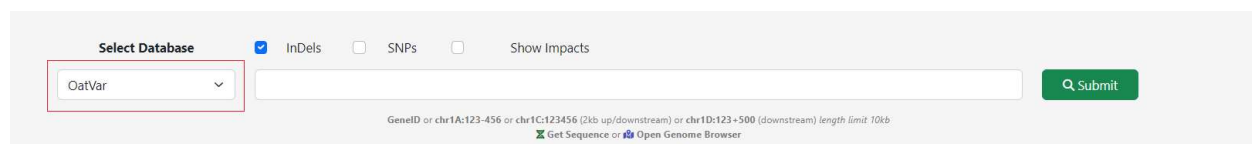


II. Oat variant database tutorials

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

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

Select Oatvar from the database list



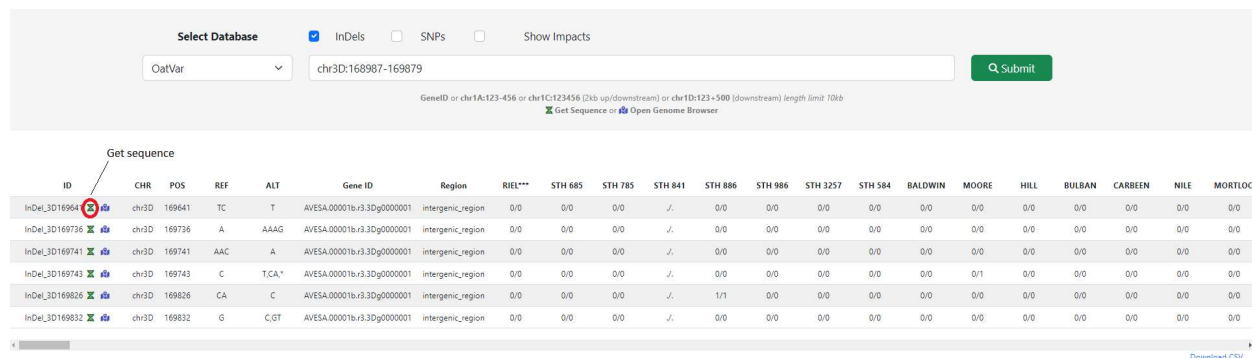
2. Query by physical positions

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



ID	CHR	POS	REF	ALT	Gene ID	Region	RIEL***	STH 685	STH 785	STH 841	STH 886	STH 986	STH 3257	STH 584	BALDWIN	MOORE	HILL	BULBAN	CARBEEN	NILE	MORTLOCI
InDel_3D16964	chr3D	169641	TC	T	AVESA.00001b.v3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
InDel_3D169736	chr3D	169736	A	AAAG	AVESA.00001b.v3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
InDel_3D169741	chr3D	169741	AAC	A	AVESA.00001b.v3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
InDel_3D169743	chr3D	169743	C	T.CA*	AVESA.00001b.v3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	0/0	0/0	0/0	0/0	0/0	0/1	0/0	0/0	0/0	0/0	0/0
InDel_3D169826	chr3D	169826	CA	C	AVESA.00001b.v3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0
InDel_3D169832	chr3D	169832	G	C.GT	AVESA.00001b.v3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0

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

Select Database ☒ InDels ☐ SNPs ☐ Show Impacts

OatVar InDel_3D169743

>chr3D:169243-170243
AGGGCTAAGCATATACAACTACATGTTTTCACATAAGGAACATATAAGGGTATCTATTAGGATTAGCATAGCAAAATATAGTAGACCTTATCATGCTGTTTCAAATCCACGAAGTGAATGAANTAGTAGGACTTGGATGATA
GTGTCACCTTCTCTTAGTAGAAGTGTGGTTCACCTCTTGATCTTGCTAATCAAACTATCTAACTTCACTACAAATCAATCAAGAAAACATAGATTCACTAGCATCCAAACAATAATCAACAATAACACACATAAATA
ATAGAAACAAGTGCATGCAAGCATGCAAAAGATAGTTTATTGCAAGGTGGTCTCTACTAGTCTAGACATGTAAGGTTCAGAGTGGTTCATTCTCTAAAGTGTAAACCATTTGCAAAAGGGTTTATCTATAAAC
ATTCTTAAATCAATCATTTATTCATGTGGTGGAAATGCTTTTAGCAGCAGCAATTTTATATGTTCACCAATAAGTCTTAAATCACAACAACTTGGTGTGGTGGTGTGATCAAAATCATTTCCCAAAAGGTTT
ACTCAAAATCATTTCCATAAATAAATCAATGTTTATTGACTAGAAATGGGTAAATCAAGTATTACTCTAACTTCACTACAAATCATTAAGGTCAGTAGGTTTCAACAACAACTTTTGTAAAGATTTCATCCCAAAAT
CATTTAGAACAAATTTTATCTAAACATGCATACATAAGTTTCTGCAAAAAAACATTTTACCAAGGTTTCTACTAAACAAAGTGCATGTTGGCTAGGGCTTGTCTTCTGAATCAATTGATATAAATTTGCAAAATTTGGGA
CGTGTAGATTAAAGTTATGCAATTTAAATGTTTGCATATAATCAGATTCAGAAATCTGTTTAAATCAAAACAGTCCACGCGCGTGATTATTGGTCGTACCG

ID	CHR	POS																	ULBAN	CARBEEN	NILE	MORTLOX
InDel_3D169641	chr3D	169641																	0/0	0/0	0/0	0/0
InDel_3D169736	chr3D	169736																	0/0	0/0	0/0	0/0
InDel_3D169741	chr3D	169741	AAC	A	AVESA.00001b.r3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0			
InDel_3D169743	chr3D	169743	C	T.CA*	AVESA.00001b.r3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	0/0	0/0	0/0	0/0	0/0	0/1	0/0	0/0	0/0			
InDel_3D169826	chr3D	169826	CA	C	AVESA.00001b.r3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0			
InDel_3D169832	chr3D	169832	G	C.GT	AVESA.00001b.r3.3Dg0000001	intergenic_region	0/0	0/0	0/0	./.	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0			

[Download CSV](#)

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

0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0 0/0

[Download CSV](#)

6. SNPs and annotations

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

Select Database ☒ InDels ☐ SNPs ☐ Show Impacts

OatVar

[Get Sequence](#) or [Open Genome Browser](#)

GeneID or chr1A:123-456 or chr1C:123456 (2kb up/downstream) or chr1D:123+500 (downstream) length limit 10kb

[Submit](#)

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

Select Database ☒ InDels ☒ SNPs ☒ Show Impacts

OatVar

[Get Sequence](#) or [Open Genome Browser](#)

GeneID or chr1A:123-456 or chr1C:123456 (2kb up/downstream) or chr1D:123+500 (downstream) length limit 10kb

[Submit](#)

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 AA	AVESA.00001b.r3.3Dg0000001	downstream_gene_variant	c*86_*88delAAA-MODIFIER c*88delA-MODIFIER c*88dupA-MODIFIER c*87_*88dupAAA-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_*91delAAA-MODIFIER c*81delA-MODIFIER c*81dupA-MODIFIER c*80_*91dupAA-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