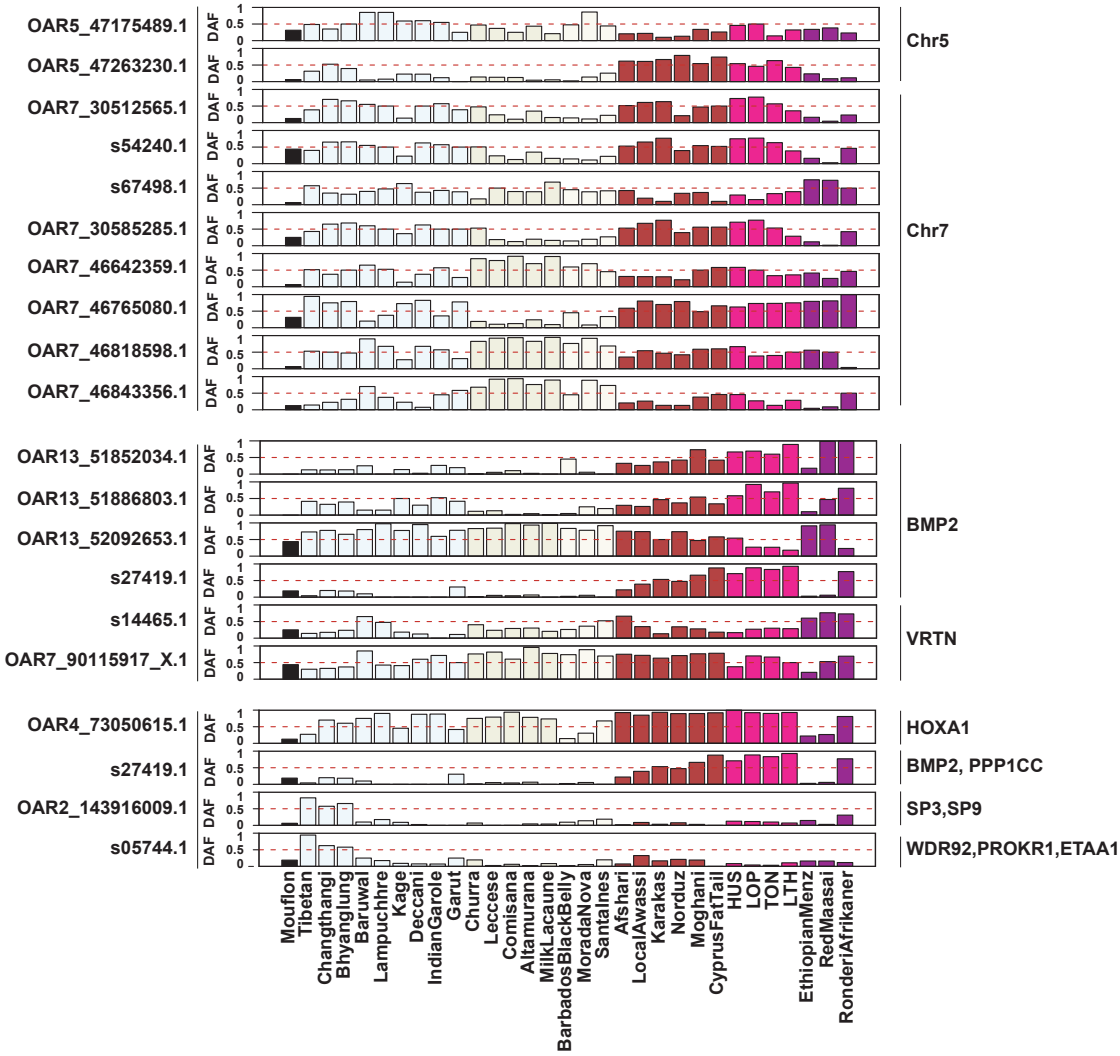
Figure S4

A DAF of the top SNPs previously proposed in each sheep breed



C Snapshot of Table 2 in study of Moioli et al.

