

Supplementary Table 1 The venn analysis of luteolin targets

TCMSP	SymMap	BATMAN-T CM	TCMSP Sym Map	TCMSP BATMAN -TCM	TCMSP SymMap BATMAN-TCM
DPP4	CDK2	ACTB	PTGS2	HSP90AA1	AKT1
	GSTP1	AHR	PRSS1	PIK3CG	TOP2A
	MAPK3	AKR1C1	AR	PRKACA	
	NOS2	ATP5A1	PTGS1	NCOA2	
	VEGFA	ATP5B	RELA		
	XIAP	ATP5C1	EGFR		
		CA1	CCND1		
		CA12	BCL2L1		
		CA14	CDKN1A		
		CA2	CASP9		
		CA3	MMP2		
		CA4	MMP9		
		CA5A	MAPK1		
		CA5B	IL10		
		CA6	RB1		
		CA7	CDK4		
		CA9	TNF		
		CBR1	JUN		
		CDK6	IL6		
		CEBPB	CASP3		
		COMT	TP53		
		CSNK2A1	NFKBIA		
		CSNK2B	XDH		
		CYP19A1	TOP1		
		CYP1B1	MDM2		
		DHFRL1	APP		
		DNMT1	MMP1		
		EIF3F	PCNA		
		ESR1	ERBB2		
		ESR2	PPARG		
		ESRRA	HMOX1		
		ESRRB	CASP7		
		GABRA1	ICAM1		
		GABRA2	MCL1		
		GABRA3	BIRC5		
		GABRA4	IL2		
		GABRA5	CCNB1		
		GABRA6	TYR		
		GABRG1	IFNG		
		GABRG2	IL4		

		GABRG3	SLC2A4		
		GPER1	INSR		
		HCK	CD40LG		
		HIBCH	PTGES		
		HSPA2	NUF2		
		IGHG1	ADCY2		
		JAK1	MET		
		KANSL3			
		MTTP			
		NCOA1			
		NQO2			
		NR1I2			
		PIM1			
		PRKCA			
		PRKCB			
		PTK2B			
		RUVBL2			
		SF3B3			
		SHBG			
		SOAT1			
		SOAT2			
		SQLE			
		STK17B			
		SYK			
		UBA1			
		UGT3A1			

Supplementary Table 2 The venn analysis of disease-related genes associated with DN

OMIM	DisGeNet	GeneCards	OMIM DisGeNet	OMIM GeneCards	DisGeNet GeneCards	OMIM DisGeNet GeneCards
GNB1	NFE2L2	ABCC8	NPPA	PTPN22	ACE	REN
PRDM16	TGFB1	GCK	SLC2A1	LMNA	ALB	AGT
TP73	MFN2	KCNJ11	LEPR	NLRP3	NOS3	PPARG
CTRC	TXNIP	HNF1B	IL1B	KLF11	SERPINE1	
CELA2A	ACE2	PDX1	CREB1	IL1RN	CCL2	
CLCNKA	CNDP1	INSR	FN1	GPD2	TGFB1	
DDOST	ELMO1	WFS1		NEUROD1	VEGFA	
ECE1	RELA	TCF7L2		CTLA4	ADIPOQ	
C1QA	GAS6	PAX4		IRS1	INS	
C1QC	CNDP2	SLC2A2		CAPN10	SOD2	
C1QB	AOC3	ENPP1			PON1	
SELENON	CDKN1A	SLC30A8			HNF1A	

