	hsa04510:Fo cal adhesion	5	17.241 37931	0.0031 72657	JUN, CAV 1, PTE N, CTN NB1, AKT 1	2 0 3	7.7221 30998	0.4462 55741	0.0127 61973	0.0067 2405
KEGG_P ATHWA Y	hsa04020:Ca lcium signaling pathway	5	17.241 37931	0.0069 37881	NOS 2, F2R, ADR A1D, ADR A1B, ADR A1A	2 5 3	6.1960 18153	0.7260 86585	0.0230 43677	0.0121 41292
KEGG_P ATHWA Y	hsa04215:Ap optosis - multiple species	4	13.793 10345	1.20E- 04	CAS P9, CAS P8, CAS P3, BAX	3 2	39.189 81481	0.0221 25036	7.71E- 04	4.06E- 04
KEGG_P ATHWA Y	hsa05416:Vir al myocarditis	4	13.793 10345	7.84E- 04	CAS P9, CAS P8,	6 0	20.901 23457	0.1357 13102	0.0042 88039	0.0022 5929

					CAS P3, CAV 1					
KEGG_P ATHWA Y	hsa05212:Pa ncreatic cancer	4	13.793 10345	0.0015 58697	CAS P9, TGF B1, BAX , AKT 1	7 6	16.500 97466	0.2518 4411	0.0070 71164	0.0037 25667
KEGG_P ATHWA Y	hsa05220:Ch ronic myeloid leukemia	4	13.793 10345	0.0015 58697	TGF B1, MYC , BAX , AKT 1	7 6	16.500 97466	0.2518 4411	0.0070 71164	0.0037 25667
KEGG_P ATHWA Y	hsa05215:Pr ostate cancer	4	13.793 10345	0.0031 32439	CAS P9, PTE N, CTN NB1, AKT 1	9 7	12.928 5987	0.4420 84659	0.0127 61973	0.0067 2405
KEGG_P ATHWA Y	hsa01522:En docrine resistance	4	13.793 10345	0.0032 248	JUN, MM P2, BAX , AKT 1	9 8	12.796 67423	0.4516 17341	0.0127 61973	0.0067 2405
KEGG_P ATHWA Y	hsa04620:To ll-like receptor signaling pathway	4	13.793 10345	0.0038 1427	JUN, CAS P8, AKT 1, MAP 3K7	1 0 4	12.058 40456	0.5087 5425	0.0144 78659	0.0076 28541
KEGG_P ATHWA Y	hsa04625:C- type lectin receptor signaling pathway	4	13.793 10345	0.0038 1427	JUN, CAS P8, AKT 1, PTG S2	1 0 4	12.058 40456	0.5087 5425	0.0144 78659	0.0076 28541
KEGG_P ATHWA Y	hsa04919:Th yroid hormone	4	13.793 10345	0.0058 27293	CAS P9, MYC ,	1 2 1	10.364 24855	0.6627 89142	0.0208 43779	0.0109 82206

	signaling pathway				CTN NB1, AKT 1					
KEGG_PATHWAY	hsa04611:Platelet activation	4	13.79310345	0.006237298	F2R, AKT 1, PIK3 CG, PTG S1	124	10.1135006	0.687693632	0.021889386	0.011533117
KEGG_PATHWAY	hsa04380:Osteoclast differentiation	4	13.79310345	0.006810363	JUN, TGF B1, AKT 1, MAP 3K7	128	9.797453704	0.719466079	0.023043677	0.012141292
KEGG_PATHWAY	hsa04218:Cellular senescence	4	13.79310345	0.011698187	TGF B1, MYC , PTE N, AKT 1	156	8.038936372	0.887936507	0.03817303	0.020112672
KEGG_PATHWAY	hsa04310:Wnt signaling pathway	4	13.79310345	0.014972267	JUN, MYC , CTN NB1, MAP 3K7	171	7.333766515	0.939547647	0.0449168	0.023665841
KEGG_PATHWAY	hsa05415:Diabetic cardiomyopathy	4	13.79310345	0.023545652	TGF B1, MMP2, PTE N, AKT 1	203	6.177704798	0.988107818	0.062469485	0.03291403
KEGG_PATHWAY	hsa05203:Viral carcinogenesis	4	13.79310345	0.02384888	JUN, CAS P8, CAS P3, BAX	204	6.147421932	0.988775355	0.062469485	0.03291403
KEGG_PATHWAY	hsa05207:Chemical carcinogenesis - receptor activation	4	13.79310345	0.026352108	JUN, MYC , AKT 1,	212	5.915443746	0.993037606	0.067143727	0.035376802

