Table S1. Least squares means (LSM) and standard error (SE) of difference between genotypes of selected gene interactions for milk fermentation ability

Interaction	Genotype	Genotype	LSM	SE	*P*-value
DGAT1 × *LEP* gene	*AA*	*MM*	14.903	0.3049	<.0001
	AA	*MW*	15.537	0.5650	<.0001
	AA	*WW*	14.978	0.8717	<.0001
	KA	*MM*	20.939	1.0385	<.0001
	KA	*MW*	16.567	1.2032	<.0001
DGAT1 × *FASN* gene	*AA*	*AG*	14.969	0.3912	<.0001
	AA	*GG*	14.857	0.2639	<.0001
	KA	*AG*	16.181	2.2756	<.0001
	KA	*GG*	18.582	0.9296	<.0001
DGAT1 × *SCD1* gene	*AA*	*CC*	14.561	0.3837	<.0001
	AA	*TC*	15.184	0.2867	<.0001
	AA	*TT*	14.676	0.5960	<.0001
	KA	*CC*	18.627	0.9936	<.0001
	KA	*TC*	16.897	1.8372	<.0001
DGAT1 × *CSN2* gene	*AA*	*AA*	13.826	1.3331	<.0001
	AA	*AB*	15.307	0.4047	<.0001
	AA	*BB*	14.738	0.2973	<.0001
	KA	*AB*	12.454	3.2089	0.0002
	KA	*BB*	18.612	0.8885	<.0001
DGAT1 × *CSN2* gene	*AA*	*A1A1*	15.638	0.5427	<.0001
	AA	*A1A2*	14.564	0.3368	<.0001
	AA	*A2A2*	15.071	0.2978	<.0001
	KA	*A1A1*	21.990	1.2858	<.0001
	KA	*A1A2*	15.729	2.3427	<.0001
	KA	*A2A2*	16.756	1.0680	<.0001
DGAT1 × *CSN3* gene	*AA*	*AA*	14.943	0.3007	<.0001
	AA	*AB*	15.022	0.3388	<.0001
	AA	*AE*	14.154	0.9150	<.0001
	AA	*BB*	15.326	0.6288	<.0001
	AA	*BC*	15.333	1.0338	<.0001
	AA	*BE*	12.644	1.4763	<.0001
	KA	*AA*	20.256	1.2230	<.0001
	KA	*AB*	16.255	1.3000	<.0001
	KA	*AE*	18.722	2.2880	<.0001
DGAT1 × *LGB* gene	*AA*	*AB*	14.997	0.2588	<.0001
	AA	*BB*	14.429	0.5782	<.0001
	KA	*AB*	18.161	0.9017	<.0001
	KA	*BB*	20.041	3.1959	<.0001
LEP × *CSN2* gene	*MM*	*A1A1*	17.119	0.6180	<.0001
	MM	*A1A2*	14.714	0.4749	<.0001
	MM	*A1A3*	14.855	0.3609	<.0001
	MW	*A1A1*	14.957	2.4804	<.0001
	MW	*A1A2*	15.225	0.7713	<.0001
	MW	*A1A3*	16.054	0.8601	<.0001
	WW	*A1A1*	13.358	1.3620	<.0001

Table S2. Least squares means (LSM) and standard error (SE) of difference between genotypes of selected gene interactions for renneting measured instrumentally