NR0B2	KDR	RETN			COL4A1	
FCN3	KLK1	AVPR2			AGER	
SDC3	MDK	AQP2			AGTR1	
CCDC28B	TGFBR2	AVP			IL6	
LCK	CST3	IGF2BP2			TNF	
TRIT1	CCN2	SLC2A4			IGF1	
ZMPSTE24	DGKH	HFE			HNF4A	
MMACHC	HAVCR1	IRS2				
PRDX1	TINAG	LIPC				
TAL1	HIF1A	AKR1B1				
ANGPTL3	ICAM1	MTNR1B				
JAK1	LCN2	AKT2				
ACADM	MIR145	PTPN1				
ALX3	MMP9	INS-IGF2				
SLC16A1	MYCN	UMOD				
VANGL1	NOX4	APOE				
NOTCH2	AXL	COL4A5				
HJV	PRKCE	MIR21				
TPM3	PTEN	MIR29A				
IL6R	PTPN11	HLA-DQB1				
MUC1	TNFAIP1	APOA1				
NCSTN	TRPC6	EPO				
CD244	VDAC1	CEL				
USF1	VDAC2	HLA-DQA1				
PPOX	ALPK1	MTHFR				
MPZ	KL	LEP				
ATF6	MTOR	MIR192				
PBX1	BMP7	CRP				
SLC19A2	MMP2	BLK				
F5	SERPINF1	APPL1				
RC3H1	PRKCB	MT-TL1				
NPHS2	PTGS2	GCG				
HMCN1	HMOX1	HLA-DRB1				
CFH	STAT3	ZFP57				
CFHR3	CAT	XPNPEP3				
CFHR1	GSK3B					
CFHR5	JAK2					
PTPRC	AGTR2					
PPP1R15B	TP53					
SLC41A1	TRPC1					
IL10	PRMT1					
HSD11B1	IGF2					
KCNH1	SPP1					

MIA3	SREBF1					
COQ8A	CASP3					
ACTA1	UTS2					
ARV1	CLU					
IRF2BP2	CYP19A1					
LPIN1	NQO1					
ADCY3	G6PD					
POMC	GHR					
DNMT3A	HSPA5					
KHK	ERRFI1					
MPV17	CCL20					
GCKR	SELP					
SIX3	SPARC					
TTC7A	TIMP2					
MSH6	C3					
ALMS1	VCAM1					
DGUOK	CUBN					
TET3	BECN1					
ST3GAL5	CD36					
CD8A	HDAC4					
EIF2AK3	EP300					
NPHP1	ESR1					
GLI2	DKK1					
RNU4ATA C	UTS2R					
PROC	HSPB1					
CXCR4	HTR2A					
ZEB2	IGF1R					
IFIH1	LAMB2					
GAD1	NOS1					
DCAF17	ATP5F1B					
SLC40A1	PROS1					
MSTN	C5					
STAT1	FGF23					
CASP10	CASP9					
CPS1	TRIP10					
SMARCAL 1	KEAP1					
SLC11A1						
COL4A4						
COL4A3						
UGT1A1						
ITPR1						

CAV3						
CIDEC						
GHRL						
PLCD1						

Supplementary Table 3 The PPI network of luteolin-DN targets

#node1	node2	experimentally_determined_interaction	database_annotated	combined_score
ACE	AGT	0.822	0.9	0.981
ADCY2	PRKACA	0.139	0.65	0.685
ADCY2	AKT1	0.058	0.6	0.607
ADIPOQ	PPARG	0	0.9	0.9
ADIPOQ	NCOA2	0	0.9	0.9
AGER	MAPK1	0	0.6	0.6
AGER	APP	0.042	0.6	0.6
AGER	RELA	0	0.9	0.9
AGT	MAPK1	0	0.9	0.9
AGT	REN	0.936	0.9	0.993
AGT	APP	0.068	0.5	0.514
AGT	NCOA2	0	0.9	0.9
AGT	AGTR1	0.501	0.9	0.947
AGTR1	SERPINE1	0.056	0.8	0.803
AKT1	MAPK1	0.148	0.8	0.822
AKT1	IL2	0	0.9	0.9
AKT1	MDM2	0.898	0.9	0.989
AKT1	RB1	0.058	0.9	0.901
AKT1	TP53	0.201	0.9	0.916
AKT1	EGFR	0.65	0	0.65
AKT1	NOS3	0.879	0.9	0.987
AKT1	BCL2L1	0.27	0.9	0.923
AKT1	INSR	0.182	0.9	0.914
AKT1	CTLA4	0.056	0.65	0.655
AKT1	IRS1	0.535	0	0.535
AKT1	CASP3	0.475	0	0.475
AKT1	CASP9	0.231	0.9	0.919
AKT1	HSP90AA1	0.946	0.9	0.994
AKT1	PIK3CG	0.184	0.9	0.914
AKT1	LMNA	0.605	0	0.605
AKT1	MCL1	0	0.9	0.9
AKT1	CD40LG	0.056	0.9	0.901
AKT1	JUN	0.057	0.8	0.803
AKT1	AR	0.87	0	0.87
AKT1	INS	0	0.9	0.9

