

Using gene networks to identify genes and pathways involved in milk production traits in Polish Holstein dairy cattle

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Supplementary Online Material (SOM)

Table S1. Gene ontology (GO) terms significant at a maximum 0.1 level after a multiple testing correction

GO symbol	GO description	Count original	Count permuted	95% CI for Odds Ratio	P-value
Milk yield					
0000796	condensin complex	4	19	21.6–168.0	< 0.00001
0046581	intercellular canaliculus	3	17	16.5–164.5	< 0.00001
0007076	mitotic chromosome condensation	4	37	11.8–83.3	< 0.00001
0031581	hemidesmosome assembly	4	57	7.8–53.4	0.00001
0030056	hemidesmosome	4	59	7.6–51.5	0.00001
0051383	kinetochore organization	2	6	23.3–431.5	0.00001
0010032	meiotic chromosome condensation	2	6	23.3–431.5	0.00001
0045132	meiotic chromosome segregation	2	11	14.4–222.7	0.00008
0032437	cuticular plate	2	17	9.9–140.3	0.00094
0016331	morphogenesis of embryonic epithelium	2	17	9.9–140.3	0.00094
0001030	RNA polymerase III type 1 promoter DNA binding	2	17	9.9–140.3	0.00094
0001031	RNA polymerase III type 2 promoter DNA binding	2	17	9.9–140.3	0.00094
0001032	RNA polymerase III type 3 promoter DNA binding	2	17	9.9–140.3	0.00094
0008503	benzodiazepine receptor activity	1	2	20.6–1184.4	0.01058
1901350	cell-cell signaling inv. in cell-cell junction organ.	1	2	20.6–1184.4	0.01058
0046339	diacylglycerol metabolic proces	1	2	20.6–1184.4	0.01058
0071000	response to magnetism	1	2	20.6–1184.4	0.01058
0050765	negative regulation of phagocytosis	2	26	6.7–90.0	0.01381
0015432	bile acid-exporting ATPase activity	1	3	16.5–756.7	0.01431
0015126	canalicular bile acid transmembrane transporter activ.	1	3	16.5–756.7	0.01431
0015722	canalicular bile acid transport	1	3	16.5–756.7	0.01431
0008554	sodium-exporting ATPase activity, phosphorylative mech.	1	3	16.5–756.7	0.01431
0036155	acylglycerol acyl-chain remodeling	1	1	27.1–2506.6	0.01536
0035336	long-chain fatty-acyl-CoA metabolic process	1	4	13.7–551.6	0.02319

Table S1 to be continued.

