



Supplementary Material

In Silico Analysis of Genome Wide Non-Synonymous Single Nucleotide Polymorphisms in Indigenous Cattle Breeds of Pakistan

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**Supplementary Table S1. Distribution of
SNPs and InDels across chromosomes.**

**Supplementary Table S2. Number of variants
by their impact.**


**Supplementary Table S3. Results of the
deleterious nsSNP analysis by SIFT tool.**

**Supplementary Table S4. Gene Ontology
biological processes (bp) enrichment by
ClueGo.**

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