



Supplementary Figure S5. Genome wide nucleotide diversity (π) for all breeds. LBG and LZG sample sets were randomly reduced to contain 3 samples per breed. To determine the significant differences between breed pairwise T-test with Bonferroni p-value adjustment was performed. Significance levels: 'ns' – non-significant, '*' – $p = [0.01, 0.05]$, '**' – $p = [0.001, 0.01]$, '***' – $p = [0, 0.001]$, '****' – $p < 0$. Abbreviations: BBL – Belgian Blue; GER – German angus; HLS – Holstein; HRF – Hereford; LBG – Latvian Brown; LMS – Limousin; LZG – Latvian Blue; TYG – Tyrolean grey.