



High imputation accuracy from informative low-to-medium density single nucleotide polymorphism genotypes is achievable in sheep

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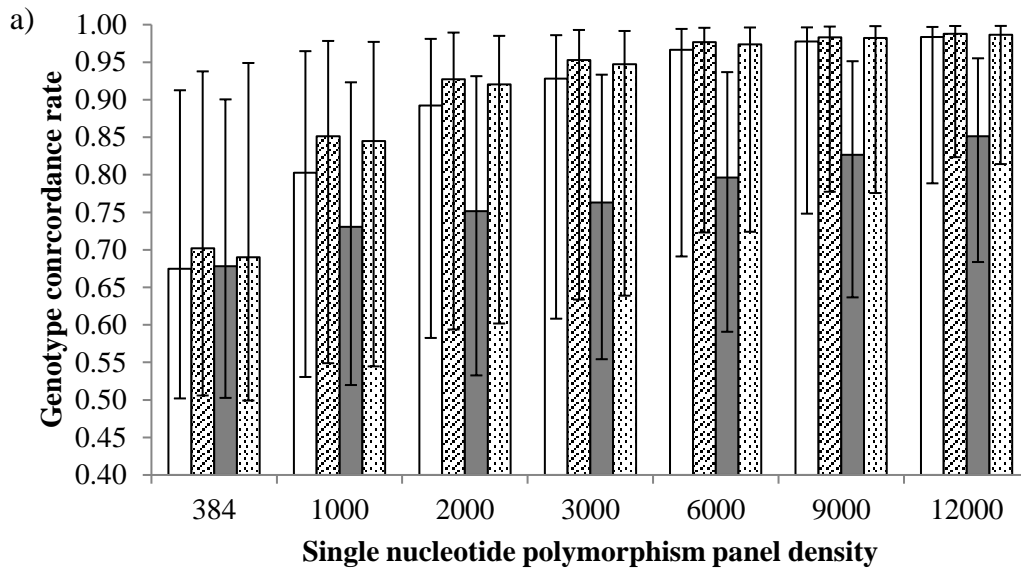
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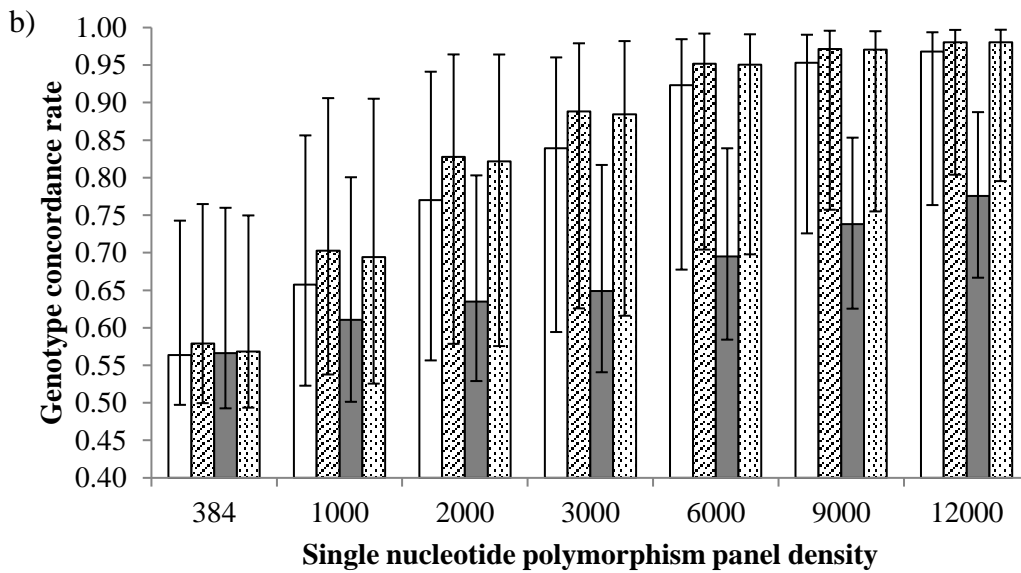
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- 1 **Supplementary Table 1.** The number of single nucleotide polymorphism (SNPs) selected
- 2 per autosome (OAR) for each of the low-density panels.

