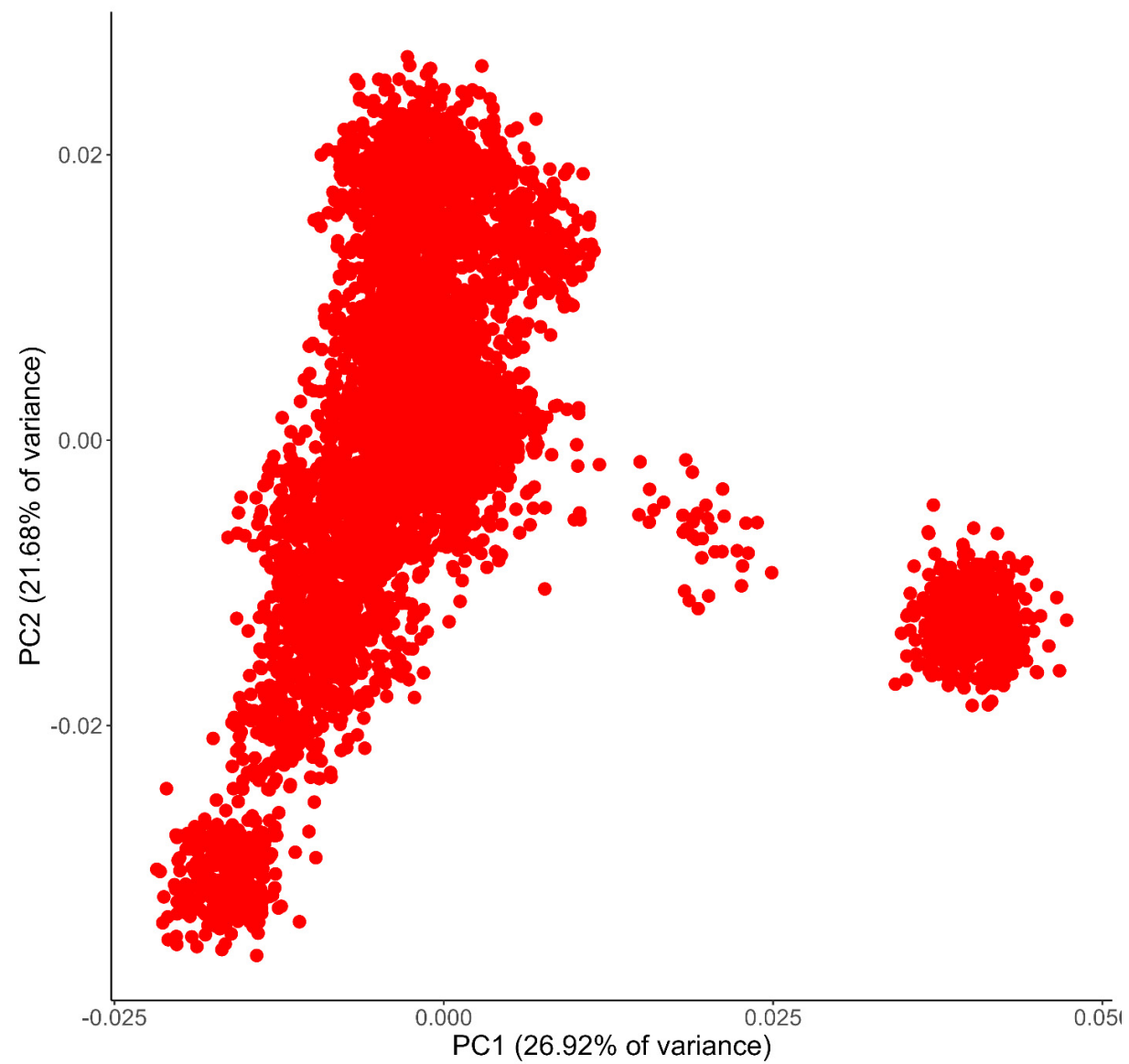
