

Supplementary materials

Table S1 Regulatory network definition of edge and node by Cytoscape. In the third column 'Up/Dn', '+' indicates the corresponding gene in the first columns is up-regulated, while '-' indicates down-regulation. The number in the column 'Group' indicates the group, with 1 for up-regulated genes, -1 for down-regulated genes, -2 for hub TFs, and 2 for TCF7L2

<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
ARSB	CAD	+	ARSB	1
COL5A1	CAD	+	ATP7B	1
GALC	CAD	+	COL5A1	1
ITGA6	CAD	+	GALC	1
THBD	CAD	+	ITGA6	1
COL5A2	CAD	+	TGFBI	1
APP	CAD	+	THBD	1
CXCL12	CAD	+	CDKN1A	1
CYP24A1	CAD	+	COL5A2	1
MAOB	CAD	+	EXT2	1
PAM	CAD	+	APP	1
PRLR	CAD	+	CXCL12	1
ATP2B1	CAD	+	LTBP1	1
SERPINA1	CAD	+	CYP24A1	1
MGLL	CAD	+	MAOB	1
TULP4	CAD	+	NPR3	1
ANO6	CAD	+	PAM	1
VEGFA	CAD	+	PPP3CA	1
GPR126	CAD	+	PRLR	1
MAP2	CAD	+	ATP2B1	1
EDN1	CAD	+	SERPINA1	1

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
FN1	CAD	+	MGLL	1
INHBA	CAD	+	TULP4	1
ITGB1	CAD	+	SHISA2	1
NT5E	CAD	+	ANO6	1
PTK7	CAD	+	VEGFA	1
RBMS1	CAD	+	GPR126	1
SORL1	CAD	+	NPNT	1
STC1	CAD	+	CYFIP2	1
YWHAZ	CAD	+	FHL2	1
DYRK2	CAD	+	MAP2	1
ENC1	CAD	+	HIPK3	1
WISP2	CAD	+	BMPR2	1
ASPH	CAD	+	CDK8	1
EPHA4	CAD	+	DGKA	1
RPS6KA3	CAD	+	DDX3X	1
ANXA3	CAD	+	CAPN2	1
RND3	CAD	+	SLC31A2	1
LMO7	CAD	+	EDN1	1
PTPN14	CAD	+	FN1	1
MAFB	CAD	+	FRK	1
ABCA1	CAD	+	GOLGA4	1
LHFPL2	CAD	+	INHBA	1
ZNF193	CAD	+	ITGB1	1
NEBL	CAD	+	LAMC1	1
TRIM16	CAD	+	LRP1	1
RAB31	CAD	+	NT5E	1
SLC35D2	CAD	+	PDE7A	1
PTPN21	CAD	+	KLK6	1
DDAH1	CAD	+	PTK7	1
MGAT4A	CAD	+	RBMS1	1
LPHN2	CAD	+	SORL1	1
C1orf9	CAD	+	SOX4	1

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Edge			Node	
Name_Node1	Name_Node2	Up/Dn	Name	Group
TNFRSF21	CAD	+	STC1	1
LMCD1	CAD	+	YWHAZ	1
SECISBP2L	CAD	+	DYRK2	1
RHOBTB3	CAD	+	ENC1	1
CPEB3	CAD	+	WISP2	1
ABLM3	CAD	+	GPRC5A	1
NMNAT2	CAD	+	STX3	1
KANK1	CAD	+	ASPH	1
ABCA12	CAD	+	COL12A1	1
NBEA	CAD	+	EPHA4	1
RRM2B	CAD	+	RPS6KA3	1
FAM49B	CAD	+	MAP4K4	1
FIGN	CAD	+	GDF15	1
STRADB	CAD	+	ANXA3	1
ERRF1	CAD	+	RND3	1
PTGFRN	CAD	+	ELK3	1
SEMA6A	CAD	+	LMO7	1
VAT1L	CAD	+	PTPN14	1
CFL2	CAD	+	MAFB	1
SUSD1	CAD	+	ABCA1	1
GPR87	CAD	+	LAMC2	1
DLC1	CAD	+	LHFPL2	1
ADPGK	CAD	+	MAP1B	1
HOOK3	CAD	+	DLC1	1
LCOR	CAD	+	PCP4	1
CCND1	CAD	+	ZNF193	1
ITGB1	CAD	+	NEBL	1
GLCCI1	CAD	+	TRIM16	1
TMEM45B	CAD	+	BTG2	1
MBNL2	CAD	+	RAB31	1
BTBD9	CAD	+	SLC35D2	1
TES	CAD	+	PTPN21	1

