

Starting with a list of SNPs

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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)

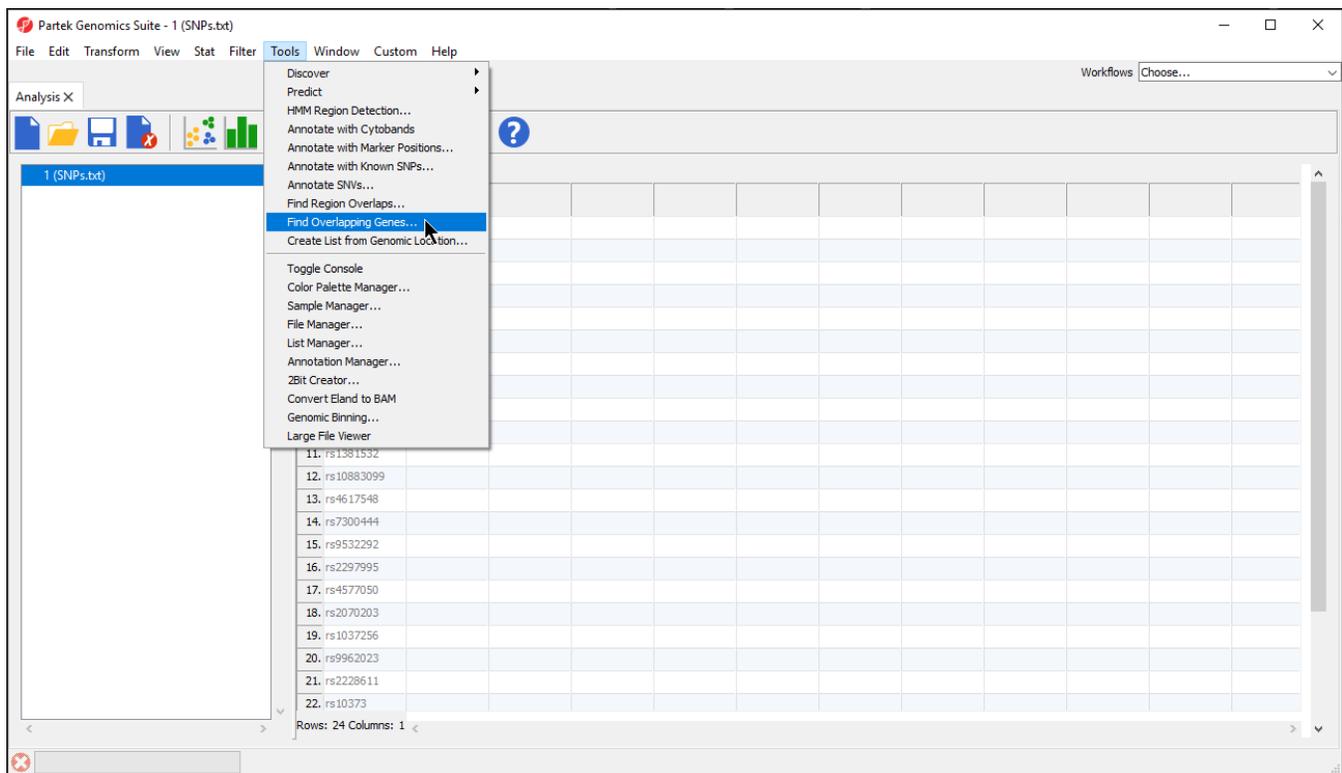


Figure 4. Adding overlapping genes to a SNP list

- 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).

Partek Genomics Suite - 1 (SNPs.txt *)

File Edit Transform View Stat Filter Tools Window Custom Help

Workflows Choose...

