

Additional file 3

Table S1 – Correlations between predictions of the different models

		Pedigree - BLUP	BovineHD - GBLUP	ImputedHD - GBLUP	Sequence - GBLUP	BovineHD - BSSVS	ImputedHD - BSSVS
SCS	BovineHD - GBLUP	0.751					
	ImputedHD - GBLUP	0.721	0.975				
	Sequence - GBLUP	0.720	0.973	0.996			
	BovineHD - BSSVS	0.792	0.995	0.969	0.967		
	ImputedHD - BSSVS	0.765	0.973	0.993	0.993	0.976	
	Sequence - BSSVS	0.765	0.974	0.992	0.995	0.977	0.998
IFL	BovineHD - GBLUP	0.700					
	ImputedHD - GBLUP	0.678	0.967				
	Sequence - GBLUP	0.680	0.967	0.996			
	BovineHD - BSSVS	0.795	0.978	0.948	0.949		
	ImputedHD - BSSVS	0.796	0.954	0.972	0.973	0.977	
	Sequence - BSSVS	0.771	0.961	0.979	0.983	0.977	0.997
PY	BovineHD - GBLUP	0.729					
	ImputedHD - GBLUP	0.717	0.965				
	Sequence - GBLUP	0.715	0.964	0.996			
	BovineHD - BSSVS	0.766	0.992	0.959	0.959		
	ImputedHD - BSSVS	0.758	0.959	0.988	0.989	0.968	
	Sequence - BSSVS	0.762	0.964	0.991	0.995	0.967	0.994

Table S2 – Estimates of genetic parameters for GBLUP model including polygenic component

Estimates of additive genetic variance (σ_g^2), heritability (h^2), regression coefficient (b), and prediction reliability (r^2) for somatic cell score using three types of genomic data.

Data	σ_g^2	h^2	$b^{(1)}$	$r^2^{(2)}$
BovineHD	18.44	0.95	1.12	0.51
ImputedHD	19.00	0.99	1.14	0.49
Sequence	18.82	0.98	1.16	0.49

¹ Standard error of the regression coefficient ranged between 0.02 and 0.03

² Standard error of the prediction reliability was 0.02.