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
KANK1	CAD	+	UBL3	1
ABCA12	CAD	+	DDAH1	1
PGM2L1	CAD	+	MGAT4A	1
JAZF1	CAD	+	LPHN2	1
LONRF2	CAD	+	SOCS5	1
ARSB	CAD	+	KSR1	1
DOCK8	CAD	+	C1orf9	1
FREM2	CAD	+	LYPD3	1
ARSB	FOXO1	+	TNFRSF21	1
ATP7B	FOXO1	+	SESN1	1
COL5A1	FOXO1	+	TNRC6A	1
ITGA6	FOXO1	+	LMCD1	1
TGFBI	FOXO1	+	SECISBP2L	1
THBD	FOXO1	+	RHOBTB3	1
CDKN1A	FOXO1	+	CPEB3	1
COL5A2	FOXO1	+	ABLIM3	1
EXT2	FOXO1	+	PHLPP2	1
APP	FOXO1	+	NMNAT2	1
LTBP1	FOXO1	+	KANK1	1
CYP24A1	FOXO1	+	TES	1
MAOB	FOXO1	+	ABCA12	1
NPR3	FOXO1	+	NBEA	1
PAM	FOXO1	+	RRM2B	1
PPP3CA	FOXO1	+	C1orf9	1
PRLR	FOXO1	+	FAM49B	1
ATP2B1	FOXO1	+	FIGN	1
SERPINA1	FOXO1	+	STRADB	1
MGLL	FOXO1	+	ERRFI1	1
SHISA2	FOXO1	+	PTGFRN	1
ANO6	FOXO1	+	SEMA6A	1
VEGFA	FOXO1	+	VAT1L	1
GPR126	FOXO1	+	CLDN1	1

Table S1 Regulatory network definition of edge and node by Cytoscape. In the third column 'Up/Dn', '+' indicates the corresponding gene in the first columns is up-regulated, while '-' indicates down-regulation. The number in the column 'Group' indicates the group, with 1 for up-regulated genes, -1 for down-regulated genes, -2 for hub TFs, and 2 for TCF7L2 (continued)

Edge			Node	
Name_Node1	Name_Node2	Up/Dn	Name	Group
FHL2	FOXO1	+	CFL2	1
MAP2	FOXO1	+	SUSD1	1
HIPK3	FOXO1	+	TNS3	1
BMPR2	FOXO1	+	AEN	1
CDK8	FOXO1	+	RNF38	1
DDX3X	FOXO1	+	OTUB2	1
CAPN2	FOXO1	+	GPR87	1
SLC31A2	FOXO1	+	DLC1	1
EDN1	FOXO1	+	FRAS1	1
FRK	FOXO1	+	DICER1	1
GOLGA4	FOXO1	+	ADPGK	1
ITGB1	FOXO1	+	C9orf5	1
LAMC1	FOXO1	+	HOOK3	1
NT5E	FOXO1	+	LCOR	1
PDE7A	FOXO1	+	KBTBD8	1
PTK7	FOXO1	+	PLEKHA8	1
RBMS1	FOXO1	+	STON2	1
STC1	FOXO1	+	CCND1	1
YWHAZ	FOXO1	+	FN1	1
DYRK2	FOXO1	+	ITGB1	1
ENC1	FOXO1	+	GLCCI1	1
WISP2	FOXO1	+	CFL2	1
GPRC5A	FOXO1	+	TMEM45B	1
STX3	FOXO1	+	RNF145	1
ASPH	FOXO1	+	MBNL2	1
COL12A1	FOXO1	+	DCP2	1
EPHA4	FOXO1	+	BTBD9	1
RPS6KA3	FOXO1	+	TES	1
MAP4K4	FOXO1	+	KANK1	1
GDF15	FOXO1	+	ABCA12	1
ANXA3	FOXO1	+	PGM2L1	1
RND3	FOXO1	+	JAZF1	1