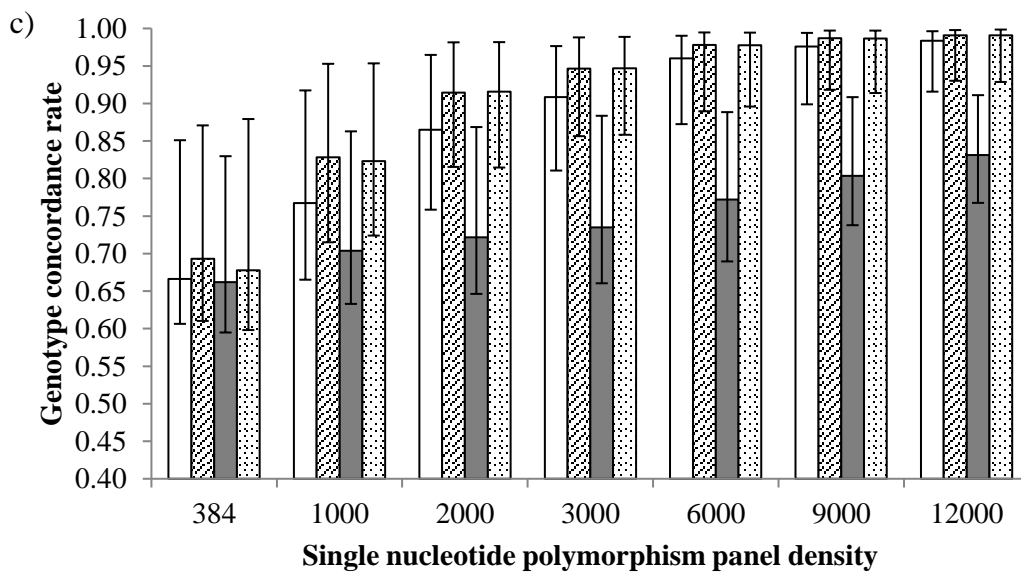
OAR	SNP panel density						
	384	1,000	2,000	3,000	6,000	9,000	12,000
1	38	113	217	332	621	994	1240
2	37	104	205	312	585	936	1168
3	34	95	187	284	532	852	1063
4	19	52	103	155	290	465	581
5	16	43	87	132	246	394	490
6	18	48	101	148	313	440	546
7	17	42	89	130	275	386	480
8	15	39	81	117	251	350	437
9	15	40	82	120	255	356	442
10	13	35	71	103	220	307	382
11	9	23	47	69	146	204	253
12	14	32	66	96	205	286	356
13	12	32	66	96	204	284	353
14	10	23	46	66	140	196	243
15	13	32	64	94	199	278	461
16	12	31	61	89	190	264	440
17	12	27	53	80	172	239	397
18	12	27	55	80	171	237	395
