Supplementary Table 1. Significant SNPs and associated genes for four traits in GWAS by using linear model GWAS (LM-GWAS) method

Trait[1]	P$_{(empirical)}$_value[2]	SNP name	Chromosome	Position (bp)	P_value	Gene	Gene function
FCR	7.48E-04	**WU_10.2_17_1001798**	17	1152272	7.80E-05	*TRMT9B*	oxidation-reduction process
		ALGA0092581	17	1703513	1.17E-04	*ENSSSCG00000006973*	cell-cell junction assembly
		WU_10.2_17_1851007	17	1956407	1.70E-04	*SGCZ*	NA
		DIAS0000567	18	20961153	2.05E-04	*GRM8*	signal transduction
		WU_10.2_17_1434901	17	1636763	2.13E-04	*C8orf48*	NA
		WU_10.2_17_1697296	17	1935638	2.23E-04	*SGCZ*	NA
		WU_10.2_13_3842462	13	3655526	3.51E-04	***PLCL2***	lipid catabolic process; lipid catabolic process
		ASGA0033576	7	45856658	4.11E-04	*PKHD1*	cellular calcium ion homeostasis
		ALGA0041464	7	45828581	5.62E-04		
		MARC0055137	18	20484602	6.31E-04	*SND1*	miRNA catabolic process
		WU_10.2_17_2202762	17	2346395	6.80E-04	*ENSSSCG00000039907*	NA
		ALGA0077090	6	39608538	6.82E-04	*ENSSSCG00000015023*	mannosylation
		ASGA0062927	14	40507969	6.82E-04	***SIRT4***	negative regulation of fatty acid oxidation; negative regulation of insulin secretion; tricarboxylic acid metabolic process; positive regulation of lipid biosynthetic process
						PLA2G1B	lipid metabolic process; fatty acid biosynthetic process; phospholipid metabolic process; lipid catabolic process
		ASGA0062929	14	40548521	7.08E-04	***PLA2G1B***	lipid metabolic process; fatty acid biosynthetic process; phospholipid metabolic process; lipid catabolic process

Trait	Marker	Chr	Position	p-value	Gene	Biological process
	ALGA0097485	18	23538749	7.33E-04	*SPAM1* *HYAL4* *ENSSSCG00000016602*	carbohydrate metabolic process
ADG 5.64E-04	**WU_10.2_10_59997776**	10	54208829	8.47E-05	*PLXDC2*	NA
	ASGA0100941	2	147068762	1.37E-04	***PRELID2***	phospholipid transport process
	WU_10.2_3_198486	3	350694	1.62E-04	*PRKAR1B*	cGMP-mediated signaling
	H3GA0054878	16	605799	1.73E-04	*CTNND2*	cell-cell adhesion
	WU_10.2_3_346336	3	521070	2.66E-04	*SUN1*	nuclear matrix anchoring at nuclear membrane
	MARC0009678	17	44751346	2.82E-04	*ENSSSCG00000038990*	peptidyl-tyrosine dephosphorylation
	WU_10.2_3_329436	3	537968	2.89E-04	***GPER1***	positive regulation of insulin secretion; negative regulation of lipid biosynthetic process
	WU_10.2_2_153522747	2	147112980	3.75E-04	***PRELID2***	phospholipid transport process
	5_6139359	5	8845224	3.99E-04		
	ALGA0030157	5	8854690	3.99E-04	*TAB1*	activation of protein kinase activity
	WU_10.2_5_6163751	5	8869294	3.99E-04		
ADFI 6.53E-04	**ALGA0065251**	12	14839808	8.11E-05	***TEX2*** ***ICAM2***	lipid transport process; insulin metabolic process
	WU_10.2_4_116973174	4	106826499	1.63E-04	*PHTF1*	signal transduction
	ASGA0039519	8	105054796	2.67E-04	*METTL14*	forebrain radial glial cell differentiation
	ALGA0049005	8	105105852	2.72E-04	*PRSS12*	zymogen activation
	WU_10.2_4_116040517	4	105851764	2.76E-04	*NRAS*	signal transduction
	ASGA0100809	9	129091764	2.77E-04	ENSSSCG00000015023	mannosylation
	M1GA0012018	8	104924079	2.81E-04	*SEC24D*	COPII-coated vesicle cargo loading

