

Analysis of Youngstock survival traits

Andreas Bøgh Poulsen

Trine Andersen

Ulrik Sander Nielsen

November 20, 2025

Table of contents

Introduction	1
Holstein	3
Genetic trends	3
Correlations	10
Legarra-Reverter test	14
Mendelian sampling	15
Reliabilities	16
Jersey	18
Genetic trends	18
Correlations	25
Legarra-Reverter test	28
Mendelian sampling	28
Reliabilities	30
RDC	31
Genetic trends	31
Correlations	38
Legarra-Reverter test	42
Mendelian sampling	43
Reliabilities	44
Note on genotype selection	46

Introduction

The Youngstock survival index for a bull is a measure of the genetic potential of his offspring to survive the early months of its life (direct effect). We use four traits to calculate this index:

1. Heifer survival, early (HP1)
2. Heifer survival, later (HP2)
3. Bull survival, early (BP1)
4. Bull survival, later (BP2)

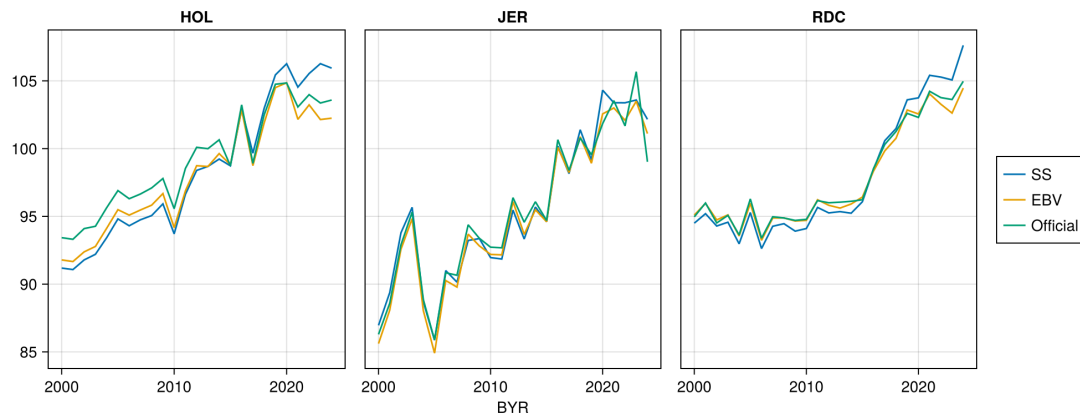
All traits are a binary 0/1 score, indicating whether the animal survived or not. Early period denotes the first 30 days of life, later period denote 30 days until a year. Since Youngstock survival is not an Interbull trait, no foreign information is included.

The model and genetic parameters are the same as those used in the current official NAV evaluation. For each breeds evaluation, we only use phenotypic data from animals with the correct breed in their `id_nor`.

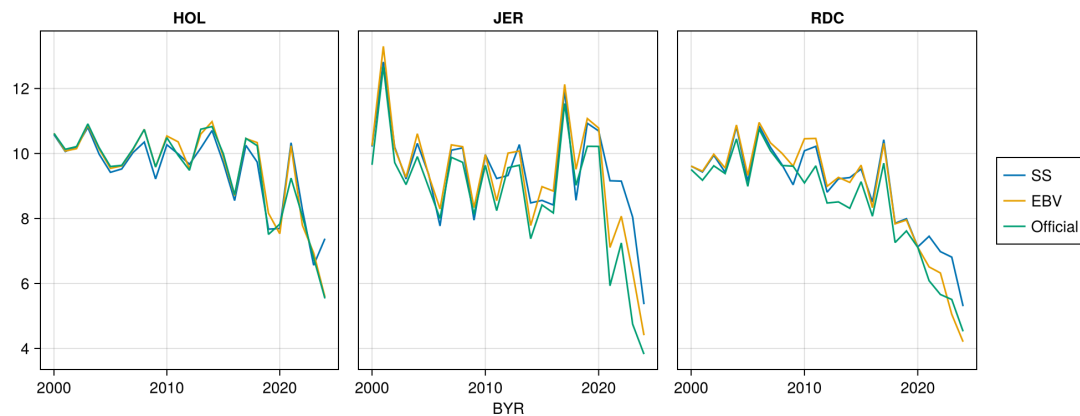
The evaluation only includes a subset of the genomic markers, compared to other single-step evaluations. This is due to systematic errors on these markers, which introduce bias in the evaluation. For more details on this, see the report “Report on systematic call errors on certain SNP markers”, SEGES 2025.

For compactness of tables, we will use abbreviations throughout. They are mentioned here:

- yss: youngstock survival
- ss: single-step breeding value
- rss: reduced information single-step breeding value
- ebv: tradition pedigree-based breeding value
- rebv: reduced information pedigree-based breeding value
- cor: correlation
- m^{*}: mean value of *
- s^{*}: standard deviation of *



(a) Genetic trend (mean and standard deviation) of combined birth index for nordic AI bulls



(b)

Figure 1:

Holstein

Genetic trends

Here, we exhibit the genetic trends of our evaluations for each trait. We see that the levels of breeding values are generally in agreement across evaluations.

Table 1: Genetic trends (Single-step (ss) vs new EBV (newebv) vs official EBV (offebv)) and correlation between single-step and official EBV for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2009	HP1	246	95.18	96.0	97.09	10.76	11.04	10.82	0.93
2010	HP1	215	92.73	93.28	94.48	11.54	11.63	11.46	0.95
2011	HP1	183	94.81	95.16	96.29	11.47	11.74	11.55	0.94
2012	HP1	196	98.37	98.34	99.38	11.52	11.33	11.12	0.95
2013	HP1	183	97.26	96.64	97.73	11.09	11.46	11.32	0.95
2014	HP1	148	99.7	99.66	100.49	12.2	12.46	12.14	0.96
2015	HP1	105	98.51	98.43	99.02	10.92	10.85	10.63	0.96
2016	HP1	99	99.65	99.61	99.58	10.11	10.37	10.18	0.95
2017	HP1	106	98.69	98.19	98.57	9.97	10.68	10.53	0.93
2018	HP1	115	101.58	101.23	101.4	10.13	10.34	10.11	0.95
2019	HP1	82	104.98	103.78	103.7	9.56	9.52	9.44	0.9
2020	HP1	71	104.06	102.97	102.51	10.25	10.64	10.39	0.93
2021	HP1	61	105.21	103.64	103.07	11.63	11.72	11.55	0.96
2022	HP1	57	105.53	103.93	103.15	10.48	10.19	10.06	0.94
2023	HP1	12	107.42	106.58	105.7	7.29	7.65	7.55	0.85
2009	HP2	244	97.22	97.8	98.44	8.62	8.86	8.86	0.94
2010	HP2	214	95.43	95.79	96.47	10.16	10.63	10.71	0.95
2011	HP2	177	97.1	97.28	97.87	9.83	10.35	10.36	0.94
2012	HP2	191	99.36	99.79	100.34	9.56	9.92	9.99	0.97
2013	HP2	177	99.14	99.34	99.8	11.06	11.38	11.39	0.96
2014	HP2	144	98.11	98.75	99.18	10.34	10.83	10.82	0.97
2015	HP2	104	98.64	98.43	98.56	9.71	10.43	10.36	0.97
2016	HP2	93	101.24	101.48	101.58	8.85	9.08	8.97	0.93
2017	HP2	96	98.85	98.41	98.44	10.74	10.65	10.66	0.95
2018	HP2	111	102.17	101.63	101.59	9.96	10.54	10.53	0.94
2019	HP2	75	103.8	102.83	102.51	7.89	8.44	8.43	0.92
2020	HP2	65	103.43	102.58	102.1	8.08	8.53	8.62	0.93

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2021	HP2	50	102.74	101.76	101.33	9.22	9.12	9.29	0.91
2022	HP2	15	102.8	102.27	101.6	7.72	8.27	8.29	0.93
2009	BP1	239	95.09	96.0	97.32	10.42	10.46	10.51	0.93
2010	BP1	209	92.32	92.72	93.95	11.71	11.65	11.78	0.95
2011	BP1	172	94.95	95.81	96.86	11.24	11.39	11.46	0.94
2012	BP1	194	98.02	97.98	98.94	11.39	10.9	10.95	0.95
2013	BP1	169	97.47	96.92	97.78	10.79	11.04	11.16	0.95
2014	BP1	139	100.31	100.47	101.02	12.35	12.47	12.43	0.96
2015	BP1	104	98.02	98.13	98.28	10.89	11.03	11.08	0.95
2016	BP1	91	100.93	100.9	100.44	9.27	9.61	9.72	0.95
2017	BP1	89	99.21	98.74	98.58	10.62	11.07	11.28	0.94
2018	BP1	103	101.38	100.83	100.65	10.36	10.0	10.18	0.95
2019	BP1	76	105.24	103.96	103.56	10.0	10.52	10.74	0.91
2020	BP1	68	105.18	103.74	103.13	10.78	11.0	11.06	0.93
2021	BP1	54	106.48	104.19	103.31	12.15	11.62	11.76	0.96
2022	BP1	50	105.28	103.5	102.48	11.22	10.59	10.68	0.93
2023	BP1	12	106.58	105.5	104.66	8.06	8.02	8.35	0.89
2009	BP2	238	97.12	97.63	98.74	8.67	8.74	8.75	0.95
2010	BP2	207	95.26	95.38	96.49	10.35	10.8	10.88	0.96
2011	BP2	169	97.22	97.7	98.69	9.63	10.06	10.0	0.95
2012	BP2	192	98.79	99.21	99.97	9.8	10.07	10.1	0.97
2013	BP2	165	99.48	99.67	100.15	11.02	11.38	11.38	0.97
2014	BP2	134	98.49	99.09	99.63	10.12	10.47	10.47	0.97
2015	BP2	101	98.67	98.56	98.56	9.45	10.05	9.98	0.96
2016	BP2	87	102.34	102.62	102.53	8.57	8.59	8.66	0.94
2017	BP2	85	99.04	98.53	98.47	10.86	10.77	10.72	0.95
2018	BP2	101	102.45	101.47	101.41	9.12	9.66	9.68	0.95
2019	BP2	73	103.01	102.03	101.64	7.94	8.14	8.04	0.93
2020	BP2	65	103.52	102.43	101.96	8.65	8.81	8.91	0.94
2021	BP2	51	102.37	100.84	100.31	8.64	8.52	8.58	0.92
2022	BP2	39	104.85	102.82	102.1	7.46	7.78	7.95	0.91
2023	BP2	3	114.33	110.33	110.06	4.04	4.04	4.29	1.0

Table 2: Genetic trends (Single-step (ss) vs new EBV (newebv) vs official EBV (offebv)) and correlation between single-step and official EBV for nordic non-genotyped cows with phenotype

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2009	HP1298424		92.89	93.36	94.59	7.13	7.16	6.94	0.97
2010	HP1303509		91.87	92.32	93.57	7.39	7.44	7.25	0.97
2011	HP1303531		92.68	93.12	94.21	7.66	7.71	7.59	0.97
2012	HP1303206		94.17	94.63	95.67	7.62	7.62	7.53	0.97
2013	HP1298589		94.18	94.6	95.51	7.3	7.3	7.35	0.96
2014	HP1300066		95.44	95.77	96.95	7.68	7.63	7.35	0.95
2015	HP1294486		94.83	95.06	96.18	9.05	9.05	8.73	0.97
2016	HP1284704		96.46	96.72	97.71	8.27	8.25	8.04	0.96
2017	HP1259664		97.1	97.3	98.19	8.25	8.23	7.93	0.96
2018	HP1249631		97.8	98.0	98.66	7.83	7.78	7.48	0.95
2019	HP1238167		98.2	98.35	98.79	8.04	8.08	7.87	0.96
2020	HP1239277		97.86	97.97	98.47	7.82	7.81	7.53	0.95
2021	HP1239231		99.49	99.52	99.7	7.97	7.93	7.76	0.96
2022	HP1231382		99.84	99.8	99.55	7.83	7.84	8.09	0.96
2023	HP1218987		100.27	100.14	99.77	8.23	8.3	8.28	0.96
2024	HP1208767		101.02	100.61	100.02	8.77	8.8	8.8	0.97
2025	HP1135468		101.76	101.06	100.39	8.38	8.28	8.3	0.96
2009	HP2286748		96.1	96.56	97.11	5.66	5.71	5.8	0.98
2010	HP2290146		94.79	95.29	95.92	6.12	6.14	6.17	0.98
2011	HP2290993		95.63	96.1	96.71	6.04	6.04	6.06	0.97
2012	HP2289872		96.22	96.69	97.28	5.88	5.89	5.98	0.97
2013	HP2282813		96.36	96.79	97.37	6.32	6.33	6.4	0.97
2014	HP2284432		97.0	97.48	98.16	6.31	6.3	6.27	0.96
2015	HP2278966		97.5	97.95	98.47	6.28	6.31	6.36	0.96
2016	HP2269637		98.27	98.72	99.19	6.49	6.5	6.5	0.96
2017	HP2246997		97.99	98.37	98.83	6.42	6.44	6.44	0.96
2018	HP2235498		99.13	99.44	99.68	6.56	6.58	6.61	0.96
2019	HP2225028		99.38	99.63	99.83	6.33	6.28	6.31	0.96
2020	HP2226833		99.22	99.41	99.68	6.36	6.35	6.26	0.95
2021	HP2224733		99.79	99.85	99.98	6.34	6.32	6.24	0.95
2022	HP2216126		99.81	99.73	99.57	6.29	6.32	6.38	0.96