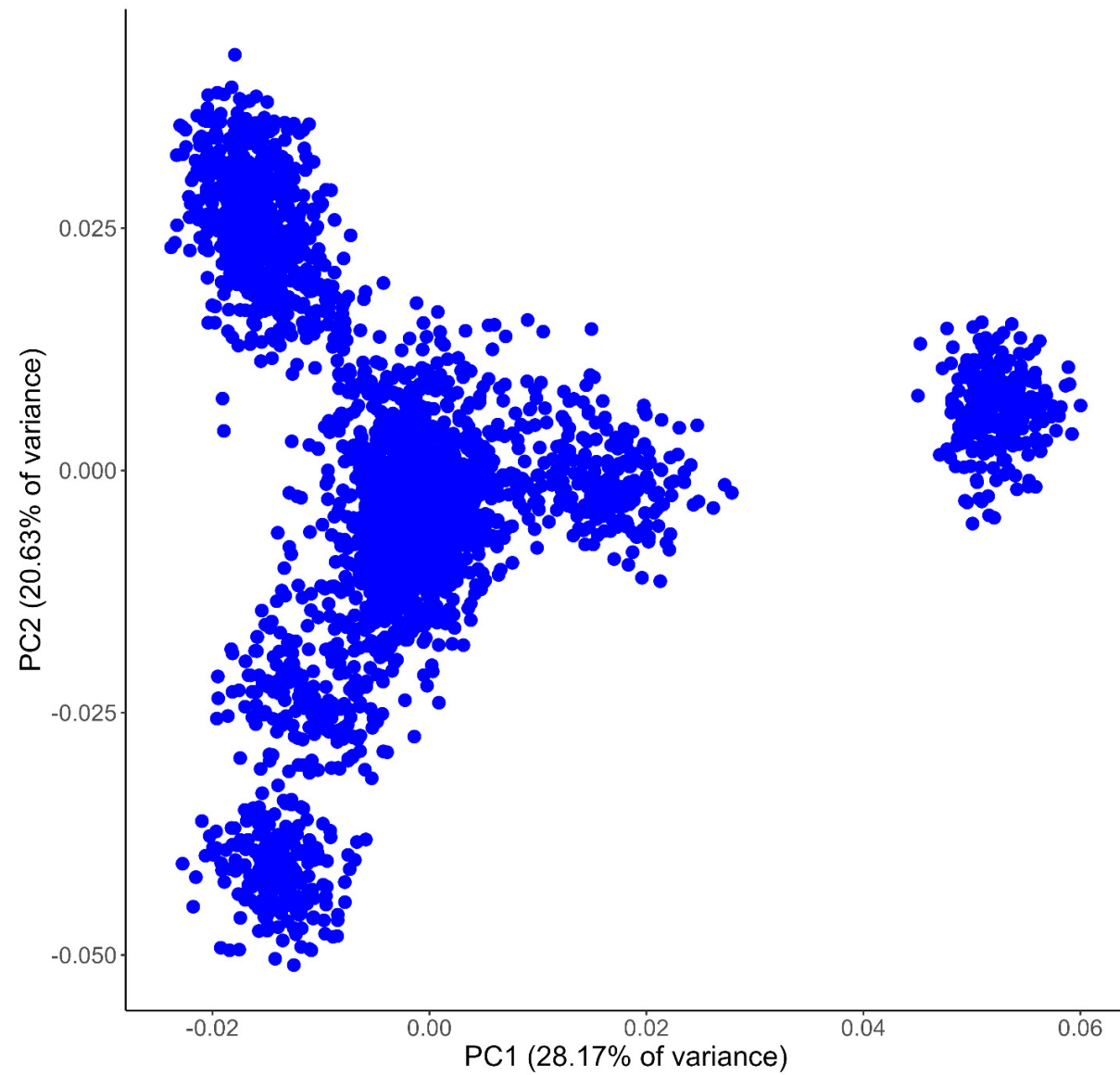