Interaction	Genotype	Genotype	LSM	SE	*P*-value
CSN3 × *DGAT1* gene	*AA*	*AA*	337.640	12.0551	<.0001
	AA	*KA*	305.230	46.7463	<.0001
	AB	*AA*	294.590	12.2865	<.0001
	AB	*KA*	354.430	44.4857	<.0001
	AE	*AA*	328.790	38.7906	<.0001
	BB	*AA*	302.640	30.9063	<.0001
	BB	*KA*	349.090	89.2432	0.0001
	BC	*AA*	218.860	62.6597	0.0006
	BE	*AA*	415.600	48.6795	<.0001
LEP × *SCD1* gene	*MM*	*CC*	314.740	17.0280	<.0001
	MM	*TC*	294.300	12.1920	<.0001
	MM	*TT*	389.330	25.4539	<.0001
	MW	*CC*	362.550	28.4093	<.0001
	MW	*TC*	324.870	21.3018	<.0001
	MW	*TT*	276.360	55.6544	<.0001
	WW	*CC*	314.230	70.2985	<.0001
	WW	*TC*	298.070	49.0867	<.0001
FASN × *SCD1* gene	*AG*	*CC*	338.740	27.6059	<.0001
	AG	*TC*	329.240	16.8870	<.0001
	AG	*TT*	390.850	52.8888	<.0001
	GG	*CC*	313.650	15.3062	<.0001
	GG	*TC*	295.980	12.1452	<.0001
	GG	*TT*	374.760	27.7025	<.0001
FASN × *CSN3* gene	*AG*	*AA*	366.070	22.2682	<.0001
	AG	*AB*	315.980	18.6091	<.0001
	AG	*AE*	307.330	70.0627	<.0001
	AG	*BB*	356.410	51.4935	<.0001
	AG	*BC*	253.630	114.140	0.0278
	GG	*AA*	330.650	12.8560	<.0001
	GG	*AB*	286.940	14.1824	<.0001
	GG	*AE*	338.470	45.9678	<.0001
	GG	*BB*	282.640	34.2320	<.0001
	GG	*BC*	203.140	73.7429	0.0066
	GG	*BE*	415.930	47.7659	<.0001
SCD1 × *CSN3* gene	*CC*	*AA*	343.180	17.3626	<.0001
	CC	*AB*	279.680	21.9140	<.0001
	CC	*AE*	373.120	58.9504	<.0001
	CC	*BC*	252.140	114.100	0.0287
	CC	*BE*	294.480	113.650	0.0105
	TC	*AA*	334.800	15.2046	<.0001
	TC	*AB*	288.980	14.5878	<.0001
	TC	*AE*	237.660	54.9668	<.0001
	TC	*BB*	308.830	28.8419	<.0001
	TC	*BC*	213.190	74.1899	0.0047
	TC	*BE*	437.260	53.1844	<.0001

	TT	*AA*	334.810	36.0084	<.0001
	TT	*AB*	372.930	29.9083	<.0001
	TT	*AE*	531.330	113.280	<.0001
CSN2 × *CSN3* gene	*AA*	*AA*	290.380	34.1290	<.0001
	AA	*AB*	261.760	64.6311	<.0001
	AA	*AE*	202.830	114.920	0.0796
	AB	*AA*	339.540	20.8502	<.0001
	AB	*AB*	269.420	18.3099	<.0001
	AB	*AE*	288.250	52.0541	<.0001
	AB	*BB*	317.060	44.1338	<.0001
	AB	*BE*	426.370	70.0711	<.0001
	BB	*AA*	338.510	13.9572	<.0001
	BB	*AB*	314.420	14.9854	<.0001
	BB	*AE*	427.180	65.7739	<.0001
	BB	*BB*	293.870	39.1712	<.0001
	BB	*BC*	224.260	62.7762	0.0005
	BB	*BE*	387.640	67.1249	<.0001
CSN3 × *CSN2* gene	*AA*	*A1A1*	282.110	38.3839	<.0001
	AA	*A1A2*	370.590	20.6416	<.0001
	AA	*A2A2*	322.030	15.4068	<.0001
	AB	*A1A1*	308.760	37.3633	<.0001
	AB	*A1A2*	286.070	19.4313	<.0001
	AB	*A2A2*	303.880	16.1578	<.0001
	AE	*A1A1*	507.120	114.990	<.0001
	AE	*A1A2*	250.070	70.5442	0.0005
	AE	*A2A2*	345.210	54.9966	<.0001
	BB	*A1A2*	380.200	50.0838	<.0001
	BB	*A2A2*	291.560	40.1093	<.0001
	BC	*A1A2*	257.120	115.910	0.0282
	BE	*A1A2*	418.640	49.0709	<.0001

