

**Supplementary Table S1.** Detected selection signatures and the association found by other authors.

Chr.	Genomic location Mbp	Animals within ROH %	Genes	Previously published results
1	83-84	44.95	<i>MAGEF1, MIR2284Y-3, EPHB3, LOC524771, THPO, POLR2H, CLCN2, FAM131A, PSMD2, ECE2, CAMK2N2, ALG3, MIR1224, ABCF3, AP2M1, HTR3C, ABCC5, PARL, MAP6D1</i>	Identified signature of selection on the genomic region 1:82 820 000-84 650 000, in a local cattle population from North Africa (Ben-Jemaa et al. 2020)
				The <i>ECE2</i> gene was associated with susceptibility to respiratory diseases in Charolais, Hereford, Red Angus and Angus cattle (Neupane et al. 2018).
1	84-85	44.95	<i>YEATS2, KLHL24, B3GNT5, LAMP3, MCCC1, DCUN1D1</i>	Serão et al. (2013) found an association of this region with residual feed intake (RFI) in Angus and Simmental cattle breeds.
7	42-43	39.74	<u><i>NLRP3</i></u>	The <i>NLRP3</i> gene is associated with resistance to infection with <i>Mycobacterium avium</i> ssp. <i>paratuberculosis</i> in HF cattle (Mallikarjunappa et al. 2018)
7	43-44	40.72	<i>MGC137030, LYPD8, SH3BP5L, ZNF692</i>	<i>LYPD8</i> is involved in the biological processes of defense responses to gram-negative bacteria and is associated with adaptive responses to environmental stimuli such as stress, infection and inflammation in cattle (Pošćić et al. 2017).
10	72-73	31.92	<i>L3HYPDH, JKAMP, CCDC175, DHRSZ, PPM1A, SIX6</i>	Gaddis et al. (2017) linked the <i>DHRS7</i> and <i>SIX6</i> genes to the number of embryos in HF cows.
10	73-74	31.92	<i>MNAT1, TRMT5, PRKCH</i>	<i>PRKCH</i> was associated with back angle in HF cows (Yan et al. 2020).
16	42-43	36.81	<i>DHRS3, VPS13D, TNFRSF1B, MIIP, MFN2, PLOD1, KLAA20I3, NPPB, NPPA, CLCN6</i>	In the Yaroslav, Kolmogor and HF breeds, a selection signature was identified in the same region (Zinovieva et al. 2020).

			<i>MTHFR</i> , <i>MIR12050</i> , <i>AGTRAP</i> , <i>DRAXIN</i> , <i>MAD2L2</i> , <i>FBXO6</i> , <i>FBXO44</i> , <i>FBXO2</i>	<i>MTHFR</i> is involved in milk protein synthesis (Menziez et al. 2009).
16	43-44	37.46	<i>DISP3</i> , <i>ANGPTL7</i> , <i>EXOSC10</i> , <i>SRM</i> , <i>MASP2</i> , <i>TARDBP</i> , <i>PEX14</i>	<i>EXOSC10</i> is associated with longevity in HF cows (Steri et al. 2019).
16	44-45	36.81	<i>DFFA</i> , <i>CORT</i> , <i>CENPS</i> , <i>PGD</i> , <i>UBE4B</i> , <i>LOC112441838</i> , <i>NMNAT1</i> , <i>CTNNBIP1</i> , <i>PIK3CD</i> , <i>TMEM201</i>	<i>NMNAT1</i> is associated with reproductive efficiency of cows (Mota et al. 2017)
16	45-46	30.29	<i>SPSB1</i> , <i>MIR34A</i> , <i>SLC2A5</i> , <i>CA6</i> , <i>ENOL</i> , <i>MIR2285CK</i> , <i>SLC45A1</i> , <i>LOC786597</i>	<i>ENO1</i> gene was significantly associated with bull fertility (Park et al. 2012)
22	21-22	30.62	<i>EDEMI</i> , <i>ARL8B</i> , <i>BHLHE40</i> , <i>ITPR1</i> , <i>MIR2285AM</i>	<i>BHLHE40</i> is associated with milk protein content (Singh et al. 2022)
22	22-23	34.20	<i>SUMF1</i> , <i>SETMAR</i> , <i>LRRN1</i>	<i>SUMF1</i> gene is associated with milk yield in HF cows (Pedrosa et al. 2021)
26	21-22	37.13	<i>CHUK</i> , <i>CWF19L1</i> , <i>SCD</i> , <i>MIR12016</i> , <i>SEC31B</i> , <i>NDUFB8</i> , <i>HIF1AN</i> , <i>SLF2</i> , <i>SEMA4G</i> , <i>MRPL43</i> , <i>TWNK</i> , <i>LZTS2</i> , <i>SFXN3</i> , <i>TLX1</i> , <i>LBX1</i>	<i>SCD</i> gene is associated with medium- and long-chain unsaturated fatty acids in a population of Chinese HF cows (Li et al. 2016).
26	22-23	42.02	<i>BTRC</i> , <i>POLL</i> , <i>DPCD</i> , <i>FBXW4</i> , <i>FGF8</i> , <i>NPM3</i> , <i>OGA</i> , <i>KCNIP2</i> , <i>HPS6</i> , <i>PPRC1</i> , <i>NOLC1</i> , <i>ELOVL3</i> , <i>PITX3</i> , <i>GBF1</i> , <i>NFKB2</i> , <i>PSD</i> , <i>FBXL15</i> , <i>CUEDC2</i> , <i>MIR146B</i> , <i>MFSD13A</i> , <i>ACTR1A</i> , <i>SUFU</i>	Wang et al. (2017) observed a significant increase in <i>MIR146B</i> expression levels in subclinical, clinical and experimental mastitis-infected bovine mammary gland tissue.
26	23-24	34.85	<i>TRIM8</i> , <i>ARL3</i> , <i>SFXN2</i> , <i>MIR2392</i> , <i>CYP17A1</i> , <i>AS3MT</i> , <i>CNNM2</i> , <i>NT5C2</i>	<i>CNNM2</i> was associated with milk yield in HF cows (Jiang et al. 2019a).