AKT1	CDKN1A	0.789	0.9	0.978
AKT1	CREB1	0.27	0.9	0.923
AKT1	SOD2	0	0.9	0.9
ALB	NCOA2	0	0.65	0.65
APP	MAPK1	0.086	0.6	0.619
APP	MMP2	0.464	0	0.463
APP	TGFB1	0.734	0	0.734
APP	PON1	0	0.72	0.72
APP	EGFR	0.642	0	0.642
APP	NPPA	0	0.5	0.499
APP	PRSS1	0.651	0	0.651
APP	INS	0	0.5	0.499
APP	COL4A1	0.451	0	0.451
APP	HSP90AA1	0.494	0	0.494
APP	RELA	0	0.9	0.9
APP	CASP3	0.682	0	0.682
AR	MAPK1	0.497	0	0.497
AR	CCND1	0.839	0.9	0.983
AR	MDM2	0.898	0	0.898
AR	RB1	0.687	0.65	0.885
AR	TP53	0.474	0	0.474
AR	EGFR	0.698	0	0.698
AR	PRKACA	0	0.9	0.9
AR	HSP90AA1	0.884	0.9	0.987
AR	JUN	0.499	0	0.499
AR	RELA	0.489	0	0.489
AR	NCOA2	0.977	0.9	0.997
BCL2L1	MAPK1	0	0.9	0.9
BCL2L1	TP53	0.977	0.9	0.997
BCL2L1	PRKACA	0	0.9	0.9
BCL2L1	MCL1	0.5	0.9	0.947
BCL2L1	CASP9	0.724	0	0.724
BIRC5	CCND1	0	0.9	0.9
BIRC5	TP53	0	0.9	0.9
BIRC5	CASP3	0.567	0	0.567
BIRC5	CASP7	0.729	0	0.729
BIRC5	CASP9	0.771	0	0.771
CASP3	MAPK1	0.057	0.8	0.803
CASP3	MDM2	0.875	0	0.875
CASP3	RB1	0.488	0.9	0.946
CASP3	MET	0.609	0	0.609
CASP3	CASP7	0.271	0.9	0.923
CASP3	TOP1	0.263	0.9	0.923

CASP3	CASP9	0.87	0.9	0.986
CASP3	CDKN1A	0.77	0.8	0.952
CASP7	RB1	0.675	0	0.675
CASP7	CASP9	0.271	0.9	0.923
CASP9	MAPK1	0.282	0.9	0.925
CCL2	RELA	0.486	0.8	0.892
CCL2	JUN	0	0.9	0.9
CCL2	IL4	0	0.9	0.9
CCL2	IL10	0	0.9	0.9
CCL2	TNF	0	0.9	0.9
CCL2	IL1B	0	0.9	0.9
CCL2	IL6	0	0.9	0.9
CCNB1	CCND1	0.078	0.9	0.903
CCNB1	RB1	0.547	0	0.547
CCNB1	LMNA	0	0.9	0.9
CCNB1	PCNA	0.685	0.36	0.789
CCNB1	CDK4	0.23	0.9	0.919
CCNB1	CDKN1A	0.898	0.9	0.989
CCND1	HNF1A	0	0.9	0.9
CCND1	CREB1	0	0.9	0.9
CCND1	RELA	0.486	0.9	0.946
CCND1	JUN	0.27	0.9	0.923
CCND1	PCNA	0.783	0.9	0.977
CCND1	RB1	0.947	0.9	0.994
CCND1	CDKN1A	0.983	0.9	0.998
CCND1	CDK4	0.998	0.9	0.999
CD40LG	NFKBIA	0.062	0.9	0.902
CD40LG	PIK3CG	0.056	0.9	0.901
CD40LG	TNF	0	0.6	0.6
CD40LG	RELA	0	0.9	0.9
CDK4	TP53	0.498	0	0.498
CDK4	HSP90AA1	0.889	0	0.889
CDK4	CDKN1A	0.985	0.9	0.998
CDK4	PCNA	0.98	0.9	0.997
CDK4	RB1	0.993	0.9	0.999
CDKN1A	MDM2	0.872	0	0.872
CDKN1A	RB1	0.37	0.9	0.934
CDKN1A	TP53	0.968	0.9	0.996
CDKN1A	HSP90AA1	0.27	0.6	0.695
CDKN1A	MCL1	0	0.9	0.9
CDKN1A	JUN	0.27	0.9	0.923
CDKN1A	PCNA	0.998	0.9	0.999
CDKN1A	RELA	0.486	0	0.485

