Getting the genes from regions of homozygosity using the UCSC browser

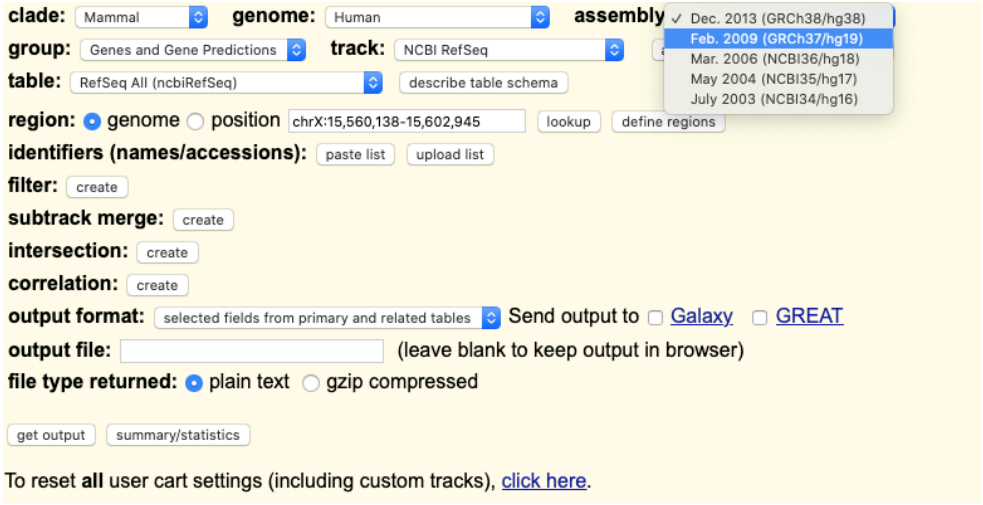
For use with SimulConsult's Regions of Homozygosity feature

The regions of homozygosity are typically reported as a BED file (Browser Extensible Data), with many lines in one of the following 2 types of format:

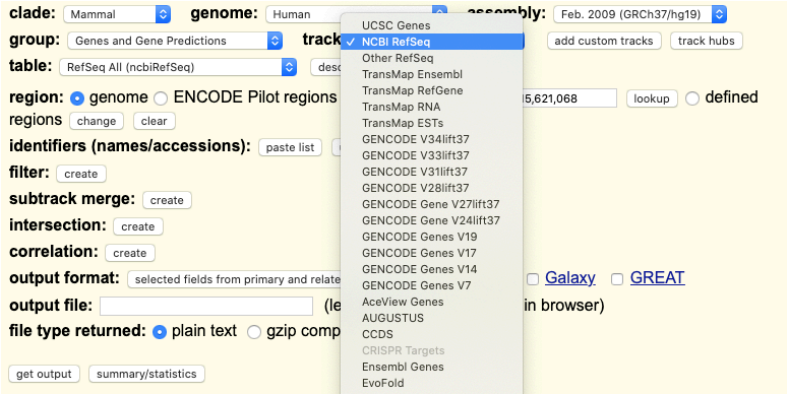
chr2 27300000 27330000 or chr2:27,300,000-27,330,000

You can use either of the 2 formats above to get a list of genes using the UCSC Table Browser using the following steps:

1. Go to https://genome.ucsc.edu/cgi-bin/hgTables. If you've used this page before, your browser will save your settings in cookies and these will persist even if you refresh the page.
2. In "**assembly**" choose the desired assembly, typically Dec. 2013 (GRCh38/hg38) or Feb. 2009 (GRCh37/hg19). The example shown uses GRCh38/hg38.

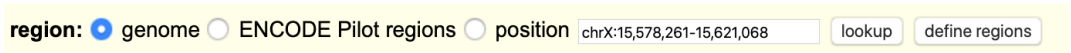


3. In "**track**" choose "NCBI RefSeq"

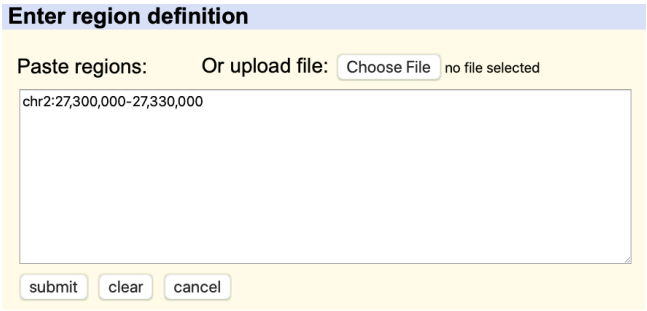


4. In "**region**":

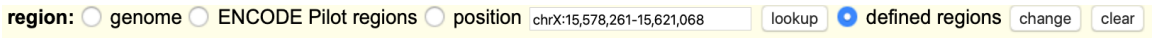
    a) On the first run click the "**define regions**" button