A. Holstein Heifer principal component analysis



B. Primiparous cow principal component analysis

Figure S1. Plots A and B show the principal component analysis (PCA) of the first two principal components (PC1 and PC2), representing the greatest genetic variance in the primiparous cow and heifer populations, respectively.

Table S1: Loci associated with fetal loss in Holstein heifers.

BTA ¹	Locus ²	Pos (Mb) ³	FDR ⁴	PVE (%) ⁵	PCG ⁶
1	1	138.8	4.98 x 10 ⁻²	0.003	
1	2	147.0	4.05 x 10 ⁻²	0.003	<i>SLC19A1, LOC100849587</i>
1		147.1	3.93 x 10 ⁻²	0.003	<i>LOC100849587, PCBP3</i>
1		147.1	3.83 x 10 ⁻²	0.003	<i>LOC100849587, PCBP3</i>
2	3	98.7	1.96 x 10 ⁻³	0.005	
3	4	115.0	1.74 x 10 ⁻³	0.005	
3		115.0	1.52 x 10 ⁻³	0.005	
7	5	32.4	2.14 x 10 ⁻³	0.004	
7		33.4	1.96 x 10 ⁻³	0.004	<i>LOC100140613</i>
14	6	13.4	1.77 x 10 ⁻³	0.004	
17	7	15.0	3.80 x 10 ⁻³	0.004	
24	8	61.9	5.30 x 10 ⁻³	0.004	<i>BCL2</i>
25	9	24.04	4.21 x 10 ⁻²	0.003	
25	10	37.2	3.94 x 10 ⁻²	0.003	
25		37.3	2.32 x 10 ⁻³	0.005	<i>TMEM225B, LOC112444278, ZNF655, ZNF789</i>
25		37.4	5.80 x 10 ⁻⁴	0.005	
25	11	38.5	2.41 x 10 ⁻³	0.004	<i>OCM, LOC100850875, CCZ1, RSPH10B</i>
25	12	39.6	1.62 x 10 ⁻²	0.004	<i>MMD2, RADIL</i>
26	13	23.9	1.72 x 10 ⁻³	0.005	<i>CNNM2</i>

26		24.2	1.44 x 10 ⁻³	0.005	<i>TAF5, ATP5MK, MIR1307, PDCD11, LOC104975977</i>
27	14	17.9	2.01 x 10 ⁻³	0.005	
27	15	17.9	1.55 x 10 ⁻³	0.005	<i>LOC112444679</i>
27		18.0	1.43 x 10 ⁻³	0.005	<i>LOC112444679, LOC107131907</i>
27		18.0	1.34 x 10 ⁻³	0.005	<i>LOC107131907, LOC781220</i>
X	16	57.7	3.48 x 10 ⁻²	0.003	<i>MORF4L2, LOC101901997, GLRA4</i>
X		57.7	1.77 x 10 ⁻³	0.004	<i>MORF4L2, LOC101901997, GLRA4</i>
X		57.7	5.00 x 10 ⁻²	0.003	<i>MORF4L2, LOC101901997, GLRA4</i>
X		57.7	4.87 x 10 ⁻²	0.003	<i>LOC101901997, GLRA4</i>
X		57.7	1.66 x 10 ⁻³	0.004	<i>LOC101901997, GLRA4</i>

¹*Bos taurus* chromosome. ²Sequentially numbered loci associated with fetal loss from BTA1 to BTAX along with their associated single nucleotide polymorphism (SNPs). The horizontal line across the table delineates each locus. ³Genomic locations of associated SNPs, given in megabase (Mb), based on nucleotide numbering in the ARS-UCD 1.2 reference genome (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.1/ (6 June 2025)). ⁴False discovery rate (FDR) adjusted P values for SNPs associated with fetal loss. ⁵Proportion of variance explained (PVE) by each SNP associated with fetal loss. ⁶Positional candidate genes located within 29 kb upstream or downstream of the SNPs associated with fetal loss based on the NCBI database and the cow genome assembly ARS-UCD2.0 (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.3/ (6 June 2025)). Positional candidate genes functional information was obtained from NCBI (<https://www.ncbi.nlm.nih.gov/> (6 June 2025)) and Ensembl (https://useast.ensembl.org/Bos_taurus/Info/Index (6 June 2025)).