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2023	HP205325		99.85	99.68	99.5	6.1	6.2	6.25	0.96
2024	HP2 90584		100.11	99.87	99.66	6.23	6.34	6.43	0.96

Table 3: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2009	HP1	224	95.07	96.99	11.07	11.19	0.98
2010	HP1	193	93.16	94.77	11.86	12.22	0.98
2011	HP1	155	94.86	96.75	11.73	11.61	0.98
2012	HP1	171	98.6	100.25	11.88	12.07	0.97
2013	HP1	151	97.67	98.81	11.35	11.67	0.96
2014	HP1	113	100.54	101.23	12.97	13.0	0.97
2015	HP1	82	98.96	99.23	10.7	10.46	0.93
2016	HP1	65	101.86	102.85	10.38	9.87	0.65
2017	HP1	66	99.64	100.36	10.07	9.13	0.56
2018	HP1	78	102.24	103.19	10.45	8.71	0.6
2019	HP1	56	106.7	104.86	9.64	5.67	0.28
2020	HP1	56	105.95	105.18	9.25	6.86	0.55
2021	HP1	46	107.67	107.17	11.03	5.83	0.33
2022	HP1	46	106.39	104.59	10.34	7.03	0.44
2023	HP1	11	107.91	101.91	7.44	7.19	0.56
2009	HP2	224	97.26	98.17	8.79	8.95	0.98
2010	HP2	193	95.58	96.21	10.26	10.41	0.98
2011	HP2	155	97.15	97.99	10.16	10.29	0.98
2012	HP2	171	99.55	100.77	9.81	9.86	0.98
2013	HP2	151	99.73	101.01	10.9	10.71	0.97
2014	HP2	113	98.84	99.73	10.64	11.04	0.97
2015	HP2	82	99.67	101.82	9.92	10.19	0.97
2016	HP2	65	103.46	105.29	8.23	7.44	0.53
2017	HP2	66	99.52	102.27	10.97	8.79	0.67
2018	HP2	78	103.24	105.5	10.08	6.44	0.41
2019	HP2	56	104.91	105.25	8.0	7.2	0.45
2020	HP2	54	104.72	106.74	7.04	6.25	0.36
2021	HP2	41	103.34	106.88	9.48	6.37	0.45

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2022	HP2	14	103.36	105.0	7.69	7.6	0.67
2009	BP1	224	94.88	97.22	10.66	10.63	0.98
2010	BP1	193	92.72	95.05	11.93	12.11	0.98
2011	BP1	154	95.32	97.79	11.45	11.17	0.98
2012	BP1	171	98.22	100.23	11.71	11.68	0.97
2013	BP1	151	97.79	99.35	10.94	11.33	0.97
2014	BP1	114	101.0	101.71	12.81	12.75	0.97
2015	BP1	82	98.78	98.85	10.84	10.56	0.95
2016	BP1	66	102.5	103.27	9.86	9.49	0.64
2017	BP1	66	100.08	100.5	10.87	8.94	0.63
2018	BP1	78	101.64	102.96	10.13	8.27	0.63
2019	BP1	56	106.61	104.21	9.91	5.84	0.2
2020	BP1	55	106.44	105.2	10.15	7.14	0.59
2021	BP1	46	107.89	106.76	11.0	6.79	0.43
2022	BP1	45	106.2	103.44	10.81	7.72	0.59
2023	BP1	11	106.91	101.64	8.37	7.67	0.61
2009	BP2	224	97.03	98.32	8.79	8.88	0.98
2010	BP2	193	95.45	96.65	10.31	10.53	0.99
2011	BP2	154	97.7	99.06	9.56	9.63	0.98
2012	BP2	171	99.06	100.69	9.98	10.05	0.98
2013	BP2	151	100.05	101.65	10.69	10.72	0.98
2014	BP2	113	99.16	100.17	10.24	10.63	0.98
2015	BP2	82	99.62	101.76	9.71	9.94	0.97
2016	BP2	66	103.85	105.77	8.25	7.09	0.56
2017	BP2	66	99.65	102.32	10.98	8.87	0.7
2018	BP2	78	102.71	105.4	9.28	5.97	0.4
2019	BP2	56	104.16	104.71	7.68	7.28	0.42
2020	BP2	55	104.58	106.33	7.35	6.61	0.42
2021	BP2	43	103.02	106.47	8.71	6.69	0.47
2022	BP2	38	105.05	106.55	7.45	6.89	0.56
2023	BP2	3	114.33	114.67	4.04	5.51	0.32

Table 4: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic cows with genotype and phenotype

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2009	HP1	979	94.78	96.65	8.18	7.94	0.92
2010	HP1	1396	92.39	94.12	8.91	8.67	0.93
2011	HP1	3041	93.4	95.28	8.97	8.85	0.94
2012	HP1	4780	95.13	96.93	8.61	8.42	0.93
2013	HP1	8320	95.74	97.48	8.23	7.97	0.92
2014	HP1	9756	96.98	98.67	8.65	8.53	0.92
2015	HP1	12507	95.72	97.04	10.42	10.57	0.94
2016	HP1	19814	98.03	99.44	9.1	8.98	0.92
2017	HP1	29716	98.6	99.56	9.0	8.62	0.91
2018	HP1	41677	100.05	101.27	8.14	7.99	0.85
2019	HP1	46882	100.48	101.79	8.57	7.74	0.78
2020	HP1	56192	99.94	101.25	8.31	7.41	0.76
2021	HP1	59989	102.56	102.84	8.17	6.82	0.7
2022	HP1	68086	102.76	102.58	8.0	6.48	0.68
2023	HP1	74969	103.34	102.71	8.7	6.56	0.65
2024	HP1	80490	104.17	103.31	9.69	6.16	0.57
2025	HP1	45504	104.4	103.73	9.14	6.18	0.59
2009	HP2	978	96.83	97.39	7.12	6.9	0.91
2010	HP2	1395	95.28	95.89	7.64	7.55	0.92
2011	HP2	3036	96.07	96.74	7.8	7.63	0.92
2012	HP2	4768	97.15	98.0	7.28	7.08	0.9
2013	HP2	8309	97.95	98.88	7.65	7.43	0.92
2014	HP2	9715	97.83	98.93	7.57	7.39	0.91
2015	HP2	12404	98.8	100.07	7.58	7.31	0.9
2016	HP2	19613	99.73	100.82	7.77	7.52	0.9
2017	HP2	29368	99.22	100.45	7.94	7.76	0.91
2018	HP2	41257	101.12	103.48	7.59	7.44	0.85
2019	HP2	46267	101.48	102.96	7.37	7.05	0.79
2020	HP2	55063	101.16	102.52	7.63	7.04	0.74
2021	HP2	58967	102.01	104.0	7.42	6.6	0.67
2022	HP2	66630	102.11	103.74	7.51	6.83	0.74
2023	HP2	73571	102.03	103.77	7.37	6.53	0.67
2024	HP2	35280	102.2	104.16	7.67	6.4	0.64

Table 5: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic bulls with genotype and phenotype

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2009	BP1	717	94.09	96.63	8.52	8.31	0.94
2010	BP1	706	91.44	93.97	9.66	9.48	0.96
2011	BP1	1338	93.92	96.33	9.39	9.14	0.95
2012	BP1	1706	95.28	97.56	8.27	8.02	0.93
2013	BP1	1801	95.77	97.91	8.17	8.01	0.93
2014	BP1	2376	97.19	99.26	9.01	8.78	0.94
2015	BP1	2012	95.77	97.26	10.55	10.8	0.95
2016	BP1	2155	99.2	100.63	8.88	8.76	0.92
2017	BP1	2446	99.12	100.25	8.95	8.23	0.91
2018	BP1	2347	101.31	102.46	8.18	7.75	0.85
2019	BP1	2516	101.53	101.85	8.31	7.2	0.75
2020	BP1	2400	102.48	102.92	8.93	7.78	0.79
2021	BP1	2198	103.37	103.38	8.6	6.71	0.63
2022	BP1	2302	104.07	102.95	8.57	6.6	0.73
2023	BP1	2246	104.76	103.61	8.86	6.59	0.63
2024	BP1	1925	105.49	103.78	9.43	6.38	0.63
2025	BP1	1256	105.53	103.62	8.61	6.48	0.65
2009	BP2	634	96.36	97.32	7.24	7.07	0.94
2010	BP2	633	94.9	96.07	8.55	8.39	0.94
2011	BP2	1157	96.77	97.96	7.58	7.6	0.93
2012	BP2	1528	96.88	98.38	7.36	7.22	0.92
2013	BP2	1555	98.29	99.79	7.58	7.48	0.93
2014	BP2	2076	97.46	98.91	8.09	7.8	0.93
2015	BP2	1804	99.44	101.12	7.72	7.53	0.92
2016	BP2	1966	100.32	101.84	7.62	7.44	0.91
2017	BP2	2276	99.95	101.74	7.97	7.78	0.92
2018	BP2	2162	101.83	104.61	7.35	6.75	0.82
2019	BP2	2297	102.12	103.5	7.34	6.73	0.78
2020	BP2	2192	102.54	103.64	7.56	6.58	0.72
2021	BP2	1993	102.75	105.04	7.07	6.29	0.65
2022	BP2	2058	103.55	104.69	7.16	6.55	0.74

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2023	BP2	2022	102.62	104.88	7.21	6.42	0.63
2024	BP2	1740	103.25	105.57	7.25	6.04	0.66
2025	BP2	430	103.64	105.54	6.36	5.95	0.7

Correlations

Here, we give correlation tables and tables of differences between the relevant evaluations. We test that we didn't change the model by comparing our new model without genomic information to the breeding values of the traditional pedigree-based model and expect very high correlations for tested animals. We test the change by incorporating genomic information, compared to a non-genomic evaluation, and expect to see some changes even in tested animals, but not too large.

