

# **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