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
ELK3	FOXO1	+	DICER1	1
LMO7	FOXO1	+	PAQR7	1
PTPN14	FOXO1	+	DLC1	1
ABCA1	FOXO1	+	RNF38	1
LHFPL2	FOXO1	+	LONRF2	1
DLC1	FOXO1	+	ARSB	1
NEBL	FOXO1	+	C2CD2	1
TRIM16	FOXO1	+	FHL2	1
BTG2	FOXO1	+	DOCK8	1
RAB31	FOXO1	+	LTBP1	1
SLC35D2	FOXO1	+	FREM2	1
PTPN21	FOXO1	+	CAD	-2
UBL3	FOXO1	+	FOXO1	-2
DDAH1	FOXO1	+	GATA3	-2
MGAT4A	FOXO1	+	TCF7L2	2
LPHN2	FOXO1	+	FBP1	-1
SOCS5	FOXO1	+	BLVRB	-1
KSR1	FOXO1	+	CRAT	-1
C1orf9	FOXO1	+	RPL37	-1
LYPD3	FOXO1	+	RPL38	-1
SESN1	FOXO1	+	RPLP1	-1
TNRC6A	FOXO1	+	ATP8B2	-1
LMCD1	FOXO1	+	DBNL	-1
SECISBP2L	FOXO1	+	ERGIC1	-1
RHOBTB3	FOXO1	+	ABR	-1
CPEB3	FOXO1	+	GMDS	-1
ABLIM3	FOXO1	+	DDR1	-1
PHLPP2	FOXO1	+	MYBL2	-1
NMNAT2	FOXO1	+	SAT1	-1
KANK1	FOXO1	+	TFF1	-1
TES	FOXO1	+	TPD52L2	-
NBEA	FOXO1	+	UNG	-1

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Edge			Node	
Name_Node1	Name_Node2	Up/Dn	Name	Group
C1orf9	FOXO1	+	NR5A2	-1
FAM49B	FOXO1	+	IER3	-1
FIGN	FOXO1	+	CSRP1	-1
STRADB	FOXO1	+	PKMYT1	-1
ERRFI1	FOXO1	+	FKBP2	-1
PTGFRN	FOXO1	+	NDUFB10	-1
SEMA6A	FOXO1	+	MB	-1
VAT1L	FOXO1	+	SFN	-1
CLDN1	FOXO1	+	POLR2I	-1
CFL2	FOXO1	+	AGPAT1	-1
SUSD1	FOXO1	+	STARD10	-1
TNS3	FOXO1	+	HNRNPUL1	-1
AEN	FOXO1	+	RPL35	-1
OTUB2	FOXO1	+	BRCA1	-1
GPR87	FOXO1	+	EPB41L1	-1
DLC1	FOXO1	+	KEAP1	-1
DICER1	FOXO1	+	SPDEF	-1
C9orf5	FOXO1	+	SSBP2	-1
LCOR	FOXO1	+	MYO16	-1
KBTBD8	FOXO1	+	ARL6IP1	-1
PLEKHA8	FOXO1	+	YBX2	-1
STON2	FOXO1	+	DCXR	-1
FN1	FOXO1	+	TREX1	-1
ITGB1	FOXO1	+	C17orf59	-1
GLCCI1	FOXO1	+	SLC35C1	-1
CFL2	FOXO1	+	ATP8B2	-1
TMEM45B	FOXO1	+	ZFAND3	-1
RNF145	FOXO1	+	GGCT	-1
MBNL2	FOXO1	+	GALNT12	-1
DCP2	FOXO1	+	ADCK4	-1
TES	FOXO1	+	C10orf81	-1
KANK1	FOXO1	+	SLC37A3	-1

