

Table S2. Posterior mean number of SNP in each distribution [0, 0.0001, 0.001 or 0.01 of the pedigree estimated genetic variance ($\sigma_{a^*}^2$)]. Data from Kemper et. al. [1].

Reference dataset	$\sigma_{a^*}^2$	Fat yield (FY)	Milk yield (MY)	Protein yield (PY)
Hol_Jer	0	627,584	627,787	627,377
	0.0001	4389	4155	4583
	0.001	23	54	37
	0.01	6	6	5
Holstein	0	627,973	628,084	627,605
	0.0001	3968	3834	4352
	0.001	53	78	40
	0.01	7	6	5
Jersey	0	628,048	628,967	628,454
	0.0001	3897	2960	3469
	0.001	49	68	73
	0.01	8	6	6