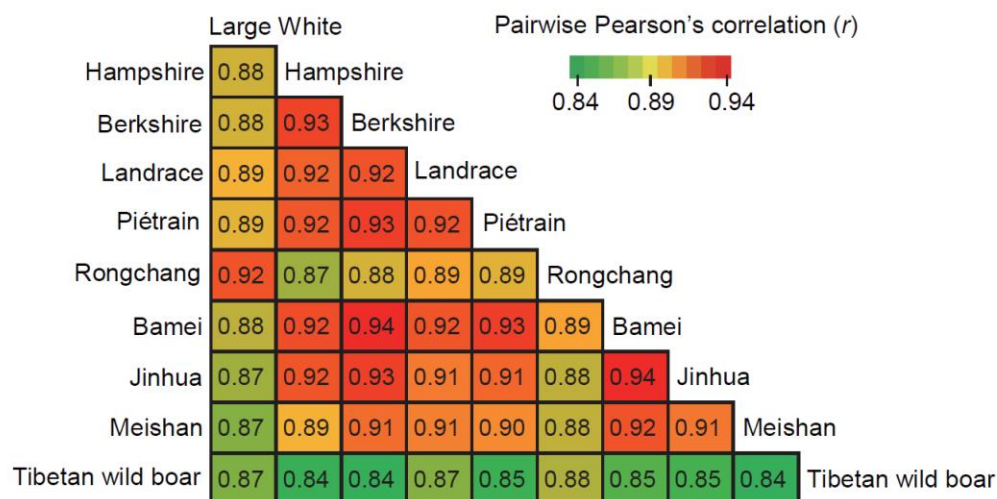


**b**



**Supplemental Fig. S31. Summary of missing sequences filled in reference assembly gaps. (a)** Length distribution of filled missing sequences across 5,317 existing gaps ( $\geq 50$  kb in length) in reference assembly. **(b)** Heat map of pairwise person's correlation ( $r$ ) of length of filled missing sequences between ten breed assemblies. The correlation rate between every two assemblies was calculated by 5,317 existing gaps ( $\geq 50$  kb in length) in reference genome.