Supplementary Materials: Maternal Chromium Restriction Leads to Glucose Metabolism Imbalance in Mice Offspring through Insulin Signaling and Wnt Signaling Pathways

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Table S1. The most enrichment GO terms ($p < 0.001$).

Term	Count	Fold Enrichment	*p*-Value	Catalogue
transcription	60	1.8330	3.07×10^{-6}	Biology Process
regulation of transcription	70	1.7016	4.52×10^{-6}	Biology Process
regulation of RNA metabolic process	51	1.8554	1.66×10^{-5}	Biology Process
regulation of transcription, DNA-dependent	50	1.8476	2.32×10^{-5}	Biology Process
positive regulation of transcription, DNA-dependent	21	2.7328	8.75×10^{-5}	Biology Process
positive regulation of RNA metabolic process	21	2.7132	9.71×10^{-5}	Biology Process
response to insulin stimulus	8	7.3404	9.90×10^{-5}	Biology Process
positive regulation of transcription from RNA polymerase II promoter	19	2.8731	1.14×10^{-4}	Biology Process
insulin receptor signaling pathway	6	11.6004	1.41×10^{-4}	Biology Process
regulation of transcription from RNA polymerase II promoter	26	2.2849	1.76×10^{-4}	Biology Process
positive regulation of nitrogen compound metabolic process	23	2.3671	2.91×10^{-4}	Biology Process
tube development	15	3.0758	3.88×10^{-4}	Biology Process
positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	22	2.3352	4.87×10^{-4}	Biology Process
positive regulation of transcription	21	2.3933	5.05×10^{-4}	Biology Process
positive regulation of cellular biosynthetic process	23	2.2556	5.60×10^{-4}	Biology Process
positive regulation of biosynthetic process	23	2.2353	6.34×10^{-4}	Biology Process
positive regulation of gene expression	21	2.3296	7.06×10^{-4}	Biology Process
ventricular cardiac muscle cell differentiation	4	19.6852	9.10×10^{-4}	Biology Process
nucleoplasm part	21	2.4608	3.34×10^{-4}	Cellular Components
nucleoplasm	23	2.3082	3.84×10^{-4}	Cellular Components
transcription regulator activity	46	2.2728	2.00×10^{-7}	Molecular Function
DNA binding	55	1.8401	6.91×10^{-6}	Molecular Function
transcription factor activity	29	2.2268	9.76×10^{-5}	Molecular Function
zinc ion binding	58	1.6418	9.96×10^{-5}	Molecular Function
transition metal ion binding	68	1.5536	1.01×10^{-4}	Molecular Function
transcription factor binding	15	3.1035	3.51×10^{-4}	Molecular Function

Table S2. Most enrichment pathways by KEGG ($p < 0.001$).

Pathway ID	Pathway	Count	Genes	Fold Enrichment	*p*-Value
mmu04310	Wnt signaling pathway	15	*Wnt5a*, *Ppp2r1a*, *Tcf7*, *Ppard*, *Ppp2r5b*, *Apc2*, *Crebbp*, *Skp1a*, *Tcf7l2*, *Porcn*, *Tcf7l1*, *Ctnnb1*, *Rac3*, *Ppp3cb*, *Frat1*	4.5484	1.81×10^{-5}
mmu05215	Prostate cancer	11	*Akt1*, *Tcf7*, *Ar*, *Creb3*, *Crebbp*, *Foxo1*, *Pik3ca*, *Ins1*, *Pik3r3*, *Tcf7l2*, *Tcf7l1*	5.5659	2.20×10^{-5}
mmu04520	Adherens junction	10	*Tcf7*, *Rac3*, *Crebbp*, *Lmo7*, *Cdh1*, *Ptpn1*, *Insr*, *Tcf7l2*, *Iqgap1*, *Tcf7l1*	5.9920	3.45×10^{-5}
mmu04910	Insulin signaling pathway	13	*Akt1*, *Irs2*, *Socs2*, *Slc2a4*, *Inpp5k*, *Tsc2*, *Foxo1*, *Pik3ca*, *Ptpn1*, *Ins1*, *Pik3r3*, *Pck2*, *Insr*	4.2899	4.00×10^{-5}
mmu04930	Type II diabetes mellitus	8	*Irs2*, *Socs2*, *Slc2a4*, *Cacna1g*, *Pik3ca*, *Ins1*, *Pik3r3*, *Insr*	7.4350	7.90×10^{-5}
mmu05213	Endometrial cancer	8	*Akt1*, *Tcf7*, *Apc2*, *Pik3ca*, *Cdh1*, *Pik3r3*, *Tcf7l2*, *Tcf7l1*	7.0061	1.17×10^{-4}
mmu05200	Pathways in cancer	19	*Wnt5a*, *Ar*, *Ppard*, *Tcf7*, *Apc2*, *Rxra*, *Crebbp*, *Itga2*, *Foxo1*, *Cdh1*, *Tcf7l2*, *Tcf7l1*, *Arnt*, *Akt1*, *Ccdc6*, *Rac3*, *Pik3ca*, *Rarb*, *Pik3r3*	2.6788	1.92×10^{-4}
mmu05216	Thyroid cancer	6	*Ccdc6*, *Tcf7*, *Rxra*, *Cdh1*, *Tcf7l2*, *Tcf7l1*	9.4220	3.53×10^{-4}

