Starting with a list of SNPs

A list of SNPs using dbSNP IDs can be imported as a text file and associated with an annotation file as described for a list of genes. The annotation file you use to annotate the SNPs should minimally contain the chromosome number and physical position of each locus.

Novel SNPs or SNPs that are not found in your annotation source must be imported as a region list. For this, follow the procedure outlined in Starting with a list of genomic regions, but use the SNP name in place of a region name.

Annotating SNPs with genes

Starting with a list of SNPs that have been associated with genomic loci using an annotation file and assigned a species with genome build, you can use *Find Overlapping Genes* to annotate these SNPs with the closest genes.

- Select **Tools** from the main toolbar
- Select **Find Overlapping Genes** (Figure 1)

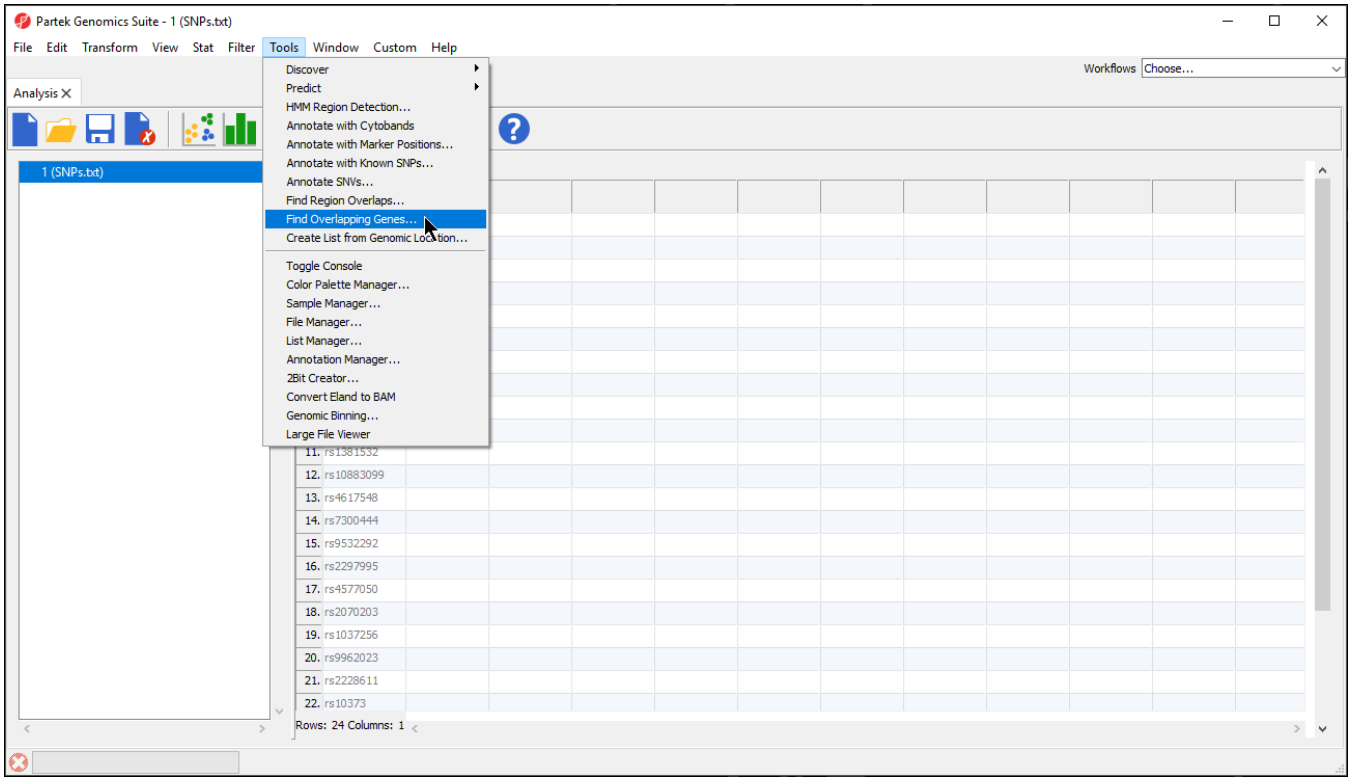

Figure 4. Adding overlapping genes to a SNP list

- Select **Add a New Column with the Gene Nearest to the Region** from the method dialog

The *Report Regions from the specified database* dialog will open.

