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Comprehensive assessment of candidate genes associated with fattening performance in Holstein–Friesian bulls

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Table S1 Detailed information about the studied genes and single nucleotide polymorphisms (SNPs)

Gene	BTA	Localization	NCBI Gene ID	Genbank Accession Number	SNP Name*	SNP Localization	Allele	Amino Acid Alterations
LEP	4	92,436,922-92,453,653	280836	AF536174.1	A80V	Exon 3	C/T	Ala/Val
					g.3691G>A	Exon 3	G/A	Val/Met
FABP4	14	44,676,542-44,681,059	281759	NC_007312.4	g.2834C>G	Intron 1	C/G	-
					g.3533T>A	Intron 2	T/A	-
DGAT1	14	603,813-612,791	282609	AY065621	K232A**	Exon 8	K/A	Lys/Ala
TG	14	8,217,490-8,453,614	280706	X05380	C422T	5'UTR	C/T	-
IGF1	5	66,191,602-66,264,083	281239	AF210383	C472T	5'UTR	C/T	-
IGF1R	21	7,780,293-8,080,394	281848	U33122	G404T	Intron 12	A/B	-
MYF5	5q13	10,284,434-10,287,669	281335	M95684	g.1911A>G	Intron 2	A/G	-
*LGB****	11q28	103,255,824-103,264,276	280838	AC_000168.1	T5261C	Exon 4 / Intron 4	A/B	Asp/Val; Gly/Ala
CAPN1	29	43,400,333-43,427,397	281661	AF252504	G316A	Exon 9	C/G	Gly/Ala
					V530I	Exon 14	A/G	Val/Ile
CAST	7	96,033,978-96,167,151	281039	AF117813	S20T	Exon 1C/1D	G/C	Ser/Thr
GHR	20q17	31,868,624-32,178,311	280805	AF140284	S555G	Exon 10	G/A	Ser/Gly
OLR1	5	99,803,497-99,815,138	281368	NM_174132	g.8232C>A	3'UTR	A/C	-

LEP – leptin. *FABP4* – fatty acid binding protein 4. *DGAT1* – diacylglycerol acyltransferase 1. *TG* – thyroglobulin. *IGF1* – insulin-like growth factor 1. *IGF1R* – insulin-like growth factor receptor 1. *MYF5* – myogenic factor 5. *LGB* – beta-lactoglobulin. *CAPN1* – micromolar calcium-activated neutral protease 1. *CAST* – calpastatin. *GHR* – growth hormone receptor. *OLR1* – oxidized low-density lipoprotein receptor.

*Marker names were selected according to genomic regions or amino acid alterations according to HGSV.

**The two SNP in the DGAT1 gene lie immediately adjacent to one another in exon 8, and the two alleles at this locus are AA and GC, encoding lysine (K) and alanine (A) at the amino acid position 232.

***Also known as progestagen-associated endometrial protein (*PAEP*).

Table S2 Estimates of variance components of the markers showing significant associations

Trait	Corresponding Markers	Additive Effect[1,2]	Dominant Effect[1,3]	Presence of Overdominance[1,4]	Overall *P* value[1,5]
DTRW2	*LEP*	-8.67***	-2.43		0.001
DTRW3	*LEP*	-7.32	8.09**		0.008
	FABP4 3691	-18.44	-16.76*		0.037
	GHR	6.75	6.31*		0.034
DTRW4	*CAPN1* 316	-13.36	-33.04**	+	0.005
DTRW5	*LEP*	-10.91**	5.77		0.006
W2-W3 FP	*FABP4* 2834	-4.37*	-0.02		0.015
	LGB	3.45	2.47*		0.047
	GHR	2.88	3.52**		0.006
W4-W5 FP	*GHR*	-3.45	9.25*	+	0.019
FW	*CAPN1* 316	21.66	18.13**		0.003
W2-W3 DMI	*CAST*	-13.89	16.67*		0.042
	GHR	17.23	15.66**		0.006
TDMI	*LEP*	-26.01	159.00*		0.018
	IGF1	55.50	-94.51*	+	0.020
	GHR	155.20***	-40.50		0.000
W1-W2 DDMI	*FABP4* 3533	0.13	-0.12**		0.004
W4-W5 DDMI	*MYF5*	0.01	0.39*	+	0.034
	GHR	0.16	-0.48*	+	0.040
TDDMI	*LEP*	-0.71***	-0.12		0.000
	FABP4 3533	-0.14	-0.28*	+	0.011
	IGF1	0.14	-0.19*	+	0.020
	LGB	-0.19	-0.26*	+	0.012
W2-W3 FCR	*CAST*	-0.16	0.18*		0.023
	GHR	0.21	0.22**		0.004
W3-W4 FCR	*OLR1*[6]	–	–		0.024
W4-W5 FCR	*FABP4* 3533	-0.06	-0.77*	+	0.031
TFCR	*LEP*	-0.18	0.19*		0.048
	IGF1	-0.42	0.30**		0.004
	CAPN1 316	-0.62	-0.56***		0.001
W2-W3 ADWG	*FABP4* 2834	0.05*	-0.01		0.019
	LGB	-0.04*	-0.02		0.036
	GHR	-0.04	-0.03**		0.009
W4-W5 ADWG	*FABP4* 3533	0.03	0.13*	+	0.019
	GHR	0.06	-0.13*		0.047
TADWG	*CAPN1* 316	0.05	0.04**		0.007

W1 – 100 kg, W2 – 200 kg, W3 – 300 kg, W4 – 400 kg, W5 – 450 kg target body weight. DTR – days to reach. FP – fattening period. FW – final weight. DMI – dry matter intake. TDMI – total dry matter intake throughout the entire experimental period. DDMI – daily dry matter intake. TDDMI – total daily dry matter intake throughout the entire experimental period. FCR – feed conversion rate. TFCR – total feed conversion rate throughout the entire experimental period. ADWG – average daily weight gain. TADG – total average daily weight gain throughout the entire experimental period.

[1]Least squares means for each genotype are shown in Tables 5-7.

[2]Additive effect is estimated as the difference between the 2 homozygous means divided by 2 (a) (Falconer and Mackay, 1996).

[3]Dominance effect is estimated as the nonadditive genetic effects or the deviation of the heterozygote from the mean of the 2 homozygotes (d) (Falconer and Mackay, 1996).

[4]The degree of dominance may be expressed as d/a. If there is over dominance, d is greater than + a or less than – a (Falconer and Mackay, 1996).

[5]Overall *P* value for marker as a fixed genotype effect.

[6]Only two genotypes were observed for *OLR1* marker, accordingly, additive and dominance effect could not be estimated.

**P*< 0.05, ***P*<0.01, ****P*<0.001