Table 6: Correlations between current EBV and new EBV for Nordic AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	224	0.998	0.997	0.998	0.997
2010	193	0.998	0.997	0.997	0.997
2011	155	0.998	0.998	0.997	0.998
2012	171	0.998	0.998	0.998	0.998
2013	151	0.998	0.998	0.997	0.998
2014	113	0.999	0.999	0.999	0.999
2015	82	0.998	0.999	0.999	0.999
2016	65	0.998	0.999	0.998	0.998
2017	66	0.999	0.999	0.999	0.999
2018	78	0.998	0.999	0.999	0.999
2019	56	0.999	0.998	0.999	0.999
2020	54	0.999	0.998	0.999	0.999
2021	41	0.999	0.999	0.999	0.998
2022	14	0.999	0.999	0.999	0.998

Table 7: Table of differences between current EBV and new EBV for Nordic AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-3.0	0	0	1	0
-2.0	10	6	16	5
-1.0	127	121	180	138
0.0	176	229	165	220

dif	dif1	dif2	dif3	dif4
1.0	59	17	11	9
2.0	1	1	1	2
3.0	1	0	0	0

Table 8: Correlations between current EBV and new Single-step for AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	224	0.944	0.944	0.936	0.948
2010	193	0.959	0.961	0.956	0.964
2011	155	0.954	0.96	0.949	0.962
2012	171	0.97	0.975	0.965	0.977
2013	151	0.959	0.968	0.952	0.968
2014	113	0.976	0.981	0.971	0.979
2015	82	0.978	0.98	0.979	0.981
2016	65	0.975	0.977	0.974	0.975
2017	66	0.962	0.985	0.967	0.981
2018	78	0.968	0.978	0.961	0.978
2019	56	0.933	0.97	0.935	0.966
2020	54	0.959	0.919	0.962	0.918
2021	41	0.966	0.943	0.959	0.932
2022	14	0.989	0.981	0.981	0.984

Table 9: Table of differences between current EBV and new Single-step for AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-13.0	0	1	2	0
-12.0	2	1	0	2
-11.0	1	0	2	0
-10.0	0	1	4	2
-9.0	3	1	2	1
-8.0	4	6	3	4
-7.0	7	1	10	6
-6.0	9	7	9	6
-5.0	10	6	20	8
-4.0	22	13	24	15

dif	dif1	dif2	dif3	dif4
-3.0	31	27	45	29
-2.0	47	57	46	58
-1.0	61	85	67	92
0.0	78	99	60	86
1.0	37	33	35	24
2.0	27	16	18	22
3.0	13	10	7	7
4.0	11	5	8	10
5.0	2	4	7	1
6.0	2	0	1	0
7.0	2	0	2	0
8.0	3	0	0	0
9.0	1	0	1	1
10.0	1	1	1	0

Table 10: Correlations between current two-step and new Single-step for genotyped nordic bulls with no offspring born after 2020

BYR	n	cor
2020	3089	0.83
2021	3050	0.809
2022	3115	0.795
2023	2990	0.797
2024	3019	0.807
2025	1831	0.778

Table 11: Table of differences between current two-step and new Single-step for genotyped nordic bulls born after 2020 with no offspring

dif	dif5
-19.0	1
-18.0	2
-17.0	3
-16.0	4
-15.0	25
-14.0	22
-13.0	49

dif	dif5
-12.0	111
-11.0	156
-10.0	235
-9.0	346
-8.0	466
-7.0	631
-6.0	791
-5.0	950
-4.0	1116
-3.0	1131
-2.0	1246
-1.0	1231
0.0	1119
1.0	1046
2.0	902
3.0	684
4.0	523
5.0	383
6.0	311
7.0	203
8.0	128
9.0	65
10.0	42
11.0	30
12.0	15
13.0	9
14.0	7
15.0	7
16.0	2
17.0	2
18.0	4
19.0	2
20.0	3

dif	dif5
21.0	0
22.0	0
23.0	1
24.0	0
25.0	1

Legarra-Reverter test

The Legarra-Reverter test is a test for bias in evaluations. We perform two calculations of breeding values, one with all information available and one where offspring of sires born after 2015 has their records removed. Then we perform a linear regression on genotyped, nordic bulls, who has no data in the reduced dataset and with more than 30 offspring in the full dataset. We also require that their sires are not in the focal group, so we remove bulls whose father meets the same criteria.

The slope of the regression indicates the bias, with a slope of one meaning no bias, a slope less than one indicating that the estimated values of unproven animals are too extreme, and a slope higher than one indicating that the estimated breeding values of unproven animals are too conservative.

As can be seen, the Legarra-Reverter scores are generally at the same level as the non-genomic model. However, it is quite far from 1. While Youngstock survival is not an Interbull trait, this would not be good enough to pass an Interbull GEBV test.

Table 12: Legarra-Reverter scores
Singlestep:

trait	b1	rsquare	n
HP1	0.725	0.413	153
HP2	0.743	0.388	151
BP1	0.771	0.446	154
BP2	0.794	0.441	154

EBV:

trait	b1	rsquare	n
HP1	0.703	0.279	153
HP2	0.647	0.19	151
BP1	0.785	0.32	154
BP2	0.713	0.234	154

Mendelian sampling

The mendelian sampling of an animal is its deviation of its breeding values from the expected breeding value, which is the average of its parents breeding values. Some mendelian sampling is expected on the individual level (this is what enables breeding), but across all animals we expect it to be close to zero. Otherwise, this indicates a bias in the set of animals in the evaluation, which violates the unbiasedness of the BLUP model.

Table 13: Average mendelian sampling by birth year. Animals are only included if they are genotyped, their sire has > 30 offspring and their dam is genotyped.

BYR	n	m1	m2	m3	m4
2010	915	-0.058	-0.092	-0.12	-0.079
2011	995	-0.039	-0.081	-0.048	-0.105
2012	1456	0.156	0.083	0.183	0.082
2013	2511	0.055	-0.011	0.051	-0.031
2014	4034	0.15	0.11	0.191	0.164
2015	5792	0.18	0.097	0.183	0.104
2016	7436	0.129	0.18	0.14	0.175
2017	9987	0.151	0.26	0.177	0.262
2018	13821	0.156	0.105	0.135	0.07
2019	19960	0.204	0.186	0.18	0.172
2020	29250	0.286	0.188	0.236	0.186
2021	37466	0.258	0.218	0.229	0.238
2022	46919	0.245	0.173	0.215	0.204
2023	51735	0.163	0.109	0.126	0.097
2024	57100	0.101	0.048	0.062	0.023

Table 14: Average mendelian sampling by birth year. Animals are only included if they are not genotyped, their sire has > 30 offspring and their dam isn't genotyped.

BYR	n	m1	m2	m3	m4
2001	393632.0	0.033	-0.015	-0.017	0.023
2002	387105.0	-0.011	0.018	-0.01	-0.019
2003	402050.0	-0.016	0.011	-0.03	-0.042
2004	446088.0	-0.013	0.004	-0.011	-0.021
2005	438062.0	-0.034	0.007	-0.013	0.0
2006	443850.0	-0.011	-0.038	0.001	0.01
2007	430691.0	-0.006	-0.015	-0.007	0.018
2008	486754.0	0.002	-0.022	0.007	0.019

BYR	n	m1	m2	m3	m4
2009	501394.0	0.013	-0.023	0.039	-0.002
2010	508661.0	0.002	-0.058	0.008	-0.004
2011	501426.0	-0.002	-0.04	0.0	0.009
2012	495998.0	0.014	-0.014	0.006	0.016
2013	489447.0	0.005	-0.016	0.002	0.004
2014	488218.0	-0.002	-0.008	0.02	-0.0
2015	481138.0	0.023	-0.034	0.001	-0.015
2016	465064.0	-0.01	0.012	0.001	-0.013
2017	430966.0	-0.001	0.042	0.002	0.014
2018	413124.0	0.009	0.017	0.007	-0.008
2019	382979.0	0.003	-0.019	0.0	-0.009
2020	373847.0	-0.004	-0.011	-0.013	0.008
2021	357920.0	-0.007	-0.014	0.001	0.02
2022	331764.0	0.004	-0.026	-0.002	0.01
2023	303504.0	0.02	-0.012	0.007	-0.004
2024	282439.0	0.024	-0.004	-0.003	-0.009

Reliabilities

Table 15: Comparison of reliabilities between single-step (ss), new EBV (ebv) and current official evaluation (cur) for nordic AI bulls with > 30 offspring and correlation between single-step and current evaluation.

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	HP1	224	71.93	61.63	61.66	7.48	11.07	11.03	0.99
2010	HP1	193	72.58	62.58	62.61	8.74	13.28	13.28	0.99
2011	HP1	155	74.04	65.23	65.3	8.03	11.14	11.11	0.98
2012	HP1	171	76.23	67.8	67.81	9.28	14.08	14.07	0.99
2013	HP1	151	76.19	67.89	67.88	9.66	14.43	14.43	1.0
2014	HP1	113	80.42	74.24	74.24	10.93	16.22	16.24	0.99
2015	HP1	82	83.58	79.64	79.62	9.3	14.02	14.05	0.99
2016	HP1	65	82.7	78.43	78.4	9.62	13.61	13.64	1.0
2017	HP1	66	83.37	79.22	79.27	9.93	14.42	14.41	0.99
2018	HP1	78	80.8	75.45	75.44	10.35	15.59	15.62	0.99
2019	HP1	56	81.0	75.82	75.88	10.27	15.45	15.4	0.99
2020	HP1	56	78.35	71.23	71.25	12.97	19.92	19.96	0.99

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2021	HP1	46	77.27	69.12	69.11	14.71	22.98	22.98	1.0
2022	HP1	46	76.82	68.7	68.83	14.77	23.23	23.29	1.0
2023	HP1	11	71.48	60.8	60.82	12.51	20.15	20.15	1.0
2009	HP2	224	71.94	61.63	72.86	7.56	11.07	9.07	0.95
2010	HP2	193	72.6	62.58	73.26	8.84	13.28	10.47	0.97
2011	HP2	155	74.06	65.23	75.82	8.1	11.14	8.94	0.97
2012	HP2	171	76.27	67.8	77.7	9.33	14.08	10.92	0.97
2013	HP2	151	76.21	67.89	77.69	9.66	14.43	11.06	0.98
2014	HP2	113	80.45	74.24	82.39	10.96	16.22	12.53	0.97
2015	HP2	82	83.9	79.64	86.77	9.66	14.02	9.94	0.98
2016	HP2	65	82.82	78.43	86.03	9.78	13.61	9.46	0.99
2017	HP2	66	83.44	79.22	85.98	10.02	14.42	10.66	0.98
2018	HP2	78	80.94	75.45	82.9	10.51	15.59	11.97	0.97
2019	HP2	56	81.12	75.82	82.59	10.4	15.45	12.41	0.97
2020	HP2	54	79.11	72.56	79.07	12.64	19.0	16.26	0.98
2021	HP2	41	79.65	72.97	77.22	13.85	21.29	19.71	0.98
2022	HP2	14	87.05	84.72	80.21	5.9	8.22	9.52	0.8
2009	BP1	224	71.89	61.63	60.41	7.38	11.07	11.05	0.99
2010	BP1	193	72.48	62.58	61.45	8.51	13.28	13.23	0.99
2011	BP1	154	74.18	65.47	64.05	6.97	10.74	10.73	0.99
2012	BP1	171	76.14	67.8	66.45	9.17	14.08	13.92	0.99
2013	BP1	151	76.03	67.89	66.28	9.49	14.43	14.26	0.99
2014	BP1	114	80.02	73.89	72.24	10.92	16.58	16.3	0.99
2015	BP1	82	83.28	79.64	77.93	9.0	14.02	14.0	0.99
2016	BP1	66	81.82	77.76	75.88	9.63	14.56	14.47	0.99
2017	BP1	66	82.86	79.22	76.98	9.38	14.42	14.4	0.99
2018	BP1	78	80.5	75.45	73.1	10.1	15.59	15.48	0.99
2019	BP1	56	80.64	75.82	73.16	9.92	15.45	15.15	0.99
2020	BP1	55	78.42	71.93	68.91	12.46	19.39	18.37	0.99
2021	BP1	46	76.93	69.12	66.43	14.55	22.98	21.75	0.99
2022	BP1	45	77.33	69.7	66.2	14.45	22.47	20.78	0.99
2023	BP1	11	71.36	60.8	58.18	12.64	20.15	18.16	0.99
2009	BP2	224	71.77	61.63	73.52	7.77	11.07	9.55	0.92

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2010	BP2	193	72.49	62.58	74.02	9.17	13.28	10.77	0.95
2011	BP2	154	74.17	65.47	76.71	7.46	10.74	8.74	0.94
2012	BP2	171	76.15	67.8	78.44	9.46	14.08	11.11	0.95
2013	BP2	151	76.12	67.89	78.23	9.74	14.43	11.37	0.96
2014	BP2	113	80.32	74.24	83.18	11.02	16.22	12.6	0.97
2015	BP2	82	83.9	79.64	87.57	9.84	14.02	9.89	0.98
2016	BP2	66	82.36	77.76	86.06	10.45	14.56	10.78	0.96
2017	BP2	66	83.42	79.22	86.61	10.2	14.42	10.72	0.97
2018	BP2	78	80.93	75.45	83.46	10.75	15.59	12.07	0.97
2019	BP2	56	81.17	75.82	82.93	10.68	15.45	12.58	0.96
2020	BP2	55	78.73	71.93	78.29	12.88	19.39	16.88	0.97
2021	BP2	43	78.6	71.36	75.88	14.46	22.07	20.48	0.97
2022	BP2	38	80.79	75.37	68.79	12.47	18.85	20.69	0.91

Table 16: Comparison of reliabilities between single-step and current official evaluation (two-step) for nordic genotyped bulls with no offspring

BYR	n	ss_rel	two_rel	s_ss_rel	s_two_rel	cor
2020	3089	52.611	62.171	2.497	2.259	0.952
2021	3050	51.966	61.647	2.797	2.591	0.958
2022	3115	52.129	61.57	2.807	2.648	0.948
2023	2990	51.38	60.612	3.521	3.426	0.961
2024	3019	51.414	59.436	3.394	3.234	0.918
2025	1831	49.498	55.888	3.975	3.481	0.84

Jersey

Genetic trends

Here, we exhibit the genetic trends of our evaluations for each trait. We see that the levels of breeding values are generally in agreement across evaluations.

