YSEQ
DNA Origins Project

Xhromato

TUTORIAL

1

Upload the two DNA files (each smaller than 50 MB) that you would like to compare. Make sure that they are saved in a **23andMe**, **AncestryDNA**, **MyHeritage**, **FTDNA Family Finder** or **VCF** format.
You can upload either two hg38 or two hg19 files.

2

Once you uploaded both files you can **analyze your results**:

Green: full match (both alleles are identical)
Yellow: half match (one allele is identical)
Red: mismatch (both alleles are different)
Blue bars: significant matching segments
cM value: total amount of matching DNA in centimorgans
Relationship: estimated relationship based on the cM value
View match on DNA Painter: visualized results

Analyze specific SNP regions by clicking on the chromosome or the blue bar. You can 1) download all SNPs for which both files contain a genotype in this segment, 2) download only the mismatching SNPs, or 3) view this region on the UCSC map or for the Y chromosome on ybrowse.org.

3

You have the option to change our default **settings**:

Remove Deaminations: remove deaminations (especially for ancient DNA)
Max gap (bp) allowed in segment: lowering this splits segments containing gaps in coverage that exceed the threshold, raising this consolidates them
Min matching segment length: shortest segment length (in centimorgans) considered as a match
Min consecutive half/full matching SNPs to consider as match no matter what: minimum number of consecutive matching SNPs required to automatically be considered a match (forgoing probabilistic determination)
Min mismatch rate (%) to consider as mismatch no matter what: the error rate at which a block is automatically considered a mismatch (forgoing probabilistic determination)
Expected mismatch rate (%) if actual mismatch: expected error rate when there is actually no match
Expected mismatch rate if actual match: expected error rate when a match actually exists

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4

To refresh the page and start a new comparison, click on ‘Home’.

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https://lab.yseq.net/chromato