Table S3. Real-time PCR primers.

Transcripts	ID	Primer Direction	Primer Sequence	Product Length
Socs2	NM_007706	F	5′-TTAGAGATAGTTCGCATTCAGA-3′	79
		R	5′-TCAATCCGCAGGTTAGTC-3′	
Akt1	NM_009652	F	5′-CAGTTTGAGACCACACAT-3′	75
		R	5′-GCGTCAGTCCTTAATAGTT-3′	
Irs2	NM_001081212	F	5′-AGGACTATGGAGACATTGAG-3′	75
		R	5′-GCATGTAGCCATCATCTG-3′	
Pik3ca	NM_008839	F	5′-TGTGGCATCTGAGTATCT-3′	132
		R	5′-TGTGGCATCTGAGTATCT-3′	
Tcf7l2	NM_001142918	F	5′-GGACACCACTCAACAATG-3′	76
		R	5′-TACAGCAAGCAACCTCTAA-3′	
Wnt5a	NM_009524	F	5′-GAGTATCGTCCTTCATTGC-3′	101
		R	5′-TCCTGGTATTCGTGGTAG-3′	
Ctnnb1 (catenin, beta 1)	NM_007614	F	5′-ATGGAGGAGATAGTAGAA-3′	98
		R	5′-AATGGAATGGTATTGAGT-3′	
FoxO1	NM_019739	F	5′-CCTTGAGCAGCCTAATGT-3′	108
		R	5′-CGATGGACGGAATGAGAG-3′	
G6pc	NM_008061	F	5′-GAAGGATGGAGGAAGGAA-3′	77
		R	5′-TTGGTAATTCACTTGGAGATAG-3′	
Ins1	NM_008386	F	5′-GGAGGTACTTTGGACTAT-3′	79
		R	5′-GATGGTCTCTGATTATAGC-3′	
Pck2 (Pepck)	NM_028994	F	5′-CCTCTGACAATCGTGCTA-3′	128
		R	5′-GTTATTATGTTCAATCCAACTCTG-3′	
Slc2a4 (Glut4)	NM_009204	F	5′-TATGTTGCGGATGCTATG-3′	82
		R	5′-TTAGGAAGGTGAAGATGAAG-3′	
Ptpn1 (Ptp1b)	NM_011201	F	5′-CCACGAACAGAGTCTAAT-3′	79
		R	5′-TGAGAGCAAGAAGAGTATT-3′	

Socs2: suppressor of cytokine signaling 2; *Akt1*: Thymoma viral proto-oncogene 1; *Irs2*: insulin receptor substrate 2; *Pik3ca*: phosphatidylinositol 3-kinase, catalytic, alpha polypeptide; *Tcf7l2*: transcription factor 7 like 2; *Wnt5a*: wingless-type MMTV integration site family, member 5A; *Ctnnb1* (catenin, beta 1): catenin (cadherin associated protein), beta 1; *FoxO1*: forkhead box O1; *G6pc*: glucose-6-phosphatase, catalytic, *Ins1*: insulin 1; *Pck2* (*Pepck*): phosphoenolpyruvate carboxykinase 2; *Slc2a4* (*Glut4*): solute carrier family 2 member 4; *Ptpn1* (*Ptp1b*): protein tyrosine phosphatase, non-receptor type 1.