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
ABCA12	FOXO1	+	AGPAT1	-1
PGM2L1	FOXO1	+	C19orf33	-1
JAZF1	FOXO1	+	SLC44A1	-1
DLC1	FOXO1	+	HNRNPUL1	-1
LONRF2	FOXO1	+	PKHD1L1	-1
ARSB	FOXO1	+	H2AFJ	-1
C2CD2	FOXO1	+	NUDT1	-1
FHL2	FOXO1	+	ABCG1	-1
DOCK8	FOXO1	+	AP1	-2
LTBP1	FOXO1	+	AP2A	-2
FREM2	FOXO1	+	PBF	-2
ARSB	GATA3	+		
COL5A1	GATA3	+		
GALC	GATA3	+		
ITGA6	GATA3	+		
TGFBI	GATA3	+		
THBD	GATA3	+		
CDKN1A	GATA3	+		
COL5A2	GATA3	+		
EXT2	GATA3	+		
APP	GATA3	+		
CXCL12	GATA3	+		
LTBP1	GATA3	+		
CYP24A1	GATA3	+		
MAOB	GATA3	+		
PAM	GATA3	+		
PPP3CA	GATA3	+		
PRLR	GATA3	+		
ATP2B1	GATA3	+		
MGLL	GATA3	+		
TULP4	GATA3	+		
ANO6	GATA3	+		

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
GPR126	GATA3	+		
NPNT	GATA3	+		
CYFIP2	GATA3	+		
FHL2	GATA3	+		
MAP2	GATA3	+		
BMPR2	GATA3	+		
DDX3X	GATA3	+		
CAPN2	GATA3	+		
SLC31A2	GATA3	+		
EDN1	GATA3	+		
FN1	GATA3	+		
FRK	GATA3	+		
ITGB1	GATA3	+		
LAMC1	GATA3	+		
LRP1	GATA3	+		
NT5E	GATA3	+		
PDE7A	GATA3	+		
RBMS1	GATA3	+		
SORL1	GATA3	+		
STC1	GATA3	+		
YWHAZ	GATA3	+		
DYRK2	GATA3	+		
ENC1	GATA3	+		
WISP2	GATA3	+		
GPRC5A	GATA3	+		
STX3	GATA3	+		
ASPH	GATA3	+		
COL12A1	GATA3	+		
EPHA4	GATA3	+		
RPS6KA3	GATA3	+		
ANXA3	GATA3	+		
RND3	GATA3	+		

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
ELK3	GATA3	+		
LMO7	GATA3	+		
PTPN14	GATA3	+		
MAFB	GATA3	+		
ABCA1	GATA3	+		
LAMC2	GATA3	+		
LHFPL2	GATA3	+		
MAP1B	GATA3	+		
DLC1	GATA3	+		
NEBL	GATA3	+		
TRIM16	GATA3	+		
BTG2	GATA3	+		
RAB31	GATA3	+		
SLC35D2	GATA3	+		
PTPN21	GATA3	+		
UBL3	GATA3	+		
MGAT4A	GATA3	+		
LPHN2	GATA3	+		
SOCS5	GATA3	+		
KSR1	GATA3	+		
C1orf9	GATA3	+		
LYPD3	GATA3	+		
TNFRSF21	GATA3	+		
SESN1	GATA3	+		
TNRC6A	GATA3	+		
LMCD1	GATA3	+		
SECISBP2L	GATA3	+		
RHOBTB3	GATA3	+		
CPEB3	GATA3	+		
ABLIM3	GATA3	+		
PHLPP2	GATA3	+		
NMNAT2	GATA3	+		

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
KANK1	GATA3	+		
TES	GATA3	+		
ABCA12	GATA3	+		
NBEA	GATA3	+		
FAM49B	GATA3	+		
FIGN	GATA3	+		
STRADB	GATA3	+		
ERRFI1	GATA3	+		
PTGFRN	GATA3	+		
SEMA6A	GATA3	+		
CLDN1	GATA3	+		
CFL2	GATA3	+		
SUSD1	GATA3	+		
TNS3	GATA3	+		
AEN	GATA3	+		
OTUB2	GATA3	+		
DLC1	GATA3	+		
C9orf5	GATA3	+		
LCOR	GATA3	+		
PLEKHA8	GATA3	+		
STON2	GATA3	+		
CCND1	GATA3	+		
FN1	GATA3	+		
ITGB1	GATA3	+		
GLCCI1	GATA3	+		
CFL2	GATA3	+		
RNF145	GATA3	+		
MBNL2	GATA3	+		
BTBD9	GATA3	+		
TES	GATA3	+		
KANK1	GATA3	+		
ABCA12	GATA3	+		

