

**Table S3.** Accuracy of genomic breeding values estimated for the three iterations investigated using a five-fold cross validation scheme.

<b>Trait</b>	<b>Iteration #</b>	<b>Mean</b>	<b>SD</b>
UTW	1	0.8366	<.000
UTW	2	0.8387	<.000
UTW	3	0.8368	<.000
TTW	1	0.7888	<.000
TTW	2	0.7934	0.001
TTW	3	0.7891	<.000

\*UTW, Untrimmed thigh weight; TTW, Trimmed thigh weight.