GO symbol	GO description	Count original	Count permuted	95% CI for Odds Ratio	P-value
0006779	porphyrin-containing compound biosynthetic process	1	4	13.7–551.6	0.02319
2000401	regulation of lymphocyte migration	1	4	13.7–551.6	0.02319
0008091	spectrin	2	29	6.1–80.4	0.02786
0007062	sister chromatid cohesion	2	30	5.9–77.6	0.03463
0060077	inhibitory synapse	1	5	11.7–432.5	0.03898
0006122	mitochondrial electron transport, ubiquinol to cyto.c	1	5	11.7–432.5	0.03898
0008121	ubiquinol-cytochrome-c reductase activity	1	5	11.7–432.5	0.03898
0007214	gamma-aminobutyric acid signaling pathway	2	32	5.5–72.6	0.05233
0004862	cAMP-dependent protein kinase inhibitor activity	1	6	10.2–355.2	0.06473
0030031	cell projection assembly	1	6	10.2–355.2	0.06473
0015961	diadenosine polyphosphate catabolic process	1	6	10.2–355.2	0.06473
0071544	diphosphoinositol polyphosphate catabolic proces	1	6	10.2–355.2	0.06473
0008486	diphosphoinositol-polyphosphate diphosphatase activity	1	6	10.2–355.2	0.06473
0052840	inositol diphosphate tetrakisphosphate diphosphatase a.	1	6	10.2–355.2	0.06473
0052846	inositol-1,5-bisdiphosphate-2,3,4,6-tetrakisphosph ...	1	6	10.2–355.2	0.06473
0052847	inositol-1,5-bisdiphosphate-2,3,4,6-tetrakisphosph ...	1	6	10.2–355.2	0.06473
0052843	inositol-1-diphosphate-2,3,4,5,6-pentakisphosphate ...	1	6	10.2–355.2	0.06473
0052848	inositol-3,5-bisdiphosphate-2,3,4,6-tetrakisphosph ...	1	6	10.2–355.2	0.06473
0052844	inositol-3-diphosphate-1,2,4,5,6-pentakisphosphate ...	1	6	10.2–355.2	0.06473
0052845	inositol-5-diphosphate-1,2,3,4,6-pentakisphosphate ...	1	6	10.2–355.2	0.06473
0016480	negative regul.of trans. from RNA polymer.III promoter	1	6	10.2–355.2	0.06473
0031056	regulation of histone modification	1	6	10.2–355.2	0.06473
0043111	replication fork arrest	1	6	10.2–355.2	0.06473
0034379	very-low-density lipoprotein particle assembly	1	6	10.2–355.2	0.06473
0034329	cell junction assembly	6	284	2.7–13.0	0.07311
0006921	cell.comp. disassembly inv. in exec. phase of apoptosis	6	289	2.7–12.8	0.08941
Fat yield					
0035278	negative regulation of translation involved in gene silencing by miRNA	7	5	15.7–141.9	> 0.00001
0000932	cytoplasmic mRNA processing body	11	38	5.4–20.0	> 0.00001
0035068	micro-ribonucleoprotein complex	5	4	12.2–147.0	0.00003
0016442	RNA-induced silencing complex	5	3	14.2–207.7	0.00004
1900153	positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	5	8	7.7–65.5	0.00011
0060213	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	5	9	7.0–57.3	0.00018
0000796	condensin complex	4	5	8.1–98.4	0.00115
0031047	gene silencing by RNA	4	6	7.2–79.7	0.00178
0007076	mitotic chromosome condensation	4	7	6.4–66.8	0.00291
0031054	pre-miRNA processing	3	3	7.9–152.2	0.02189
0045947	negative regulation of translational initiation	3	5	5.8–84.1	0.04872
0030422	production of siRNA involved in RNA interference	3	1	11.9–546.4	0.05380
0030056	hemidesmosome	4	13	4.0–33.5	0.05622
0046581	intercellular canaliculus	3	6	5.1–68.3	0.08159

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Table S1 to be continued.

GO symbol	GO description	Count original	Count permuted	95% CI for Odds Ratio	P-value
Protein yield					
0019886	antigen processing and presentation of ...	7	114	5.8–25.7	< 0.00001
0030131	clathrin adaptor complex	5	31	13.2–80.9	< 0.00001
0030665	clathrin-coated vesicle membrane	4	27	11.3–82.9	< 0.00001
0006892	post-Golgi vesicle-mediated transport	7	86	7.7–34.3	< 0.00001
0050690	regulation of defense response to virus by vir.	6	77	7.0–35.0	< 0.00001
0032588	trans-Golgi network membrane	6	51	10.4–53.5	< 0.00001
0005765	lysosomal membrane	5	81	5.3–30.0	0.00008
0016044	cellular membrane organization	9	267	3.5–12.7	0.00009
0006897	endocytosis	7	190	3.5–15.3	0.00076
0048488	synaptic vesicle endocytosis	3	33	6.5–58.7	0.00110
0030276	clathrin binding	2	12	9.6–145.2	0.00154
0007093	mitotic cell cycle checkpoint	2	13	8.9–133.3	0.00235
0071480	cellular response to gamma radiation	2	14	8.4–123.2	0.00352
0000940	condensed chromosome outer kinetochore	2	17	7.1–100.4	0.01053
0030118	clathrin coat	2	18	6.7–94.5	0.01466
0030659	cytoplasmic vesicle membrane	4	83	3.9–26.0	0.01635
0006886	intracellular protein transport	6	183	3.0–14.5	0.01977
0004677	DNA-dependent protein kinase activity	2	19	6.4–89.3	0.02008
0007051	spindle organization	2	20	6.1–84.6	0.02712
0000139	Golgi membrane	7	250	2.7–11.6	0.03054
0048268	clathrin coat assembly	2	21	5.8–80.4	0.03613
0030132	clathrin coat of coated pit	2	21	5.8–80.4	0.03613
0043517	positive regulation of DNA damage response	2	21	5.8–80.4	0.03613
0042132	fructose 1,6-bisphosphate 1-phosphatase activ.	1	2	14.8–846.9	0.04259
0004331	fructose-2,6-bisphosphate 2-phosphatase activ.	1	2	14.8–846.9	0.04259
0032438	melanosome organization	2	23	5.4–73.2	0.06180
0007063	regulation of sister chromatid cohesion	1	3	11.8–541.1	0.06180
0005905	coated pit	4	99	3.3–21.8	0.08481