Table S3. Least squares means (LSM) and standard error (SE) of difference between genotypes of selected gene interactions for renneting measured subjectively

Interaction	Genotype	Genotype	LSM	SE	*P*-value
SCD1 × *FASN* gene	*CC*	*AG*	493.720	48.6845	<.0001
	CC	*GG*	502.560	27.3609	<.0001
	TC	*AG*	566.720	31.4552	<.0001
	TC	*GG*	487.960	22.1275	<.0001
	TT	*AG*	544.840	83.2348	<.0001
	TT	*GG*	678.860	49.1391	<.0001
CSN2 × *SCD1* gene	*AA*	*CC*	721.170	106.780	<.0001
	AA	*TC*	451.330	65.4750	<.0001
	AB	*CC*	471.770	40.4708	<.0001
	AB	*TC*	507.330	31.9470	<.0001
	AB	*TT*	484.510	69.6248	<.0001
	BB	*CC*	496.240	30.1167	<.0001
	BB	*TC*	522.050	22.9887	<.0001
	BB	*TT*	698.830	50.1108	<.0001
CSN2 × *SCD1* gene	*A1A1*	*CC*	435.960	78.8870	<.0001
	A1A1	*TC*	669.390	71.6962	<.0001
	A1A1	*TT*	421.180	95.7888	<.0001
	A1A2	*CC*	517.560	47.5240	<.0001
	A1A2	*TC*	529.580	30.2828	<.0001
	A1A2	*TT*	567.990	67.3376	<.0001
	A2A2	*CC*	502.790	32.0337	<.0001
	A2A2	*TC*	499.590	26.9266	<.0001
	A2A2	*TT*	713.760	58.8342	<.0001

Table S4. Least squares means (LSM) and standard error (SE) of difference between genotypes of selected gene interactions for ethanol test

Interaction	Genotype	Genotype	LSM	SE	*P*-value
LEP × *FASN* gene	*MM*	*AG*	0.7497	0.1181	<.0001
	MM	*GG*	0.8937	0.0636	<.0001
	MW	*AG*	1.2737	0.1655	<.0001
	MW	*GG*	0.7301	0.1327	<.0001
	WW	*AG*	1.6081	0.2940	<.0001
	WW	*GG*	1.0407	0.4626	0.0256
DGAT1 × *CSN2* gene	*AA*	*AA*	0.4312	0.2156	0.0467
	AA	*AB*	0.6952	0.0869	<.0001
	AA	*BB*	1.0494	0.0637	<.0001
	KA	*AB*	1.0142	0.3097	0.0012
	KA	*BB*	1.1401	0.2576	<.0001
LEP × *CSN2* gene	*MM*	*AA*	0.1406	0.3493	0.6879
	MM	*AB*	0.7008	0.0939	<.0001
	MM	*BB*	0.975	0.0692	<.0001
	MW	*AA*	0.7149	0.4087	0.0819
	MW	*AB*	0.5804	0.1660	0.0006
	MW	*BB*	1.1567	0.1329	<.0001
	WW	*AB*	0.6253	0.8932	0.4847
	WW	*BB*	1.5022	0.2488	<.0001
FASN × *CSN2* gene	*AG*	*AA*	0.9384	0.5639	0.0975
	AG	*AB*	0.7024	0.1746	<.0001
	AG	*BB*	1.1487	0.1095	<.0001
	GG	*AA*	0.3704	0.2309	0.1101
	GG	*AB*	0.7264	0.0929	<.0001
	GG	*BB*	1.0192	0.0733	<.0001
SCD1 × *CSN2* gene	*CC*	*AA*	0.5002	0.3702	0.1780
	CC	*AB*	0.7154	0.1482	<.0001
	CC	*BB*	1.0661	0.1075	<.0001
	TC	*AA*	0.4048	0.2590	0.1194
	TC	*AB*	0.6934	0.1015	<.0001
	TC	*BB*	1.0715	0.0790	<.0001
	TT	*AB*	0.8947	0.2387	0.0002
	TT	*BB*	0.9172	0.1879	<.0001
CSN2 × *LEP* gene	*A1A1*	*MM*	0.7906	0.1755	<.0001
	A1A1	*MW*	0.7999	0.3752	0.0344
	A1A1	*WW*	1.0395	0.6529	0.1131
	A1A2	*MM*	0.8818	0.0971	<.0001
	A1A2	*MW*	0.6334	0.1767	0.0004
	A1A2	*WW*	0.6582	0.8967	0.4639
	A2A2	*MM*	0.8527	0.0761	<.0001
	A2A2	*MW*	1.201	0.1449	<.0001
	A2A2	*WW*	2.0871	0.3469	<.0001
CSN3 × *LEP* gene	*AA*	*MM*	0.905	0.0789	<.0001