Table S2: Loci associated with fetal loss in primiparous cows.

BTA ¹	Locus ²	Pos (Mb) ³	FDR ⁴	PVE ⁵	PCG ⁶
1	1	3.1	3.43 x 10 ⁻²	0.007	<i>SCAF4, SOD1, TRNAG-CCC</i>
2	2	8.0	3.36 x 10 ⁻²	0.007	<i>GULP1</i>
2	3	22.4	3.85 x 10 ⁻²	0.007	<i>SCRN3, CIR1</i>

2		22.5	3.77×10^{-2}	0.007	<i>LOC112443637</i>
2	4	97.9	1.81×10^{-3}	0.013	<i>MAP2</i>
2	5	108.4	3.82×10^{-2}	0.007	
3	6	10.2	2.85×10^{-2}	0.008	<i>TRNAG-UCC, OR10J30P, APCS</i>
6	7	91.3	5.54×10^{-3}	0.01	
8	8	4.6	3.07×10^{-2}	0.007	<i>GALNTL6</i>
8	9	36.9	4.08×10^{-2}	0.007	<i>LOC132345943</i>
8		37.0	3.65×10^{-2}	0.007	<i>LOC132345943</i>
8	10	88.2	8.24×10^{-3}	0.01	
8		88.3	2.35×10^{-2}	0.008	
8		88.4	2.31×10^{-2}	0.008	<i>SYK</i>
8		88.4	8.33×10^{-3}	0.01	<i>SYK</i>
8	11	102.5	2.53×10^{-2}	0.008	<i>ECPAS</i>
9	12	99.1	3.12×10^{-2}	0.007	<i>PRKN</i>
9		99.1	3.08×10^{-2}	0.007	<i>PRKN</i>
10	13	17.2	3.71×10^{-2}	0.007	
11	14	2.6	3.39×10^{-2}	0.007	<i>KANSL3, FER1L5</i>
12	15	79.3	3.76×10^{-2}	0.007	<i>FARP1, LOC112449164</i>
14	16	33.7	5.58×10^{-3}	0.01	<i>CPA6</i>
14		33.8	4.88×10^{-3}	0.01	<i>CPA6</i>
14		33.8	4.34×10^{-3}	0.01	<i>CPA6</i>
14	17	41.8	3.74×10^{-2}	0.007	
14	18	54.5	3.96×10^{-2}	0.007	
15	20	33.3	3.82×10^{-2}	0.007	<i>LOC101903557, LOC100848689, MIR125B-1</i>
15	19	76.2	3.07×10^{-2}	0.008	<i>LOC132342364</i>
18	21	27.0	2.17×10^{-2}	0.008	
18	22	29.9	3.10×10^{-2}	0.012	
18	23	51.7	3.26×10^{-2}	0.007	<i>ARHGEF1, CD79A, RPS19, DMRTC2, LYPD4</i>
18	24	52.0	2.28×10^{-2}	0.008	<i>PHLDB3, ETHE1, ZNF575, XRCC1, PINLYP</i>
18		52.0	2.25×10^{-2}	0.008	<i>ETHE1, ZNF575, XRCC1, PINLYP</i>