CI = confidence interval

Trait	Genes in significant KEGG pathways
Milk yield	ACTB ACTC1 ACTG1 ACTN1 ACTN2 ACTN3 ACTN4 ADCY1 ADCY2 ADCY3 ADCY4 ADCY5 ADCY6 ADCY7 ADCY8 ADCY9 ADRB1 AKT1 AKT2 AKT3 AMOTL1 ASH1L CACNA1C CACNA1D CACNA1F CACNA1S CACNA2D1 CACNA2D2 CACNA2D3 CACNA2D4 CACNB1 CACNB2 CACNB3 CACNB4 CACNG1 CACNG2 CACNG3 CACNG4 CACNG5 CACNG6 CACNG7 CACNG8 CASK CDC42 CDH2 CDK4 CGN CLDN1 CLDN10 CLDN11 CLDN14 CLDN15 CLDN16 CLDN17 CLDN18 CLDN19 CLDN2 CLDN22 CLDN23 CLDN24 CLDN25 CLDN3 CLDN4 CLDN5 CLDN6 CLDN7 CLDN8 CLDN9 CRR3 CSDA CSNK2A1 CSNK2A2 CSNK2B CTNNA1 CTNNA3 CTNNB1 CTTN DAG1 DES DSC2 DSG2 DSP EMD EPB41 EPB41L1 EPB41L2 EPB41L3 EXOC3 EXOC4 F11R GJA1 GNAI1 GNAI2 GNAI3 GNAS HCLS1 HRAS IGF1 IGSF5 INADL ITGA1 ITGA10 ITGA11 ITGA2 ITGA2B ITGA3 ITGA4 ITGA5 ITGA6 ITGA7 ITGA8 ITGA9 ITGAV ITGB1 ITGB3 ITGB4 ITGB5 ITGB6 ITGB7 ITGB8 IgM JAM2 JAM3 JUP KRAS LEF1 LGL1 LGL2 LMNA MAGI1 MAGI2 MAGI3 MLLT4 MPDZ MPP5 MRAS MYBPC3 MYH1 MYH10 MYH11 MYH13 MYH14 MYH15 MYH2 MYH3 MYH4 MYH6 MYH7 MYH8 MYH9 MYL10 MYL12A MYL12B MYL2 MYL3 MYL7 MYL9 MYLPF NRAS OCLN PARD3 PARD6A PARD6B PARD6G PKP2 PLN PPP2CA PPP2CB PPP2R1A PPP2R1B PPP2R2A PPP2R2B PPP2R2C PRKACA PRKACB PRKCA PRKCB PRKCD PRKCE PRKCG PRKCH PRKCI PRKCQ PRKCZ PRKX PTEN RAB13 RAB3B RHOA RRAS RRAS2 RYR2 SGCA SGCB SGCD SGCG SRC SYMPK TCF7 TCF7L1 TCF7L2 TGFB1 TGFB2 TGFB3 TJAP1 TJP1 TJP2 TJP3 TNFB TNNC1 TNNI3 TNNT2 TPM1 TPM2 TPM3 TPM4 TTN VAPA YES1 ZAK
Fat yeild	BTG1 BTG2 BTG3 BTG4 C1D CNOT1 CNOT10 CNOT2 CNOT3 CNOT4 CNOT6 CNOT6L CNOT7 CNOT8 DCPIA DCP1B DCP2 DCPS DDX6 DHX36 DIS3 EDC3 EDC4 ENO1 ENO2 ENO3 EXOSC1 EXOSC10 EXOSC2 EXOSC3 EXOSC4 EXOSC5 EXOSC6 EXOSC8 EXOSC9 HSPA9 HSPD1 LSM1 LSM2 LSM3 LSM4 LSM5 LSM6 LSM7 MPHOSPH6 NAA38 NUDT16 PABPC1 PABPC1L PABPC1L2 PABPC1L2 PABPC4 PABPC5 PAN2 PAN3 PAPD7 PARN PATL1 PNPT1 RQCD1 SKIV2L2 TOB1 TOB1 TOB2 TTC37 WDR61 XRN1 XRN2 ZCCHC7
