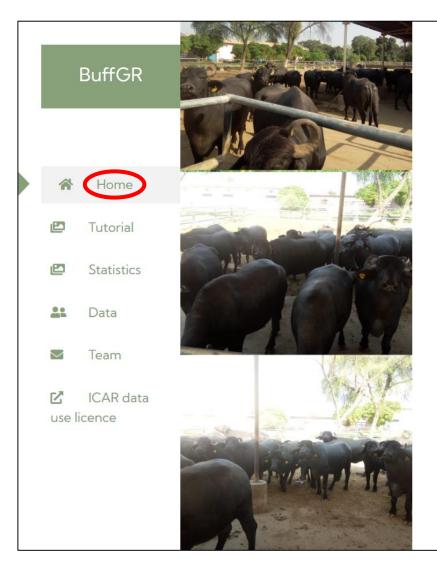
# HOMEPAGE: http://backlin.cabgrid.res.in/buffgr/



## apples ICAR

## Introduction

*BuffGR* is a first comprehensive web genomic resource of buffalo that catalogues 6028881 SNPs and 613403 InDels extracted from the set of 31 buffalo tissues while collectively a total of 7727122 SNPs and 634124 InDels were distributed in Murrah, Bangladesh, Jaffarabadi and Egyptian breeds with reference to Mediterranean breed. It also houses 4504691 SSR markers from all the breeds along with 1702 circRNAs, 37712 IncRNAs and 938 miRNAs. This comprehensive web-resource can widely used by the buffalo community across the globe in studies involving marker trait association, genetic diversity, as biomarker in adultery and breed traceability, in various diseases and other stress conditions. This resource can also be useful in buffalo improvement programs and disease/breed management.

Visitors: 0 0 0 0 0 7 1 6

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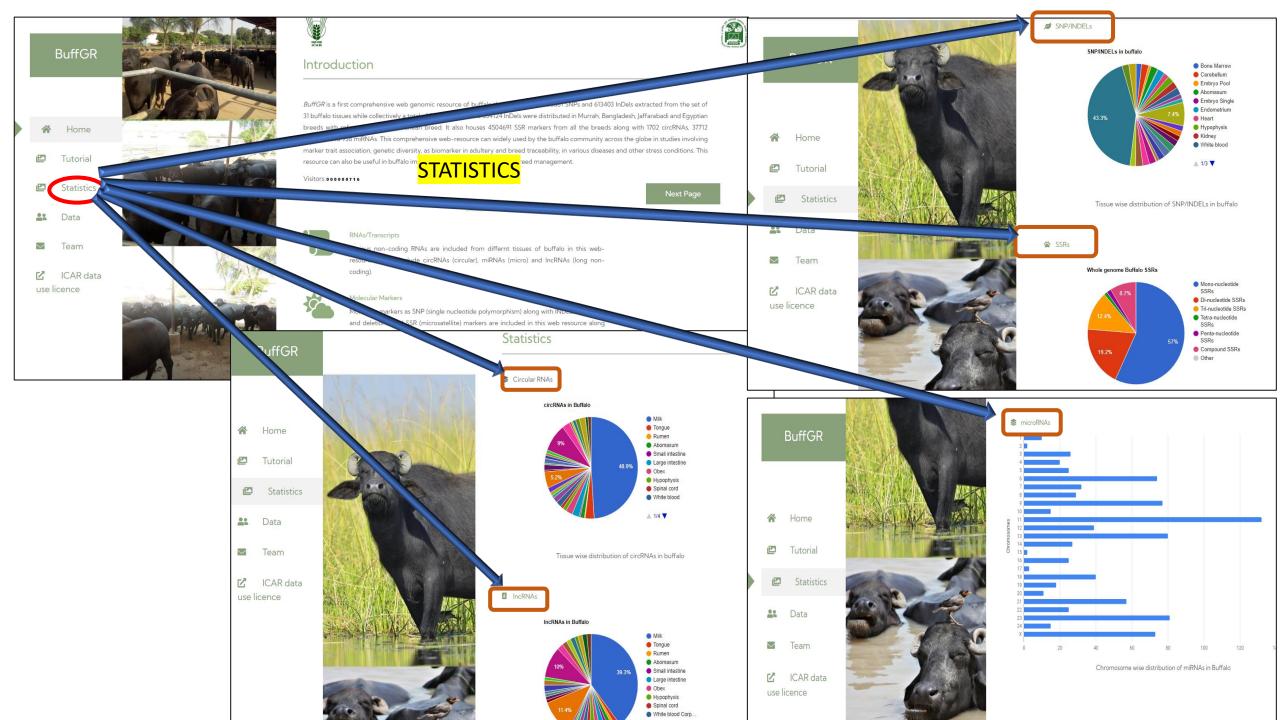
### RNAs/Transcripts