					CYP 3A4					
KEGG_P ATHWA Y	hsa05208:Ch emical carcinogenes is - reactive oxygen species	4	13.793 10345	0.0300 18677	JUN, PTE N, AKR 1C3, AKT 1	2 2 3	5.6236 50556	0.9965 48665	0.0738 28395	0.0388 98832
KEGG_P ATHWA Y	hsa05131:Shi gellosis	4	13.793 10345	0.0389 17064	JUN, BAX , AKT 1, MAP 3K7	2 4 7	5.0772 22972	0.9993 78385	0.0904 82174	0.0476 73404
KEGG_P ATHWA Y	hsa05020:Pri on disease	4	13.793 10345	0.0499 26794	CAS P9, CAS P3, CAV 1, BAX	2 7 3	4.5936 77927	0.9999 27085	0.1118 84142	0.0589 49709
KEGG_P ATHWA Y	hsa05016:Hu ntington disease	4	13.793 10345	0.0658 82203	CAS P9, CAS P8, CAS P3, BAX	3 0 6	4.0982 81288	0.9999 96876	0.1358 8104	0.0715 93236
KEGG_P ATHWA Y	hsa05206:Mi croRNAs in cancer	4	13.793 10345	0.0679 61529	MYC , CAS P3, PTE N, PTG S2	3 1 0	4.0454 00239	0.9999 97936	0.1359 23059	0.0716 15375
KEGG_P ATHWA Y	hsa05014:A myotrophic lateral sclerosis	4	13.793 10345	0.0989 06874	CAS P9, NOS 2, CAS P3, BAX	3 6 4	3.4452 58445	0.9999 99996	0.1858 25035	0.0989 06874
KEGG_P ATHWA Y	hsa05216:Th yroid cancer	3	10.344 82759	0.0056 55797	MYC , BAX , CTN NB1	3 7	25.420 42042	0.6517 9518	0.0206 27025	0.0108 68002

KEGG_PATHWAY	hsa05219:Bladder cancer	3	10.344 82759	0.0069 11371	MM P1, MYC, MM P2	4 1	22.940 3794	0.7247 23156	0.0230 43677	0.0121 41292
KEGG_PATHWAY	hsa05134:Legionellosis	3	10.344 82759	0.0130 53497	CAS P9, CAS P8, CAS P3	5 7	16.500 97466	0.9131 8157	0.0418 61215	0.0220 55909
KEGG_PATHWAY	hsa04923:Regulation of lipolysis in adipocytes	3	10.344 82759	0.0134 94348	AKT 1, PTG S2, PTG S1	5 8	16.216 4751	0.9201 04661	0.0425 41505	0.0224 14341
KEGG_PATHWAY	hsa04370:VEGF signaling pathway	3	10.344 82759	0.0139 41653	CAS P9, AKT 1, PTG S2	5 9	15.941 61959	0.9265 67867	0.0432 19125	0.0227 71367
KEGG_PATHWAY	hsa00590:Arachidonic acid metabolism	3	10.344 82759	0.0148 55462	AKR 1C3, PTG S2, PTG S1	6 1	15.418 94353	0.9381 99577	0.0449 168	0.0236 65841
KEGG_PATHWAY	hsa05211:Renal cell carcinoma	3	10.344 82759	0.0187 60805	JUN, TGF B1, AKT 1	6 9	13.631 23994	0.9704 79133	0.0545 23589	0.0287 27482
KEGG_PATHWAY	hsa05230:Central carbon metabolism in cancer	3	10.344 82759	0.0192 76458	MYC, PTE N, AKT 1	7 0	13.436 50794	0.9732 28807	0.0551 60325	0.0290 62967
KEGG_PATHWAY	hsa05223:Non-small cell lung cancer	3	10.344 82759	0.0203 25658	CAS P9, BAX, AKT 1	7 2	13.063 2716	0.9780 61724	0.0564 26454	0.0297 30067
KEGG_PATHWAY	hsa05218:Melanoma	3	10.344 82759	0.0203 25658	PTE N, BAX, AKT 1	7 2	13.063 2716	0.9780 61724	0.0564 26454	0.0297 30067