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
PGM2L1	GATA3	+		
JAZF1	GATA3	+		
PAQR7	GATA3	+		
DLC1	GATA3	+		
LONRF2	GATA3	+		
FHL2	GATA3	+		
LTBP1	GATA3	+		
FREM2	GATA3	+		
ITGA6	TCF7L2	+		
TGFBI	TCF7L2	+		
THBD	TCF7L2	+		
CDKN1A	TCF7L2	+		
COL5A2	TCF7L2	+		
EXT2	TCF7L2	+		
APP	TCF7L2	+		
CXCL12	TCF7L2	+		
LTBP1	TCF7L2	+		
CYP24A1	TCF7L2	+		
MAOB	TCF7L2	+		
NPR3	TCF7L2	+		
PAM	TCF7L2	+		
PPP3CA	TCF7L2	+		
PRLR	TCF7L2	+		
SERPINA1	TCF7L2	+		
MGLL	TCF7L2	+		
TULP4	TCF7L2	+		
SHISA2	TCF7L2	+		
VEGFA	TCF7L2	+		
GPR126	TCF7L2	+		
CYFIP2	TCF7L2	+		
FHL2	TCF7L2	+		
HIPK3	TCF7L2	+		

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Edge			Node	
Name_Node1	Name_Node2	Up/Dn	Name	Group
BMPR2	TCF7L2	+		
CDK8	TCF7L2	+		
DDX3X	TCF7L2	+		
SLC31A2	TCF7L2	+		
EDN1	TCF7L2	+		
FN1	TCF7L2	+		
FRK	TCF7L2	+		
ITGB1	TCF7L2	+		
LAMC1	TCF7L2	+		
LRP1	TCF7L2	+		
NT5E	TCF7L2	+		
PDE7A	TCF7L2	+		
PTK7	TCF7L2	+		
RBMS1	TCF7L2	+		
SORL1	TCF7L2	+		
DYRK2	TCF7L2	+		
ENC1	TCF7L2	+		
GPRC5A	TCF7L2	+		
STX3	TCF7L2	+		
ASPH	TCF7L2	+		
COL12A1	TCF7L2	+		
EPHA4	TCF7L2	+		
RPS6KA3	TCF7L2	+		
MAP4K4	TCF7L2	+		
RND3	TCF7L2	+		
LMO7	TCF7L2	+		
PTPN14	TCF7L2	+		
ABCA1	TCF7L2	+		
LAMC2	TCF7L2	+		
LHFPL2	TCF7L2	+		
DLC1	TCF7L2	+		
PCP4	TCF7L2	+		

Table S1 Regulatory network definition of edge and node by Cytoscape. In the third column 'Up/Dn', '+' indicates the corresponding gene in the first columns is up-regulated, while '-' indicates down-regulation. The number in the column 'Group' indicates the group, with 1 for up-regulated genes, -1 for down-regulated genes, -2 for hub TFs, and 2 for TCF7L2 (continued)

<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
NEBL	TCF7L2	+		
BTG2	TCF7L2	+		
RAB31	TCF7L2	+		
SLC35D2	TCF7L2	+		
PTPN21	TCF7L2	+		
UBL3	TCF7L2	+		
DDAH1	TCF7L2	+		
MGAT4A	TCF7L2	+		
LPHN2	TCF7L2	+		
SOCS5	TCF7L2	+		
KSR1	TCF7L2	+		
C1orf9	TCF7L2	+		
TNFRSF21	TCF7L2	+		
SESN1	TCF7L2	+		
LMCD1	TCF7L2	+		
RHOBTB3	TCF7L2	+		
PHLPP2	TCF7L2	+		
KANK1	TCF7L2	+		
NBEA	TCF7L2	+		
RRM2B	TCF7L2	+		
FAM49B	TCF7L2	+		
FIGN	TCF7L2	+		
STRADB	TCF7L2	+		
PTGFRN	TCF7L2	+		
SEMA6A	TCF7L2	+		
VAT1L	TCF7L2	+		
CLDN1	TCF7L2	+		
SUSD1	TCF7L2	+		
TNS3	TCF7L2	+		
AEN	TCF7L2	+		
ADPGK	TCF7L2	+		
C9orf5	TCF7L2	+		