Table 17: Genetic trends (Single-step (ss) vs new EBV (newebv) vs official EBV (offebv)) and correlation between single-step and official EBV for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2009	HP1	53	96.15	95.98	96.5	6.69	6.47	6.04	0.96
2010	HP1	60	94.65	95.32	95.93	10.97	11.57	10.7	0.98

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2011	HP1	50	89.68	89.78	90.75	8.71	8.86	8.29	0.96
2012	HP1	52	95.48	95.62	96.35	8.25	8.43	7.83	0.96
2013	HP1	52	93.52	93.54	94.41	9.49	9.51	8.81	0.98
2014	HP1	48	96.67	96.73	97.35	7.84	7.47	6.96	0.96
2015	HP1	34	96.12	95.91	96.66	7.88	8.65	8.02	0.98
2016	HP1	30	100.03	100.0	100.4	7.32	7.45	6.85	0.97
2017	HP1	38	99.24	99.08	99.36	7.61	8.3	7.73	0.98
2018	HP1	28	98.25	98.25	98.56	7.49	7.47	6.92	0.93
2019	HP1	32	101.12	101.59	101.38	9.45	9.68	8.96	0.99
2020	HP1	31	102.0	100.81	100.7	7.84	8.0	7.36	0.95
2021	HP1	16	105.56	105.38	105.06	5.63	5.16	4.9	0.98
2022	HP1	18	100.61	100.11	99.97	8.37	8.37	7.66	0.98
2023	HP1	5	105.4	104.6	104.18	4.04	5.32	4.94	0.97
2009	HP2	53	92.45	92.23	92.59	10.16	11.0	10.86	0.95
2010	HP2	59	92.36	92.37	92.76	9.99	9.36	9.15	0.93
2011	HP2	49	95.45	96.14	96.48	10.28	9.98	9.73	0.96
2012	HP2	52	95.69	96.63	96.93	12.67	12.2	11.98	0.94
2013	HP2	51	94.61	95.55	95.83	11.73	11.07	10.86	0.93
2014	HP2	47	99.28	99.02	99.17	10.17	9.62	9.53	0.94
2015	HP2	33	95.61	95.12	95.18	11.21	11.32	11.07	0.98
2016	HP2	29	101.41	101.34	101.22	9.93	9.93	9.78	0.93
2017	HP2	37	98.14	98.22	98.15	18.11	18.73	18.44	0.99
2018	HP2	27	99.93	99.15	99.06	11.66	12.0	11.8	0.96
2019	HP2	30	98.9	99.17	98.92	14.67	14.71	14.48	0.98
2020	HP2	30	102.97	101.8	101.44	13.1	13.51	13.34	0.98
2021	HP2	13	106.85	106.46	105.85	11.58	11.29	11.19	0.99
2022	HP2	6	102.67	100.5	100.16	9.05	8.31	8.26	0.89
2009	BP1	41	96.49	96.1	96.52	6.28	6.04	5.82	0.96
2010	BP1	35	94.4	94.63	95.08	10.55	11.36	10.69	0.99
2011	BP1	22	93.64	93.41	94.02	6.91	6.59	6.25	0.95
2012	BP1	16	98.69	97.94	98.39	7.01	7.23	6.95	0.97
2013	BP1	17	95.18	95.35	95.86	7.62	8.16	7.53	0.99
2014	BP1	17	97.35	97.29	97.85	8.03	7.45	7.17	0.99

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2015	BP1	29	95.9	95.52	96.03	7.47	8.1	7.71	0.99
2016	BP1	18	101.06	100.72	101.0	7.18	6.87	6.43	0.98
2017	BP1	26	99.88	99.81	99.89	7.54	8.06	7.65	0.99
2018	BP1	14	100.86	101.43	101.36	7.72	7.71	7.33	0.99
2019	BP1	28	101.32	101.25	100.99	9.03	9.64	9.05	1.0
2020	BP1	26	102.27	101.19	100.99	7.76	7.57	7.3	0.96
2021	BP1	13	105.46	105.0	104.4	5.46	5.37	5.23	0.99
2022	BP1	14	99.93	99.43	99.07	7.74	8.05	7.75	0.99
2023	BP1	1	110.0	110.0	109.47	NaN	NaN	NaN	NaN
2009	BP2	34	93.68	92.59	93.02	8.96	9.7	9.51	0.97
2010	BP2	30	92.2	92.57	92.91	8.83	8.25	7.95	0.93
2011	BP2	18	96.28	97.39	97.62	7.04	7.16	6.93	0.94
2012	BP2	15	96.2	96.93	97.02	14.77	15.22	14.82	0.99
2013	BP2	15	98.73	100.87	100.6	4.57	5.5	5.46	0.73
2014	BP2	16	101.25	100.56	100.62	10.95	10.87	10.5	0.99
2015	BP2	28	97.61	97.18	97.0	10.63	10.81	10.46	0.98
2016	BP2	18	100.56	100.5	100.19	10.35	10.63	10.49	0.99
2017	BP2	24	100.0	100.0	99.64	19.38	19.68	19.24	1.0
2018	BP2	12	101.75	101.92	101.63	11.47	11.84	11.47	1.0
2019	BP2	27	98.89	98.85	98.41	14.78	14.81	14.5	0.99
2020	BP2	23	103.78	103.35	102.89	12.39	12.81	12.66	0.99
2021	BP2	12	105.42	104.42	103.84	10.99	10.82	10.55	0.98
2022	BP2	10	97.8	97.8	97.44	11.08	10.51	10.61	0.93

Table 18: Genetic trends (Single-step (ss) vs new EBV (newebv) vs official EBV (offebv)) and correlation between single-step and official EBV for nordic non-genotyped cows with phenotype

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2009	HP132514		93.04	92.78	93.52	5.96	6.03	5.57	0.99
2010	HP130005		92.5	92.37	93.16	7.03	7.09	6.6	0.99
2011	HP129816		91.02	90.84	91.78	7.43	7.43	6.93	0.99
2012	HP130230		92.31	92.26	93.14	7.5	7.56	7.07	0.99
2013	HP130123		91.24	91.21	92.18	7.11	7.14	6.72	0.99
2014	HP129552		91.91	91.85	92.8	6.15	6.13	5.77	0.98

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2015	HP128286		93.82	93.94	94.8	5.91	5.89	5.52	0.98
2016	HP127183		93.73	93.71	94.64	5.4	5.32	5.03	0.97
2017	HP124779		94.92	94.84	95.68	5.58	5.63	5.29	0.97
2018	HP126646		96.15	96.03	96.77	5.03	5.03	4.73	0.97
2019	HP125887		97.38	97.33	97.93	4.89	4.87	4.59	0.97
2020	HP127874		97.95	97.99	98.48	4.86	4.86	4.59	0.97
2021	HP127971		99.61	99.64	99.92	5.65	5.63	5.29	0.98
2022	HP128984		100.11	100.06	100.25	5.62	5.7	5.35	0.98
2023	HP126314		100.59	100.33	100.43	5.92	5.99	5.6	0.98
2024	HP125240		101.8	101.55	101.49	5.07	5.17	4.82	0.98
2025	HP117093		101.36	101.03	100.97	5.21	5.34	4.97	0.98
2009	HP230051		92.42	91.54	91.97	6.09	6.01	5.92	0.97
2010	HP227469		92.04	91.43	91.95	6.37	6.32	6.3	0.97
2011	HP226968		92.92	92.32	92.83	5.77	5.77	5.82	0.96
2012	HP227714		92.86	92.42	92.97	6.9	6.8	6.85	0.96
2013	HP226965		94.24	93.98	94.53	7.96	7.81	7.82	0.97
2014	HP226935		93.94	93.84	94.35	7.37	7.18	7.18	0.96
2015	HP225446		95.2	95.3	95.67	7.67	7.55	7.5	0.96
2016	HP223283		96.13	95.95	96.31	6.6	6.47	6.5	0.95
2017	HP222610		96.26	96.11	96.39	7.16	7.07	7.04	0.96
2018	HP224235		99.12	99.11	99.23	6.42	6.38	6.35	0.96
2019	HP223737		97.76	97.68	97.8	9.43	9.44	9.35	0.98
2020	HP225559		99.33	99.42	99.44	10.01	10.02	9.89	0.99
2021	HP225359		99.93	99.98	99.94	8.53	8.59	8.49	0.98
2022	HP225819		101.01	100.94	100.82	8.77	8.75	8.65	0.98
2023	HP223703		102.4	102.31	102.1	8.4	8.38	8.27	0.98
2024	HP210858		102.13	101.81	101.53	7.48	7.54	7.44	0.98

Table 19: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2009	HP1	50	96.02	97.24	6.74	6.94	0.98
2010	HP1	55	94.93	96.25	11.03	11.5	0.99
2011	HP1	47	89.96	91.23	8.81	8.47	0.97

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2012	HP1	47	95.66	96.68	8.13	7.98	0.98
2013	HP1	50	93.52	94.56	9.66	9.46	0.98
2014	HP1	36	96.53	96.78	7.55	7.09	0.94
2015	HP1	30	95.57	95.8	7.97	8.73	0.96
2016	HP1	26	100.27	98.73	7.74	5.86	0.77
2017	HP1	29	100.1	99.48	7.52	7.07	0.58
2018	HP1	20	99.2	97.4	7.82	6.2	0.61
2019	HP1	29	101.76	99.83	9.49	6.29	0.43
2020	HP1	25	101.84	99.64	8.52	4.64	0.46
2021	HP1	14	106.14	99.14	5.78	4.4	0.76
2022	HP1	17	100.41	99.35	8.59	4.62	0.52
2023	HP1	5	105.4	100.6	4.04	2.51	0.49
2009	HP2	50	92.66	93.46	10.35	10.78	0.98
2010	HP2	55	92.65	93.24	9.97	9.23	0.97
2011	HP2	47	95.3	96.26	10.47	10.05	0.97
2012	HP2	47	96.6	97.26	12.28	11.79	0.98
2013	HP2	50	94.7	95.5	11.83	11.09	0.96
2014	HP2	36	99.5	99.39	9.98	10.03	0.95
2015	HP2	30	95.77	95.9	11.74	11.0	0.95
2016	HP2	26	100.58	99.35	9.97	6.54	0.55
2017	HP2	29	99.21	100.31	19.32	8.8	0.57
2018	HP2	20	101.9	101.7	11.02	6.82	0.73
2019	HP2	29	99.07	100.55	14.9	6.68	0.43
2020	HP2	24	104.12	100.29	13.61	7.74	0.42
2021	HP2	13	106.85	101.85	11.58	4.56	0.46
2022	HP2	6	102.67	103.33	9.05	4.32	0.57
2009	BP1	41	96.49	97.8	6.28	6.45	0.98
2010	BP1	35	94.4	95.4	10.55	10.81	0.99
2011	BP1	22	93.64	94.55	6.91	6.71	0.96
2012	BP1	16	98.69	99.31	7.01	6.74	0.97
2013	BP1	17	95.18	96.65	7.62	7.26	0.97
2014	BP1	16	98.0	97.38	7.82	8.32	0.97
2015	BP1	29	95.9	96.38	7.47	8.15	0.97

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2016	BP1	19	101.21	99.37	7.01	5.74	0.76
2017	BP1	26	100.31	99.65	7.09	6.74	0.58
2018	BP1	14	100.86	98.43	7.72	6.38	0.65
2019	BP1	26	101.42	100.35	9.37	5.78	0.49
2020	BP1	21	101.9	99.76	8.48	5.05	0.42
2021	BP1	13	105.46	99.08	5.46	3.75	0.84
2022	BP1	14	99.93	99.14	7.74	3.68	0.43
2023	BP1	1	110.0	101.0	NaN	NaN	NaN
2009	BP2	34	93.68	94.38	8.96	9.61	0.98
2010	BP2	30	92.2	92.7	8.83	8.16	0.97
2011	BP2	18	96.28	97.44	7.04	7.64	0.95
2012	BP2	15	96.2	96.67	14.77	15.12	0.99
2013	BP2	15	98.73	100.2	4.57	4.49	0.82
2014	BP2	16	101.25	100.31	10.95	11.46	0.98
2015	BP2	28	97.61	97.86	10.63	9.64	0.94
2016	BP2	19	100.95	99.74	10.21	6.93	0.51
2017	BP2	25	99.64	101.36	19.06	7.94	0.57
2018	BP2	12	101.75	101.92	11.47	6.99	0.88
2019	BP2	26	98.54	101.08	14.96	6.29	0.46
2020	BP2	20	103.85	100.35	13.11	7.4	0.35
2021	BP2	12	105.42	102.0	10.99	3.44	0.63
2022	BP2	10	97.8	101.4	11.08	4.77	0.52