CDKN1A	CREB1	0	0.9	0.9
COL4A1	MMP9	0.442	0	0.442
CREB1	MAPK1	0	0.9	0.9
CREB1	HMOX1	0	0.9	0.9
CREB1	TP53	0.805	0	0.805
CREB1	NOS3	0	0.9	0.9
CREB1	PRKACA	0.487	0.9	0.946
CREB1	JUN	0.492	0.9	0.947
CREB1	IL6	0	0.9	0.9
CREB1	IL10	0	0.9	0.9
CREB1	VEGFA	0.27	0.9	0.923
EGFR	MAPK1	0.44	0.9	0.941
EGFR	IL2	0	0.6	0.6
EGFR	IFNG	0	0.6	0.6
EGFR	IL4	0	0.6	0.6
EGFR	MDM2	0	0.6	0.6
EGFR	ERBB2	0.982	0.9	0.998
EGFR	PRKACA	0.487	0	0.487
EGFR	INSR	0.107	0.5	0.534
EGFR	LMNA	0.486	0	0.485
EGFR	PTPN22	0.682	0	0.682
EGFR	IL10	0	0.6	0.6
EGFR	IL6	0	0.6	0.6
EGFR	IGF1	0	0.6	0.6
EGFR	INS	0	0.8	0.8
EGFR	VEGFA	0	0.6	0.6
EGFR	MET	0.887	0	0.887
EGFR	IRS1	0.251	0.6	0.687
EGFR	HSP90AA1	0.884	0.9	0.987
ERBB2	IRS1	0.251	0.6	0.687
ERBB2	INS	0	0.6	0.6
ERBB2	PRKACA	0	0.9	0.9
ERBB2	VEGFA	0	0.6	0.6
ERBB2	IGF1	0	0.6	0.6
ERBB2	IL6	0	0.9	0.9
ERBB2	HSP90AA1	0.907	0.9	0.99
FN1	MAPK1	0	0.6	0.6
FN1	IL4	0	0.9	0.9
FN1	IGF1	0	0.9	0.9
FN1	IRS1	0	0.9	0.9
FN1	PRKACA	0	0.9	0.9
FN1	LMNA	0.074	0.6	0.613
HMOX1	IL4	0	0.9	0.9

