

SUPPLEMENTARY MATERIALS

to the article M.G. Smaragdov "Identification of homozygosity-rich regions in the Holstein genome"

Supplementary Material 1

Estimated mean ROH number (\pm SE) in the herds based on 15 SNPs consecutive runs (detectRUNS)

ROH number	Herd						Mean
	1	2	3	4	5	6	
Zero heterozygous SNP in ROH							
The mean number of ROH	190.3 \pm 11.1	175.4 \pm 1.5	178.0 \pm 1.7	190.7 \pm 16.6	178.2 \pm 1.7	179.8 \pm 2.0	182.1 \pm 3.4
Maximum	629	205	249	929	211	215	
Minimum	12	143	149	105	151	145	

Supplementary Material 2

Estimated mean ROH number (\pm SE) across the herds in length classes based on consecutive runs (detectRUNS)

N*	Class (Mb)				
	1-2	2-4	4-8	8-16	>16
Consecutive runs with 20 SNPs					
0	3585 \pm 277	1155 \pm 9	662 \pm 63	319 \pm 32	113 \pm 17
1	6792 \pm 560	1391 \pm 103	704 \pm 63	344 \pm 34	123 \pm 17
2	12382 \pm 1080	1840 \pm 142	750 \pm 69	362 \pm 31	131 \pm 18
Consecutive runs with 15 SNPs					
0	8994 \pm 734	1172 \pm 90	662 \pm 63	319 \pm 32	113 \pm 17

* The number of allowed heterozygous SNPs in the ROH segments.

Supplementary Material 3

Estimated mean ROH number (\pm SE) across the herds in the length classes based on 20 SNPs sliding runs

N*	Class (Mb)				
	1-2	2-4	4-8	8-16	>16
Sliding runs based on detectRUNS					
0	3190 \pm 241	1048 \pm 83	643 \pm 61	309 \pm 32	111 \pm 16
1	6488 \pm 554	1419 \pm 122	690 \pm 66	358 \pm 31	139 \pm 15
2	12205 \pm 1100	2444 \pm 220	81 \pm 88	385 \pm 39	152 \pm 14
Sliding runs based on Plink					
0	2415 \pm 198	1145 \pm 86	655 \pm 63	328 \pm 33	118 \pm 15

* The number of allowed heterozygous SNPs in ROH segments.

Supplementary Material 4

Chromosomes rank by ROH coverage (consecutive runs)

BTA*	Size of BTA (Mb)**	Proportion of the chromosomes size in cow genome	Proportion of ROH in chromosomes	Rank of chromosomes
1	158.53	0.0636	0.071	1.116
2	136.23	0.0547	0.05	0.914
3	121.01	0.0486	0.0464	0.955
4	120.0	0.0482	0.0505	1.048
5	120.09	0.0482	0.0439	0.911
6	117.81	0.0473	0.0478	1.011
7	110.68	0.0445	0.055	1.236
8	113.32	0.0455	0.054	1.187
9	105.45	0.0424	0.038	0.896
10	103.31	0.0415	0.038	0.916
11	106.98	0.043	0.0397	0.923
12	87.22	0.035	0.032	0.914
13	83.47	0.0335	0.0375	1.119
14	82.4	0.0331	0.044	1.329
15	85.01	0.0342	0.027	0.789
16	81.01	0.0325	0.042	1.292
17	73.17	0.0294	0.031	1.054
18	65.82	0.0264	0.02	0.758
19	63.45	0.0255	0.026	1.02
20	71.97	0.0289	0.0296	1.024
21	69.86	0.0281	0.027	0.961
22	60.77	0.0244	0.0239	0.98
23	52.5	0.0211	0.017	0.806
24	62.32	0.025	0.024	0.96
25	42.35	0.017	0.0149	0.876
26	51.99	0.021	0.025	1.191
27	45.61	0.183	0.0137	0.749
28	45.94	0.0185	0.0125	0.676
29	51.1	0.0205	0.0173	0.844

* *Bos taurus* autosome; ** cow genome 2489.37 Mb.