- Select your preferred database. Be sure to match the species and genome build of your SNP list
- Select **OK**

This will add 3 columns to the list of SNPs spreadsheet including Nearest Feature, which will indicate the nearest gene and strand (Figure 2).

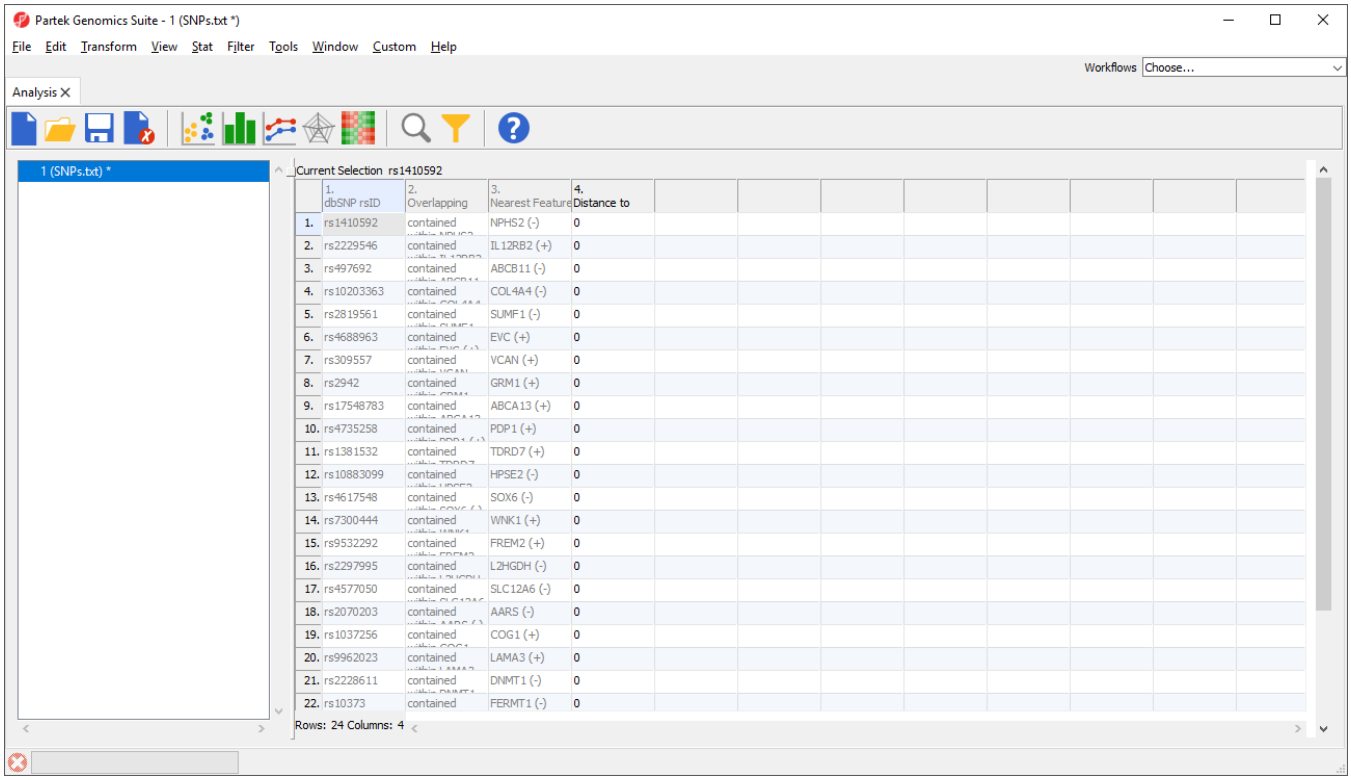

Figure 5. Find Overlapping Genes adds three columns to a SNP list: overlapping features, nearest feature, and distance to nearest feature (bps)

To allow gene list operations such as GO Enrichment or Pathway Enrichment to be performed on the SNP list, we can set the *Nearest Feature* column as the gene symbol column for the spreadsheet.

