Additional notes for decoding *ARRDC3*, *NFIA*, and *JMJD1C* marker genotype information

Assembled by M.P. Heaton 3/21/2024.

The *ARRDC3* and *NFIA* information was extracted from Table 5 of the revised article:
Heaton MP, Harhay GP, Bassett AS et al. Association of *ARRDC3* and *NFIA* variants with bovine congestive heart failure in feedlot cattle [version 2]. F1000Research 2024, 11:385 (https://doi.org/10.12688/f1000research.109488.2)

The *JMJD1C* information was extracted from Table 1 of the FigShare data release:
Heaton, Michael; Harhay, Gregory; PL Smith, Timothy; Kuhn, Kristin; Kalbfleisch, Theodore S.; Jobman, Erin; et al. (2022). Table 1. Genome sequence context for *JMJD1C* SNPs associated with bovine congestive heart failure (BCHF). figshare. Dataset. (https://doi.org/10.6084/m9.figshare.19780558.v1)

Marker BCHF5 (*ARRDC3*)

Top strand ARS-UCD1.2 genome assembly reference sequence (chr7:90,845,941):
5'-AGCAA-[T/C]-AGAGA-3' where "[T/C]" denotes either a "T" or "C" nucleotide at that position.

Top strand ARS-UCD1.2 genome assembly reference diploid genotypes:
TT = increased disease risk
TC, CC = normal disease risk

Reverse complement ARS-UCD1.2 genome assembly reference genotypes:
5'-TCTCT-[A/G]-TTGCT]-3'
AA = increased disease risk
AG, GG = normal disease risk

Marker BCHF31 (*NFIA*)

Note: BCHF31 is tightly linked to BCHF32 (r2 = 0.94), but it does not perfectly predict the BCHF32 genotype. Although each marker had a slightly different set of informative case-control pairs used to calculate the odds ratio, the ratios were identical and thus, both markers are equivalently associated with BCHF risk.

Top strand ARS-UCD1.2 genome assembly reference sequence (chr3:84,578,325):
5'-TCCAC-[G/A]-ATGTA-3' where "[G/A]" denotes either a "G" or "A" nucleotide at that position.

Top strand ARS-UCD1.2 genome assembly reference diploid genotypes:
GG = increased disease risk
GA, AA = normal disease risk

Reverse complement ARS-UCD1.2 genome assembly reference genotypes:
5'-TACAT-[C/T]-GTGGA-3'
CC = increased disease risk
CT, TT = normal disease risk

Marker BCHF32 (*NFIA*)

Note: BCHF32 is tightly linked to BCHF31 (r^2 = 0.94), but it does not perfectly predict the BCHF31 genotype. Although each marker had a slightly different set of informative case-control pairs used to calculate the odds ratio, the ratios were identical and thus, both markers are equivalently associated with BCHF risk.

Top strand ARS-UCD1.2 genome assembly reference sequence (chr3:84,580,655):
5'-TTACA-[T/C]-GAAGA-3' where "[T/C]" denotes either a "T" or "C" nucleotide at that position.

Top strand ARS-UCD1.2 genome assembly reference diploid genotypes:
TT = increased disease risk
TC,TT = normal disease risk

Reverse complement ARS-UCD1.2 genome assembly reference genotypes:
5'-TCTTC-[A/G]-TGTAA-3'
AA = increased disease risk
AG, GG = normal disease risk

Marker BCHF40 (*JMJD1C*)

Top strand ARS-UCD1.2 genome assembly reference sequence (chr28:19,391,236):
5'-TCACA-[G/A]-TTCTC-3' where "[G/A]" denotes either a "G" or "A" nucleotide at that position.

Top strand ARS-UCD1.2 genome assembly reference diploid genotypes:
GG = normal disease risk
GA, AA = Protective from disease

Reverse complement ARS-UCD1.2 genome assembly reference genotypes:
5'-GAGAA-[C/T]-TGTGA]-3'
CC = normal disease risk
CT, TT = Protective from disease

Marker BCHF42 (*JMJD1C*)

Top strand ARS-UCD1.2 genome assembly reference sequence (chr28:19,418,234):
5'-CTTGT-[T/C]-CTATA-3' where "[T/C]" denotes either a "T" or "C" nucleotide at that position.

Top strand ARS-UCD1.2 genome assembly reference diploid genotypes:
TT = normal disease risk
TC, CC = Protective from disease

Reverse complement ARS-UCD1.2 genome assembly reference genotypes:
5'-TATAG-[A/G]-ACAAG]-3'
AA = normal disease risk
AG, GG = Protective from disease