Table 2. Genomic regions encoding putative candidate genes of the fat tail phenotype

Chromosome	Marker	Position on Chromosome v3.1[1]	Gene Symbol	Gene Start	Gene Stop	Accession no.
2	OAR2_115949202	107805210	–			
	OAR2_116017982	107866879				
	OAR2_116054738	107911874				
6	OAR6_44329387	39650297	SLIT2	39691904	40093085	EF627036
	OAR6_44345133	39662841				
7	s14465.1	82694743	VRTN	82585586	82587626	XM_004010786
	OAR7_90115917_X.1	82749607				
	s73063.1	82851545				
10	s68983.1	30618253	ALOX5AP	30365140	30388562	XM_004012141
	s12004.1	30674002				
10	s27955.1	35596332	FGF9	35583697	35610038	XM_004012161
	s26969.1	35629123				
13	OAR13_51852034.1	48623826	BMP2	48460133	48473737	XM_004014353
	OAR13_51886803.1	48657027				
	OAR13_52092653.1	48832966				
	s27419.1	48968332				

B Snapshot of Table 3 in study of Moradi et al.

Table 3 The table of significant test for Zel-Lori Bakhtiri and ovine HapMap data set.

SNP_Name	Chr	Coordinate	Zel-Lori Bakhtiri data set		HapMap data set		Fisher's combined
			windowed F_{ST}	P-value	windowed F_{ST}	P-value	P-value
OAR2_55861669.1	2	55861669	0.24	0.00051	0.06	0.08192	0.0004593
s63030.1	2	55922894	0.25	0.00042	0.06	0.07696	0.0003646
s20468.1	2	56248983	0.24	0.00048	0.10	0.01297	0.0000814*
s58048.1	2	56288982	0.23	0.00053	0.10	0.01303	0.0000886*
OAR2_56300406.1	2	56300406	0.22	0.00064	0.10	0.01441	0.0001157
s42805.1	2	73631109	0.23	0.00055	0.02	0.52322	0.0026316
OAR2_73687773.1	2	73687773	0.25	0.00044	0.02	0.46291	0.0019329
OAR2_73744625.1	2	73744625	0.29	0.00024	0.02	0.42839	0.0010538
OAR2_73784818.1	2	73784818	0.26	0.00040	0.03	0.38720	0.0014986
s35724.1	3	146673736	0.22	0.00066	0.01	0.71086	0.0040613
s55322.1	5	47149400	0.26	0.00037	0.13	0.00505	0.0000267*
OAR5_47175489.1	5	47175489	0.28	0.00029	0.17	0.00140	0.0000063*
OAR5_47263230.1	5	47263230	0.29	0.00022	0.12	0.00669	0.0000212*
OAR7_30512565.1	7	30512565	0.22	0.00068	0.02	0.45742	0.0028276
s54240.1	7	30525058	0.29	0.00026	0.03	0.25759	0.0007199
s67498.1	7	30572812	0.27	0.00035	0.04	0.19337	0.0007205
OAR7_30585285.1	7	30585285	0.22	0.00062	0.04	0.17072	0.0010675
OAR7_46642359.1	7	46642359	0.27	0.00033	0.15	0.00282	0.0000138*
OAR7_46765080.1	7	46765080	0.34	0.00015	0.16	0.00177	0.0000044*
OAR7_46818598.1	7	46818598	0.28	0.00031	0.17	0.00161	0.0000077*
OAR7_46843356.1	7	46843356	0.25	0.00046	0.13	0.00476	0.0000308*
OARX_58621412.1	X	58621412	0.22	0.00057	0.05	0.09020	0.0005604
OARX_59194976.1	X	59194976	0.30	0.00020	0.12	0.00647	0.0000186*
OARX_59257971.1	X	59257971	0.38	0.00013	0.19	0.00088	0.0000020*
OARX_59327581.1	X	59327581	0.44	0.00009	0.21	0.00048	0.0000008*
OARX_59383635.1	X	59383635	0.55	0.00004	0.27	0.00019	0.0000002*
OARX_59571364.1	X	59571364	0.58	0.00002	0.27	0.00017	0.0000001*
OARX_59578440.1	X	59578440	0.49	0.00007	0.22	0.00038	0.0000005*
OARX_59912586.1	X	59912586	0.38	0.00011	0.17	0.00144	0.0000026*
s38079.1	X	60149273	0.34	0.00018	0.16	0.00179	0.0000050*
OARX_60238540.1	X	60238540	0.21	0.00070	0.07	0.03783	0.0003069
s31917.1	X	61452816	0.22	0.00059	0.04	0.19923	0.0011873

Position, windowed F_{ST}, empirical P-values and Fisher's combined P-values of observed peaks in Zel-Lori Bakhtiri data set (windowed F_{ST} > 0.20) and comparison to independent experiment using Ovine HapMap data

* Significant P-Value < 0.0001

D Snapshot of Table 1 and Table 2 in study of Yuan et al.