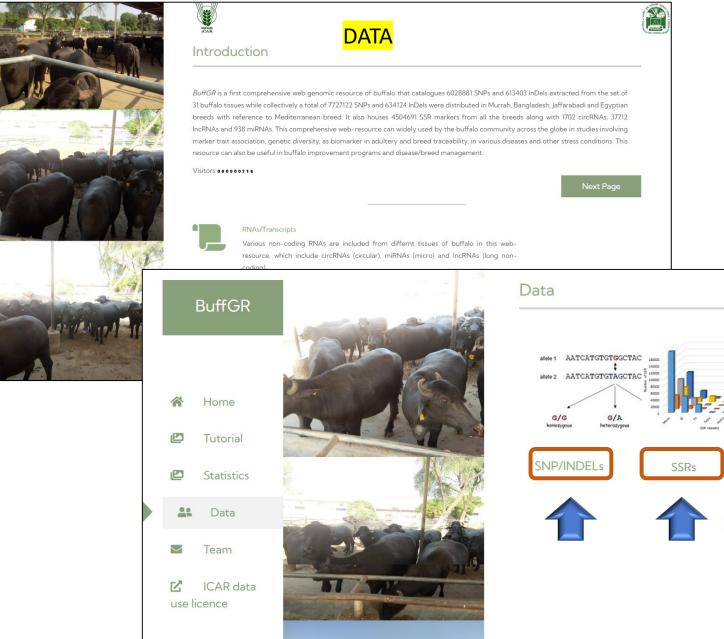
Various non-coding RNAs are included from differnt tissues of buffalo in this webresource, which include circRNAs (circular), miRNAs (micro) and IncRNAs (long noncoding).

# Ŝ

#### Molecular Markers

Molecular markers as SNP (single nucleotide polymorphism) along with INDELs (incertion and deletions) and SSR (microsatellite) markers are included in this web resource along with their distribution in various tissues and breeds of buffalo.





**BuffGR** 

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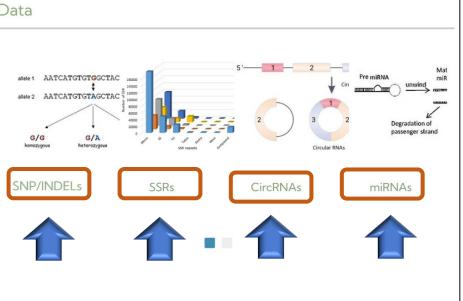
Team