18		52.1	2.14×10^{-2}	0.008	<i>XRCC1, PINLYP</i>
18		52.1	2.11×10^{-2}	0.008	
18		52.1	2.07×10^{-2}	0.008	<i>XRCC1, PINLYP, IRGQ</i>
18		52.1	2.04×10^{-2}	0.008	<i>PINLYP, IRGQ, ZNF576, ZNF428, SRRM5</i>
18		52.1	2.99×10^{-2}	0.008	<i>IRGQ, ZNF576, ZNF428, SRRM5, CADM4, PLAUR</i>
18	25	52.2	3.74×10^{-2}	0.007	<i>LOC512005, LOC526915, IRGC, LOC616722</i>
18		52.2	3.83×10^{-2}	0.007	<i>LOC616722, SMG9, LOC104974883, KCNN4</i>
18		52.3	3.80×10^{-2}	0.007	<i>SMG9, LOC104974883, KCNN4</i>
18		52.3	3.77×10^{-2}	0.007	<i>SMG9, LOC104974883, KCNN4, LYPD5</i>
18		52.3	4.30×10^{-3}	0.011	<i>SMG9, LOC104974883, KCNN4, LYPD5</i>
18		52.3	2.87×10^{-3}	0.011	<i>LYPD5, ZNF283</i>
18		52.3	7.27×10^{-3}	0.01	<i>ZNF283</i>
18	26	52.4	1.48×10^{-2}	0.008	<i>ZNF226, ZNF227, ZNF233</i>
18		52.5	3.74×10^{-2}	0.007	<i>ZNF227, ZNF233</i>
18	27	53.8	1.97×10^{-2}	0.008	<i>NOVA2, LOC112442342</i>
18		53.8	1.93×10^{-2}	0.008	<i>NOVA2, LOC112442342</i>
19	28	56.1	3.18×10^{-2}	0.007	<i>RNF157, FOXJ1</i>
21	29	35.5	3.08×10^{-2}	0.007	<i>STXBP6</i>
21	30	48.4	3.06×10^{-2}	0.008	<i>TTC6</i>
22	31	7.5	3.72×10^{-2}	0.007	<i>CRTAP, SUSD5</i>
22		7.6	3.68×10^{-2}	0.007	<i>SUSD5, FBXL2, LOC112443433</i>
22		7.6	3.65×10^{-2}	0.007	<i>SUSD5, FBXL2, LOC112443433</i>
23	32	49.3	1.77×10^{-2}	0.008	<i>LYRM4, PPP1R3G</i>
24	33	3.8	2.67×10^{-2}	0.008	<i>ZNF407</i>
24	34	4.3	3.76×10^{-2}	0.007	<i>DIPK1C, C24H18orf63, SPACDR</i>
24	35	5.7	2.89×10^{-2}	0.008	
24	36	5.8	3.09×10^{-2}	0.008	
24	37	6.1	3.05×10^{-2}	0.008	
24	38	7.4	1.42×10^{-2}	0.008	<i>RTTN</i>
24	39	7.6	1.39×10^{-2}	0.008	<i>CD226</i>

24		7.6	1.36 × 10 ⁻²	0.008	CD226
24	40	12.6	3.42 × 10 ⁻²	0.007	SERPINB8, TRNAK-UUU, LOC112444149
25	41	36.6	3.20 × 10 ⁻²	0.007	NYAP1, TSC22D4, SPACDR, PPP1R35, MEPCE, ZCWPW1
29	42	2.1	8.53 × 10 ⁻²	0.01	FAT3
29		2.5	3.75 × 10 ⁻²	0.007	FAT3, LOC112444945
29	43	43.6	3.89 × 10 ⁻²	0.007	MEN1, TRNAE-CUC, CDC42BPG, EHD1
X	44	145.6	3.46 × 10 ⁻²	0.007	
X		145.8	3.42 × 10 ⁻²	0.007	LOC101902122, TRNAC-ACA

¹*Bos taurus* chromosome. ²Sequentially numbered loci from BTA1 to BTAX associated fetal loss, along with their corresponding single nucleotide polymorphism (SNPs). The horizontal line across the table delineates each locus. ³Genomic locations of associated SNPs, given in megabase (Mb), based on nucleotide numbering in the ARS-UCD 1.2 reference genome (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.1/ (6 June 2025)). ⁴False discovery rate (FDR) adjusted P values for SNPs associated with fetal loss. ⁵Proportion of variance explained (PVE) by each SNP associated with fetal loss. ⁶Positional candidate genes located within 29 kb upstream or downstream of the SNPs associated with fetal loss based on the NCBI database and the cow genome assembly ARS-UCD2.0 (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.3/ (6 June 2025)). Positional candidate genes functional information was obtained from NCBI (<https://www.ncbi.nlm.nih.gov/>) and Ensembl (https://useast.ensembl.org/Bos_taurus/Info/Index (6 June 2025)).