Table 1 Candidate regions and genes identified by hapFLK.

Region	Chr.	Start	Stop	Size (Mb)	Peak SNP	*P*-value	No. of genes	Peak gene	Genes
1	2	133.2	137.10	3.90	OAR2_143941600 9.1	4.11E-06	23	*CDCA7*	*ATP5G3, ATF2, RPL17, CHN1, CHRNA1, GPR155, SCRN3, CIR1, SP9OLA1, SP3, CDCA7, MLTK, RAPGEF4, AIMP1, PDK1, ITGA6, DLX2, DLX1, METAP1D, HAT1, SLC25A12, DYNC1I2, CYBRD1*
2	3	37.17	43.07	5.90	s05744.1	8.99E-5	37	*WDR92*	*LCLAT1, CAPN13, GALNT14, CAPN14, EHD3, SNRPG, PCYOX1, GLRX5, TIAT, CFDP2, PCBP1, ASPRV1, MXD1, SNRNP27, GMCL1, BMP2K, NFU1, GFPT1, HERC5, ANTXR1, GKN1, POL, GKN2, BMP10, ARHGAP25, PROKR1, APLF, FBXO48, PLEK, CNRIP1, PPP3R1, PNO1, WDR92, ETAA1, MBS2, GSR, SPRED2*
3	4	66.84	70.32	3.48	OAR4_73050615.1	2.76E-05	29	*HOXA1, SKAP2*	*CPVL, TRIL, CREB5, RPS19A, CREB5, JAZF1, TAX1BP1, RAN, HIBADH, RPS18, EVX1, HOXA11, HOXA10, HOXA9, HOXA7, HOXA6, HOXA5, HOXA3, HOXA4, HOXA2, HOXA1, SKAP2, SNX10, CBX3, HNRNPA2B1, NFE2L3, SLC30A9, SLC30A9, STK32B*
4	10	26.82	32.28	5.6	OAR10_29511510.1	1.61E-14	33	*RXFP2*	*SLC25A5, RFC3, CFDP2, STARD13, KL, PDS5B, N4BP2L2, M4BP2L1, BRCA2, ZAR1L, FRY, EEF1A1, RXFP2, B3GALTL, HSPH1, C13ORF26, ALOX5AP, USPL1, HMGB1, HMGB1, KATNAL1, UBL3, SLCFA1, MTUS2, MTUS2, SLC46A3, POMP, FLT1, PAN3, FLT3, PRHOXNB, CDX2, GSX1, POLR1D, HSPE1, LNX2, MTIF3, GTF3A*
5	13	44.11	52.89	8.78	OAR13_51852034.1	2.64E-13	67	*BMP2 - PPP1CC*	*PFK, ADARB2, F5, WDR37, ID1, GTPBP4, LARP4B, DIP2C, CFDP2, ZMYND11, PRNP, PRND, RASSF2, SLC23A2, PCNA, CDS2, PROKR2, GPCPD1, CHGB, TRMT6, MCM8, CRLS1, LRRN4, FERMT1, BMP2, PPP1CC, MUTED, UBA52, HAO1, ADRA1D, SMOX, RNF24, PANK2, MAVS, C20ORF29, CDC25B, CENPB, SPEF1, HSPA12B, SIGLEC1, ADAM33, ATRN, WDR45L, C20ORF194, SLC4A11, ITPA, DDRGK1, PROSAPIP1, PROSAPIP1, FASTKD5, UBOX5, PTPRA, VPS16, FAM113A, C20ORF141, CPXM1, IDH3B, NOP56, TMC2, SNRPB, TGM6, TGM3, STK35, PDYN, SIRPA, SIRPA, FAM108C1*
6	15	2.50	5.77	3.28	OAR15_2999185.1	2.25E-06	11	*PDGFD*	*MRPL32, CASP13, DD1, PDGFD, DYNC2H1, DCUN1D5, MMP13, MMP12, MMP3, MMP1, MMP27*
7	22	38.22	41.73	3.51	s02448.1	1.47E-4	22	*FGFR2*	*FAM45A, SFXN4, PRDX3, GRK5, TIAL1, BAG3, INPP5F, MCMBP, SEC23IP, PPARDC1A, WDR11, IL11, FGFR2, ATE1, ZNRD1AS, TACC2, TACC2, BTBD16, HTRA1, DMBT1, DMBT1, IKZFP5TK*

Table 2 Candidate regions and genes identified by F_{ST}.