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Edge			Node	
Name_Node1	Name_Node2	Up/Dn	Name	Group
KBTBD8	TCF7L2	+		
PLEKHA8	TCF7L2	+		
STON2	TCF7L2	+		
ITGB1	TCF7L2	+		
GLCCI1	TCF7L2	+		
RNF145	TCF7L2	+		
MBNL2	TCF7L2	+		
DCP2	TCF7L2	+		
TES	TCF7L2	+		
JAZF1	TCF7L2	+		
DLC1	TCF7L2	+		
RNF38	TCF7L2	+		
LONRF2	TCF7L2	+		
FHL2	TCF7L2	+		
DOCK8	TCF7L2	+		
LTBP1	TCF7L2	+		
FREM2	TCF7L2	+		
FBP1	AP1	-		
BLVRB	AP1	-		
CRAT	AP1	-		
RPL38	AP1	-		
RPLP1	AP1	-		
ATP8B2	AP1	-		
DBNL	AP1	-		
ERGIC1	AP1	-		
ABR	AP1	-		
GMDS	AP1	-		
DDR1	AP1	-		
MYBL2	AP1	-		
SAT1	AP1	-		
TFF1	AP1	-		
TPD52L2	AP1	-		

Table S1 Regulatory network definition of edge and node by Cytoscape. In the third column 'Up/Dn', '+' indicates the corresponding gene in the first columns is up-regulated, while '-' indicates down-regulation. The number in the column 'Group' indicates the group, with 1 for up-regulated genes, -1 for down-regulated genes, -2 for hub TFs, and 2 for TCF7L2 (continued)

<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
UNG	AP1	-		
NR5A2	AP1	-		
IER3	AP1	-		
CSRP1	AP1	-		
PKMYT1	AP1	-		
FKBP2	AP1	-		
MB	AP1	-		
AGPAT1	AP1	-		
STARD10	AP1	-		
RPL35	AP1	-		
EPB41L1	AP1	-		
SSBP2	AP1	-		
MYO16	AP1	-		
ARL6IP1	AP1	-		
DCXR	AP1	-		
ZFAND3	AP1	-		
ADCK4	AP1	-		
SLC37A3	AP1	-		
AGPAT1	AP1	-		
C19orf33	AP1	-		
HNRNPUL1	AP1	-		
PKHD1L1	AP1	-		
ABCG1	AP1	-		
RPL37	AP2A	-		
RPL38	AP2A	-		
RPLP1	AP2A	-		
ATP8B2	AP2A	-		
DBNL	AP2A	-		
ERGIC1	AP2A	-		
ABR	AP2A	-		
DDR1	AP2A	-		
MYBL2	AP2A	-		

Table S1 Regulatory network definition of edge and node by Cytoscape. In the third column 'Up/Dn', '+' indicates the corresponding gene in the first columns is up-regulated, while '-' indicates down-regulation. The number in the column 'Group' indicates the group, with 1 for up-regulated genes, -1 for down-regulated genes, -2 for hub TFs, and 2 for TCF7L2 (continued)

Edge			Node	
Name_Node1	Name_Node2	Up/Dn	Name	Group
SAT1	AP2A	-		
TFF1	AP2A	-		
TPD52L2	AP2A	-		
UNG	AP2A	-		
IER3	AP2A	-		
CSRP1	AP2A	-		
PKMYT1	AP2A	-		
FKBP2	AP2A	-		
NDUFB10	AP2A	-		
MB	AP2A	-		
SFN	AP2A	-		
POLR2I	AP2A	-		
STARD10	AP2A	-		
HNRNPUL1	AP2A	-		
RPL35	AP2A	-		
KEAP1	AP2A	-		
SPDEF	AP2A	-		
MYO16	AP2A	-		
ARL6IP1	AP2A	-		
YBX2	AP2A	-		
DCXR	AP2A	-		
ATP8B2	AP2A	-		
ZFAND3	AP2A	-		
GALNT12	AP2A	-		
ADCK4	AP2A	-		
SLC37A3	AP2A	-		
AGPAT1	AP2A	-		
PKHD1L1	AP2A	-		
NUDT1	AP2A	-		
ABCG1	AP2A	-		
BLVRB	GATA3	-		
CRAT	GATA3	-		

