



Supplemental Fig. S29. Comparisons of mapping ratio (a) and coverage ratio (b) of orphan reads against missing sequences between their respective assembly and other nine assemblies. Notably, the relatively lower mapping ratio of orphan reads derived from Tibetan wild boar assembly may be attributed to the idiosyncrasies of the different sequencing platform (i.e. the Illumina HiSeq 2000 used for Tibetan wild boar and HiSeq 2500 used for other nine breeds).