Region	Chr	Position (Mb)	Peak SNP (F_{ST})	Top SNP	Peak gene	Genes
1	1	14.69–14.93	OAR1_14614448.1 (0.35)	1	*SMAP2*	*COL9A2, SMAP2, ZNF642, DEM1, ZNF684, GTF2F2, RIMS3*
2	1	94.84–95.27	OAR1_100921673.1 (0.46)	2	–	–
3	1	215.05–215.35	OAR1_232334848.1(0.38)	1	*PHC3*	*SKIL, PRKCI, RPL17, PHC3, GPR160*
4	2	134.30–135.45	OAR2_143916009.1 (0.49)	4	*SP3*	*CHN1, CHRNA1, GPR155, SCRN3, CIR1, SP9, OLA1, SP3*
5	3	39.58–40.91	s05744.1 (0.65)	5	*WDR92*	*PROKR1, APLF, FBXO48, PLEK, CNRIP1, PPP3R1, PNO1, WDR92, ETAA1*
6	3	78.37–78.52	s26507.1 (0.37)	1	–	–
7	3	93.33–93.98	s64982.1 (0.49)	2	*DYSF*	*DYSF, CYP26B1*
8	3	154.16–154.26	OAR3_165009241.1 (0.47)	1	*MSRB3*	*MSRB3*
9	4	48.42–48.95	OAR4_51489408.1 (0.46)	1	*BCAP29*	*COC5, GPR22, DUS4L, BCAP29, SLC26A4, SLC26A3, DLD*
10	4	68.36–69.21	OAR4_72720594.1 (0.57)	3	*RPS18*	*TAX1BP1, RAN, HIBADH, RPS18, VX1, HOXA11, HOXA10, HOXA9, HOXA7, HOXA6, HOXA5, HOXA3, HOXA4, HOXA2, HOXA1, SKAP2*
11	4	87.51–87.73	OAR4_93067608.1 (0.41)	1	*SLC13A1*	*SLC13A1, IQUB*
12	6	36.28–36.66	OAR6_40780034.1 (0.39)	1	*ABCG2*	*HERC6, PPM1K, ABCG2, PKD2*
13	6	96.61–96.84	OAR6_106396859.1 (0.39)	1	*VAMP714*	*VAMP714, HNRNPD, NAP1L1, HNRPDL, ENOPH1*
14	7	96.61–96.84	s55494.1 (0.46)	1	*VSX2*	*QTSA11302, ALDH6A1, LIN52, VSX2, ABCD4, VRTN, TMEM90A, NPC2, ISCA, LTBP2*
15	8	56.03–56.29	s12519.1 (0.38)	1	–	–
16	9	1.30–1.46	OAR9_1100990.1 (0.41)	1	–	–
17	9	93.46–93.80	OAR9_99601991.1 (0.39)	1	*ENPP2*	*ENPP2, TAF2, DSCC1*
18	10	29.24–29.61	OAR10_29469450.1 (0.71)	3	*RXFP2*	*FRY, EEF1A1, RXFP2, B3GALTL*
19	11	18.24–18.58	OAR11_18701428.1(0.44)	3	*NF1*	*NF1, EVI2A, EVI2B, OMG*
20	13	47.77–49.21	s27419.1 (0.65)	5	*PPP1CC*	*BMP2, PPP1CC, MUTED, UBA52*
21	13	62.77–63.46	s12884.1 (0.38)	1	*RALY*	*RALY, EIF2S2, ASIP, AHCY, AHCY, ITCH*
22	15	3.24–3.99	OAR15_3091174.1 (0.61)	2	*PDGFD*	*PDGFD, DD1*
23	16	16.99–17.14	OAR16_18729547.1 (0.37)	1	*IPO11*	*IPO11, DIMT1L, KIF2A*
24	22	36.65–36.90	s19503.1 (0.36)	1	*EMX2*	*PDZD8, EMX2*
25	25	7.20–7.69	s25195.1 (0.40)	2	*EIF2S2*	*SLC35F3, C1ORF31, TARBP1, EIF2S2, IRF2BP2*
26	25	38.63–38.83	s21601.1 (0.38)	1	*GHITM,*	*GHITM, CDHR1, LRIT2, LRIT1*