

Supplementary Table S1. QTL positions and candidate genes. Significantly associated QTL (Bonferroni < 0.05) with chromosome and base pair position, as well as potential candidate genes for all models are given. The implied role of each locus on the basis of their respective candidate genes, in either udder and teat morphology, mastitis immune responses, or other processes (N/A) is also summarized. Asterisks (*) indicate novel QTL.

Trait	Chromosome ¹	Position (bp) ¹	Candidate Genes ²	Implied Role
Front Teat Length	10	50107685-50117321	<i>FOXB1, LOC112448464</i>	N/A
Front Teat Width	23	19946762	PLA2G7 , <i>ANKRD66, TRD6, SLC25A27</i>	immunology
	23	20566460-20576922	<i>TNFRSF21, CD2AP, ADGRF2</i>	morphology; immunology
Fore Udder Attachment	2	126354670-126359098	<i>WASF2, GPR3, CD164L2, FCN3, MAP3K6, SYTL1, TMEM222, WDTC1, SLC9A1, FAM46B, TRNP1, KDF1, NUDC, NR0B2, GPN2, SFN, ZDHHC18, PIGV, LOC112443408, ARID1A, RPS6KA1, HMGN2, LIN28A, ZNF683, CRYBG2, UBXN11, CEP85</i>	morphology; immunology
	X	121461599-121477381	<i>PHEX, LOC112445297, SMS, LOC112445297, MBTPS2, SMPX, KLHL34, TRNAC-GCA, LOC112445299, CNKSR2</i>	N/A
Risk PC1	15*	7287030*	<i>CEP126, ANGPTL5, TRPC6</i>	morphology; immunology
Rear Teat Length	2	112245780	<i>SCG2, AP1S3, WDFY1, MRPL44, SERPINE2, FAM124B, CUL3</i>	
Rear Teat End Shape	26	50630351	KNDC1 , <i>SYCE1, TCERG1L, CYP2E1, LOC528422, LOC112444506, ADGRA1, LOC100850437, LOC101906198, LOC112444503, CFAP46, LOC112444502, LOC112444507, NKX6-2, INPP5A, LOC112444505</i>	morphology; immunology
Rear Teat Width ³	25*	38568564*	<i>LOC618554, LOC101906717</i>	N/A
Rear Teat Width ⁴	10		CTDSPL2 , <i>EIF3J, SPG11, LOC112448593, PATL2</i>	N/A
	11*	104129366*	<i>LOC112448855, LHX3, QSOX2, LOC787891, GPSM1, LOC101902280, DNLZ, CARD9, SNAPC4, ENTR1,</i>	morphology; immunology

		PMPCA, INPP5E, SEC16A, NOTCH1, LOC112448856, EGFL7, MIR126, LOC101902839, LOC101902895, FAM69B, LOC112448928, LOC107132967, LOC100848307, LOC112448857, ABO, LOC112448956, SURF6, LOC11244890, MED22, RPL7A, LOC100139115, LOC100112448907, LOC100112448908, LOC100112448904, LOC100112448903, LOC100112448905, SURF2, SURF4, STKLD1, LOC107132968, REXO4, ADAMTS13, CACFD1, SLC2A6, LOC112448858, TRNAC-GCA, MYMK, ADAMTSL2, FAM163B, DBH, SARDH, VAV2	
16	61802991-62196774	CEP350, QSOX1, LOC112441858, LHX4, ACBD6, MIR669, XPR1, TRNAC-ACA, LOC107133256, KIAA1614, STX6, MR1, IER5, CACNA1E, LOC104974498, ZNF648, LOC101905162, GLUL, TEDDM1, RGSL1, RNASEL,	morphology; immunology
16*	63823597*	RGS16, RGS8, LOC101905664, NPL, DHX9, SHCBP1L, LAMC1, LAMC2, NMNAT2	morphology; immunology
18	17655467	LOC112442233, CBLN1, C18H16orf78, ZNF423, TRNAG-CCC	N/A
18	20537778	LOC516179, TOX3	N/A
18	42468232	MIR2899, LOC112442482, TRNAG-CCC, LOC617301, ZNF507, DPY19L3	N/A
19	22640468	VPS53, MIR2336, RFLNB, C19H17orf97, TRNAG-UCC, RPH3AL, LOC104975006, DOC2B, LOC112442619, YWHAE, TRNAE-UUC, CRK, MYO1C, INPP5K , PITPNA, SLC43A2, SCARF1, RILP, PRPF8, TLCD2, MIR22, WDR81, SMYD4, SERPINF1, RPA1, RTN4RL1, LOC112442621, DPH1, OVCA1, MIR132, MIR212, HIC1, SMG6, LOC112442776	morphology; immunology
19	23978522-23997890	RAP1GAP2, OR1D5, LOC101906737, LOC618593, OR1G1, LOC540082, LOC532238, LOC522582, LOC112442765, LOC520835 , LOC59525, LOC59526	N/A

	19	29058547- 29063744	<i>GLP2R, RCVRN, GAS7</i>	immunology
	25*	35208040*	<i>CUX1, TRNAW-CCA, MIR2388, LOC112444316, LOC112444338, MYL10, COL26A1, LOC104970468, IFT22, FIS1, PLOD3, LOC618076, NAT16, VGF, AP1S1, LOC101902751, SERPINE1, TRIM56, LOC101902689, LOC101909082, LOC107131854</i>	morphology; immunology
	25	40126743- 40190566	SDK1	immunology
Udder Depth	5	113268242	TCF20 , LOC104976976	morphology
Udder Height	6	102964124- 102982437	LOC100298890	N/A
	14	27024015	<i>CLVS1, ASPH</i>	morphology
	15	15545765- 15782913	AMOTL1, LOC112441606	N/A
	18	62273143- 62481417	<i>TNNT1, PPP1R12C, LOC112442386, LOC112442387, EPS8L1, RDH13, LOC100848752, GP6, NLRP2, LOC100336589, LOC100852077, LOC112442414</i>	morphology; immunology
	22	46733454	CACNA2D3 , LOC112443534	N/A
Udder Width	15	75722222	<i>PRDM11, LOC101906676, SYT13, LOC107133190, LOC112441655, CHST1, LOC104974324, LOC107133191, SLC35C1, CRY2, MAPK8IP1, C15H11orf94, PEX16, LARGE2, PHF21A, CREB3L1</i>	morphology; immunology
Front Teat Placement ⁵	9	58002055- 58079933	<i>LOC101902249, LOC112448054</i>	N/A
Udder Depth ^{5,6}	17	34476230- 34552407	<i>SPRY1, SPATA5, LOC112442097, NUDT6, FGF2</i>	morphology

¹Positions based on ARS_UCD 1.2

²Genes in LD with significantly associated SNP, or +/- 500 kb of associated SNP in case of no LD, bolded text indicates associated SNP is within the gene

³case-control GWA of narrow versus wide rear teats divided at the median value

⁴linear GWA of quantitative rear teat width scores

⁵primiparous only subset of cows (n = 144)

⁶not passing Bonferroni correction, QTL significantly associated at $FDR < 0.05$