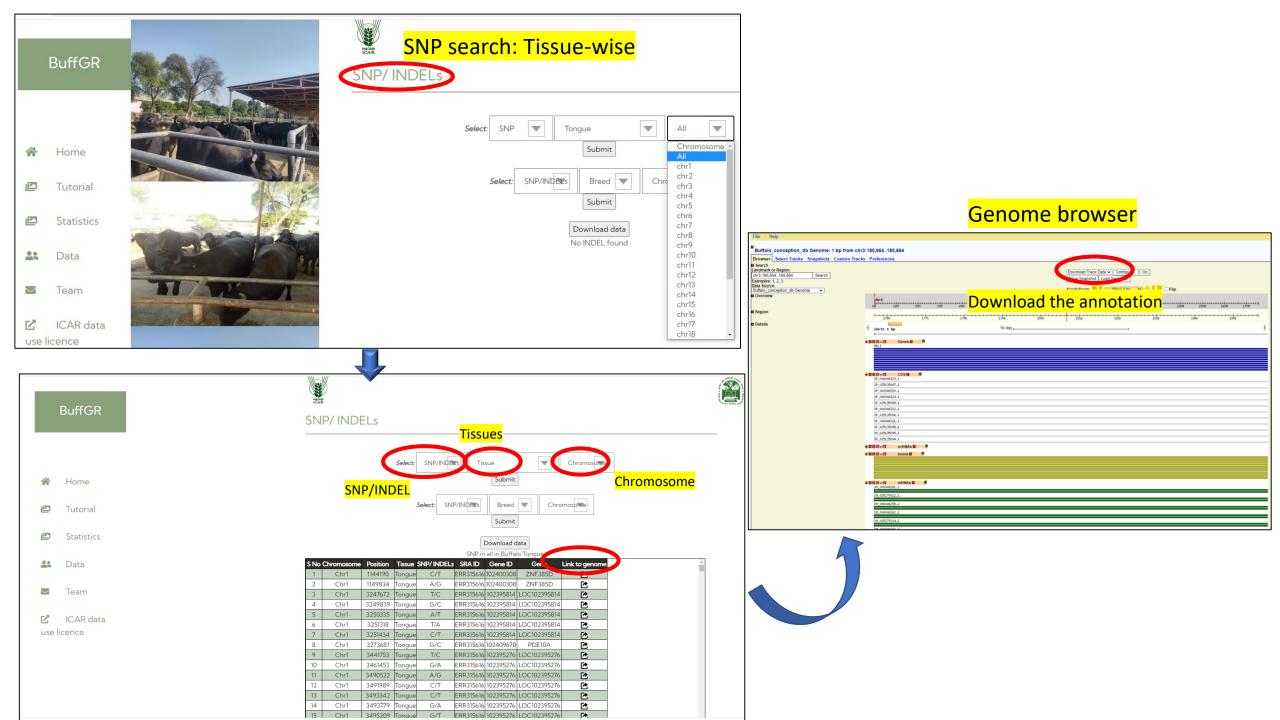
ICAR data

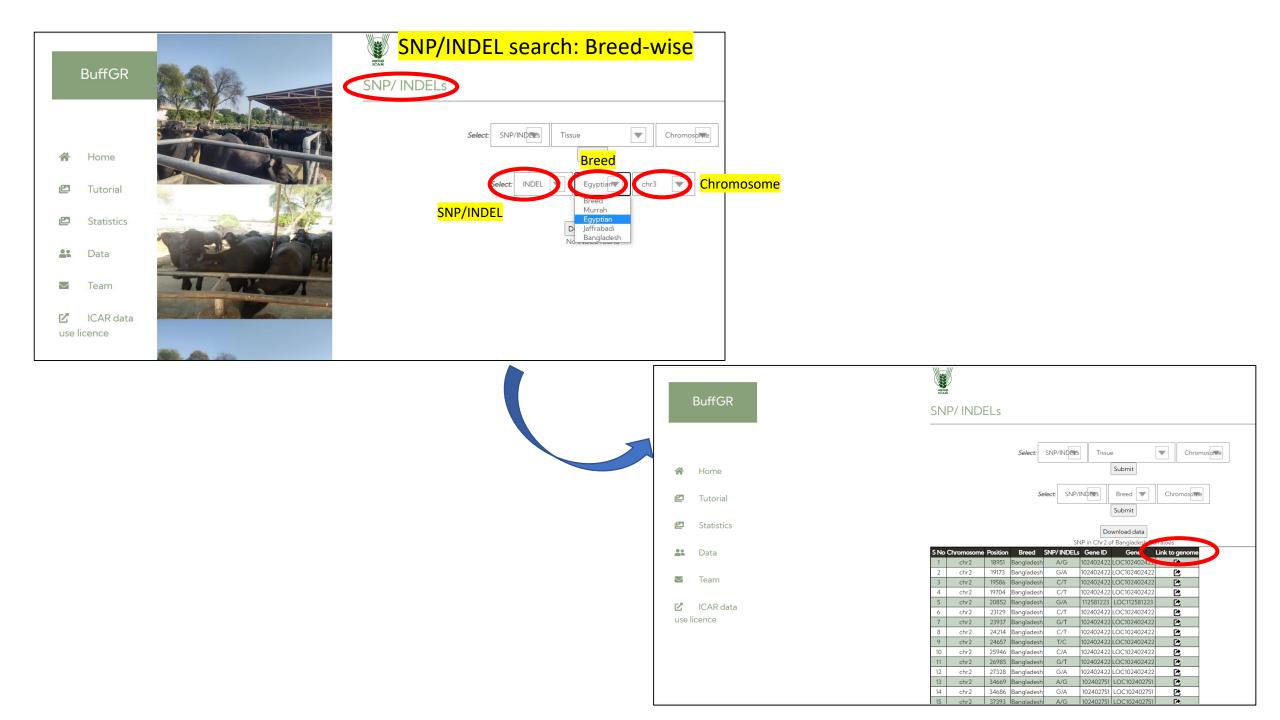
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