		ASGA0084451	2	31158784	2.86E-04	*ENSSSCG00000034018*	translation
		WU_10.2_6_122065838	6	131840097	2.87E-04	*ADGRL2*	cell surface receptor signaling pathway
		ASGA0005581	1	203367107	4.05E-04	***ACER2***	lipid metabolic process
		WU_10.2_8_113454144	8	105564831	4.83E-04	*ENSSSCG00000009116*	Rab protein signal transduction
		WU_10.2_4_115704336	4	105565718	4.87E-04	*SYCP1*	regulation of protein localization
		WU_10.2_9_141498530	9	128772045	5.44E-04	*KCNK2*	G protein-coupled receptor signaling pathway
		MARC0077909	10	40140575	1.28E-04	*BAMBI*	cell migration
		ASGA0050023	11	16074356	1.69E-04	*ENSSSCG00000033483*	NA
		M1GA0015002	11	16080206	1.89E-04		
		ALGA0060467	11	5379554	2.14E-04	***PDX1***	glucose metabolic process; insulin secretion
		WU_10.2_6_122065838	6	131840097	2.21E-04	*ADGRL2*	cell surface receptor signaling pathway
		WU_10.2_16_7550558	16	7078401	2.80E-04	*NSSSCG00000016796*	NA
		H3GA0031138	11	6366025	3.34E-04	*MTUS2*	NA
RFI	7.58E-04	**WU_10.2_1_18721969**	1	16417185	3.73E-04	*PPIL4*	protein peptidyl-prolyl isomerization
		WU_10.2_4_116973174	4	106826499	3.89E-04	*PHTF1*	signal transduction
		WU_10.2_4_116864084	4	106658685	4.72E-04	*AP4B1*	vesicle-mediated transport
		WU_10.2_5_8988909	5	11256612	4.75E-04	*FOXRED2*	ubiquitin-dependent ERAD pathway
		ALGA0037549	6	158658647	4.96E-04	*GLIS1*	negative regulation of transcription by RNA polymerase II
		ASGA0092485	8	102881678	5.63E-04	*TNIP3*	cellular response to lipopolysaccharide
		ALGA0048953	8	102999435	5.63E-04		
		H3GA0017183	5	94558952	5.93E-04	*C12orf50*	Poly (A)+ mRNA export from nucleus
		H3GA0031439	11	16032696	6.28E-04	*ENSSSCG00000033483*	NA

[1]FCR = feed conversion ratio, ADG = average daily gain, ADFI = average daily feed intake, RFI = residual feed intake.

$^{2}P_{(empirical)}$ _value = the empirical p-values of a multiple testing based on FDR adjusted at the genome-wide significance level of 0.01.

The bold data in SNP name column represents common SNPs identified by linear model GWAS (LM-GWAS) and single-step GWAS (ssGWAS) methods.

The underscore data in SNP name column represents common SNPs related to ADFI and RFI traits.

The bold data in Gene column represent genes related to four feed efficiency related traits.

Supplementary Table 2. Significant SNPs and associated genes for four traits in GWAS by using single-step GWAS (ssGWAS) method

Trait[1]	P(empirical)_value[2]	SNP name	Chromosome	Position (bp)	P_value	Gene	Gene function
FCR	7.17E-04	**WU_10.2_17_1001798**	17	1152272	4.76E-05	*TRMT9B*	oxidation-reduction process
		WU_10.2_17_1697296	17	1935638	5.65E-05	*SGCZ*	NA
		ALGA0092581	17	1703513	8.11E-05	*ENSSSCG00000006973*	cell-cell junction assembly
		DIAS0000567	18	20961153	1.15E-04	*GRM8*	signal transduction
		WU_10.2_17_1434901	17	1636763	1.68E-04	*C8orf48*	NA
		WU_10.2_17_1851007	17	1956407	1.80E-04	*SGCZ*	NA
		MARC0055137	18	20484602	4.14E-04	*SND1*	miRNA catabolic process
		WU_10.2_13_3842462	13	3655526	4.26E-04	***PLCL2***	lipid catabolic process; lipid catabolic process
		WU_10.2_17_2592359	17	2686699	5.36E-04	*SGCZ*	NA
ADG	5.24E-04	**WU_10.2_10_59997776**	10	54208829	4.28E-05	*PLXDC2*	NA
		WU_10.2_3_198486	3	350694	9.29E-05	*PRKAR1B*	cGMP-mediated signaling
		ASGA0100941	2	147068762	1.18E-04	***PRELID2***	phospholipid transport process
		WU_10.2_5_6163751	5	8869294	2.18E-04	*TAB1*	activation of protein kinase activity
		WU_10.2_3_329436	3	537968	2.46E-04	***GPER1***	positive regulation of insulin secretion; negative regulation of lipid biosynthetic process
		5_6139359	5	8845224	2.54E-04	*TAB1*	activation of protein kinase activity
		ALGA0030157	5	8854690	2.54E-04		
		H3GA0054878	16	605799	2.71E-04	*CTNND2*	cell-cell adhesion
		WU_10.2_2_153522747	2	147112980	3.68E-04	***PRELID2***	phospholipid transport process
		MARC0009678	17	44751346	3.75E-04	*ENSSSCG00000038990*	peptidyl-tyrosine dephosphorylation
		WU_10.2_3_346336	3	521070	3.83E-04	*SUN1*	nuclear matrix anchoring at nuclear membrane