Table 20: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic cows with genotype and phenotype

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2009	HP1	194	94.8	95.89	5.96	5.91	0.95
2010	HP1	2263	91.72	92.88	8.02	8.0	0.97
2011	HP1	4200	91.14	92.29	7.97	8.06	0.97
2012	HP1	4797	92.66	93.83	8.06	8.06	0.97
2013	HP1	3801	91.71	92.76	7.64	7.66	0.96
2014	HP1	4753	92.16	93.31	6.62	6.51	0.95
2015	HP1	5686	94.23	95.32	6.36	6.15	0.94
2016	HP1	6765	94.09	94.91	5.93	5.61	0.93

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2017	HP1	8439	95.32	96.12	6.07	5.9	0.93
2018	HP1	10369	96.46	96.34	5.64	5.16	0.87
2019	HP1	12609	97.67	97.41	5.53	5.25	0.77
2020	HP1	15319	98.48	97.36	5.54	5.24	0.71
2021	HP1	14922	100.39	98.88	6.13	4.99	0.69
2022	HP1	15725	100.78	98.43	6.15	4.52	0.56
2023	HP1	15401	101.04	98.72	6.59	4.27	0.62
2024	HP1	16337	102.13	98.85	5.67	4.02	0.64
2025	HP1	10527	101.85	99.33	5.73	3.69	0.63
2009	HP2	194	93.19	93.3	7.76	7.4	0.92
2010	HP2	2262	92.3	92.46	7.72	6.97	0.92
2011	HP2	4200	93.05	93.4	7.55	6.74	0.91
2012	HP2	4797	93.17	93.76	8.78	7.83	0.93
2013	HP2	3782	94.69	95.06	9.74	8.7	0.94
2014	HP2	4713	94.31	94.87	8.97	8.23	0.92
2015	HP2	5617	95.26	95.99	9.44	8.56	0.92
2016	HP2	6331	96.44	96.54	8.22	7.35	0.9
2017	HP2	8177	96.19	96.64	8.64	7.69	0.89
2018	HP2	10193	99.59	98.92	7.99	6.46	0.8
2019	HP2	12211	97.99	99.01	10.52	6.55	0.66
2020	HP2	14996	98.86	99.97	12.09	6.69	0.72
2021	HP2	14424	99.74	99.93	10.26	6.19	0.62
2022	HP2	15170	100.98	100.43	10.25	5.71	0.6
2023	HP2	14994	101.99	100.63	9.81	5.43	0.64
2024	HP2	7587	101.85	100.87	8.93	4.94	0.58

Table 21: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic bulls with genotype and phenotype

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2009	BP1	132	96.47	97.77	5.83	5.7	0.97
2010	BP1	214	93.8	95.06	7.99	7.96	0.97
2011	BP1	359	92.51	93.75	7.09	6.93	0.97
2012	BP1	393	94.72	95.91	7.21	7.11	0.96
2013	BP1	408	93.59	94.74	6.98	6.81	0.97

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2014	BP1	432	94.82	95.87	6.18	6.01	0.95
2015	BP1	491	96.2	96.93	5.51	5.26	0.93
2016	BP1	423	96.59	97.07	5.35	5.05	0.91
2017	BP1	467	96.85	97.4	5.59	5.38	0.92
2018	BP1	308	98.32	97.79	5.44	4.82	0.82
2019	BP1	370	98.66	98.94	4.92	4.24	0.63
2020	BP1	346	99.6	98.21	5.04	4.57	0.7
2021	BP1	213	100.5	99.21	5.84	4.27	0.66
2022	BP1	281	101.04	98.6	5.78	3.94	0.57
2023	BP1	319	100.1	98.64	5.22	3.62	0.58
2024	BP1	355	101.68	99.35	5.37	3.71	0.61
2025	BP1	231	101.64	99.52	5.09	3.25	0.61
2009	BP2	132	94.37	94.66	7.99	7.92	0.94
2010	BP2	214	92.19	92.64	7.67	7.15	0.93
2011	BP2	357	94.89	95.41	7.49	6.82	0.92
2012	BP2	385	96.12	97.05	8.9	8.12	0.93
2013	BP2	401	95.82	96.25	9.21	8.55	0.94
2014	BP2	421	96.4	97.09	8.18	7.39	0.91
2015	BP2	470	96.37	97.1	8.38	7.91	0.92
2016	BP2	393	98.23	98.4	8.28	7.19	0.89
2017	BP2	458	96.75	97.48	8.87	7.36	0.86
2018	BP2	304	100.47	100.26	7.9	6.3	0.81
2019	BP2	362	98.52	100.53	10.33	6.08	0.71
2020	BP2	337	102.04	100.85	8.91	6.01	0.7
2021	BP2	209	98.7	100.37	9.42	5.62	0.59
2022	BP2	264	102.18	101.11	9.51	5.17	0.57
2023	BP2	284	100.48	100.47	9.18	4.89	0.6
2024	BP2	327	100.57	101.45	8.58	4.69	0.56
2025	BP2	80	101.85	101.38	7.77	4.84	0.62

Correlations

Here, we give correlation tables and tables of differences between the relevant evaluations. We test that we didn't change the model by comparing our new model without genomic information to the breeding values of the traditional pedigree-based model and expect very high correlations for tested animals. We test the change by incorporating genomic informa-

tion, compared to a non-genomic evaluation, and expect to see some changes even in tested animals, but not too large.

Table 22: Correlations between current EBV and new EBV for Nordic AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	50	0.999	1.0	0.999	0.999
2010	55	1.0	0.999	1.0	0.999
2011	47	0.999	0.999	0.999	0.999
2012	47	0.999	1.0	0.999	0.999
2013	50	0.999	0.999	0.999	0.999
2014	36	0.999	0.999	0.999	0.999
2015	30	0.999	1.0	0.999	1.0
2016	26	0.999	0.999	0.999	0.999
2017	29	0.999	1.0	0.999	1.0
2018	20	0.999	1.0	0.999	0.999
2019	29	1.0	1.0	0.999	1.0
2020	24	0.999	1.0	0.999	1.0
2021	13	0.999	1.0	0.998	1.0

Table 23: Table of differences between current EBV and new EBV for Nordic AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-2.0	4	0	0	0
-1.0	32	36	36	61
0.0	79	106	86	81
1.0	26	5	24	5
2.0	6	0	1	0

Table 24: Correlations between current EBV and new Single-step for AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	50	0.964	0.958	0.965	0.955
2010	55	0.985	0.932	0.984	0.922
2011	47	0.96	0.959	0.958	0.962
2012	47	0.964	0.963	0.966	0.96
2013	50	0.982	0.929	0.982	0.921

BYR	n	cor1	cor2	cor3	cor4
2014	36	0.984	0.97	0.979	0.965
2015	30	0.989	0.984	0.988	0.983
2016	26	0.976	0.965	0.977	0.964
2017	29	0.988	0.997	0.986	0.997
2018	20	0.961	0.968	0.965	0.966
2019	29	0.993	0.985	0.995	0.983
2020	24	0.977	0.986	0.98	0.986
2021	13	0.989	0.995	0.991	0.992

Table 25: Table of differences between current EBV and new Single-step for AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-10.0	0	1	0	1
-9.0	0	0	0	0
-8.0	1	2	0	1
-7.0	0	0	1	1
-6.0	0	1	0	0
-5.0	0	4	0	3
-4.0	4	5	1	7
-3.0	1	9	4	8
-2.0	17	14	16	20
-1.0	36	33	38	33
0.0	42	38	53	39
1.0	28	23	20	18
2.0	11	7	10	8
3.0	5	4	2	2
4.0	0	2	1	2
5.0	1	0	1	0
6.0	1	2	0	2
7.0	0	0	0	1
8.0	0	2	0	0
9.0	0	0	0	1

Youngstock survival is not implemented in two-step, so we do not compare to it here

Legarra-Reverter test

The Legarra-Reverter test is a test for bias in evaluations. We perform two calculations of breeding values, one with all information available and one where offspring of sires born after 2015 has their records removed. Then we perform a linear regression on genotyped, nordic bulls, who has no data in the reduced dataset and with more than 30 offspring in the full dataset. We also require that their sires are not in the focal group, so we remove bulls whose father meets the same criteria.

The slope of the regression indicates the bias, with a slope of one meaning no bias, a slope less than one indicating that the estimated values of unproven animals are too extreme, and a slope higher than one indicating that the estimated breeding values of unproven animals are too conservative.

As can be seen, we have some issues with the Legarra-Reverter test. We're looking into it.

Table 26: Legarra-Reverter scores
Singlestep:

trait	b1	rsquare	n
HP1	0.884	0.502	58
HP2	1.148	0.331	58
BP1	0.708	0.448	43
BP2	1.119	0.304	41

EBV:

trait	b1	rsquare	n
HP1	0.894	0.391	58
HP2	1.078	0.243	58
BP1	0.653	0.285	43
BP2	0.966	0.172	41

Mendelian sampling

The mendelian sampling of an animals is its deviation of its breeding values from the expected breeding value, which is the average of its parents breeding values. Some mendelian samling is expected on the individual level (this is what enables breeding), but across all animals we expect it to be close to zero. Otherwise, this indicates a bias in the set of animals in the evaluation, which violates the unbiasedness of the BLUP model. We conclude that the mendelian sampling is generally close to 0.

Table 27: Average mendelian sampling by birth year. Animals are only included if they are genotyped, their sire has > 30 offspring and their dam is genotyped.

BYR	n	m1	m2	m3	m4
2010	171	0.529	0.275	0.518	0.272

BYR	n	m1	m2	m3	m4
2011	285	-0.121	0.298	-0.096	0.225
2012	1096	0.315	0.401	0.37	0.244
2013	1745	0.254	0.452	0.246	0.328
2014	2581	0.226	0.211	0.235	0.141
2015	3220	0.241	0.364	0.173	0.322
2016	3539	0.191	0.073	0.147	0.114
2017	4550	0.25	0.28	0.217	0.19
2018	5619	0.129	0.104	0.148	0.007
2019	7709	0.16	0.192	0.151	0.129
2020	10977	0.201	0.128	0.195	0.069
2021	12759	0.261	0.214	0.21	0.222
2022	14310	0.211	0.122	0.195	0.085
2023	14556	0.193	0.094	0.173	0.1
2024	15322	0.126	0.017	0.103	0.036

Table 28: Average mendelian sampling by birth year. Animals are only included if they are not genotyped, their sire has > 30 offspring and their dam isn't genotyped.

BYR	n	m1	m2	m3	m4
2001	42612.0	0.021	0.017	0.043	0.074
2002	39068.0	0.072	0.003	-0.008	0.071
2003	39691.0	0.077	0.016	-0.027	0.019
2004	37567.0	0.042	0.038	-0.024	-0.042
2005	35388.0	-0.01	-0.017	-0.043	0.048
2006	37227.0	-0.013	0.014	-0.061	0.047
2007	35415.0	0.087	0.041	0.04	0.037
2008	35232.0	0.083	0.024	0.013	0.002
2009	37146.0	0.057	0.015	-0.021	-0.008
2010	35117.0	0.052	0.01	0.016	0.008
2011	34313.0	0.038	0.047	0.019	-0.015
2012	34397.0	0.017	0.081	0.034	-0.024
2013	32289.0	0.025	0.068	0.031	-0.033
2014	30611.0	0.026	0.069	0.027	-0.0
2015	29327.0	0.035	0.022	-0.0	0.011
2016	27998.0	0.013	-0.023	-0.008	0.023

	BYR	n	m1	m2	m3	m4
2017	25785.0	-0.026	0.005	-0.009	-0.044	
2018	27463.0	-0.028	-0.003	0.004	-0.07	
2019	25982.0	-0.02	0.027	-0.01	-0.01	
2020	27442.0	-0.028	0.008	-0.005	-0.034	
2021	26870.0	0.011	-0.02	-0.011	0.025	
2022	25275.0	0.005	0.002	0.004	0.006	
2023	22663.0	0.025	-0.012	0.02	0.006	
2024	22153.0	0.002	-0.024	-0.004	0.013	

Reliabilities

Table 29: Comparison of reliabilities between single-step (ss), new EBV (ebv) and current official evaluation (cur) for nordic AI bulls with > 30 offspring and correlation between single-step and current evaluation.