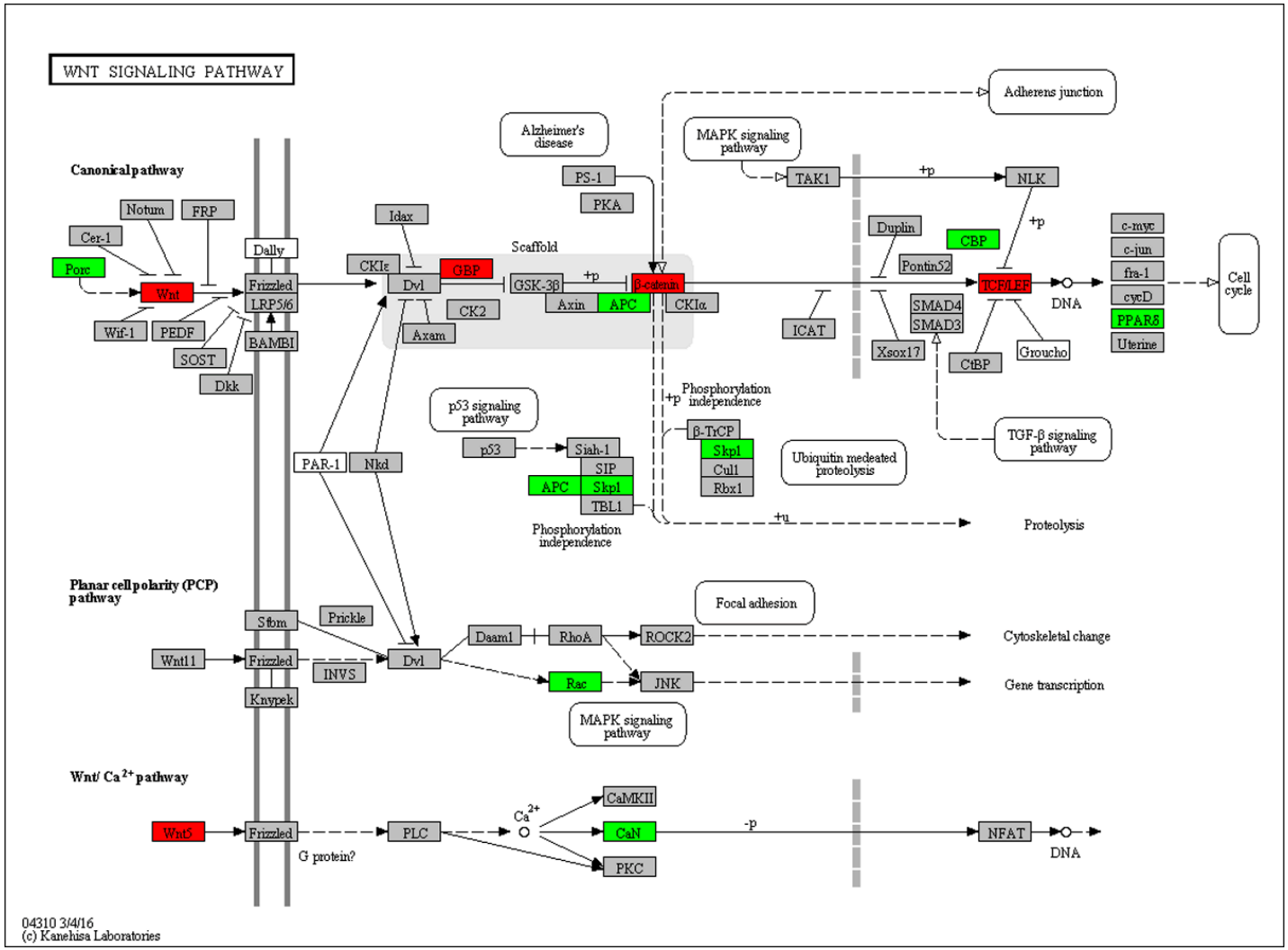

Figure S1. Wnt pathway. Red represents up-regulated; green represents down-regulated; grey represents no significant change. Arrows with dashed line show possible interaction of genes. Arrows with solid line show interaction of genes. T bars show inhibition of genes.