Protein yield	ABCA2 ABCB9 ABL1 ACAP1 ACAP3 ADRB1 ADRB2 ADRB3 ADRBK1 ADRBK2 AGA AGAP1 AGAP2 AGAP3 AKR1B1 AKR1B10 ALDOA ALDOB ALDOC ANAPC1 ANAPC10 ANAPC11 ANAPC13 ANAPC2 ANAPC4 ANAPC5 ANAPC7 AP-4 AP1B1 AP1G1 AP1G2 AP1M1 AP1M2 AP1S1 AP1S2 AP1S3 AP2A1 AP2A2 AP2B1 AP2M1 AP2S1 AP3B1 AP3B2 AP3D1 AP3M1 AP3M2 AP3S1 AP3S2 AP4B1 AP4M1 AP4S1 ARAP1 ARAP2 ARAP3 ARF6 ARFGAP1 ARFGAP2 ARFGAP3 ARRB1 ARRB2 ARSA ARSB ARSG ASAH1 ASAP1 ASAP2 ASAP3 ATM ATP6AP1 ATP6V0A1 ATP6V0A2 ATP6V0A4 ATP6V0B ATP6V0C ATP6V0D1 ATP6V0D2 ATP6V0E1 ATP6V0E2 ATP6V1A ATP6V1B1 ATP6V1B2 ATP6V1C1 ATP6V1C2 ATP6V1D ATP6V1E1 ATP6V1E2 ATP6V1F ATP6V1G1 ATP6V1G2 ATP6V1G3 ATP6V1H ATR <i>AdaPtin</i> BOLA BOLA BOLA-A BOLA-N BUB1 BUB1B BUB3 C5H12orf CACNA1A CACNA1B CAV1 CAV2 CAV3 CBL CBLB CBLC CCNA1 CCNA2 CCNB1 CCNB2 CCND1 CCND2 CCND3 CCNE1 CCNE2 CCNH CCR5 CD164 CD63 CD68 CDC14A CDC14B CDC16 CDC20 CDC23 CDC25A CDC25B CDC25C CDC26 CDC27 CDC42 CDC45 CDC6 CDC7 CDK1 CDK2 CDK4 CDK6 CDK7 CDKN1A CDKN1B CDKN1C CDKN2A CDKN2B CDKN2C CDKN2D CHEK1 CHEK2 CHMP1A CHMP1A CHMP1B CHMP2A CHMP2B CHMP3 CHMP4A CHMP4B CHMP4C CHMP5 CHMP6 CHMP7 CLN3 CLN5 CLTA CLTB CLTC CPLX1 CPLX2 CPLX3 CPLX4 CREBBP CSF1R CTNS CTSA CTSB CTSC CTSD CTSE CTSG CTSH CTSK CTSL2 CTSO CTSS CTSW CTSZ CUL1 CXCR1 CXCR2 CXCR2 CXCR4 DAB2 DBF4 DERA DNAJC6 DNASE2 DNASE2B DNM1 DNM2 DNM3 E2F1 E2F2 E2F3 E2F4 E2F5 EEA1 EGF EGFR EHD1 EHD2 EHD3 EHD4 ENTPD4 EPN1 EPN1 EPN2 EPN3 EPS15 ERBB3 ERBB4 ESPL1 F2R FAM125B FBP1 FBP2 FGFR2 FGFR3 FGFR4 FLT1 FOLR1 FOLR2 FPGT FUK FZR1 G2/mitot G6PD GAA GADD45A GADD45B GADD45G GALT GALNS GBA