

## **A comprehensive comparison of high-density SNP panels and an alternative ultra-high-density panel for genomic analyses in Nellore cattle**

*Ricardo V. Ventura<sup>A,B,C,K</sup>, Luiz F. Brito<sup>A,D</sup>, Gerson A. Oliveira Junior<sup>A,J</sup>, Hans D. Daetwyler<sup>E,F</sup>, Flavio S. Schenkel<sup>A</sup>, Mehdi Sargolzaei<sup>G</sup>, Gordon Vandervoort<sup>A,B</sup>, Fabyano Fonseca e Silva<sup>H</sup>, Stephen P. Miller<sup>A,I</sup>, Minos E. Carvalho<sup>J</sup>, Miguel H. A. Santana<sup>J</sup>, Elisangela C. Mattos<sup>J</sup>, Pablo Fonseca<sup>A</sup>, Joanir P. Eler<sup>J</sup> and Jose Bento Sterman Ferraz<sup>J</sup>*

<sup>A</sup>Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, 1 Stone Road West, Guelph, Ontario, N1G 2W1, Canada.

<sup>B</sup>AgSights, 294 Mill St East, Suite 209, Elora, N0B 1S0 Ontario, Canada.

<sup>C</sup>Department of Animal Nutrition and Production, School of Veterinary Medicine and Animal Science, University of São Paulo, Pirassununga, São Paulo, 13635-900, Brazil.

<sup>D</sup>Department of Animal Sciences, Purdue University, 270 S. Russell Street, West Lafayette, Indiana, 47907, USA.

<sup>E</sup>Agriculture Victoria, AgriBio, Centre for AgriBioscience, Bundoora, Vic. 3083, Australia.

<sup>F</sup>School of Applied Systems Biology, La Trobe University, Bundoora, Vic. 3086, Australia.

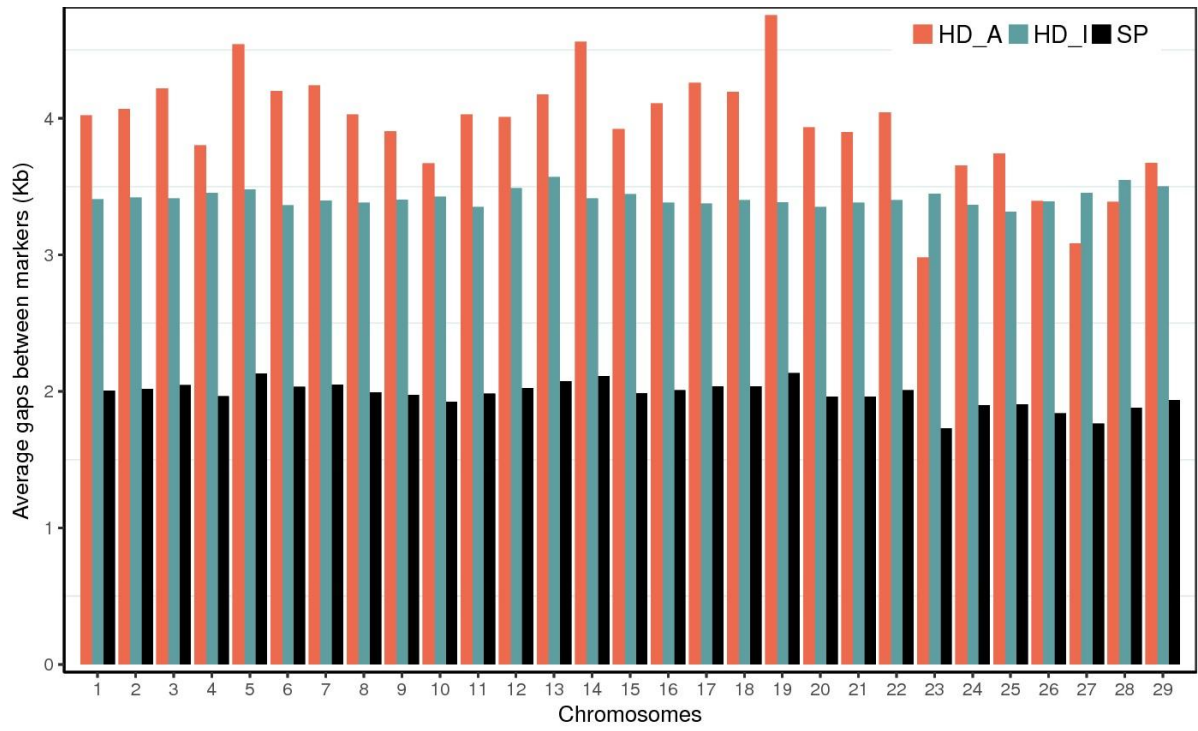
<sup>G</sup>Select Sires Inc., Plain City, Ohio, 43064, USA

<sup>H</sup>Department of Animal Science, Universidade Federal de Vicosa, Vicosa, Minas Gerais, 36570-900, Brazil.