		ALGA0023779	4	18464440	5.44E-04	*SNTB1*	NA
		MARC0021142	4	121957530	5.46E-04	*ENSSSCG00000050922*	NA
		ALGA0065251	12	14839808	5.60E-05	***TEX2***	lipid transport process
						ICAM2	insulin metabolic process
		ALGA0049005	8	105105852	7.47E-05	*PRSS12*	zymogen activation
		WU_10.2_4_132878400	4	121005694	1.99E-04	*PTBP2*	regulation of neural precursor cell proliferation
		ASGA0084451	2	31158784	2.67E-04	*ENSSSCG00000034018*	translation
		ASGA0039519	8	105054796	3.06E-04	*METTL14*	forebrain radial glial cell differentiation
		ASGA0093786	4	121249272	3.09E-04	*ENSSSCG00000049773*	NA
ADFI	6.16E-04	**WU_10.2_6_122065838**	6	131840097	3.46E-04	*ADGRL2*	cell surface receptor signaling pathway
		WU_10.2_4_132842339	4	120993942	3.49E-04	*PTBP2*	regulation of neural precursor cell proliferation
		WU_10.2_8_113454144	8	105564831	3.55E-04	*ENSSSCG00000009116*	Rab protein signal transduction
		WU_10.2_4_116973174	4	106826499	3.63E-04	*PHTF1*	signal transduction
		M1GA0012018	8	104924079	3.87E-04	*SEC24D*	COPII-coated vesicle cargo loading
		4_133002201	4	121131168	4.07E-04	*U6*	NA
		WU_10.2_9_141498530	9	128772045	4.91E-04	*KCNK2*	G protein-coupled receptor signaling pathway
		ASGA0100809	9	129091764	4.96E-04	ENSSSCG00000015023	mannosylation
		WU_10.2_4_116864084	4	106658685	5.38E-04	*AP4B1*	regulation of apoptotic process
		ASGA0022698	4	120818459	6.01E-04	*ENSSSCG00000043509*	NA
		ALGA0019602	3	68298863	6.14E-04	***HK2***	glucose metabolic process; glycolytic process
		WU_10.2_2_139099797	2	133780841	1.77E-04	*ENSSSCG00000014267*	signal transduction
RFI	5.89E-04	**WU_10.2_6_122065838**	6	131840097	2.62E-04	*ADGRL2*	cell surface receptor signaling pathway
		WU_10.2_1_18721969	1	16417185	2.77E-04	*PPIL4*	protein peptidyl-prolyl isomerization
		ALGA0049005	8	105105852	2.90E-04	*PRSS12*	zymogen activation

ALGA0019602	3	68298863	3.47E-04	*HK2*	glucose metabolic process; glycolytic process
WU_10.2_9_123609853	9	112285807	3.90E-04	*ENSSSCG00000045606*	NA
WU_10.2_9_123578317	9	112254271	4.03E-04		
WU_10.2_11_4727497	11	5092611	4.76E-04	*PDX1*	glucose metabolic process; insulin secretion
MARC0071589	9	102094613	5.27E-04	*MAGI2*	positive regulation of signal transduction
WU_10.2_9_123469671	9	112313852	5.50E-04	*ENSSSCG00000045606*	NA
ALGA0060467	11	5379554	5.66E-04	*PDX1*	glucose metabolic process; insulin secretion

[1]FCR = feed conversion ratio; ADG = average daily gain; ADFI = average daily feed intake; RFI = residual feed intake.

[2]$P_{(empirical)}$ _value = the empirical p-values of a multiple testing based on FDR adjusted at the genome-wide significance level of 0.01.

The bold data in SNP name column represents common SNPs identified by linear model GWAS (LM-GWAS) and single-step GWAS (ssGWAS) methods.

The underscore data in SNP name column represents common SNPs related to ADFI and RFI traits.

The bold data in Gene column represents genes related to four feed efficiency related traits.