



## LOHPaired Documentation

**Description:** Detects Loss of Heterozygosity (LOH)  
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### Summary

The LOHPaired module detects loss of heterozygosity (LOH). It takes as input a GenePattern .snp file that contains paired normal-target samples with genotype calls. (LOHPaired accepts only non-allele-specific .snp files; .snp files that contain one intensity value per probe.) It returns as output a GenePattern .loh file that contains, for each probe, the LOH calls for each array pair.

LOH call values are:

L	LOH: AB in normal and A or B in tumor
R	Retention: AB in both normal and tumor or No Call in normal and AB in tumor
C	Conflict: A or B in normal and AB in tumor
N	Non-informative call: A or B in normal No call: No Call in normal or tumor

Or, in other words:

		Tumor			
		A	B	AB	No Call
Normal	A	N	N	C	N
	B	N	N	C	N
	AB	L	L	R	N
	No Call	N	N	R	N

### References

1. Ming Lin, Lee-Jen Wei, William R. Sellers, Marshall Lieberfarb, Wing Hung Wong\*, and Cheng Li\* (2004). dChipSNP: Significance Curve and Clustering of SNP-Array-Based Loss-of-Heterozygosity Data. *Bioinformatics*. 20: 1233-1240.

### Parameters

Name	Description
input filename	GenePattern .snp file that contains paired normal-target samples and genotype calls. Use the SNPFileCreator module to create a GenePattern .snp file from a set of CEL files generated using an Affymetrix SNP chip.

# GenePattern

**Note:** LOHPaired accepts only non-allele-specific .snp files (.snp files that contain one intensity value per probe).

sample info  
filename

Name of a sample information file (for example, a dChip format sample information file). This is a tab-delimited file where

- The first row contains labels identifying the content of each column.
- Each remaining row describes one sample.

LOH detection requires columns with the following label, all other columns are ignored:

- **Paired:** indicates the normal/target pairs. For the normal array, *Paired* is Yes; for the target sample, *Paired* is the array name of the normal sample.
- **Array:** contains the array name.

output file

Name of the output file. By default, the output file is named *input-file.loh*.

## Output Files

1. .loh file (LOH call per probe per normal-target sample pair)

## Platform Dependencies

<b>Module type:</b>	SNP Analysis
<b>CPU type:</b>	any
<b>OS:</b>	any
<b>Language:</b>	Java