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	HP1	26	71.11	65.37	66.65	9.13	11.23	10.94	1.0
2010	HP1	26	70.67	64.85	66.12	9.73	12.58	12.43	1.0
2011	HP1	16	69.18	62.8	63.94	8.24	11.15	11.08	0.99
2012	HP1	29	69.76	63.65	64.76	11.29	14.29	14.12	1.0
2013	HP1	18	64.2	56.01	56.94	8.27	11.0	10.92	0.99
2014	HP1	17	73.17	67.76	68.71	15.16	19.46	19.28	1.0
2015	HP1	17	86.47	85.23	86.06	9.97	11.8	11.44	1.0
2016	HP1	15	80.82	77.92	78.87	13.11	16.29	15.9	1.0
2017	HP1	15	93.79	93.38	93.73	3.24	3.12	2.89	0.95
2019	HP1	14	88.22	87.17	87.57	10.06	12.2	11.88	1.0
2009	HP2	26	71.09	65.37	66.65	8.77	11.23	2.82109e7	-0.24
2010	HP2	26	70.76	64.85	66.12	9.7	12.58	4.35665e7	-0.33
2011	HP2	16	69.27	62.8	63.94	8.22	11.15	2.8686e7	-0.23
2012	HP2	29	69.84	63.65	64.76	11.26	14.29	8.35208e9	-0.07
2013	HP2	18	64.31	56.01	56.94	8.25	11.0	3.00715e7	0.0
2014	HP2	17	73.25	67.76	68.71	15.12	19.46	4.07125e7	-0.32
2015	HP2	17	86.31	85.23	86.06	9.79	11.8	4.71772e9	-0.32
2016	HP2	15	80.87	77.92	78.87	13.07	16.29	2.64824e7	0.03
2017	HP2	15	93.8	93.38	93.73	3.23	3.12	2.6038e7	-0.41
2019	HP2	14	88.26	87.17	87.57	10.03	12.2	2.51968e7	-0.15

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	BP1	24	71.56	65.95	1466.58	9.0	11.51	6569.29	0.16
2010	BP1	17	73.8	68.98	499.76	10.78	13.76	1524.86	-0.17
2015	BP1	17	86.48	85.23	111.59	9.97	11.8	157.66	0.31
2016	BP1	12	85.52	83.75	74.83	9.56	11.71	105.49	0.52
2017	BP1	15	93.8	93.38	3766.6	3.23	3.12	14256.9	0.18
2019	BP1	14	88.25	87.17	85.5	10.04	12.2	102.68	0.26
2009	BP2	18	73.36	68.43	88.0	9.02	12.22	32.01	0.11
2010	BP2	15	75.03	70.54	85.8	10.93	13.94	34.83	-0.06
2015	BP2	16	87.02	86.41	80.44	8.91	11.1	39.91	0.27
2016	BP2	12	85.53	83.75	99.0	9.55	11.71	0.0	NaN
2017	BP2	15	93.57	93.38	79.2	3.13	3.12	40.99	0.16
2019	BP2	14	88.27	87.17	84.86	10.03	12.2	35.95	-0.24

RDC

Genetic trends

Here, we exhibit the genetic trends of our evaluations for each trait. We see that the levels of breeding values are generally in agreement across evaluations.

Table 30: Genetic trends (Single-step (ss) vs new EBV (newebv) vs official EBV (offebv)) and correlation between single-step and official EBV for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2009	HP1	158	94.87	95.98	96.53	8.73	9.27	8.78	0.95
2010	HP1	169	93.12	94.02	94.53	9.77	9.98	9.26	0.96
2011	HP1	174	95.42	96.08	96.48	9.98	10.35	9.58	0.96
2012	HP1	174	96.77	97.64	97.93	8.87	9.25	8.71	0.94
2013	HP1	130	95.68	96.12	96.17	10.31	10.73	9.76	0.95
2014	HP1	90	96.62	97.3	97.5	9.75	10.15	9.39	0.96
2015	HP1	77	96.57	96.79	96.74	11.32	12.31	11.55	0.98
2016	HP1	71	99.23	99.45	99.98	9.22	9.75	9.25	0.96
2017	HP1	66	102.41	101.35	101.02	12.34	12.63	11.87	0.98
2018	HP1	56	100.84	100.09	99.85	8.95	9.35	8.66	0.97
2019	HP1	54	104.41	103.94	103.22	8.41	8.45	8.94	0.95
2020	HP1	53	103.58	102.7	102.16	7.92	8.01	7.51	0.96
2021	HP1	48	104.98	103.9	104.33	7.45	7.35	6.89	0.93

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2022	HP1	40	104.95	103.15	103.58	8.24	8.29	7.92	0.94
2023	HP1	8	103.12	101.62	101.54	5.91	5.45	5.33	0.68
2009	HP2	158	93.81	94.35	94.39	9.26	9.79	9.85	0.96
2010	HP2	168	94.26	94.61	94.29	9.84	10.47	10.25	0.96
2011	HP2	174	96.25	96.29	96.15	10.29	10.62	10.31	0.97
2012	HP2	174	94.95	95.29	95.22	9.39	9.84	9.82	0.95
2013	HP2	129	94.87	95.43	95.01	10.64	11.14	10.69	0.96
2014	HP2	89	96.1	96.26	96.37	9.56	10.26	9.79	0.97
2015	HP2	75	96.03	95.93	96.2	10.5	11.04	10.62	0.98
2016	HP2	71	99.51	99.25	99.62	8.57	8.82	8.76	0.96
2017	HP2	66	100.89	100.3	100.11	10.94	11.32	11.2	0.98
2018	HP2	56	102.48	102.09	102.1	7.58	8.14	8.04	0.98
2019	HP2	54	103.15	102.59	101.72	7.89	8.16	9.37	0.92
2020	HP2	51	103.96	103.24	103.19	7.67	7.81	7.73	0.97
2021	HP2	40	104.82	103.9	103.97	7.18	7.32	6.94	0.97
2022	HP2	8	106.62	104.5	104.4	9.33	9.09	9.48	0.97
2009	BP1	158	95.32	96.28	97.08	8.53	9.03	8.67	0.95
2010	BP1	167	94.2	95.17	95.75	9.39	9.51	8.96	0.95
2011	BP1	173	95.95	96.49	96.84	9.33	9.65	9.14	0.96
2012	BP1	176	96.7	97.41	97.71	8.75	8.99	8.64	0.94
2013	BP1	130	96.48	96.97	96.94	9.89	10.32	9.58	0.96
2014	BP1	88	96.97	97.47	97.48	9.38	9.83	9.25	0.96
2015	BP1	77	96.78	96.9	96.78	10.63	11.49	10.94	0.98
2016	BP1	70	99.27	99.21	99.63	8.91	9.18	8.74	0.97
2017	BP1	66	102.12	100.97	100.64	11.92	12.07	11.55	0.98
2018	BP1	57	100.7	100.25	99.66	8.55	9.05	8.48	0.97
2019	BP1	55	104.35	103.73	102.91	8.32	8.3	8.92	0.95
2020	BP1	52	103.75	102.83	102.1	7.31	7.32	7.09	0.96
2021	BP1	46	105.04	103.72	103.89	7.32	7.1	6.72	0.94
2022	BP1	41	104.85	102.95	103.07	8.21	8.46	8.17	0.94
2023	BP1	8	102.88	101.38	100.94	5.62	5.24	5.15	0.71
2009	BP2	158	94.36	94.96	94.43	9.27	9.63	9.71	0.96
2010	BP2	167	94.98	95.47	94.5	10.85	11.18	11.06	0.97

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2011	BP2	172	96.76	96.92	96.37	10.36	10.53	10.27	0.97
2012	BP2	175	95.13	95.7	95.25	9.37	9.63	9.73	0.95
2013	BP2	130	94.91	95.62	95.03	10.44	10.85	10.59	0.96
2014	BP2	87	96.28	96.51	96.39	9.72	9.8	9.44	0.97
2015	BP2	76	96.67	96.41	96.62	9.88	10.42	10.15	0.98
2016	BP2	70	99.79	99.4	99.17	8.9	9.15	9.01	0.98
2017	BP2	66	101.14	100.56	100.13	10.8	10.95	10.91	0.98
2018	BP2	57	102.02	101.88	101.88	7.74	7.94	8.16	0.99
2019	BP2	54	103.15	102.56	101.79	7.81	8.03	8.8	0.92
2020	BP2	49	102.41	101.76	101.62	8.54	8.67	8.59	0.98
2021	BP2	40	105.3	104.5	104.34	7.17	7.47	7.28	0.96
2022	BP2	32	104.47	102.97	103.22	6.76	7.28	7.89	0.85

Table 31: Genetic trends (Single-step (ss) vs new EBV (newebv) vs official EBV (offebv)) and correlation between single-step and official EBV for nordic non-genotyped cows with phenotype

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2009	HP1130334		93.87	94.62	95.56	7.52	7.62	7.01	0.98
2010	HP1122756		93.21	93.95	94.84	6.83	6.92	6.38	0.98
2011	HP1118031		93.58	94.4	95.15	6.82	6.96	6.43	0.98
2012	HP1109712		94.4	95.17	95.72	6.64	6.74	6.2	0.98
2013	HP1105822		94.01	94.71	95.31	6.56	6.68	6.13	0.97
2014	HP1 99890		93.9	94.63	95.1	6.82	6.9	6.37	0.97
2015	HP1 88083		94.88	95.62	95.97	6.75	6.83	6.36	0.97
2016	HP1 75691		95.35	96.14	96.21	6.66	6.75	6.32	0.97
2017	HP1 63643		96.0	96.64	96.74	6.01	6.22	5.94	0.96
2018	HP1 55915		96.37	96.94	96.9	6.11	6.35	6.04	0.96
2019	HP1 48385		97.89	98.14	98.32	7.08	7.3	6.88	0.97
2020	HP1 43067		99.48	99.61	99.35	7.11	7.22	6.92	0.97
2021	HP1 37677		99.56	99.61	99.47	6.07	6.15	5.89	0.96
2022	HP1 31546		99.99	99.9	99.74	5.91	5.96	5.8	0.96
2023	HP1 25756		100.27	100.06	99.9	5.98	6.14	5.86	0.97
2024	HP1 21233		102.61	102.5	102.52	5.56	5.72	5.54	0.96
2025	HP1 12904		103.27	102.94	102.95	5.23	5.37	5.17	0.95

BYR	trait	n	ss_m	ebv_m	offebv_m	ss_s	ebv_s	offebv_s	cor
2009	HP2125058		94.62	95.03	95.06	6.58	6.59	6.43	0.98
2010	HP2117053		94.51	94.92	94.91	6.33	6.35	6.18	0.98
2011	HP2113074		95.05	95.47	95.4	6.35	6.35	6.19	0.98
2012	HP2104986		95.16	95.55	95.38	6.17	6.19	6.03	0.98
2013	HP2100787		95.3	95.65	95.5	6.06	6.02	5.84	0.97
2014	HP2 94566		94.81	95.13	95.02	6.48	6.44	6.23	0.97
2015	HP2 83150		95.31	95.75	95.58	6.28	6.26	6.02	0.97
2016	HP2 71353		96.0	96.38	96.2	6.4	6.42	6.17	0.97
2017	HP2 60191		96.72	97.04	96.91	5.67	5.66	5.49	0.97
2018	HP2 52765		97.36	97.61	97.56	5.36	5.29	5.12	0.96
2019	HP2 45757		98.11	98.25	98.23	6.06	6.05	5.91	0.97
2020	HP2 40920		99.62	99.77	99.68	5.62	5.54	5.45	0.97
2021	HP2 35619		99.68	99.73	99.5	5.03	4.96	4.89	0.96
2022	HP2 29684		100.13	100.06	99.94	5.27	5.11	5.05	0.96
2023	HP2 24199		100.91	100.73	100.59	5.12	4.96	4.88	0.96
2024	HP2 8873		101.92	101.74	101.56	4.98	4.81	4.74	0.97