Table S3. Loci associated with fetal loss in Holstein heifers that were shared in previous fertility studies.

BTA ¹	Locus ²	Pos (Mb) ³	FDR ⁴	PVE (%) ⁵	PCG ⁶	Study ⁷	Breed ⁸	Trait ⁹
3	4	115.0	1.74 × 10 ⁻³	0.005		Kiser et al. 2019 [59]	Holstein	HCR1
3	4	115.0	1.74 × 10 ⁻³	0.005		Kiser et al. 2019 [59]	Holstein	TBRD
3	4	115.0	1.74 × 10 ⁻³	0.005		Galliou et al. 2020 [47]	Holstein	TBRD

3	4	115.0	1.52×10^{-3}	0.005		Kiser et al. 2019 [59]	Holstein	HCR1
3	4	115.0	1.52×10^{-3}	0.005		Kiser et al. 2019 [59]	Holstein	TBRD
3	4	115.0	1.52×10^{-3}	0.005		Galliou et al. 2020 [47]	Holstein	TBRD
17	7	15.0	3.80×10^{-3}	0.004		Cole et al. 2011 [61]	Holstein	DPR
17	7	15.0	3.80×10^{-3}	0.004		Cole et al. 2011 [61]	Holstein	DPR
17	7	15.0	3.80×10^{-3}	0.004		Suarez et al. 2024 [30]	Holstein	SA
25	10	37.2	3.94×10^{-2}	0.003		Suarez et al. 2024 [30]	Holstein	SA
25	12	39.6	1.62×10^{-2}	0.004	MMD2, RADIL	McDanel et al. 2014 [60]	Braford, Brangus, Simbrah	CR

¹*Bos taurus* chromosome. ²Sequentially numbered loci from BTA1 to BTAX associated fetal loss, along with their corresponding single nucleotide polymorphism (SNPs). ³Genomic locations of associated SNPs, given in megabase (Mb), based on nucleotide numbering in the ARS-UCD 1.2 reference genome (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.1/ (6 June 2025)). ⁴False discovery rate (FDR) adjusted P values for SNPs associated with fetal loss. ⁵Proportion of variance explained (PVE) by each SNP associated with fetal loss. ⁶Positional candidate genes located within 29 kb upstream or downstream of the SNPs associated with fetal loss based on the NCBI database and the cow genome assembly ARS-UCD2.0 (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.3/ (6 June 2025)). ⁷Previous fertility studies. ⁸Cattle breed evaluated in previous study. ⁹Fertility trait associated in a previous study as defined by: HCR1 (heifer conception rate at first service), TBRD (number of times bred by artificial insemination before a pregnancy was achieved), DPR (daughter pregnancy rate), SA (spontaneous abortion or fetal loss) and CR (conception rate). Positional candidate genes functional information was obtained from NCBI (<https://www.ncbi.nlm.nih.gov/> (6 June 2025)) and Ensembl (https://useast.ensembl.org/Bos_taurus/Info/Index (6 June 2025)).

Table S4. Loci associated with fetal loss in primiparous cows that were shared in previous fertility studies.