Analysis X

1 (SNPs.txt) *

Current Selection rs1410592

1.	2.	3.	4.						
dbSNP rsID	Overlapping	Nearest Feature	Distance to						
1. rs1410592	contained	NPHS2 (-)	0						
2. rs2229546	contained	IL12RB2 (+)	0						
3. rs497692	contained	ABCB11 (-)	0						
4. rs10203363	contained	COL4A4 (-)	0						
5. rs2819561	contained	SUMF1 (-)	0						
6. rs4688963	contained	EVC (+)	0						
7. rs309557	contained	VCAN (+)	0						
8. rs2942	contained	GRM1 (+)	0						
9. rs17548783	contained	ABCA13 (+)	0						
10. rs4735258	contained	PDP1 (+)	0						
11. rs1381532	contained	TDRD7 (+)	0						
12. rs10883099	contained	HPSE2 (-)	0						
13. rs4617548	contained	SOX6 (-)	0						
14. rs7300444	contained	WINK1 (+)	0						
15. rs9532292	contained	FREM2 (+)	0						
16. rs2297995	contained	L2HGDH (-)	0						
17. rs4577050	contained	SLC12A6 (-)	0						
18. rs2070203	contained	AARS (-)	0						
19. rs1037256	contained	COG1 (+)	0						
20. rs9962023	contained	LAMA3 (+)	0						
21. rs2228611	contained	DNMT1 (-)	0						
22. rs10373	contained	FERMT1 (-)	0						

Rows: 24 Columns: 4

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**

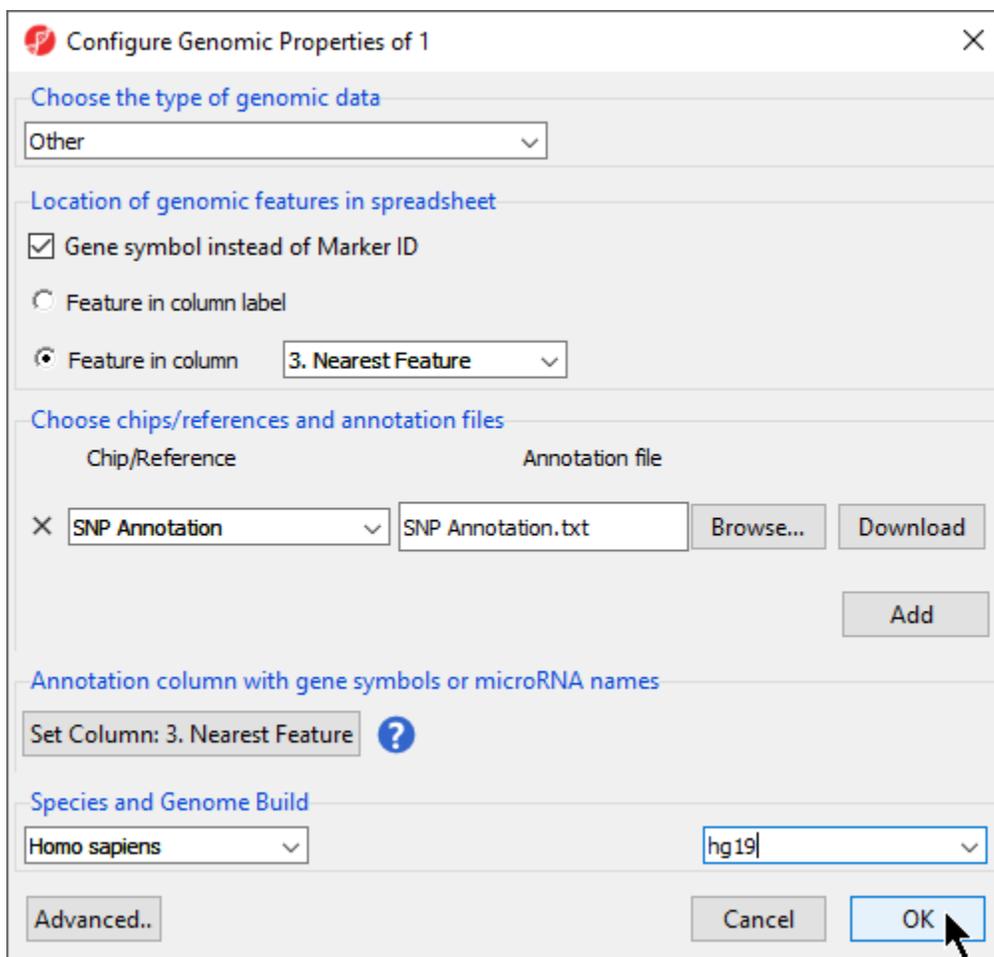


Figure 6. Setting Nearest Feature as the gene symbol allows gene list functions to be performed on a SNP list

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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