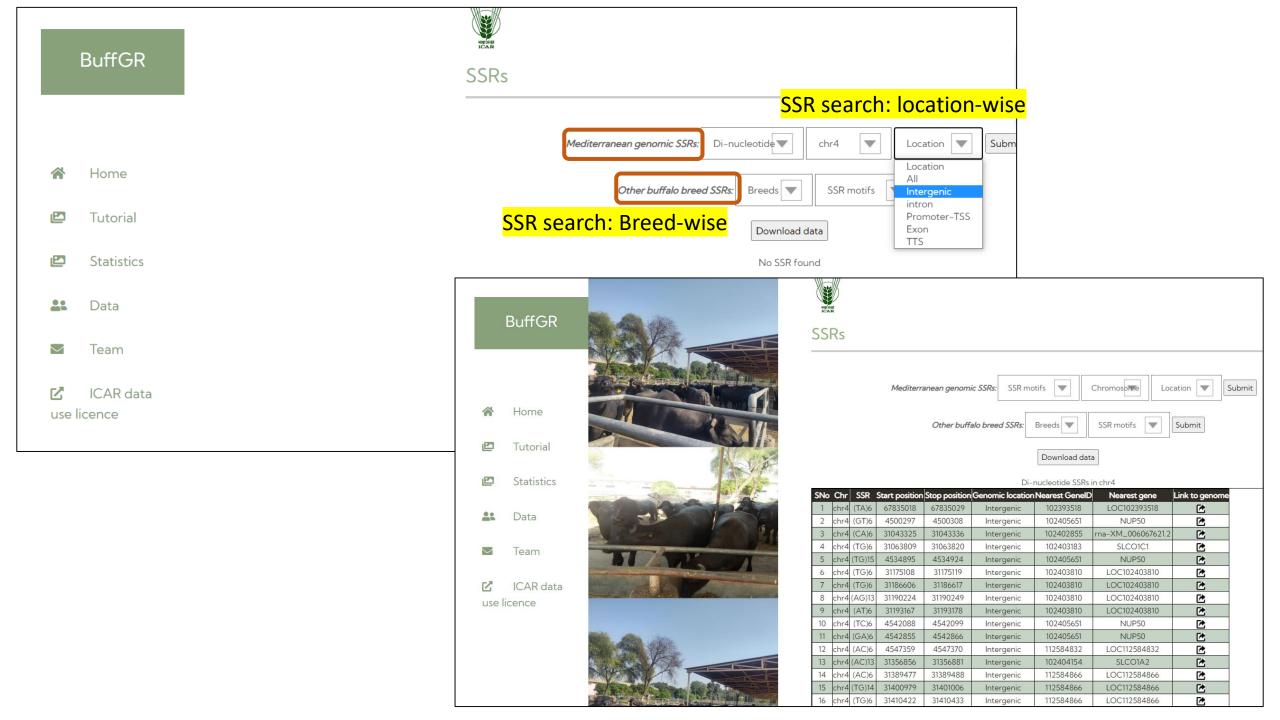
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