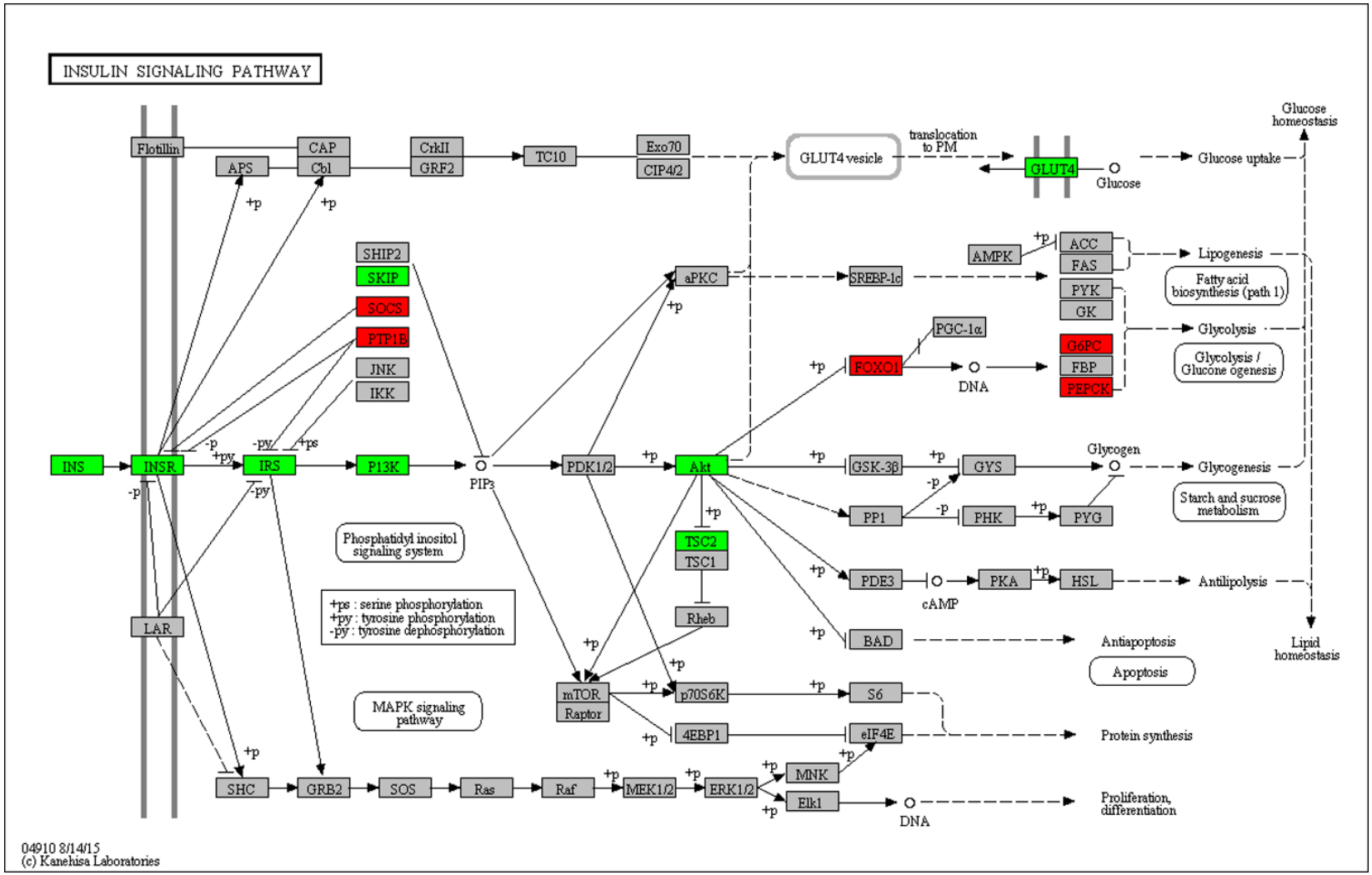

Figure S2. Insulin signaling pathway. Red represents up-regulated; green represents down-regulated; grey represents no significant change. Arrows with dashed line show possible interaction of genes. Arrows with solid line show interaction of genes. T bars show inhibition of genes.