HMOX1	JUN	0	0.9	0.9
HNF1A	MAPK1	0	0.9	0.9
HNF1A	HNF4A	0.241	0.9	0.92
HNF4A	TP53	0.43	0	0.43
HNF4A	NCOA2	0.831	0	0.831
HSP90AA1	MAPK1	0.365	0.9	0.933
HSP90AA1	IL2	0	0.9	0.9
HSP90AA1	IFNG	0	0.9	0.9
HSP90AA1	MDM2	0.675	0	0.675
HSP90AA1	RB1	0.128	0.9	0.909
HSP90AA1	TP53	0.899	0.9	0.989
HSP90AA1	NOS3	0.76	0.9	0.974
HSP90AA1	PRKACA	0.654	0.9	0.963
HSP90AA1	MET	0.55	0	0.55
HSP90AA1	MCL1	0.128	0.9	0.909
HSP90AA1	VEGFA	0.27	0.9	0.923
HSP90AA1	NLRP3	0.27	0.8	0.847
ICAM1	RELA	0.681	0	0.681
ICAM1	IL10	0	0.9	0.9
IFNG	LEPR	0	0.6	0.6
IFNG	RELA	0	0.9	0.9
IFNG	JUN	0	0.9	0.9
IGF1	MAPK1	0	0.9	0.9
IGF1	MMP2	0	0.9	0.9
IGF1	MET	0	0.6	0.6
IGF1	MMP1	0	0.9	0.9
IGF1	IRS1	0	0.9	0.9
IGF1	INS	0	0.8	0.8
IGF1	INSR	0.945	0.8	0.988
IL10	MMP2	0	0.9	0.9
IL10	TGFB1	0	0.9	0.9
IL10	IL1RN	0	0.9	0.9
IL10	IL1B	0	0.9	0.9
IL10	MMP1	0	0.9	0.9
IL10	LEPR	0	0.6	0.6
IL10	MMP9	0	0.9	0.9
IL10	TNF	0	0.9	0.9
IL10	VEGFA	0	0.9	0.9
IL1B	IL4	0	0.9	0.9
IL1B	IL1RN	0	0.9	0.9
IL1B	JUN	0	0.8	0.8
IL1B	RELA	0	0.9	0.9
IL1B	TNF	0	0.5	0.499

IL1B	NLRP3	0	0.8	0.8
IL1B	IL6	0	0.9	0.9
IL2	MAPK1	0	0.9	0.9
IL2	LEPR	0	0.6	0.6
IL2	IRS1	0	0.9	0.9
IL2	JUN	0.27	0.9	0.923
IL2	RELA	0.486	0.9	0.946
IL4	LEPR	0	0.6	0.6
IL4	IRS1	0	0.9	0.9
IL4	RELA	0	0.9	0.9
IL4	JUN	0	0.9	0.9
IL4	IL6	0	0.9	0.9
IL4	TNF	0	0.9	0.9
IL6	MAPK1	0	0.9	0.9
IL6	MMP2	0	0.9	0.9
IL6	TGFB1	0	0.9	0.9
IL6	MMP1	0	0.9	0.9
IL6	LEPR	0.076	0.6	0.614
IL6	JUN	0	0.9	0.9
IL6	MMP9	0	0.9	0.9
IL6	RELA	0.27	0.9	0.923
IL6	VEGFA	0	0.9	0.9
IL6	TNF	0	0.9	0.9
INS	RB1	0.463	0	0.463
INS	INSR	0.972	0.9	0.997
INS	IRS1	0	0.9	0.9
INS	MET	0	0.6	0.6
INS	NPPA	0	0.5	0.499
INSR	VEGFA	0	0.6	0.6
INSR	IRS1	0.922	0.9	0.991
IRS1	MAPK1	0.213	0.9	0.917
IRS1	LEPR	0	0.6	0.6
IRS1	MET	0.132	0.6	0.637
IRS1	PIK3CG	0.391	0.8	0.872
JUN	MAPK1	0.867	0.9	0.986
JUN	NFKBIA	0	0.9	0.9
JUN	TGFB1	0	0.9	0.9
JUN	RB1	0.486	0.9	0.946
JUN	TP53	0.149	0.6	0.645
JUN	PPARG	0.066	0.9	0.902
JUN	NOS3	0	0.9	0.9
JUN	PRKACA	0	0.8	0.8
JUN	MMP1	0.628	0	0.628

