



Online Resource 2. Summary of sequencing and bioinformatic processing for Allegro Targeted Genotyping of 279 targets for 48 fecal swab samples collected from feral horses on Sable Island, Nova Scotia, Canada. Presented are the number of raw reads generated and then, as a proportion of each bar representing a sample, the number of reads retained following processing steps: trimming, alignment to the EquCab2 reference genome, the number of reads assigned to a target site before variant calling, and the number of reads after variant calling.

Article: Targeted genome-wide SNP genotyping in feral horses using non-invasive fecal swabs

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