BTA ¹	Locus ²	Pos ³ (Mb)	FDR ⁴	PVE (%) ⁵	PCG ⁶	Study ⁷	Breed ⁸	Trait ⁹
11	14	2.6	3.39 × 10 ⁻²	0.007	<i>KANSL3, FER1L5</i>	Rezende et al. 2018 [106]	Jersey	CR
14	17	41.8	3.74 × 10 ⁻²	0.007		Galliou et al. 2020 [47]	Holstein	TBRD
14	17	41.8	3.70 × 10 ⁻²	0.007		Galliou et al. 2020 [47]	Holstein	TBRD
14	17	41.8	3.67 × 10 ⁻²	0.007		Galliou et al. 2020 [47]	Holstein	TBRD
18	24	52.0	2.28 × 10 ⁻²	0.008	<i>PHLDB3, ETHE1, ZNF575, XRCC1, PINLYP</i>	Cole et al. 2011 [61]	Holstein	DPR
18	24	52.0	2.28 × 10 ⁻²	0.008	<i>PHLDB3, ETHE1, ZNF575, XRCC1, PINLYP</i>	Nayeri et al. 2017 [107]	Holstein	LPL
18	24	52.0	2.25 × 10 ⁻²	0.008	<i>ETHE1, ZNF575, XRCC1, PINLYP</i>	Cole et al. 2011 [61]	Holstein	DPR
18	24	52.0	2.21 × 10 ⁻²	0.008	<i>ETHE1, ZNF575, XRCC1, PINLYP</i>	Cole et al. 2011 [61]	Holstein	DPR
22	31	7.5	3.72 × 10 ⁻²	0.007	<i>CRTAP, SUS5D</i>	Parker Gaddis et al. 2016 [58]	Holstein	CR
22	31	7.6	3.68 × 10 ⁻²	0.007	<i>SUS5D, FBXL2, LOC112443433</i>	Parker Gaddis et al. 2016 [58]	Holstein	PR
22	31	7.6	3.65 × 10 ⁻²	0.007	<i>SUS5D, FBXL2, LOC112443433</i>	Parker Gaddis et al. 2016 [58]	Holstein	CR

¹*Bos taurus* chromosome. ²Sequentially numbered loci from BTA1 to BTAX that were associated with fetal loss, along with their corresponding single nucleotide polymorphism (SNPs). ³Genomic locations of associated SNPs, given in megabase (Mb), based on nucleotide numbering in the ARS-UCD 1.2 reference genome (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.1/ (6 June 2025)). ⁴False discovery rate (FDR) adjusted P values for SNPs associated with fetal loss. ⁵Proportion of variance explained (PVE) for each SNP associated with fetal loss. ⁶Positional candidate genes located within 29 kb upstream or downstream of the SNPs associated with fetal loss based on the NCBI database and the cow genome assembly ARS-UCD2.0 (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.3/ (6 June 2025)). ⁷Previous fertility studies. ⁸Cattle breed evaluated in previous studies. ⁹Fertility trait associated in previous studies as defined by: CR

(conception rate), TBRD (number of times bred by artificial insemination before a pregnancy was achieved), DPR (daughter pregnancy rate), LPL (length of productive life), and PR (pregnancy rate). Positional candidate genes functional information was obtained from NCBI (<https://www.ncbi.nlm.nih.gov/> (6 June 2025)) and Ensembl (https://useast.ensembl.org/Bos_taurus/Info/Index (6 June 2025)).

Table S5. Loci associated with fetal loss in Holstein heifers and primiparous cows that were shared in previous production trait studies.

BTA ¹	Locus ²	Location (Mb) ³	PVE (%) ⁴	PCG ⁵	Study ⁶	Breed ⁷	Trait ⁸
26	13	23.6	0.005	<i>CNNM2</i>	Pedrosa et al. 2021 [97]	Nordic-Red	Milk fat yield
26	13	23.9	0.005	<i>TAF5, ATP5MK, MIR1307, PDCD11, LOC104975977</i>	Gebreyesus et al. 2019 [98]	Holstein	Milk fatty acid yield

¹*Bos taurus* chromosome. ²Sequentially numbered loci from BTA1 to BTAX associated fetal loss, along with their corresponding single nucleotide polymorphism (SNPs). ³Genomic locations of associated SNPs, given in megabase (bp), based on nucleotide numbering in the ARS-UCD 1.2 reference genome (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.1/ (6 June 2025)). ⁴Proportion of variance explained (PVE) by each SNP associated with fetal loss. ⁵Positional candidate genes located within 29 kb upstream or downstream of the SNPs associated with fetal loss based on the NCBI database and the cow genome assembly ARS-UCD2.0 (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.3/). ⁶Previous production trait studies. ⁷Cattle breed evaluated in previous study. ⁸Production trait associated in the previous study. Positional candidate genes functional information was obtained from NCBI (<https://www.ncbi.nlm.nih.gov/> (6 June 2025)) and Ensembl (https://useast.ensembl.org/Bos_taurus/Info/Index (6 June 2025)).