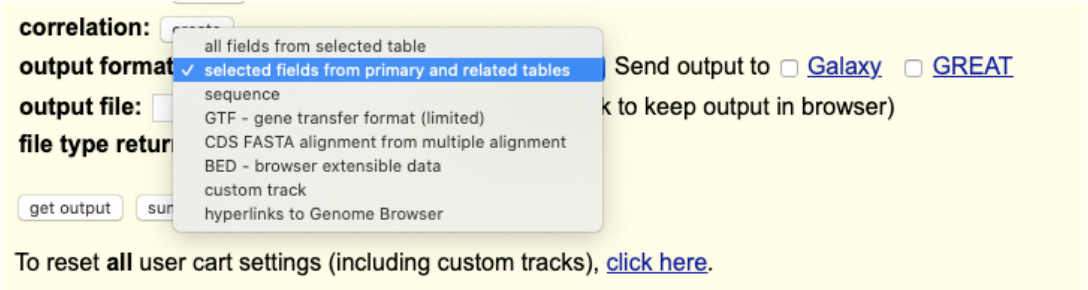
    On the resulting screen, paste many lines of regions such as " chr2:27,300,000-27,330,000" into the text area.



    b) Note: On subsequent runs, "**defined regions**" will be remembered by the browser and already selected; choose "**change**" or "**clear**" if you want to change the regions.

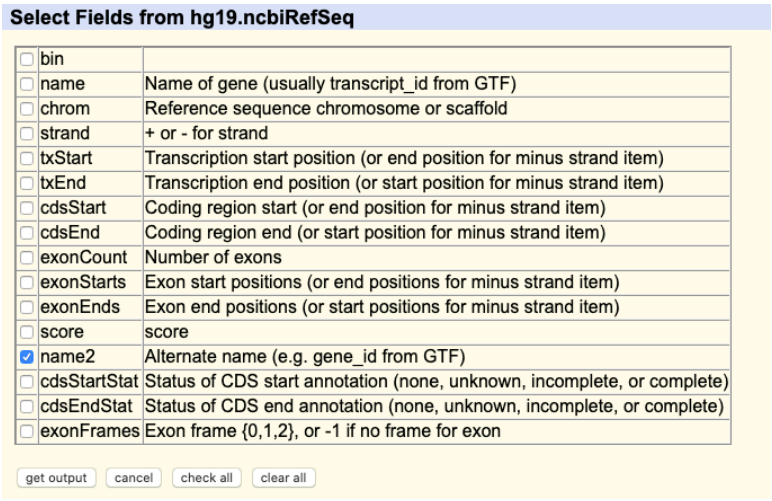


5. Click the "**submit**" button
6. In "**output format**", choose "**selected fields from primary and related tables**"



7. Click the "**get output**" button

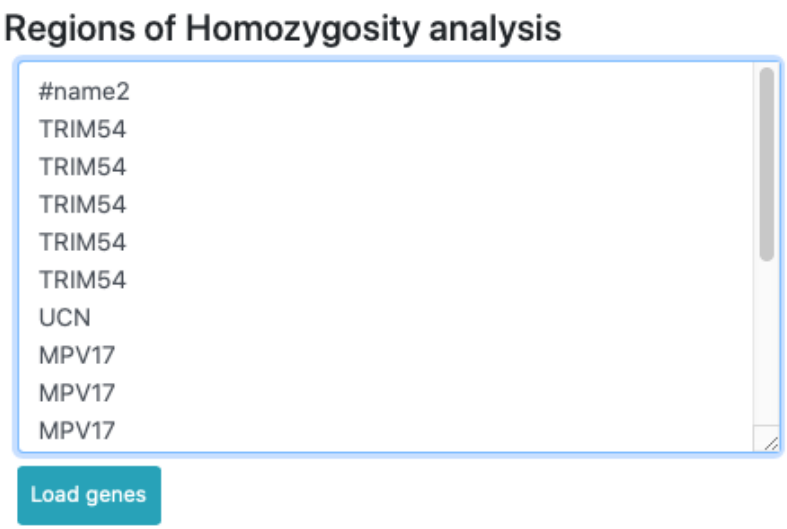
8. Check the "**name2**" checkbox



9. Click the "**get output**" button
10. Paste the full output from the UCSC tool into the text area at the top of the SimulConsult "Regions of Homozygosity analysis" screen accessible under the helix symbol on the top menu. Don't bother to remove the header or the repeated HGNC symbols; the Regions of Homozygosity analysis removes these automatically.

```
#name2
TRIM54
TRIM54
TRIM54
TRIM54
TRIM54
UCN
MPV17
MPV17
MPV17
MPV17
MPV17
MPV17
MPV17
GTF3C2
GTF3C2
GTF3C2
GTF3C2
```

Copy & paste



When the parents are first cousins, thousands of lines of HGNC gene symbols are obtained, with many repeated symbols but typically ~2,000 unique genes, of which only hundreds will have known human biallelic phenotypes. From the tiny gene list above, the last time we checked, only the MPV17 gene has a known human phenotype.

When you click the Next button on the “Regions of Homozygosity analysis” screen in SimulConsult, you will see the "Genotype" tab of the Diagnose screen. If you’ve already entered a robust set of findings for the patient, the genes with highest pertinence for the differential diagnosis for the patient will be high in the list of pertinent genes. You can enter additional pertinent positive or pertinent negative findings to help distinguish among the most pertinent genes and choose which to sequence. The useful findings suggested on the "Add findings" and "Add tests" tabs of the Diagnose screens can help choose findings on which to comment or other types of testing that can be helpful.