Adding a Variant Annotation Database

Click the **green plus** (+) icon next to the *Variant annotations* section header on the library file management page. Alternatively, click the **Add library file** button and choose **Variant annotations** from the *Library type* drop-down list.

If you are using a human - hg19 assembly, variant annotation databases from various sources will appear in the *Variant annotation* drop-down list (Figure 1). Available variant annotation database sources include:

- dbSNP
- Kaviar
- NHLBI Variant Server
- 1000 Genomes

Multiple versions of the above databases are available. For human - hg38, only dbSNP is currently available. This list is periodically updated.

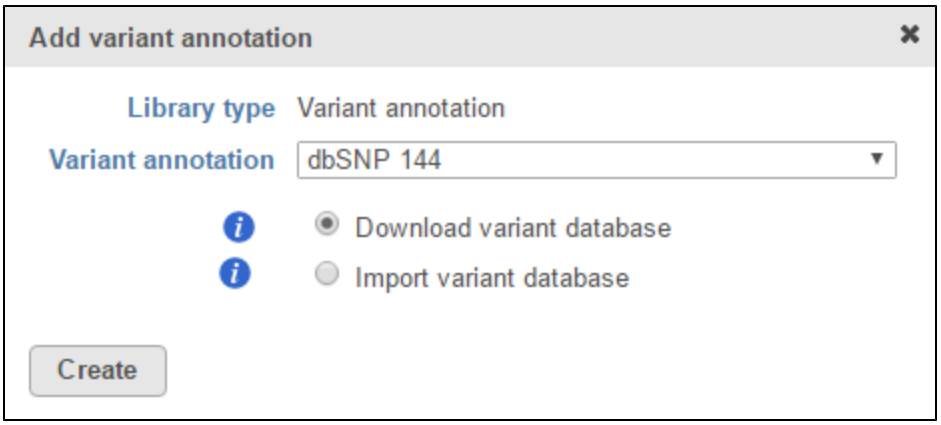

Figure 1. For human - hg19, automatic downloads of various variant annotation databases are available from the Partek repository

Choose a database from the drop-down list, select the **Download variant database** radio button and click **Create**.

If you prefer to add a custom variant annotation database, perhaps from another source or 'gold-standard' validated variants, choose **Add variant database** from the *Variant annotation* drop-down list (Figure 2). Name the variant annotation database by typing into the *Custom Name* box and click **Creat** . Characters such as $ * | \ : " < > ? / % cannot be used in custom names. A variant annotation database can be added from the *Partek Flow Server*, *My Computer* or a *URL* download link. The behavior of each option is similar to when importing a reference sequence (see *Adding a Reference Sequence*). When browsing for files on the Partek Flow server, only the files with relevant file extensions will be visible (.vcf and various compressed formats).

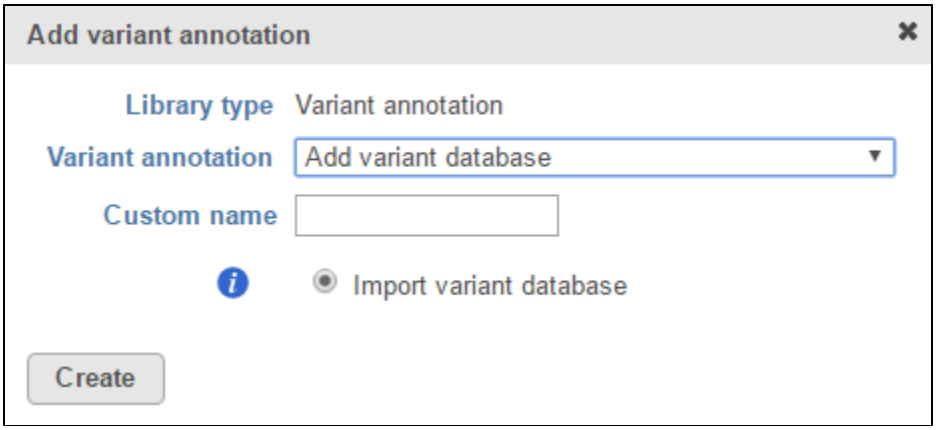

Figure 2. Add a custom variant annotation database

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

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