II. Oat variant database tutorials

1. The variant database can be accessed using the following link

http://database.oatpangenome.com/search/

Select Oatvar from the database list

2. Query by physical positions

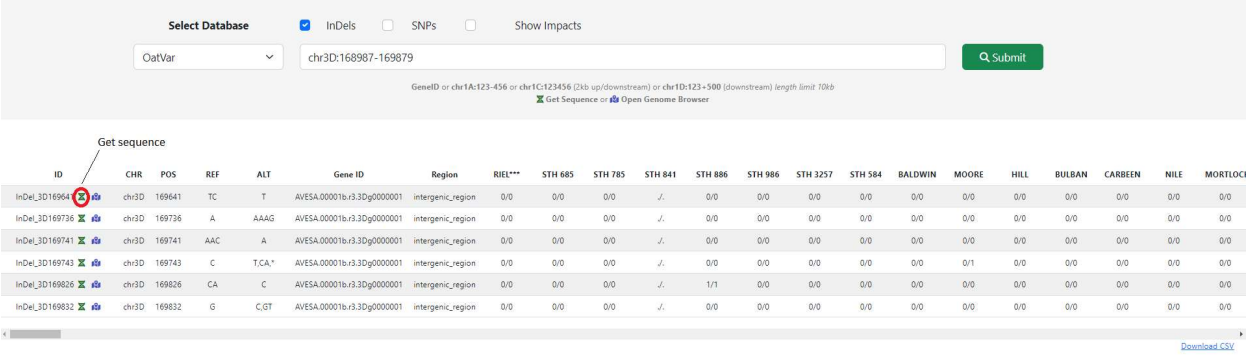
For physical position query, different format can be used

- Chromosome:start-end (chr1A:123-456)

- Chromosome:position to query 2kb up and downstream (chr1C:123456)

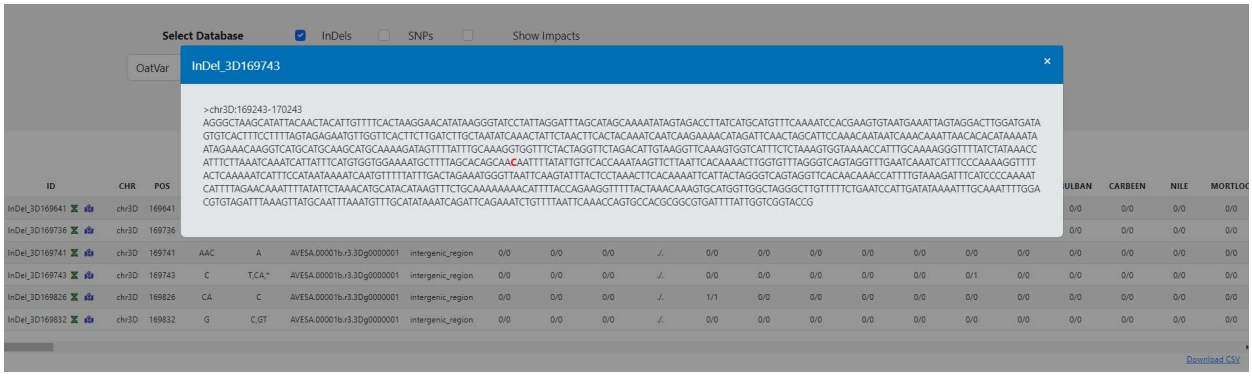
- Chromosome:start+length to query an exact region from start position (chr1D:123+500)

3. The result is display in a table format



4. The sequence around the variant can be retrieve using the sequence icon next to the variant ID

The sequence is pre-formated in fasta format and the variant is in red



5. The whole result table can be exported into csv format

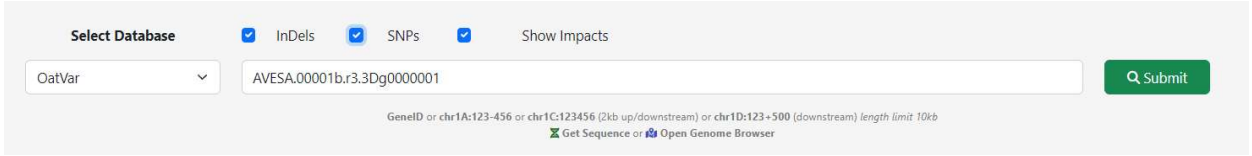
6. SNPs and annotations

By default, only Indels is pre-selected. SNPs and variant annotations data can be enable using the check boxes

7. Query by geneIDs

All variants within the gene regions can be query using gene IDs

The example gene ID format is AVESA.00001b.r3.3Dg0000001



8. Distinguish SNPs and Indels from the result

Indels and SNPs (if enable) can be distinguish using their variants ID on the left column

InDel_3D286921	chr3D	286921	GAAA	G,GAAAA,GAA,GAAAA	AVESA.00001b.r3.3Dg0000001	downstream_gene_variant	c.*86_*88delAAA:MODIFIER c.*88delA:MODIFIER c.*88dupA:MODIFIER c.*87_*88dupAA:MODIFIER c.*657_*659delAAA:MODIFIER c.*659delA:MODIFIER c.*659dupA:MODIFIER c.*658_*659dupAA:MODIFIER c.*1252_*1254delAAA:MODIFIER c.*1254delA:MODIFIER c.*1254dupA:MODIFIER c.*1253_*1254dupAA:MODIFIER c.-623_-621delAAA:MODIFIER c.-621delA:MODIFIER c.-621dupA:MODIFIER c.-622_-621dupAA:MODIFIER c.-650_-648delAAA:MODIFIER c.-648delA:MODIFIER c.-648dupA:MODIFIER c.-649_-648dupAA:MODIFIER c.*79_*81delAAA:MODIFIER c.*81delA:MODIFIER c.*81dupA:MODIFIER c.*80_*81dupAA:MODIFIER c.*1109_*1111delAAA:MODIFIER c.*1111delA:MODIFIER c.*1111dupA:MODIFIER c.*1110_*1111dupAA:MODIFIER	0|0	0|0	0/0	0/3	1/3	0|1	0/1	0|0	0/0
SNP_3D282413	chr3D	282413	T	C,*	AVESA.00001b.r3.3Dg0000001	upstream_gene_variant	c.-132T>C:MODIFIER	0/0	0/0	0/0	2/2	1|1	1|1	0/0	0/0	0/0