

SNPFileSorter Documentation

Module name:SNPFileSorterDescription:Sorts SNPs by chromosome and physical locationAuthor:David Twomey, gp-help@broad.mit.edu

Summary

The SNPFileSorter module sorts SNPs by chromosome and physical location. Sorting the SNPs is a prerequisite for using certain other tools, such as SNPViewer.

- The input file can be any of the following GenePattern files: .snp, .xcn, .cn, or .loh. If you used the SNPFileCreator module to create a sorted .snp file, you do not need to resort the SNPs.
- The output file is the input GenePattern file, sorted by chromosome and physical location.
- Features (rows) in the input file that do not have genome location information are ignored; they
 are not included in the output file. The stdout.txt file lists all rows that were ignored. The
 stderr.txt file contains an error message for each row that was ignored.

References

None.

Parameters	
Name	Description
snp filename	GenePattern .snp (allele-specific or non-specific), .xcn, .cn. or .loh file.
output file	Name of the output file. By default, the output file is named <i>input-file</i> .sorted.snp. If you are sorting a .cn or .loh file, change the default file extension.

Return Value

1. .snp, .xcn, .cn, or .loh file (sorted by chromosome and physical location)

Platform Dependencies

Task type:	SNP Analysis
CPU type:	any
OS:	any
Language:	R