	AA	*MW*	0.9802	0.1531	<.0001
	AA	*WW*	0.8063	0.3167	0.0117
	AB	*MM*	0.7985	0.0829	<.0001
	AB	*MW*	0.8339	0.1475	<.0001
	AB	*WW*	2.2842	0.3651	<.0001
	AE	*MM*	0.5765	0.2706	0.0345
	AE	*MW*	1.2072	0.6370	0.0596
	BB	*MM*	1.0878	0.2485	<.0001
	BB	*MW*	2.3783	0.5151	<.0001
	BC	*MM*	0.9453	0.4479	0.0362
	BE	*MM*	1.6114	0.4066	0.0001
	BE	*MW*	0.5474	0.3991	0.1719
	EE	*MM*	0.9186	0.8913	0.3041
CSN3 × *CSN2* gene	*AA*	*AA*	0.3826	0.2336	0.1029
	AA	*AB*	0.7885	0.1245	<.0001
	AA	*BB*	1.0593	0.0838	<.0001
	AB	*AA*	0.7293	0.4750	0.1261
	AB	*AB*	0.6822	0.1049	<.0001
	AB	*BB*	0.9803	0.0956	<.0001
	AE	*AA*	0.4943	0.9618	0.6079
	AE	*AB*	0.5222	0.3864	0.1779
	AE	*BB*	0.8940	0.3954	0.0247
	BB	*AB*	0.8998	0.3013	0.0031
	BB	*BB*	2.0418	0.2661	<.0001
	BC	*BB*	1.0408	0.4715	0.0283
	BE	*AB*	0.3986	0.5474	0.4673
	BE	*BB*	1.0628	0.3153	0.0009
	EE	*AB*	0.7662	0.9633	0.4272
LGB × *LEP* gene	*AA*	*MM*	0.8434	0.3156	0.0082
	AA	*MW*	1.2727	0.8814	0.1504
	AA	*WW*	0.7977	0.6334	0.2095
	AB	*MM*	0.8084	0.0626	<.0001
	AB	*MW*	0.9401	0.1106	<.0001
	AB	*WW*	0.8287	0.2950	0.0055
	BB	*MM*	1.1743	0.1377	<.0001
	BB	*MW*	0.8317	0.2579	0.0015
	BB	*WW*	3.6888	0.5162	<.0001
LGB × *CSN2* gene	*AA*	*AB*	1.3640	0.6901	0.0493
	AA	*BB*	0.8542	0.3318	0.0107
	AB	*AA*	0.3509	0.2297	0.1281
	AB	*AB*	0.6878	0.0866	<.0001
	AB	*BB*	1.0100	0.0750	<.0001
	BB	*AA*	0.9250	0.5587	0.0992
	BB	*AB*	1.1177	0.3579	0.0020
	BB	*BB*	1.2291	0.1336	<.0001