Table 32: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic AI bulls with at least 30 offspring in the full dataset

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2009	HP1	158	95.01	96.23	8.56	8.7	0.98
2010	HP1	165	93.22	94.3	9.8	9.71	0.98
2011	HP1	168	95.38	96.2	9.98	10.01	0.98
2012	HP1	169	96.72	97.88	8.79	8.75	0.98
2013	HP1	122	95.6	96.04	10.42	10.0	0.97
2014	HP1	85	96.66	98.06	10.01	10.3	0.97
2015	HP1	71	96.8	96.9	11.37	11.7	0.97
2016	HP1	70	99.31	99.63	9.28	6.56	0.49
2017	HP1	66	102.41	102.33	12.34	6.76	0.55
2018	HP1	52	100.88	100.31	9.17	6.14	0.39
2019	HP1	50	105.02	101.22	8.35	5.82	0.42
2020	HP1	53	103.58	99.68	7.92	4.45	0.27
2021	HP1	46	105.2	101.2	7.43	5.22	0.43
2022	HP1	40	104.95	100.15	8.24	3.9	0.42

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2023	HP1	8	103.12	101.5	5.91	3.25	0.14
2009	HP2	158	93.84	94.05	9.24	9.3	0.99
2010	HP2	165	94.21	94.44	9.91	9.97	0.98
2011	HP2	168	96.26	96.17	10.38	10.32	0.98
2012	HP2	169	94.97	95.6	9.34	9.47	0.98
2013	HP2	122	94.61	95.09	10.53	10.56	0.98
2014	HP2	85	95.96	96.76	9.75	10.24	0.98
2015	HP2	71	95.73	95.9	10.64	10.77	0.98
2016	HP2	70	99.5	99.57	8.63	6.17	0.48
2017	HP2	66	100.89	101.77	10.94	5.98	0.57
2018	HP2	52	102.63	100.42	7.8	5.92	0.15
2019	HP2	50	103.98	101.94	7.54	5.45	0.54
2020	HP2	51	103.96	100.43	7.67	4.57	0.25
2021	HP2	40	104.82	102.05	7.18	5.81	0.44
2022	HP2	8	106.62	102.5	9.33	3.25	-0.12
2009	BP1	158	95.48	96.75	8.37	8.56	0.99
2010	BP1	165	94.31	95.55	9.39	9.33	0.98
2011	BP1	168	95.9	96.79	9.44	9.47	0.98
2012	BP1	169	96.7	97.96	8.69	8.64	0.98
2013	BP1	123	96.47	97.14	9.97	9.63	0.97
2014	BP1	84	96.93	98.32	9.6	9.85	0.98
2015	BP1	71	96.9	97.25	10.69	10.98	0.97
2016	BP1	70	99.37	99.87	8.94	6.69	0.51
2017	BP1	66	102.12	102.21	11.92	6.67	0.55
2018	BP1	52	100.83	100.69	8.8	6.07	0.37
2019	BP1	50	105.12	101.72	8.21	5.65	0.44
2020	BP1	52	103.75	100.02	7.31	4.58	0.32
2021	BP1	46	105.04	101.61	7.32	5.26	0.41
2022	BP1	41	104.85	100.51	8.21	3.84	0.45
2023	BP1	8	102.88	101.88	5.62	2.95	0.04
2009	BP2	158	94.3	94.23	9.31	9.28	0.99
2010	BP2	165	95.08	94.91	10.86	10.87	0.99
2011	BP2	168	96.79	96.46	10.43	10.34	0.99

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2012	BP2	169	95.22	95.4	9.45	9.5	0.98
2013	BP2	123	94.73	94.88	10.61	10.65	0.98
2014	BP2	84	96.13	96.36	9.84	10.1	0.98
2015	BP2	71	96.61	96.45	10.15	10.19	0.98
2016	BP2	70	99.83	99.59	8.9	6.19	0.59
2017	BP2	66	101.14	101.67	10.8	6.41	0.7
2018	BP2	52	102.27	100.19	8.0	5.48	0.17
2019	BP2	50	103.9	101.88	7.5	5.19	0.54
2020	BP2	49	102.41	99.96	8.54	4.2	0.33
2021	BP2	40	105.3	102.2	7.17	5.39	0.48
2022	BP2	32	104.47	101.56	6.76	3.66	0.28

Table 33: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic cows with genotype and phenotype

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2009	HP1	441	94.73	95.99	7.26	7.18	0.95
2010	HP1	3428	92.87	93.99	7.62	7.5	0.96
2011	HP1	6066	93.64	94.83	7.99	7.8	0.96
2012	HP1	6830	94.5	95.67	7.65	7.4	0.96
2013	HP1	7243	94.18	95.04	7.4	7.15	0.95
2014	HP1	8039	94.44	95.59	7.67	7.37	0.95
2015	HP1	10571	95.19	96.06	7.5	7.15	0.94
2016	HP1	14776	95.69	96.76	7.44	7.14	0.94
2017	HP1	17598	96.64	97.12	7.13	6.82	0.92
2018	HP1	19923	96.86	97.38	6.92	6.56	0.81
2019	HP1	20207	98.93	99.23	8.31	5.72	0.65
2020	HP1	22514	100.68	98.63	7.97	5.44	0.65
2021	HP1	22694	100.92	99.3	6.94	5.6	0.66
2022	HP1	23572	101.21	99.23	6.8	4.92	0.61
2023	HP1	21878	101.4	99.87	6.95	4.63	0.56
2024	HP1	22252	103.88	100.18	6.47	4.4	0.52
2025	HP1	11813	104.17	100.4	6.1	4.24	0.52
2009	HP2	441	93.95	94.24	7.09	6.91	0.94
2010	HP2	3425	94.25	94.4	7.47	7.25	0.95

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2011	HP2	6058	95.17	95.36	7.56	7.31	0.95
2012	HP2	6818	94.9	95.12	7.46	7.19	0.95
2013	HP2	7211	95.38	95.57	7.2	6.92	0.94
2014	HP2	7980	94.8	95.24	7.85	7.57	0.94
2015	HP2	10412	95.41	95.61	7.49	7.25	0.93
2016	HP2	14540	96.22	96.79	7.53	7.37	0.93
2017	HP2	17205	97.17	97.42	7.0	6.69	0.92
2018	HP2	19500	97.88	97.49	6.61	6.32	0.83
2019	HP2	19804	98.8	98.71	7.48	5.95	0.75
2020	HP2	22099	100.65	98.53	6.68	5.73	0.66
2021	HP2	22242	100.76	99.12	6.26	5.79	0.66
2022	HP2	23059	101.4	99.4	6.25	5.28	0.68
2023	HP2	21381	102.03	100.21	6.11	5.16	0.68
2024	HP2	9771	103.36	100.91	6.01	4.9	0.65

Table 34: Genetic trends (Single-step full dataset (f) vs single-step reduced dataset (r)) for nordic bulls with genotype and phenotype

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2009	BP1	403	94.84	96.22	8.1	7.89	0.97
2010	BP1	690	92.5	93.79	7.79	7.56	0.96
2011	BP1	1425	94.87	96.12	7.68	7.6	0.96
2012	BP1	1815	95.59	96.8	7.07	6.72	0.95
2013	BP1	1838	94.99	95.83	6.82	6.49	0.94
2014	BP1	1839	94.66	95.97	7.21	6.97	0.95
2015	BP1	1781	95.72	96.56	7.27	6.97	0.95
2016	BP1	1707	96.48	97.66	7.33	6.98	0.93
2017	BP1	1984	97.27	97.79	7.21	6.75	0.91
2018	BP1	1916	98.77	99.33	6.63	5.71	0.75
2019	BP1	1891	100.16	100.63	7.85	5.3	0.62
2020	BP1	2162	100.45	99.73	6.97	5.22	0.61
2021	BP1	1948	102.36	100.98	6.3	4.94	0.58
2022	BP1	1833	102.9	100.21	6.18	4.48	0.59
2023	BP1	1703	103.11	101.06	6.1	4.45	0.58
2024	BP1	1435	105.16	101.46	6.11	4.15	0.51

BYR	trait	n	f_m	r_m	f_s	r_s	cor
2025	BP1	854	104.53	101.15	5.74	3.99	0.53
2009	BP2	338	92.68	92.57	8.85	8.81	0.98
2010	BP2	575	94.95	94.7	9.16	9.01	0.97
2011	BP2	1123	96.65	96.5	8.3	8.02	0.97
2012	BP2	1385	95.07	94.89	7.59	7.39	0.96
2013	BP2	1355	95.36	95.2	7.22	7.14	0.95
2014	BP2	1452	94.79	94.87	8.27	8.11	0.96
2015	BP2	1420	95.52	95.43	7.98	7.82	0.96
2016	BP2	1382	96.6	96.83	8.18	7.95	0.95
2017	BP2	1655	98.13	98.12	7.15	6.7	0.92
2018	BP2	1628	99.82	99.38	6.82	5.82	0.77
2019	BP2	1622	99.28	99.46	7.45	5.75	0.77
2020	BP2	1837	100.91	99.3	6.25	5.23	0.69
2021	BP2	1617	101.6	100.35	6.37	5.22	0.69
2022	BP2	1503	101.85	100.03	6.41	4.88	0.67
2023	BP2	1400	102.74	100.66	6.19	4.92	0.68
2024	BP2	1188	104.61	102.03	6.02	4.32	0.63
2025	BP2	248	103.83	101.34	5.8	4.32	0.59

Correlations

Here, we give correlation tables and tables of differences between the relevant evaluations. We test that we didn't change the model by comparing our new model without genomic information to the breeding values of the traditional pedigree-based model and expect very high correlations for tested animals. We test the change by incorporating genomic information, compared to a non-genomic evaluation, and expect to see some changes even in tested animals, but not too large.

Table 35: Correlations between current EBV and new EBV for Nordic AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	158	0.989	0.991	0.992	0.989
2010	165	0.994	0.992	0.994	0.992
2011	168	0.995	0.994	0.994	0.992
2012	169	0.994	0.991	0.994	0.99
2013	122	0.994	0.993	0.994	0.991
2014	85	0.995	0.995	0.995	0.993

BYR	n	cor1	cor2	cor3	cor4
2015	71	0.996	0.997	0.996	0.994
2016	70	0.993	0.993	0.995	0.991
2017	66	0.997	0.996	0.996	0.995
2018	52	0.995	0.994	0.993	0.991
2019	50	0.994	0.997	0.993	0.994
2020	51	0.995	0.996	0.994	0.993
2021	40	0.996	0.996	0.996	0.993

Table 36: Table of differences between current EBV and new EBV for Nordic AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-4.0	2	1	1	1
-3.0	4	0	6	6
-2.0	29	14	26	28
-1.0	84	80	97	93
0.0	110	155	118	128
1.0	77	71	69	64
2.0	24	14	17	13
3.0	7	1	3	4
4.0	0	1	0	0

Table 37: Correlations between current EBV and new Single-step for AI bulls with > 30 offspring

BYR	n	cor1	cor2	cor3	cor4
2009	158	0.95	0.958	0.95	0.958
2010	165	0.957	0.959	0.954	0.967
2011	168	0.965	0.973	0.964	0.971
2012	169	0.939	0.956	0.943	0.957
2013	122	0.956	0.96	0.957	0.96
2014	85	0.96	0.977	0.964	0.972
2015	71	0.987	0.985	0.984	0.982
2016	70	0.975	0.982	0.978	0.981
2017	66	0.984	0.984	0.985	0.982
2018	52	0.977	0.986	0.976	0.988
2019	50	0.978	0.972	0.977	0.969

BYR	n	cor1	cor2	cor3	cor4
2020	51	0.96	0.968	0.953	0.973
2021	40	0.967	0.965	0.966	0.962

Table 38: Table of differences between current EBV and new Single-step for AI bulls with > 30 offspring born after 2015

dif	dif1	dif2	dif3	dif4
-9.0	1	1	0	0
-8.0	0	0	2	1
-7.0	1	1	0	0
-6.0	4	2	3	4
-5.0	6	3	9	3
-4.0	16	13	13	18
-3.0	33	27	44	28
-2.0	50	40	52	45
-1.0	68	81	67	76
0.0	56	93	64	91
1.0	49	48	39	39
2.0	36	13	32	21
3.0	11	8	7	4
4.0	3	3	2	4
5.0	1	4	2	3
6.0	0	0	0	0
7.0	1	0	0	0
8.0	1	0	1	0

Table 39: Correlations between current two-step and new Single-step for genotyped nordic bulls with no offspring born after 2020

BYR	n	cor
2020	2751	0.787
2021	2704	0.749
2022	2502	0.782
2023	2258	0.773
2024	2190	0.737
2025	1197	0.673

Table 40: Table of differences between current two-step and new Single-step for genotyped nordic bulls born after 2020 with no offspring

dif	dif5
-19.0	1
-18.0	0
-17.0	1
-16.0	1
-15.0	5
-14.0	17
-13.0	40
-12.0	55
-11.0	85
-10.0	166
-9.0	243
-8.0	383
-7.0	545
-6.0	674
-5.0	853
-4.0	1003
-3.0	1060
-2.0	1020
-1.0	1012
0.0	956
1.0	801
2.0	596
3.0	480
4.0	298
5.0	197
6.0	134
7.0	92
8.0	56
9.0	35
10.0	14
11.0	7

dif	dif5
12.0	5
13.0	1
14.0	2
15.0	2
16.0	2
17.0	4
18.0	1
19.0	1
20.0	1
21.0	1
22.0	0
23.0	1

Legarra-Reverter test

The Legarra-Reverter test is a test for bias in evaluations. We perform two calculations of breeding values, one with all information available and one where offspring of sires born after 2015 has their records removed. Then we perform a linear regression on genotyped, nordic bulls, who has no data in the reduced dataset and with more than 30 offspring in the full dataset. We also require that their sires are not in the focal group, so we remove bulls whose father meets the same criteria.

