Supplementary Table 3. Summary statistics for the whole genome sequence of three Welsh sheep after strict quality control.

Animal ID	Uniquely aligned (Mb)	Heterozygous false negative error rate[a]	Heterozygous false positive error rate	Mean read depth	Estimated true heterozygosity[b]
DWM1[c]	30,767	0.422	4.95×10^{-5}	12	0.002773
TWM1[d]	27,245	0.533	4.50×10^{-5}	11	0.002836
WHSF1[e]	32,368	0.364	6.24×10^{-5}	13	0.002816

[a] Calculated as the proportion of heterozygous sites that are missed in the sequence data.

[b] True heterozygosity estimated from the observed heterozygosity and corrected for false negative error rate: True heterozygosity = observed heterozygosity/[1-False Negative Error Rate]).

[c] Dolgellau Welsh Mountain, [d] Tregaron Welsh Mountain, [e] Welsh Hardy Speckled Faced