19	11	24	50	77	152	213	353
20	10	23	43	68	137	191	316
21	7	18	34	52	102	143	236
22	9	21	42	67	132	183	305
23	9	22	45	70	138	240	320
24	6	15	30	45	91	157	207
25	9	20	38	61	121	210	279
26	7	19	37	57	112	195	257



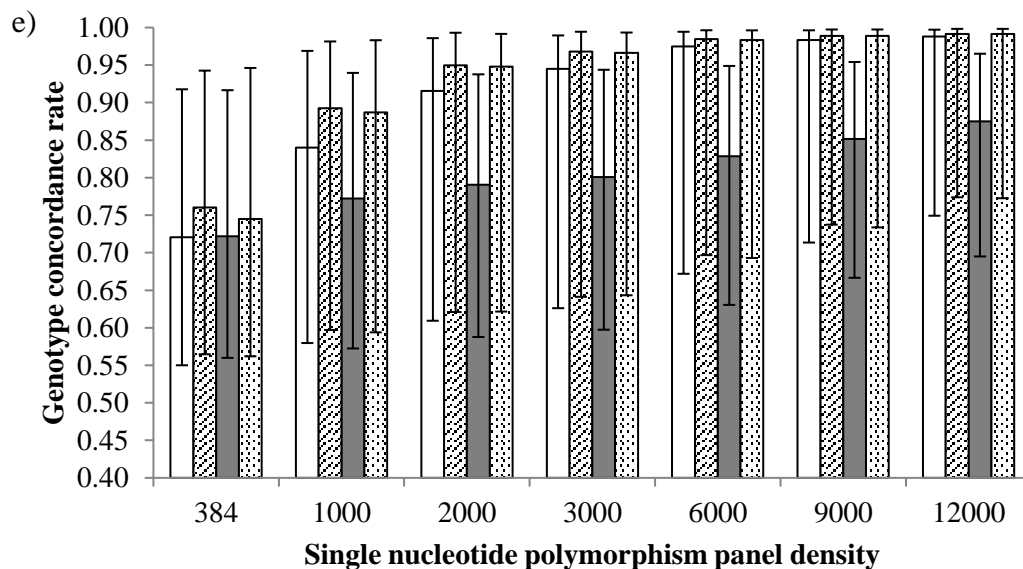
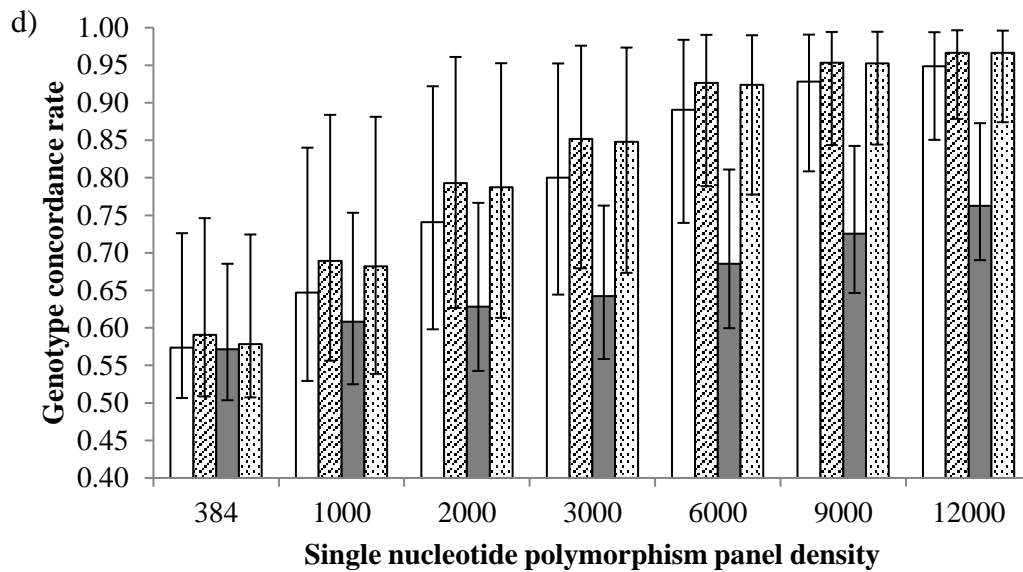
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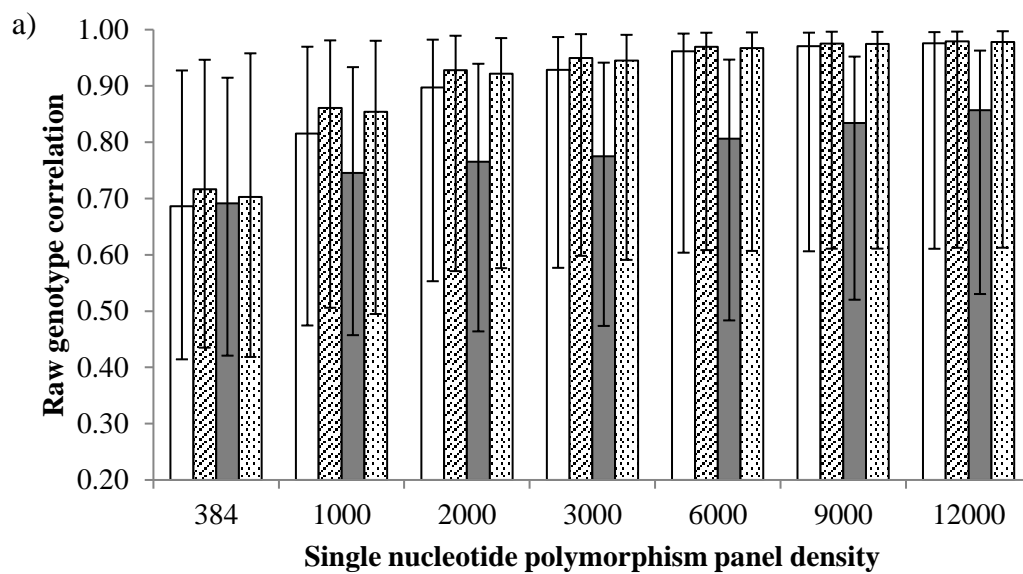
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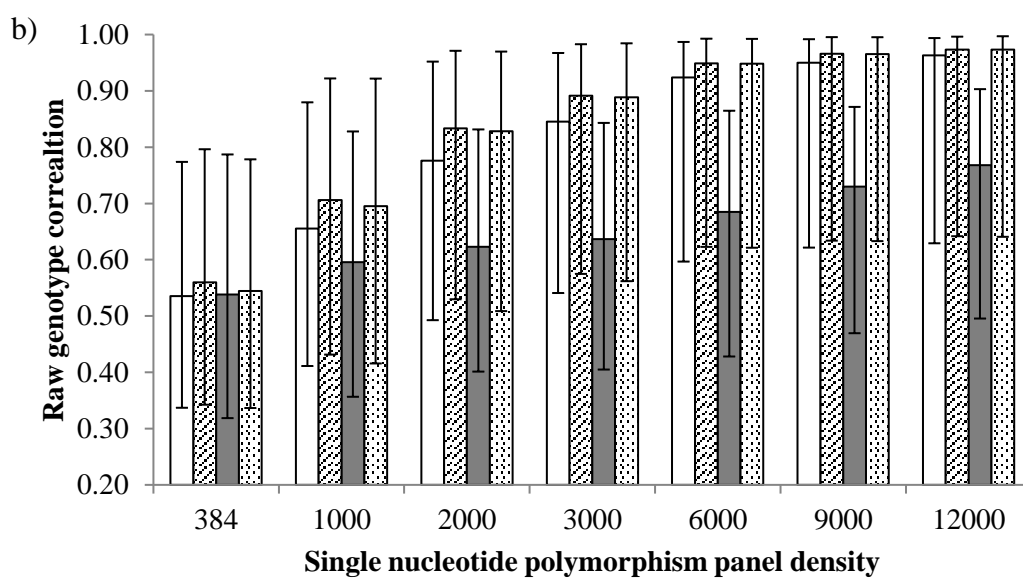
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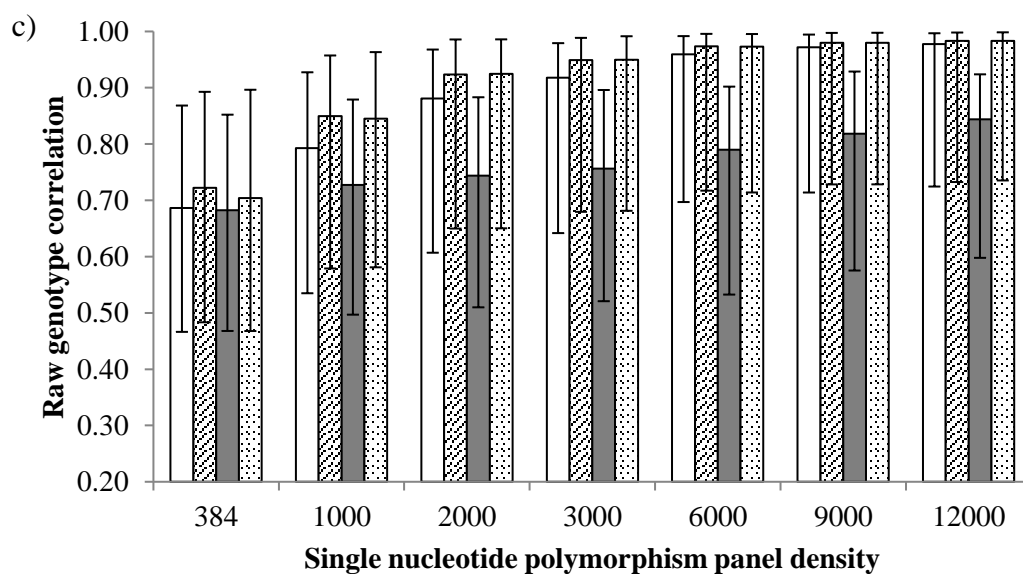
Supplementary Figure 1. Mean genotype concordance rate per animal across multiple SNP panel densities. One breed is represented per graph; a) Belclare, b) Charollais, c) Suffolk, d) Texel and e) Vendeen. SNPs were selected randomly (white bar), using the block method (striped bar), using the EquiMAF method (dark grey bar) and using the Wellman method (spotted bar; Wellman et al., 2013). SNP panels were created within each breed separately and the reference and validation populations were composed only of animals of that breed (Scenario 1). The error bars represent the best and worst mean allele concordance rate per animal.