The slope of the regression indicates the bias, with a slope of one meaning no bias, a slope less than one indicating that the estimated values of unproven animals are too extreme, and a slope higher than one indicating that the estimated breeding values of unproven animals are too conservative.

As can be seen, we have some issues with the Legarra-Reverter test. We're looking into it.

Table 41: Legarra-Reverter scores
Singlestep:

trait	b1	rsquare	n
HP1	0.896	0.319	143
HP2	0.869	0.292	143
BP1	0.84	0.299	141
BP2	0.995	0.41	140

EBV:

trait	b1	rsquare	n
HP1	0.731	0.165	143

trait	b1	rsquare	n
HP2	0.59	0.096	143
BP1	0.652	0.134	141
BP2	0.804	0.196	140

Mendelian sampling

The mendelian sampling of an animal is its deviation of its breeding values from the expected breeding value, which is the average of its parents breeding values. Some mendelian sampling is expected on the individual level (this is what enables breeding), but across all animals we expect it to be close to zero. Otherwise, this indicates a bias in the set of animals in the evaluation, which violates the unbiasedness of the BLUP model. We conclude that the mendelian sampling is generally close to 0.

Table 42: Average mendelian sampling by birth year. Animals are only included if they are genotyped, their sire has > 30 offspring and their dam is genotyped.

BYR	n	m1	m2	m3	m4
2010	355	-0.283	-0.179	-0.263	-0.137
2011	623	-0.144	-0.142	-0.152	-0.104
2012	1491	-0.039	0.042	-0.037	0.106
2013	2895	0.299	0.336	0.245	0.293
2014	4036	0.161	0.221	0.146	0.172
2015	5644	0.125	0.139	0.106	0.107
2016	6462	0.077	0.138	0.087	0.154
2017	7556	0.15	0.191	0.157	0.13
2018	9463	0.054	0.077	-0.01	0.103
2019	11268	0.231	0.229	0.153	0.201
2020	14009	0.198	0.181	0.182	0.189
2021	15983	0.217	0.292	0.223	0.222
2022	18283	0.268	0.278	0.263	0.239
2023	17721	0.185	0.209	0.169	0.17
2024	18709	0.114	0.12	0.131	0.15

Table 43: Average mendelian sampling by birth year. Animals are only included if they are not genotyped, their sire has > 30 offspring and their dam isn't genotyped.

BYR	n	m1	m2	m3	m4
2001	126540.0	0.035	-0.029	-0.026	0.021
2002	135856.0	0.048	-0.029	0.011	-0.002
2003	146442.0	0.022	-0.012	-0.001	0.007

BYR	n	m1	m2	m3	m4
2004	246075.0	0.005	-0.019	-0.009	-0.013
2005	234341.0	-0.015	-0.015	-0.01	-0.014
2006	227023.0	-0.013	-0.029	-0.014	-0.012
2007	214555.0	0.011	-0.018	-0.01	-0.027
2008	251447.0	0.02	0.006	-0.004	-0.019
2009	243677.0	0.03	0.012	-0.015	-0.009
2010	229627.0	0.03	0.025	-0.005	-0.011
2011	218364.0	0.023	0.035	-0.009	0.006
2012	201983.0	0.008	0.027	0.018	0.014
2013	190385.0	0.022	0.052	0.007	0.016
2014	180247.0	0.013	0.039	-0.002	-0.003
2015	159444.0	0.031	0.023	0.009	-0.001
2016	137934.0	0.01	0.013	0.012	0.043
2017	115679.0	-0.005	0.028	-0.005	0.008
2018	103080.0	-0.0	0.024	-0.036	0.049
2019	86700.0	0.026	0.033	-0.028	0.027
2020	75811.0	0.005	-0.028	-0.001	0.006
2021	63836.0	-0.025	-0.001	0.003	-0.003
2022	51517.0	-0.004	-0.002	0.003	-0.011
2023	41856.0	-0.018	-0.005	-0.03	-0.014
2024	34619.0	-0.025	-0.029	-0.007	0.005

Reliabilities

Table 44: Comparison of reliabilities between single-step (ss), new EBV (ebv) and current official evaluation (cur) for nordic AI bulls with > 30 offspring and correlation between single-step and current evaluation.

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2009	HP1	158	69.18	62.97	63.48	6.41	8.2	8.03	0.99
2010	HP1	165	67.68	60.59	61.13	7.2	9.26	9.09	0.99
2011	HP1	168	69.08	62.67	63.18	8.31	10.85	10.65	0.99
2012	HP1	169	69.05	62.79	63.25	9.04	11.65	11.41	1.0
2013	HP1	122	71.02	65.36	65.83	10.44	13.46	13.18	1.0
2014	HP1	85	75.1	71.01	71.35	10.35	13.07	12.84	1.0
2015	HP1	71	77.59	74.31	74.58	9.24	11.5	11.31	1.0

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2016	HP1	70	76.19	72.3	72.63	9.74	11.86	11.69	0.96
2017	HP1	66	76.34	72.77	73.06	10.41	13.04	12.81	1.0
2018	HP1	52	76.38	73.11	73.38	10.02	12.19	11.99	1.0
2019	HP1	50	76.21	72.83	73.06	10.66	13.34	13.09	1.0
2020	HP1	53	74.46	70.61	70.83	11.65	15.12	14.94	1.0
2021	HP1	46	70.79	65.61	65.87	13.5	18.05	17.82	1.0
2022	HP1	40	64.02	56.96	57.45	14.68	19.34	19.1	1.0
2009	HP2	158	68.92	62.97	75.68	6.46	8.2	7.79	0.97
2010	HP2	165	67.41	60.59	72.86	7.26	9.26	8.1	0.96
2011	HP2	168	68.83	62.67	75.07	8.38	10.85	9.65	0.96
2012	HP2	169	68.8	62.79	74.98	9.11	11.65	10.31	0.97
2013	HP2	122	70.77	65.36	77.09	10.52	13.46	11.61	0.98
2014	HP2	85	74.89	71.01	82.61	10.44	13.07	10.64	0.97
2015	HP2	71	77.4	74.31	85.59	9.32	11.5	8.63	0.98
2016	HP2	70	75.98	72.3	84.17	9.82	11.86	8.99	0.94
2017	HP2	66	76.14	72.77	84.05	10.49	13.04	10.18	0.98
2018	HP2	52	76.18	73.11	84.44	10.1	12.19	8.94	0.99
2019	HP2	50	76.0	72.83	83.94	10.75	13.34	10.88	0.98
2020	HP2	51	75.18	71.92	82.73	10.94	13.84	12.68	0.97
2021	HP2	40	73.65	69.89	79.2	11.67	15.12	14.05	0.97
2009	BP1	158	69.19	62.97	64.2	6.41	8.2	8.24	0.99
2010	BP1	165	67.69	60.59	61.78	7.19	9.26	9.22	0.99
2011	BP1	168	69.1	62.67	63.91	8.31	10.85	10.87	0.99
2012	BP1	169	69.07	62.79	64.05	9.04	11.65	11.67	0.99
2013	BP1	123	70.76	65.06	66.33	10.8	13.82	13.8	1.0
2014	BP1	84	75.39	71.41	72.71	10.09	12.61	12.42	1.0
2015	BP1	71	77.6	74.31	75.65	9.24	11.5	11.43	1.0
2016	BP1	70	76.2	72.3	73.51	9.74	11.86	11.72	0.96
2017	BP1	66	76.35	72.77	74.0	10.4	13.04	12.95	1.0
2018	BP1	52	76.39	73.11	74.21	10.02	12.19	11.94	1.0
2019	BP1	50	76.22	72.83	73.84	10.66	13.34	13.11	1.0
2020	BP1	52	74.93	71.24	72.21	11.28	14.56	14.34	1.0
2021	BP1	46	70.8	65.61	66.24	13.49	18.05	17.9	1.0

BYR	trait	n	rel_ss	rel_ebv	rel_cur	s_rel_ss	s_rel_ebv	s_rel_cur	cor
2022	BP1	41	63.53	56.29	56.27	14.84	19.58	18.93	1.0
2009	BP2	158	68.88	62.97	74.2	6.47	8.2	8.04	0.93
2010	BP2	165	67.37	60.59	71.53	7.26	9.26	8.28	0.93
2011	BP2	168	68.79	62.67	73.37	8.39	10.85	9.91	0.95
2012	BP2	169	68.76	62.79	73.53	9.12	11.65	10.77	0.95
2013	BP2	123	70.47	65.06	75.51	10.89	13.82	12.42	0.97
2014	BP2	84	75.14	71.41	81.64	10.19	12.61	10.54	0.97
2015	BP2	71	77.37	74.31	84.79	9.33	11.5	9.02	0.97
2016	BP2	70	75.95	72.3	82.96	9.83	11.86	9.37	0.94
2017	BP2	66	76.11	72.77	83.03	10.51	13.04	10.52	0.98
2018	BP2	52	76.15	73.11	83.19	10.11	12.19	9.45	0.98
2019	BP2	50	75.97	72.83	82.5	10.76	13.34	11.35	0.98
2020	BP2	49	76.06	73.19	82.0	10.16	12.54	11.34	0.97
2021	BP2	40	73.77	70.05	77.53	11.38	14.77	14.15	0.97
2022	BP2	32	67.21	61.63	60.78	14.37	18.6	18.47	0.95

Table 45: Comparison of reliabilities between single-step and current official evaluation (two-step) for nordic genotyped bulls with no offspring

BYR	n	ss_rel	two_rel	s_ss_rel	s_two_rel	cor
2020	2751	43.588	52.115	2.408	2.194	0.921
2021	2704	42.911	51.492	2.513	2.32	0.918
2022	2502	42.335	50.884	2.529	2.313	0.931
2023	2258	42.103	50.378	2.832	2.846	0.944
2024	2190	40.624	47.508	3.812	4.033	0.949
2025	1197	38.014	43.145	4.036	3.793	0.893

Note on genotype selection

In previous experiments and developments, it was observed that there is a bias in which animals are genotyped. Specifically, animals which die in the early period are very unlikely to be genotyped. Since this was observed together with an increase in genetic trend, it was assumed that this “genotyping selection” was the cause of the increased trend.

The proposed solution to this problem was to only include genotypes of tested AI bulls in the single-step evaluation and estimate SNP solutions based on their genotypes. Other genomically tested animals would then receive an indirect genomic breeding value, similar to a two-step setup, and similar to what is done in our current monthly evaluations.

However, we had severe problems getting this to work. Correlations to pedigree-based breeding values were essentially zero, and we saw huge variances of genomic breeding values.

After correspondance with MiX99 authors and failing to resolve the issues, it was determined that using a modified marker set would also solve the original issues, and would likely bring higher accuracy to genomic breeding values by including a much larger genomic reference population. Hence, this approach of including only genotypes from AI bulls was ultimately abandoned.