JUN	MMP9	0.486	0	0.485
JUN	VEGFA	0.182	0.9	0.914
JUN	TNF	0	0.9	0.9
JUN	RELA	0.481	0.9	0.945
KLF11	MAPK1	0.514	0	0.514
LMNA	MAPK1	0.251	0.6	0.687
LMNA	RB1	0.75	0	0.75
MAPK1	MCL1	0.463	0	0.463
MAPK1	PPARG	0.699	0	0.699
MAPK1	PRKACA	0.18	0.8	0.828
MAPK1	MET	0.148	0.9	0.911
MAPK1	TGFB1	0.058	0.9	0.901
MAPK1	RB1	0.213	0.9	0.917
MAPK1	RELA	0.118	0.9	0.908
MAPK1	NFKBIA	0.134	0.9	0.909
MAPK1	TP53	0.876	0.8	0.974
MCL1	TP53	0.298	0.9	0.926
MDM2	PCNA	0.486	0	0.485
MDM2	RB1	0.881	0.9	0.987
MDM2	TP53	0.998	0.9	0.999
MET	VEGFA	0	0.6	0.6
MMP1	MMP2	0	0.9	0.9
MMP1	TGFB1	0	0.9	0.9
MMP1	PRSS1	0	0.9	0.9
MMP1	MMP9	0	0.9	0.9
MMP1	VEGFA	0	0.9	0.9
MMP2	MMP9	0	0.9	0.9
MMP2	VEGFA	0	0.9	0.9
MMP2	TGFB1	0.634	0.9	0.961
MMP9	TGFB1	0.634	0.9	0.961
MMP9	PRSS1	0	0.9	0.9
MMP9	VEGFA	0	0.9	0.9
NCOA2	PPARG	0.954	0.9	0.995
NFKBIA	PRKACA	0.056	0.8	0.803
NFKBIA	TP53	0.615	0	0.615
NFKBIA	TNF	0.27	0.9	0.923
NFKBIA	RELA	0.998	0.9	0.999
NLRP3	RELA	0	0.9	0.9
NOS3	PRKACA	0.154	0.9	0.911
NOS3	VEGFA	0	0.9	0.9
PCNA	RB1	0	0.9	0.9
PCNA	TP53	0.486	0.65	0.812
PCNA	TOP1	0.955	0	0.955

PPARG	TGFB1	0	0.9	0.9
PPARG	RB1	0.297	0.9	0.926
PPARG	TP53	0.292	0.65	0.741
PPARG	TNF	0	0.9	0.9
PPARG	SLC2A4	0.056	0.9	0.901
PPARG	RELA	0.768	0.9	0.975
PRKACA	VEGFA	0	0.9	0.9
PRKACA	RELA	0.767	0.9	0.975
PTGES	PTGS1	0	0.9	0.9
PTGES	PTGS2	0	0.9	0.9
PTGS1	PTGS2	0.27	0.8	0.847
PTGS2	TP53	0.874	0	0.874
RB1	TP53	0.486	0.9	0.946
RELA	TGFB1	0	0.9	0.9
RELA	TP53	0.451	0	0.451
RELA	SOD2	0	0.9	0.9
RELA	TNF	0.501	0.9	0.948
SLC2A1	TP53	0.13	0.8	0.818
SLC2A1	SLC2A4	0	0.8	0.8
TGFB1	VEGFA	0	0.5	0.499
TOP1	TP53	0.735	0	0.735
TOP1	TOP2A	0.919	0	0.919

Supplementary Table 4 The venn analysis of important PPI network through MCC, MNC, DMNC algorithm

DMNC	MNC	MCC DMNC	MCC MNC	DMNC MNC	MCC DMNC MNC
MCL1	APP	CCL2	JUN	ERBB2	TP53
NOS3	CASP3	CDK4	IL6		RB1
PPARG	INS	IL10	RELA		TNF
NFKBIA		CCNB1	AKT1		IL1B
INSR			IL4		AR
AGER			MAPK1		CDKN1A
BIRC5			HSP90AA1		TGFB1
CD40LG			VEGFA		MMP1
BCL2L1			EGFR		MMP9
IL2			IRS1		MDM2
MET			PRKACA		MMP2
			CREB1		PCNA
					CCND1
					IGF1