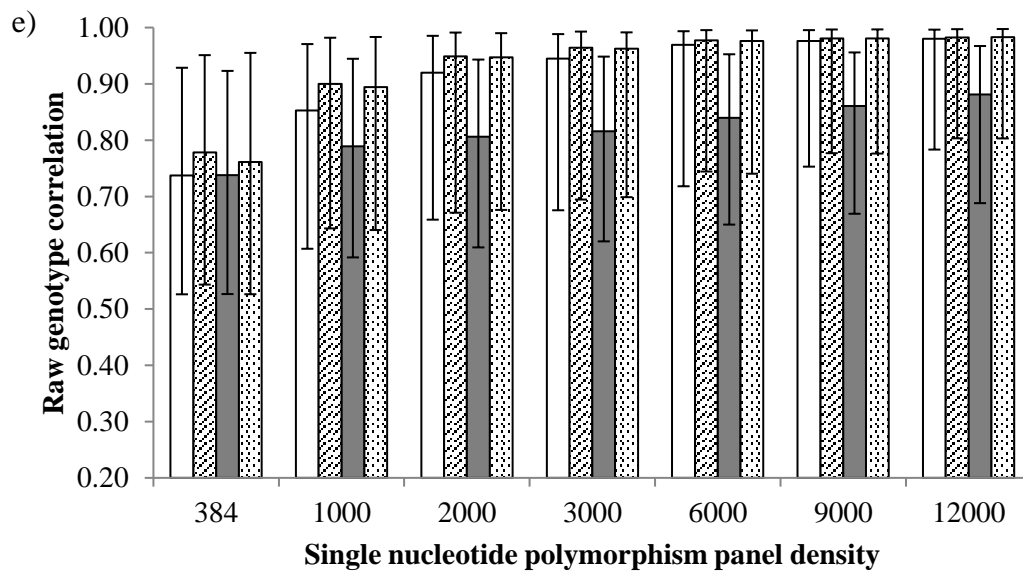
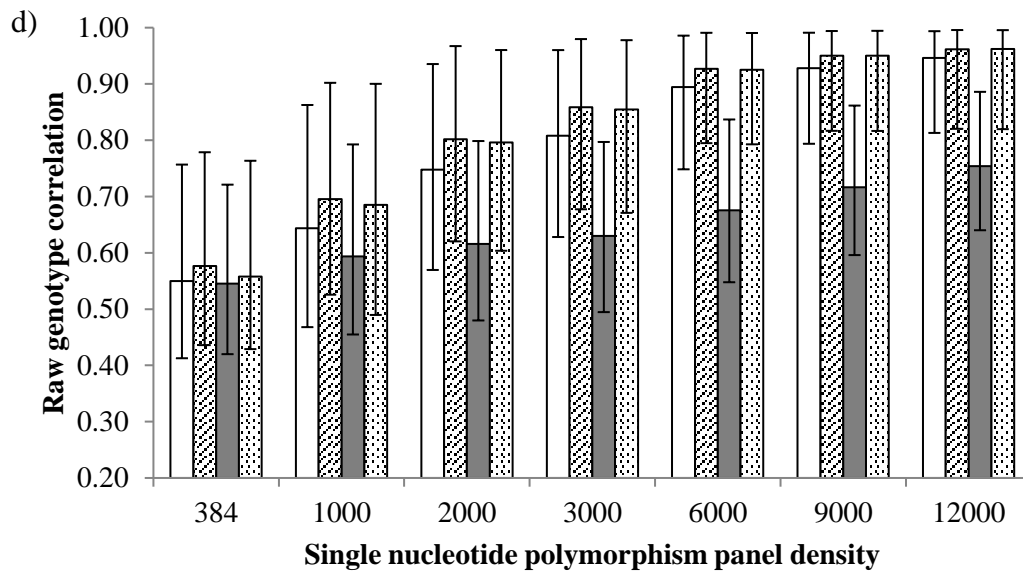
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Supplementary Figure 2. The mean raw genotype correlation per animal across multiple SNP panels densities. One breed is represented per graph; a) Belclare, b) Charollais, c) Suffolk, d) Texel and e) Vendéen. SNPs were selected randomly (white bar), using the block method (striped bar), using the EquiMAF method (dark grey bar) and using the Wellman method (spotted bar; Wellman et al., 2013). SNP panels were created within each breed separately and the reference and validation populations were composed only of animals of that breed (Scenario 1). The error bars represent the best and worst mean allele concordance rate per animal.