

1 **Bayesian-genome wide association study and post-GWAS on reproductive traits of Holstein**
2 **dairy cattle**

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5 **SUPPLEMENTARY FILE**

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9 Table S1. Summary of the pedigree file and number of animals

Information	Number of Records
Individuals in total	2,774,183
Inbred animals in total	2,020,760
Sires in total	28,498
Dams in total	1,332,556
Individuals with progeny	1,361,054
Individuals with no progeny	1,413,129
founders	278,081

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12 Table S2. Summarized basic statistics of reproductive traits' records

Trait	Number of Records	Mean	Min.	Max.	S.D.
CI	943480	412.45	300.00	700.00	83.371
AFC	1355824	773.88	630.00	1200.0	97.340
DO	1283493	132.43	40.000	350.00	71.750
PR	902031	25.163	-27.750	48.000	17.792

13 AFC, age at first calving(days); CI, calving interval(days); DO, days open(days); RP, pregnancy rate (%)

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1 Table S3. The number of SNPs and animals remained after quality control for each chip are used in the final analysis.

Chip	No. of unspecified physical position	Mind>0.01	MAF <0.01	Geno>0.01	HWE <10 ⁻⁵ -10 ⁻⁶	SNP	No. of animals
54001	7834	0	4053	3268	116	38730	601
5901	347	0	78	10	0	5466	46
7116	433	0	191	13	2	6477	88
7292	456	0	143	16	6	6671	129
24396	1750	0	1802	30	2	20812	65
24484	1831	0	1201	170	19	21263	432
36197	2918	4	1636	152	31	31460	332
36586	3574	0	2760	159	3	30090	81
36668	4266	4	3588	3238	83	25493	124
45650	6328	0	5292	158	194	33678	502

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5 Table S4. GO terms (biological process) significantly enriched for genes associated with reproductive traits in
6 Iranian Holstein dairy cattle

Trait	GO ID	Description	Count in gene set	FDR
AFC	GO:0006412	Translation	16 of 465	1.55e-12
	GO:0044249	Cellular biosynthetic process	22 of 2121	3.19e-09
	GO:1901566	biosynthetic process	18 of 1248	3.89e-09
	GO:1901576	Organic substance biosynthetic process	22 of 2208	5.35e-09
	GO:0044271	Cellular nitrogen compound biosynthetic process	17 of 1260	4.05e-08
	GO:0034645	cellular macromolecule biosynthetic process	17 of 1340	9.56e-08
	GO:0010467	Gene expression	18 of 1854	1.34e-06
	GO:0046500	metabolic process	4 of 14	2.79e-05
	GO:0034641	Cellular nitrogen compound metabolic process	20 of 2979	5.18e-05
	GO:0006556	S-adenosylmethionine biosynthetic process	3 of 6	0.00039
	GO:0044272	Sulfur compound biosynthetic process	5 of 99	0.0010
	GO:0006555	Methionine metabolic process	3 of 13	0.0023
	GO:0043624	Cellular protein complex disassembly	4 of 58	0.0035
	GO:0070126	Mitochondrial translational termination	3 of 16	0.0035
	GO:0032543	Mitochondrial translation	4 of 69	0.0061

	GO:0006579	Amino-acid betaine catabolic process	2 of 2	0.0108
	GO:1901564	Organonitrogen compound metabolic process	21 of 4795	0.0164
	GO:0030326	Embryonic limb morphogenesis	4 of 102	0.0209
	GO:0006730	Embryonic limb morphogenesis	3 of 38	0.0244
	GO:0044237	Cellular metabolic process	25 of 6875	0.0293
DO	GO:0000077	DNA damage checkpoint	8 of 88	1.32e-08
	GO:0006281	DNA repair	11 of 445	1.11e-07
	GO:0006974	Cellular response to DNA damage stimulus	12 of 649	1.80e-07
	GO:0071479	Cellular response to ionizing radiation	6 of 53	5.59e-07
	GO:0010212	Response to ionizing radiation	7 of 109	5.62e-07
	GO:0071478	Cellular response to radiation	7 of 124	1.16e-06
	GO:0051726	Regulation of cell cycle	12 of 893	3.26e-06
	GO:0009314	Response to radiation	8 of 299	1.31e-05
	GO:0035329	Hippo signaling	4 of 19	3.00e-05
	GO:0003365	Establishment of cell polarity involved in ameboid cell migration	3 of 3	4.48e-05
	GO:0090304	Nucleic acid metabolic process	14 of 1856	8.78e-05
	GO:0006975	DNA damage induced protein phosphorylation	3 of 5	0.00011
	GO:0033044	Regulation of chromosome organization	7 of 311	0.00021
PR	GO:0010564	Regulation of cell cycle process	8 of 500	0.00033
	GO:0032012	Regulation of arm protein signal transduction	4 of 19	0.00020
	GO:0015833	Peptide transport	10 of 1214	0.0058
	GO:0006810	Transport	15 of 3496	0.0073
	GO:0034394	Protein localization to cell surface	3 of 23	0.0091
	GO:0071702	Organic substance transport	11 of 1857	0.0099
	GO:0015031	Protein transport	9 of 1195	0.0112
	GO:0032097	Positive regulation of response to food	2 of 3	0.0161
	GO:0051179	Localization	8 of 1126	0.0164
	GO:0051649	Establishment of localization in cell	9 of 1504	0.0367