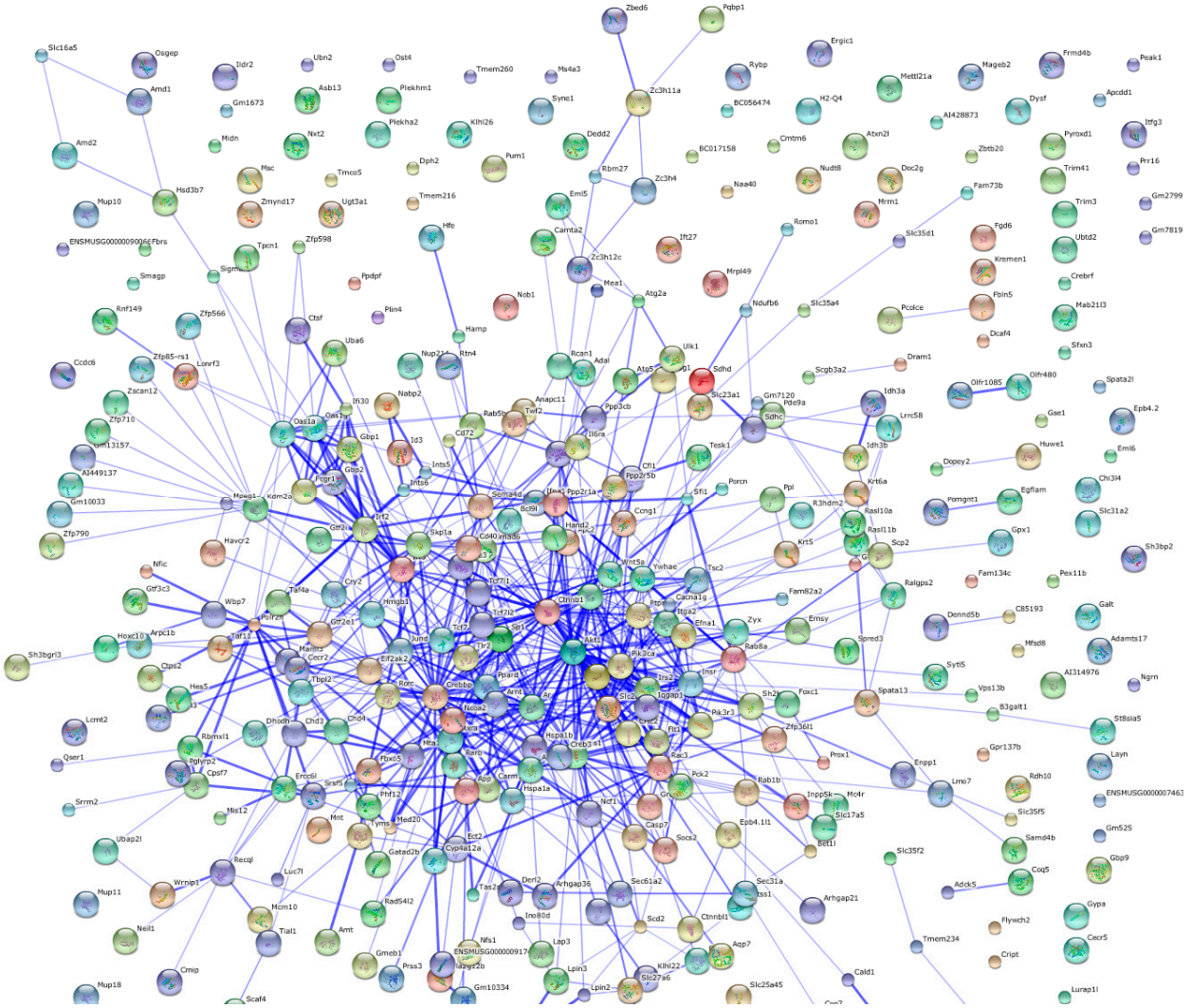

Figure S3. Interaction networks maps of differentially expressed genes. There were 13 nodes with ≥10 joint-edges in the map, including 190 joint-edges, which accounted for 88% of the total. Stronger associations are represented by thicker lines.

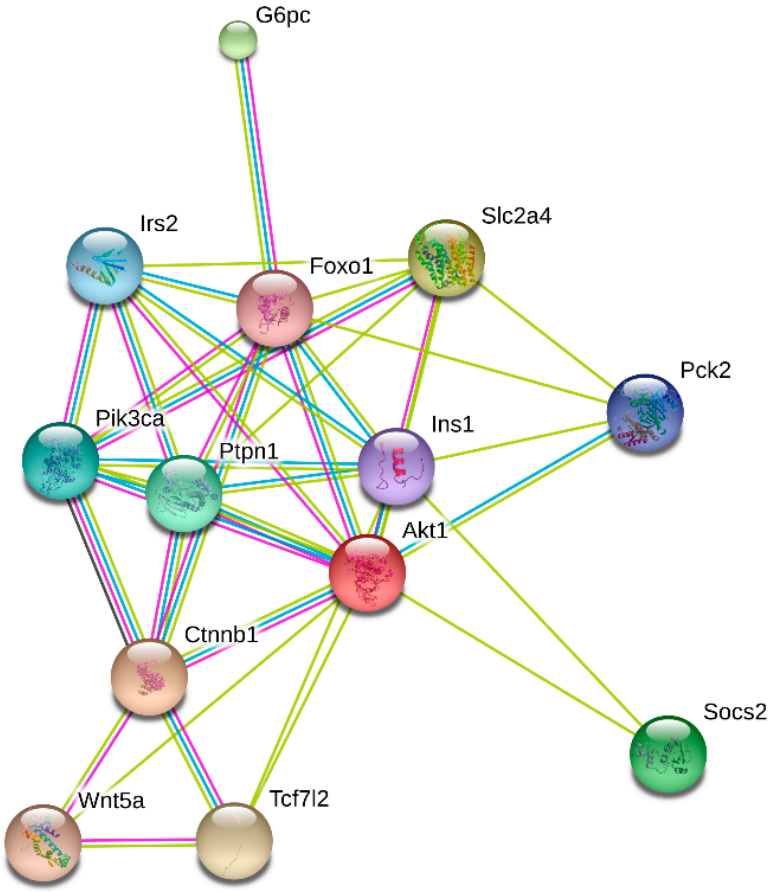

Figure S4. Interaction networks maps of differentially expressed genes in insulin signaling pathway and Wnt pathway. *Socs2*: suppressor of cytokine signaling 2; *Akt1*: Thymoma viral proto-oncogene 1; *Irs2*: insulin receptor substrate 2; *Pik3ca*: phosphatidylinositol 3-kinase, catalytic, alpha polypeptide; *Tcf7l2*: transcription factor 7 like 2; *Wnt5a*: wingless-type MMTV integration site family, member 5A; *Ctnnb1* (catenin, beta 1): catenin (cadherin associated protein), beta 1; *FoxO1*: forkhead box O1; *G6pc*: glucose-6-phosphatase, catalytic, *Ins1*: insulin 1; *Pck2* (*Pepck*): phosphoenolpyruvate carboxykinase 2; *Slc2a4* (*Glut4*): solute carrier family 2 member 4; *Ptpn1* (*Ptp1b*): protein tyrosine phosphatase, non-receptor type 1. Violet lines show experimentally determined interactions. Sky blue lines show known interactions from curated databases. Olive lines show interaction from text mining. Black lines show co-expression interaction.