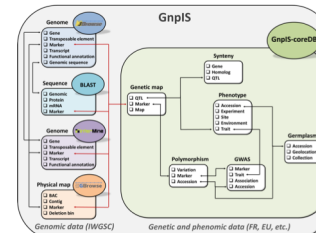
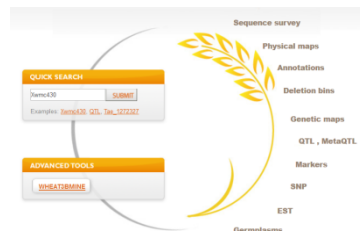


How to provide updated gene annotations for inclusion in IWGSC RefSeq annotation v2.0

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Process

1. Follow the guidelines to generate your GFF3
2. Send your file to GDEC
3. File validation by GDEC
4. GDEC send the data to URGI to display in the next release in the browser

<https://wheat-urgi.versailles.inra.fr/Seq-Repository/Manually-curated-genes>

Guidelines

CONTACTS

- Questions about gene annotation and **recipients of the file**: [Hélène Rimbert](#) , [Frédéric Choulet](#) .
- Questions about the browser and the website: [Thomas Letellier](#) , [Michael Alaux](#) .

GUIDELINES

- The manually curated genes must be transferred in GFF3 format following The Sequence Ontology specifications. See description [here](#) .
- Please make sure your GFF3 file contains at least gene/mRNA/exon/CDS features with uniq ID and Parent attributes. The only case where an ID is not necessary concerns CDS & CDS features if they have Parent attribute defined.
- All attributes and feature types are case sensitive! i.e. Id is not the same as ID.
- Please make sure the chromosome names you are using are the same as the official release IWGSC RefSeq v1 annotations and sequences.
- Please, be as precise and complete as possible. Every feature which is not described in your annotation compared to the previous one will be lost.
- Once transferred, your file will be validated and added to the [browser](#) in the next release.

DOWNLOAD

[example of minimal gff3.txt \(1.90 kB\)](#)



Other needs ?

If needed, we can also set-up a software to help the teams without bioinformatics facilities to perform their manual annotation:
Web Apollo