GGA1 GGA2 GGA3 GIT1 GIT2 GLA GLB1 GM2A GMDS GMPA GMPPA GMPPB GNPTAB GNPTG GNS GPI GRK1 GRK4 GRK5 GRK6 GRK7 GSK3B GUSB H6PD HDAC1 HDAC2 HEXA HEXB HGS HGSNAT HK1 HK2 HKDC1 HRAS HSPA1A HSPA1A HSPA1L HSPA2 HSPA6 HSPA8 IDS IDUA IGF1R IGF2R IL2RA IL2RB IL2RG IQSEC1 IQSEC2 IQSEC3 ITCH JSP1 KDR KHK KIT LAMP1 LAMP2 LAMP3 LAPTM4A LAPTM4B LAPTM5 LDLR LDLRAP1 LGMN LIPA M6PR MAD1L1 MAD2 <i>mit</i> MAD2L1 MAD2L2 MAN2B1 MANBA MCM2 MCM3 MCM4 MCM5 MCM6 MCM7 MCOLN1 MDM2 MET MFSD8 MPI MTMR2 MTMR6 MTMR7 MVB12A MYC NAGA NAGLU NAGA NAPA NAPA NAPS A NEDD4 NEDD4L NEU1 NPC1 NPC2 NSF NTRK1 ORC1 ORC2 ORC3 ORC4 ORC5 ORC6 PARD3 PARD6A PARD6B PARD6G PCNA PDCCD6IP PDGFRA PFKFB1 PFKFB2 PFKFB3 PFKFB4 PFKL PFKM PFKP PGD PGLS PGM1 PGM2 PHPT1 PIP5K1A PIP5K1B PIP5K1C PIP5KL1 PKMYT1 PLA2G15 PLD1 PLD2 PLK1 PML PMM1 PMM2 PPT1 PPT2 PRKCI PRKCZ PRKDC PRPS1 PRPS2 PSAP PSAPL1 PSD PSD2 PSD3 PSD4 PTTG1 RAB11A RAB11B RAB11FIP RAB11FIP RAB11FIP RAB11FIP RAB22A RAB31 RAB3A RAB4A RAB5A RAB5B RAB5C RAB7A RABEP1 RAD21 RB1 RBKS RBL1 RBL2 RBX1 RET RGN RHOA RIMS1 RNF41 RPE RPIA RUFY1 <i>S-phase</i> SCARB2 SFN SGSH SH3GL1 SH3GL2 SH3GL3 SH3GLB1 SH3GLB2 SH3KBP1 SKP1 SKP2 SLC11A1 SLC11A2 SLC17A5 SLC17A6 SLC17A7 SLC17A8 SLC18A1 SLC18A2 SLC18A3 SLC32A1 SMAD2 SMAD3 SMAD4 SMAD6 SMAD7 SMAP1 SMAP2 SMC1A SMC1B SMC3 SMPD1 SMURF1 SMURF2 SNF8 SORD SORT1 SRC STAG1 STAG2 STAM STAM2 STAMPB STX1A STX1B STX2 STX3 STXBPI SUMF1 SUMF1 SYT1 TALDO1 TCIRG1 TFDPI TFRC TGFB1 TGFB2 TGFB3 TGFB3 TGFB3 TKT TKTL1 TKTL2 TP53 TP11 TPP1 TRAF6 TSG101 TSTA3 TTK UNC13A UNC13B UNC13C USP8 VAMP2 VPS25 VPS28 VPS36 VPS37A VPS37B VPS37C VPS37D VPS45 VPS4A VPS4B VTA1 WEE1 WEE2 WWP1 YWHAB YWHAE YWHAG YWHAH YWHAQ YWHAZ ZBTB17 ZFYVE16 ZFYVE20 ZFYVE9