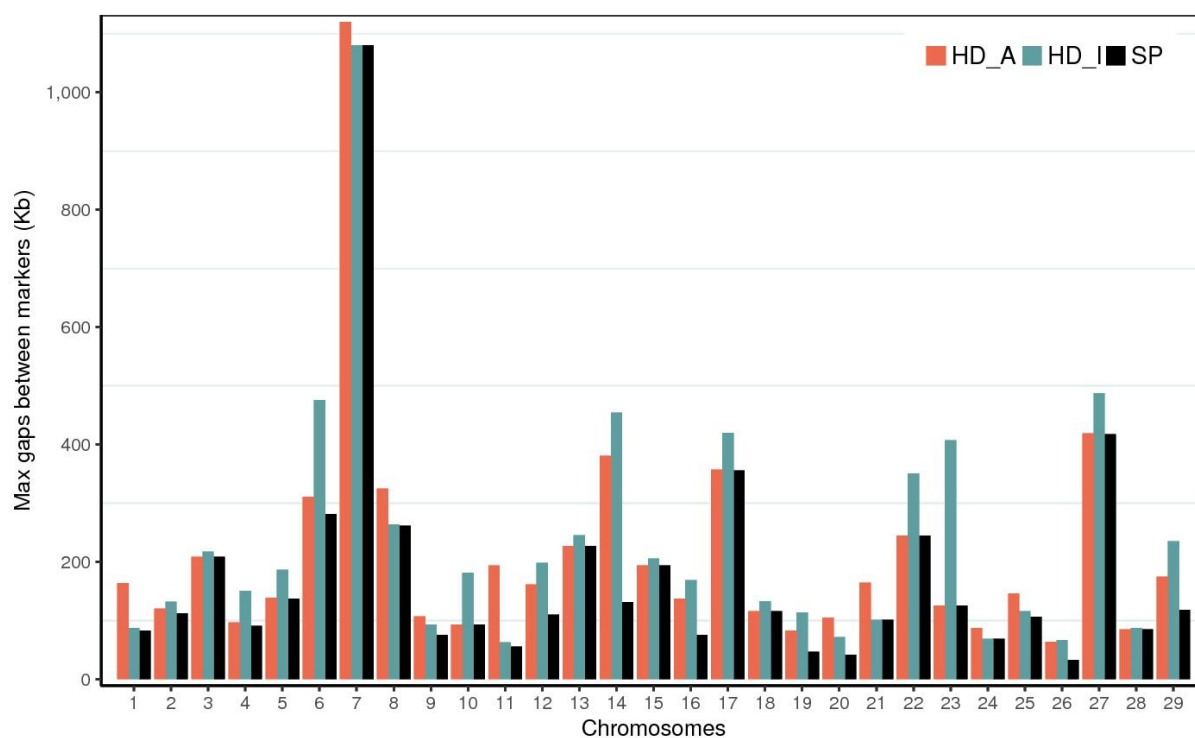
<sup>I</sup>Angus Genetics Inc., 3201 Frederick Avenue, Saint Joseph, St Joseph, Missouri, 64506, USA.

<sup>J</sup>Department of Veterinary Medicine, School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, São Paulo, 13635-900, Brazil.

<sup>K</sup>Corresponding author. Email: [rvventura@usp.br](mailto:rvventura@usp.br)



**Fig. S1.** Average gaps between markers (in Kb) for three SNP chip panels.



**Fig. S2.** Maximum gaps between markers (in Kb) for three SNP chip panels.

**Table S1.** Gap (Kb) description (Mean and Max) per chromosome and overall average values for the six investigated SNP panels