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
RPL37	GATA3	-		
RPL38	GATA3	-		
ATP8B2	GATA3	-		
ERGIC1	GATA3	-		
GMDS	GATA3	-		
DDR1	GATA3	-		
SAT1	GATA3	-		
TFF1	GATA3	-		
UNG	GATA3	-		
NR5A2	GATA3	-		
IER3	GATA3	-		
PKMYT1	GATA3	-		
FKBP2	GATA3	-		
MB	GATA3	-		
SFN	GATA3	-		
POLR2I	GATA3	-		
AGPAT1	GATA3	-		
STARD10	GATA3	-		
HNRNPUL1	GATA3	-		
RPL35	GATA3	-		
BRCA1	GATA3	-		
SPDEF	GATA3	-		
SSBP2	GATA3	-		
MYO16	GATA3	-		
ARL6IP1	GATA3	-		
DCXR	GATA3	-		
SLC35C1	GATA3	-		
ATP8B2	GATA3	-		
ZFAND3	GATA3	-		
GALNT12	GATA3	-		
ADCK4	GATA3	-		
C10orf81	GATA3	-		

Table S1 Regulatory network definition of edge and node by Cytoscape. In the third column 'Up/Dn', '+' indicates the corresponding gene in the first columns is up-regulated, while '-' indicates down-regulation. The number in the column 'Group' indicates the group, with 1 for up-regulated genes, -1 for down-regulated genes, -2 for hub TFs, and 2 for TCF7L2 (continued)

<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
AGPAT1	GATA3	-		
C19orf33	GATA3	-		
SLC44A1	GATA3	-		
PKHD1L1	GATA3	-		
H2AFJ	GATA3	-		
FBP1	PBF	-		
CRAT	PBF	-		
RPL37	PBF	-		
RPL38	PBF	-		
RPLP1	PBF	-		
ATP8B2	PBF	-		
ERGIC1	PBF	-		
GMDS	PBF	-		
SAT1	PBF	-		
TFF1	PBF	-		
TPD52L2	PBF	-		
UNG	PBF	-		
NR5A2	PBF	-		
IER3	PBF	-		
CSRP1	PBF	-		
PKMYT1	PBF	-		
FKBP2	PBF	-		
NDUFB10	PBF	-		
SFN	PBF	-		
STARD10	PBF	-		
HNRNPUL1	PBF	-		
BRCA1	PBF	-		
EPB41L1	PBF	-		
MYO16	PBF	-		
ARL6IP1	PBF	-		
DCXR	PBF	-		
TREX1	PBF	-		

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<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
C17orf59	PBF	-		
SLC35C1	PBF	-		
ZFAND3	PBF	-		
GGCT	PBF	-		
GALNT12	PBF	-		
ADCK4	PBF	-		
C10orf81	PBF	-		
SLC37A3	PBF	-		
AGPAT1	PBF	-		
C19orf33	PBF	-		
HNRNPUL1	PBF	-		
PKHD1L1	PBF	-		
H2AFJ	PBF	-		
NUDT1	PBF	-		
ABCG1	PBF	-		
CRAT	TCF7L2	-		
RPL38	TCF7L2	-		
RPLP1	TCF7L2	-		
DBNL	TCF7L2	-		
ERGIC1	TCF7L2	-		
ABR	TCF7L2	-		
GMDS	TCF7L2	-		
SAT1	TCF7L2	-		
UNG	TCF7L2	-		
NR5A2	TCF7L2	-		
IER3	TCF7L2	-		
STARD10	TCF7L2	-		
BRCA1	TCF7L2	-		
EPB41L1	TCF7L2	-		
KEAP1	TCF7L2	-		
SSBP2	TCF7L2	-		
MYO16	TCF7L2	-		

Table S1 Regulatory network definition of edge and node by Cytoscape. In the third column 'Up/Dn', '+' indicates the corresponding gene in the first columns is up-regulated, while '-' indicates down-regulation. The number in the column 'Group' indicates the group, with 1 for up-regulated genes, -1 for down-regulated genes, -2 for hub TFs, and 2 for TCF7L2 (continued)

<i>Edge</i>			<i>Node</i>	
<i>Name_Node1</i>	<i>Name_Node2</i>	<i>Up/Dn</i>	<i>Name</i>	<i>Group</i>
ARL6IP1	TCF7L2	-		
ATP8B2	TCF7L2	-		
ADCK4	TCF7L2	-		
AGPAT1	TCF7L2	-		
C19orf33	TCF7L2	-		
SLC44A1	TCF7L2	-		
PKHD1L1	TCF7L2	-		