KEGG_P ATHWAY	hsa05214:Glioma	3	10.344 82759	0.0219 43619	PTE N, BAX , AKT 1	7 5	12.540 74074	0.9838 68168	0.0600 22252	0.0316 24627
KEGG_P ATHWAY	hsa05133:Peritussis	3	10.344 82759	0.0224 94563	JUN, NOS 2, CAS P3	7 6	12.375 73099	0.9854 73272	0.0606 37517	0.0319 48799
KEGG_P ATHWAY	hsa01521:EGFR tyrosine kinase inhibitor resistance	3	10.344 82759	0.0241 81736	PTE N, BAX , AKT 1	7 9	11.905 76653	0.9894 65274	0.0624 69485	0.0329 1403
KEGG_P ATHWAY	hsa04012:Erbb signaling pathway	3	10.344 82759	0.0277 07272	JUN, MYC , AKT 1	8 5	11.065 35948	0.9946 26602	0.0696 42601	0.0366 93414
KEGG_P ATHWAY	hsa05235:PD-L1 expression and PD-1 checkpoint pathway in cancer	3	10.344 82759	0.0301 66441	JUN, PTE N, AKT 1	8 9	10.568 03995	0.9966 45092	0.0738 28395	0.0388 98832
KEGG_P ATHWAY	hsa05323:Rheumatoid arthritis	3	10.344 82759	0.0327 09972	JUN, TGF B1, MM PI	9 3	10.113 5006	0.9979 41513	0.0780 00702	0.0410 97144
KEGG_P ATHWAY	hsa04970:Salivary secretion	3	10.344 82759	0.0327 09972	ADR A1D, ADR A1B, ADR A1A	9 3	10.113 5006	0.9979 41513	0.0780 00702	0.0410 97144
KEGG_P ATHWAY	hsa05146:Amoebiasis	3	10.344 82759	0.0387 29717	TGF B1, NOS 2, CAS P3	1 0 2	9.2211 32898	0.9993 55436	0.0904 82174	0.0476 73404
KEGG_P ATHWAY	hsa04660:T cell receptor signaling pathway	3	10.344 82759	0.0401 21355	JUN, AKT 1, MAP 3K7	1 0 4	9.0438 03419	0.9995 07692	0.0921 30519	0.0485 41887

KEGG_P ATHWAY	hsa04726:Serotonergic synapse	3	10.344 82759	0.0481 08284	CASP3, PTGS2, PTGS1	1 1 5	8.1787 43961	0.9998 9594	0.1091 23669	0.0574 95266
KEGG_P ATHWAY	hsa04722:Neurotrophin signaling pathway	3	10.344 82759	0.0511 46783	JUN, BAX, AKT1	1 1 9	7.9038 28198	0.9999 42586	0.1132 53592	0.0596 71247
KEGG_P ATHWAY	hsa04152:AMPK signaling pathway	3	10.344 82759	0.0526 91783	AKT1, ADRA1A, MAP3K7	1 2 1	7.7731 8641	0.9999 57598	0.1139 61298	0.0600 44125
KEGG_P ATHWAY	hsa04071:Sphingolipid signaling pathway	3	10.344 82759	0.0526 91783	PTEIN, BAX, AKT1	1 2 1	7.7731 8641	0.9999 57598	0.1139 61298	0.0600 44125
KEGG_P ATHWAY	hsa04068:FoxO signaling pathway	3	10.344 82759	0.0606 64398	TGFB1, PTEIN, AKT1	1 3 1	7.1798 13401	0.9999 91196	0.1296 96299	0.0683 34609
KEGG_P ATHWAY	hsa04270:Vascular smooth muscle contraction	3	10.344 82759	0.0631 33709	ADRA1D, ADRA1B, ADRA1A	1 3 4	7.0190 7131	0.9999 94604	0.1334 41702	0.0703 07994
KEGG_P ATHWAY	hsa05135:Yersinia infection	3	10.344 82759	0.0656 37378	JUN, AKT1, MAP3K7	1 3 7	6.8653 69019	0.9999 9672	0.1358 8104	0.0715 93236
KEGG_P ATHWAY	hsa04915:Estrogen signaling pathway	3	10.344 82759	0.0664 79434	JUN, MM2, AKT1	1 3 8	6.8156 19968	0.9999 97226	0.1358 8104	0.0715 93236
KEGG_P ATHWAY	hsa04371:Apelin signaling pathway	3	10.344 82759	0.0673 25191	NOS2, AKT1, PIK3CG	1 3 9	6.7665 86731	0.9999 97657	0.1359 23059	0.0716 15375

KEGG_PATHWAY	hsa04140:Autophagy - animal	3	10.34482759	0.069027697	PTE N, AKT 1, MAP 3K7	1 4 1	6.670606777	0.999998332	0.13658672	0.071965046
KEGG_PATHWAY	hsa04550:Signaling pathways regulating pluripotency of stem cells	3	10.34482759	0.070744668	MYC , CTN NB1, AKT 1	1 4 3	6.577311577	0.999998817	0.138510614	0.07297871
KEGG_PATHWAY	hsa04072:Phospholipase D signaling pathway	3	10.34482759	0.075098906	F2R, AKT 1, PIK3 CG	1 4 8	6.355105105	0.999999506	0.14550413	0.076663466
KEGG_PATHWAY	hsa04921:Oxytocin signaling pathway	3	10.34482759	0.080436597	JUN, PTG S2, PIK3 CG	1 5 4	6.107503608	0.999999832	0.154239249	0.081265841
KEGG_PATHWAY	hsa04390:Hippo signaling pathway	3	10.34482759	0.083149802	TGF B1, MYC , CTN NB1	1 5 7	5.990799717	0.999999903	0.15781493	0.083149802