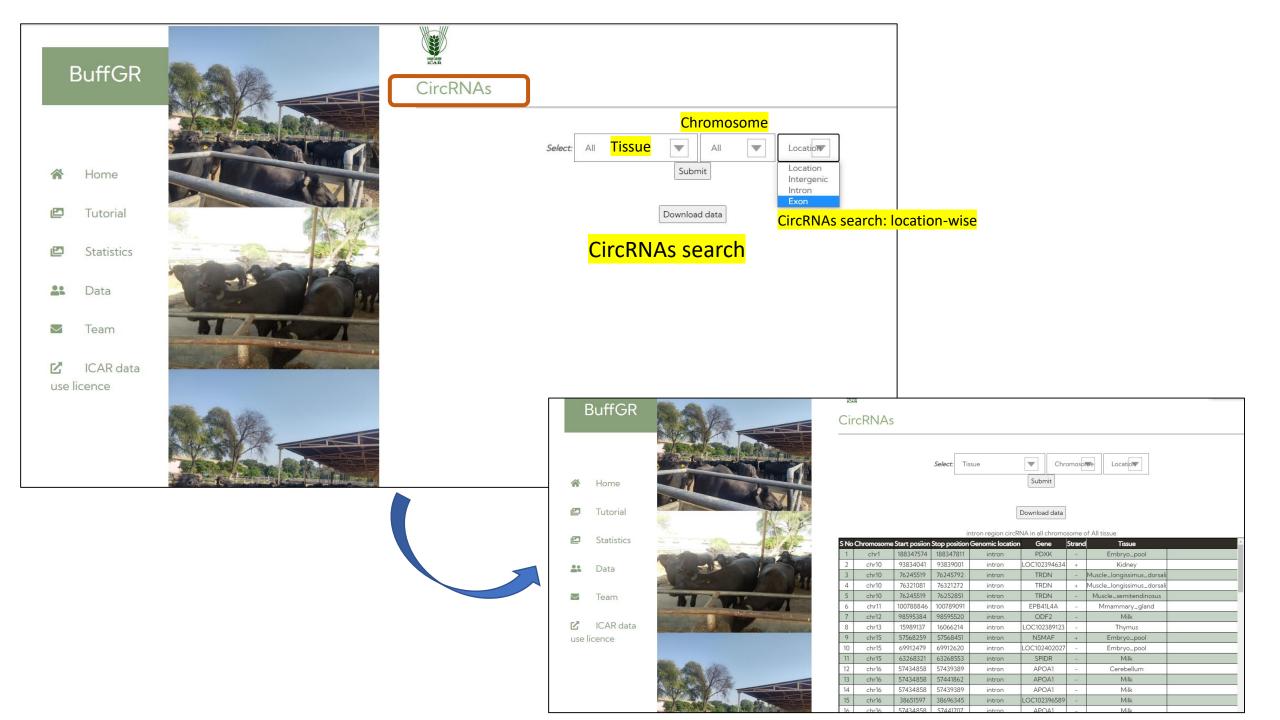
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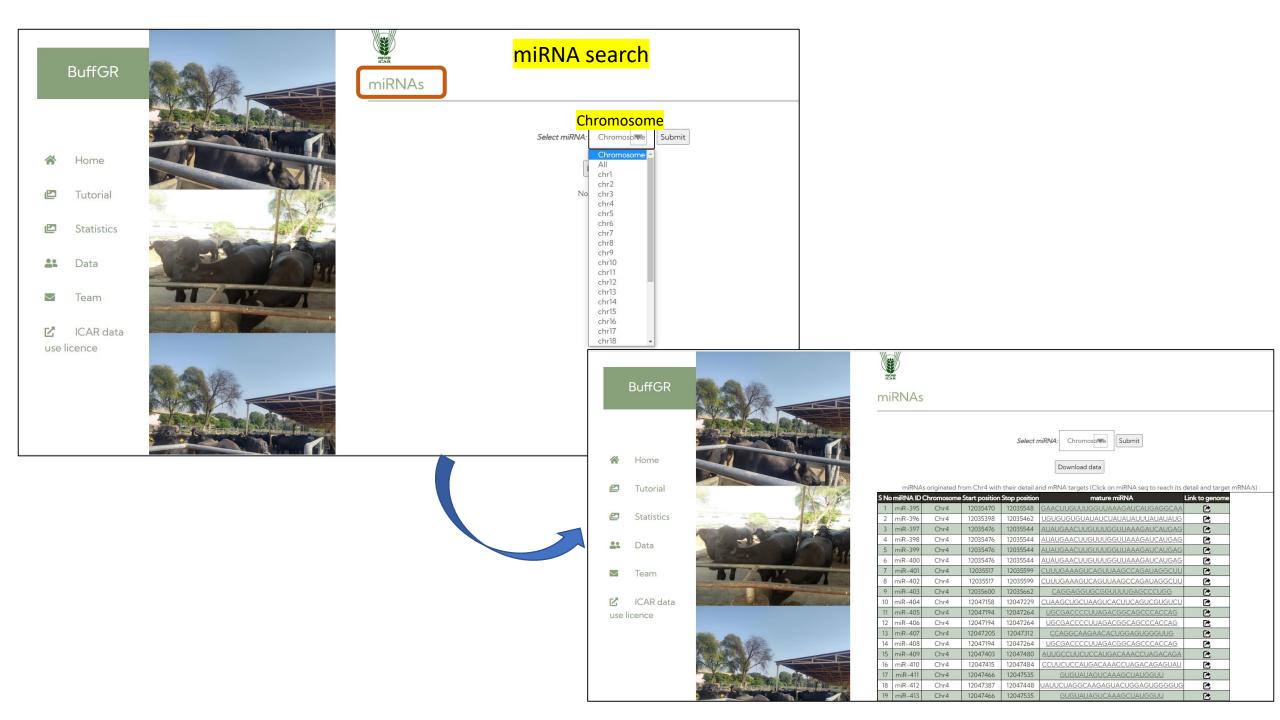