Supplementary Table 5 The list of top 20 GO term

category	Term	ID	count	p_value	Rich_factor
BP	GO:1904707	positive regulation of vascular smooth muscle cell proliferation	5	4.43E-08	0.089285714
MF	GO:0019899	enzyme binding	7	1.13E-07	0.017948718
BP	GO:0001934	positive regulation of protein phosphorylation	6	1.81E-07	0.028301887
BP	GO:0010628	positive regulation of gene expression	7	5.69E-07	0.013333333
BP	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	8	1.05E-06	0.008221994
BP	GO:0051726	regulation of cell cycle	6	1.48E-06	0.018518519
BP	GO:0097421	liver regeneration	4	2.69E-06	0.095238095
BP	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	8	4.54E-06	0.00661157
BP	GO:1902895	positive regulation of pri-miRNA transcription from RNA polymerase II promoter	4	5.15E-06	0.076923077
BP	GO:0043491	protein kinase B signaling	4	5.15E-06	0.076923077
BP	GO:0071466	cellular response to xenobiotic stimulus	4	1.01E-05	0.061538462
BP	GO:0048661	positive regulation of smooth muscle cell proliferation	4	1.27E-05	0.057142857
BP	GO:0030335	positive regulation of cell migration	5	2.21E-05	0.018939394
BP	GO:0007265	Ras protein signal transduction	4	2.70E-05	0.044444444
BP	GO:0042493	response to drug	5	3.32E-05	0.017064846
BP	GO:2000679	positive regulation of transcription regulatory region DNA binding	3	4.36E-05	0.2
BP	GO:0010629	negative regulation of gene expression	5	4.46E-05	0.015822785
BP	GO:0043065	positive regulation of apoptotic process	5	5.40E-05	0.015060241
BP	GO:0045893	positive regulation of transcription, DNA-templated	6	7.28E-05	0.008287293
BP	GO:0030308	negative regulation of cell growth	4	7.72E-05	0.03125

Supplementary Table 6 The list of top 20 KEGG pathway

category	ID	Term	count	p_value	Rich_factor
KEGG	hsa05215	Prostate cancer	8	4.20E-11	0.082474227
KEGG	hsa01522	Endocrine resistance	8	4.52E-11	0.081632653
KEGG	hsa05205	Proteoglycans in cancer	9	1.53E-10	0.043902439
KEGG	hsa05200	Pathways in cancer	11	2.85E-10	0.020715631
KEGG	hsa04110	Cell cycle	7	1.92E-08	0.05511811
KEGG	hsa05218	Melanoma	6	5.51E-08	0.083333333
KEGG	hsa05214	Glioma	6	6.78E-08	0.08
KEGG	hsa05220	Chronic myeloid leukemia	6	7.25E-08	0.078947368
KEGG	hsa05161	Hepatitis B	7	8.27E-08	0.043209877
KEGG	hsa05163	Human cytomegalovirus infection	7	5.81E-07	0.031111111
KEGG	hsa04218	Cellular senescence	6	2.65E-06	0.038461538
KEGG	hsa04115	p53 signaling pathway	5	3.88E-06	0.068493151
KEGG	hsa05212	Pancreatic cancer	5	4.56E-06	0.065789474
KEGG	hsa05169	Epstein-Barr virus infection	6	9.43E-06	0.02970297
KEGG	hsa04933	AGE-RAGE signaling pathway in diabetic complications	5	1.37E-05	0.05
KEGG	hsa05166	Human T-cell leukemia virus 1 infection	6	1.49E-05	0.027027027
KEGG	hsa04068	FoxO signaling pathway	5	3.97E-05	0.038167939
KEGG	hsa05418	Fluid shear stress and atherosclerosis	5	5.01E-05	0.035971223
KEGG	hsa05224	Breast cancer	5	6.24E-05	0.034013605
KEGG	hsa05226	Gastric cancer	5	6.57E-05	0.033557047