Chr	20K		50K		70K		HD_A		HD_I		SP	
	Mean	Max	Mean	Max	Mean	Max	Mean	Max	Mean	Max	Mean	Max
1	140.55	499.48	46.90	1,767.83	37.17	187.70	5.01	181.12	3.83	162.14	2.33	162.14
2	143.57	609.56	49.12	1,323.05	37.08	187.43	5.11	120.35	3.90	77.38	2.37	60.11
3	142.52	600.26	49.19	3,128.70	36.19	338.50	5.15	208.70	3.85	217.08	2.36	208.70
4	137.38	438.74	46.95	336.47	37.02	188.82	4.79	122.97	3.94	140.26	2.31	87.15
5	146.39	516.65	54.88	3,506.41	36.75	312.82	5.84	145.25	4.03	275.10	2.55	137.27
6	138.57	2,016.56	46.26	1,520.19	37.89	1,919.86	5.45	583.71	3.87	613.93	2.43	583.09
7	136.76	1,106.45	47.80	1,123.52	36.81	1,082.92	5.20	1,135.40	3.76	1,080.18	2.34	1,080.18
8	137.84	543.11	47.62	1,964.30	37.33	441.79	5.01	324.32	3.77	356.94	2.30	324.32
9	141.67	449.17	50.39	666.90	36.38	203.14	4.91	120.53	3.84	100.03	2.31	75.27
10	134.20	545.96	47.24	1,962.28	36.79	366.54	4.52	183.23	3.92	190.27	2.25	122.81
11	134.48	387.47	46.72	505.41	37.17	281.72	5.00	334.65	3.89	110.67	2.34	99.70
12	134.60	738.18	51.32	998.67	36.88	702.06	5.18	314.70	4.08	602.53	2.44	288.26
13	132.21	499.02	45.35	615.15	36.42	299.59	5.16	243.69	4.11	245.39	2.43	243.65
14	133.13	489.27	45.45	489.27	36.00	454.01	5.70	556.64	3.83	454.01	2.44	398.72
15	136.10	595.03	47.95	662.97	34.83	211.35	4.89	195.43	3.93	205.13	2.33	195.43
16	139.09	595.26	47.10	979.32	35.56	595.26	4.98	239.73	3.77	443.54	2.29	233.57
17	136.85	547.18	46.88	813.74	35.98	510.62	5.29	360.57	3.85	502.36	2.38	355.34
18	142.54	593.25	47.80	647.49	34.82	206.10	5.19	146.41	3.95	186.69	2.40	117.39
19	139.86	510.52	44.77	299.44	34.08	252.61	5.97	171.26	4.00	161.09	2.54	161.09
20	137.87	449.93	45.94	339.36	34.50	156.94	4.97	154.61	3.84	101.09	2.31	45.82
21	139.22	607.61	47.97	763.72	34.58	207.80	4.92	260.82	3.92	189.27	2.33	141.90
22	127.04	421.24	46.27	376.16	34.70	369.24	4.85	347.67	3.86	353.11	2.31	347.67
23	132.48	587.43	47.86	448.47	32.65	246.13	3.54	183.29	3.98	628.37	2.01	183.29
24	127.99	423.01	48.21	717.09	34.77	213.95	4.48	135.74	3.78	213.02	2.19	112.78
25	115.33	380.51	43.18	513.82	33.09	157.97	4.47	237.36	3.96	115.79	2.25	106.37
26	126.11	481.24	46.26	536.74	34.22	182.59	4.15	148.49	3.91	70.77	2.16	51.05
27	123.52	846.39	46.25	914.35	33.53	809.36	3.74	489.64	3.96	565.86	2.06	489.64
28	122.56	460.45	47.12	345.18	32.90	173.91	4.16	128.79	4.03	199.52	2.19	122.69
29	124.70	480.63	47.40	729.89	33.70	368.95	4.54	174.86	4.14	361.57	2.31	151.83
Aver.	134.66	600.67	47.45	999.86	35.51	401.02	4.90	274.13	3.91	307.69	2.32	230.59

**Table S2.** Number of markers excluded per chromosome during the SNP pruning based on linkage disequilibrium for HD\_A, HD\_I and SP

Chr.	HD_A		HD_I		SP	
	Pruned out	Remaining	Pruned out	Remaining	Pruned out	Remaining
BTA1	4,598	26,965	17,975	23,333	26,413	41,475
BTA2	4,195	22,526	15,729	19,259	23,117	34,453
BTA3	3,445	20,099	13,832	17,654	20,193	31,160
BTA4	3,848	21,295	12,993	17,579	19,739	32,285
BTA5	3,820	16,893	14,251	15,766	20,680	26,818
BTA6	3,946	17,904	14,369	16,417	21,161	27,805
BTA7	3,340	18,280	13,434	16,463	19,322	28,698
BTA8	3,722	18,862	13,133	16,899	20,120	28,994
BTA9	3,255	18,211	11,992	15,489	18,025	27,623
BTA10	3,637	19,398	11,518	15,061	17,639	28,519
BTA11	3,139	18,298	12,496	15,050	17,950	27,769
BTA12	2,676	14,899	9,485	12,819	14,222	23,060
BTA13	2,597	13,699	8,550	11,903	13,327	21,219
BTA14	2,058	12,671	8,936	13,054	13,344	21,134

BTA15	2,678	14,711	9,016	12,646	13,729	22,728
BTA16	2,072	14,250	9,044	12,610	13,258	22,268
BTA17	1,763	12,355	7,967	11,528	11,479	20,024
BTA18	2,042	10,660	7,535	9,124	10,962	16,464
BTA19	1,503	9,196	6,912	9,074	9,505	15,604
BTA20	2,268	12,203	8,141	10,595	12,101	18,920
BTA21	2,322	12,208	8,152	10,099	12,132	18,557
BTA22	1,864	10,771	6,736	9,139	9,938	16,610
BTA23	1,972	12,847	4,809	8,340	8,160	17,961
BTA24	2,096	11,855	7,092	9,450	10,848	17,643
BTA25	1,304	8,264	4,313	6,474	6,594	12,406
BTA26	1,658	10,774	5,306	7,869	8,258	15,636
BTA27	1,568	10,546	4,316	7,143	7,158	14,861
BTA28	1,652	9,454	4,386	7,078	7,142	13,902
BTA29	1,795	9,530	5,104	7,310	8,075	14,174
Total	76,833	429,624	277,522	365,225	414,591	658,770