- Right click the spreadsheet in the spreadsheet tree
- Select **Properties** from the pop-up menu
- Select **Gene symbol instead of Marker ID**
- Select **Feature in column** and select **Nearest Feature** (Figure 3)
- Select **OK**

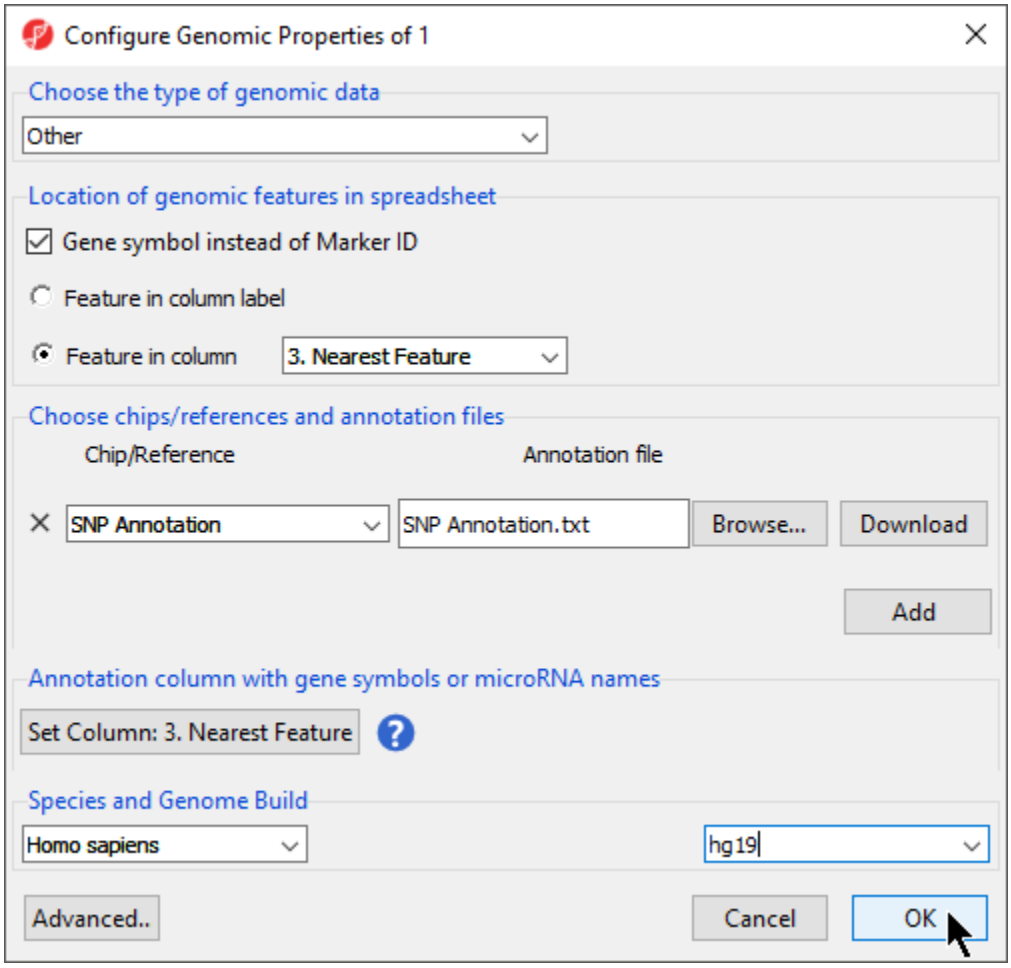

Figure 6. Setting Nearest Feature as the gene symbol allows gene list functions to be performed on a SNP list

Annotating a Partek Genomics Suite-generated SNP list with SNVs

If you have a SNP spreadsheet that was generated using Partek Genomics Suite (not imported as a .txt file), you can annotate the SNP list with gene, transcript, exon, and information about the predicted effect of the SNPs.

- Select **Tools** from the main command toolbar
- Select **Annotate SNVs**

« Starting with a list of genomic regions Importing a BED file »

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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