Table S2 Comparison of linear canonical analyses determining significantly misclassified (p<0.05) grandson-maternal grandsire pairs using SNP allele matches and genomic relationship scores.

Bull_MGS	SNP allele matches[1]			Genomic Relationship[2]			SNP allele matches & Genomic Relationship		
		Probabilities			Probabilities			Probabilities	
	Predicted Group	Predicted group	Third group	Predicted Group	Predicted group	Third group	Predicted Group	Predicted group	Third group
7171_3274	unrelated	0.9362	0	unrelated	0.9996	0	unrelated	0.9995	0
7413_3376	unrelated	0.9478	0	unrelated	0.9973	0	unrelated	0.9977	0
7358_3833	unrelated	0.9965	0	unrelated	0.9950	0	unrelated	0.9983	0
3333_783	unrelated	0.9958	0	unrelated	0.8562	0	unrelated	0.9664	0
3474_2122	unrelated	0.9658	0	unrelated	0.9069	0	unrelated	0.9538	0
3535_783	unrelated	0.9958	0	unrelated	0.9961	0	unrelated	0.9987	0
3763_2287	unrelated	0.9265	0	unrelated	0.9160	0	unrelated	0.9478	0
3807_2283	unrelated	0.9687	0	unrelated	0.9987	0	unrelated	0.9989	0
7228_3376	unrelated	0.9566	0	unrelated	0.9880	0	unrelated	0.9917	0
7416_3274	unrelated	0.8565	0.00001	unrelated	0.9990	0	unrelated	0.9985	0
7495_3421	unrelated	0.9238	0.00001	unrelated	0.9877	0	unrelated	0.9899	0
7203_3241	unrelated	0.8355	0.00002	unrelated	0.9954	0	unrelated	0.9942	0
7137_3274	unrelated	0.8352	0.00003	unrelated	0.9620	0	unrelated	0.9646	0
7241_3274	unrelated	0.8342	0.00004	unrelated	0.9965	0	unrelated	0.9953	0
7243_3376	unrelated	0.762	0.00009	unrelated	0.6374	0.00004	unrelated	0.7027	0.00001
7346_3376	unrelated	0.7153	0.00013	unrelated	0.8710	0	unrelated	0.8740	0
7330_3908	unrelated	0.7272	0.00016	unrelated	0.9836	0	unrelated	0.9783	0
7126_3259	unrelated	0.5413	0.0004	unrelated	0.7212	0.00002	unrelated	0.7080	0.00001
7351_3304	unrelated	0.5415	0.00093	fourth	0.7207	0.00035	fourth	0.6887	0.00013
3656_2132	fourth	0.7405	0.00122	fourth	0.9540	0.00391	fourth	0.9496	0.00031
3788_3089	fourth	0.5823	0.00138	fourth	0.9741	0.01330	fourth	0.9772	0.00174
7021_3586	fourth	0.7317	0.0022	unrelated	0.9986	0	unrelated	0.9952	0
7338_3274	fourth	0.8079	0.00486	unrelated	0.5981	0.00005	fourth	0.5308	0.00005
7322_5224	fourth	0.7529	0.00493	fourth	0.8931	0.00139	fourth	0.9009	0.00061
3304_783	fourth	0.9001	0.01275				fourth	0.9788	0.01992
3434_783	fourth	0.9239	0.01683	fourth	0.9734	0.01646	fourth	0.9876	0.00400
2219_783	fourth	0.9426	0.03637				fourth	0.9708	0.02854
3292_783	fourth	0.8792	0.04628						
3680_3156				fourth	0.9740	0.01243			
7144_5186				fourth	0.9705	0.02202	fourth	0.9779	0.01635
7422_3833				fourth	0.9684	0.02509	fourth	0.9858	0.01051
7568_3651				fourth	0.9642	0.03046	fourth	0.9532	0.04461
3805_3070				fourth	0.9522	0.04426			
3917_5172				fourth	0.9482	0.04865	fourth	0.9711	0.02655
7324_3421				fourth	0.9479	0.04897			
7008_3070							fourth	0.9661	0.03189
3677_3156							fourth	0.9567	0.04248

[1] Following Table 1, Grandson-maternal grandsire pairs as listed in the herd-book for which the probabilities of assignment to the third group < 0.05.
[2] Following VanRaden (2008), the genomic relationship scores were calculated and used as the covariant in the discriminant analysis.