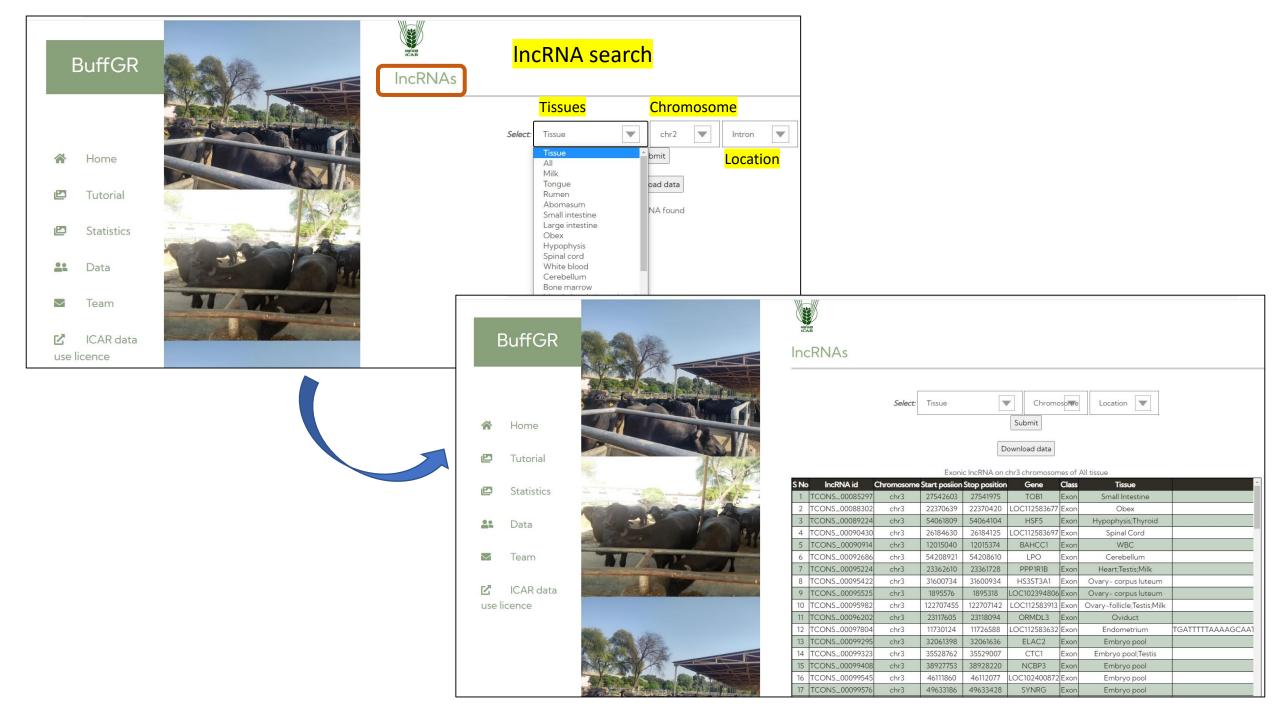


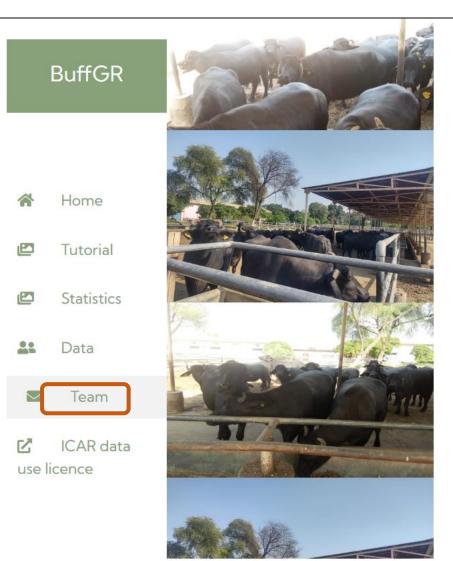












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