

Table S1 Data Files

Contents	File Type	File Name(s)
Mapped reads	bam	<line>_GDL_WGS.bam*
Variant sites and genotypes	vcf	GDL_Ch<#>_SNPs.vcf* GDL_Ch<#>_Indels.vcf*
Uncallable genome intervals	bed	GDL_uncallable_intervals.bed*
Regions IBD between populations	bed	GDL_IBD_regions.bed*
Heterozygous blocks	bed	GDL_HetBlocks.bed*
Multi-species alignment	MAF	view at http://genome-mirror.cshl.edu/

* SRA #SRP050151