Carl Zimmer ARGweaver results

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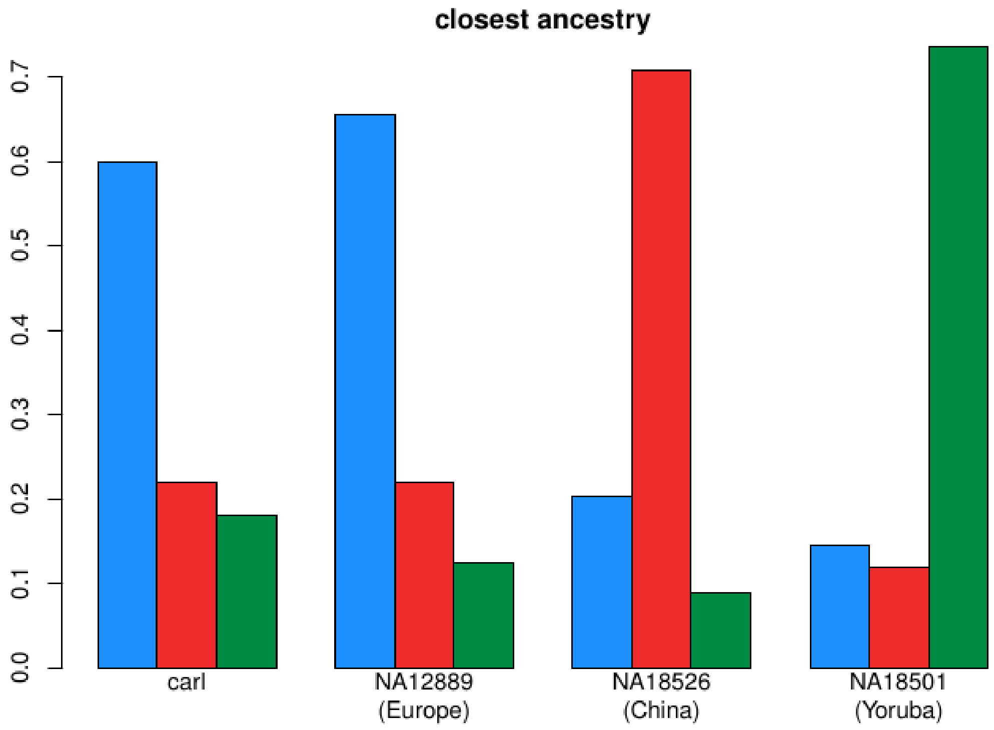
2/29/2016

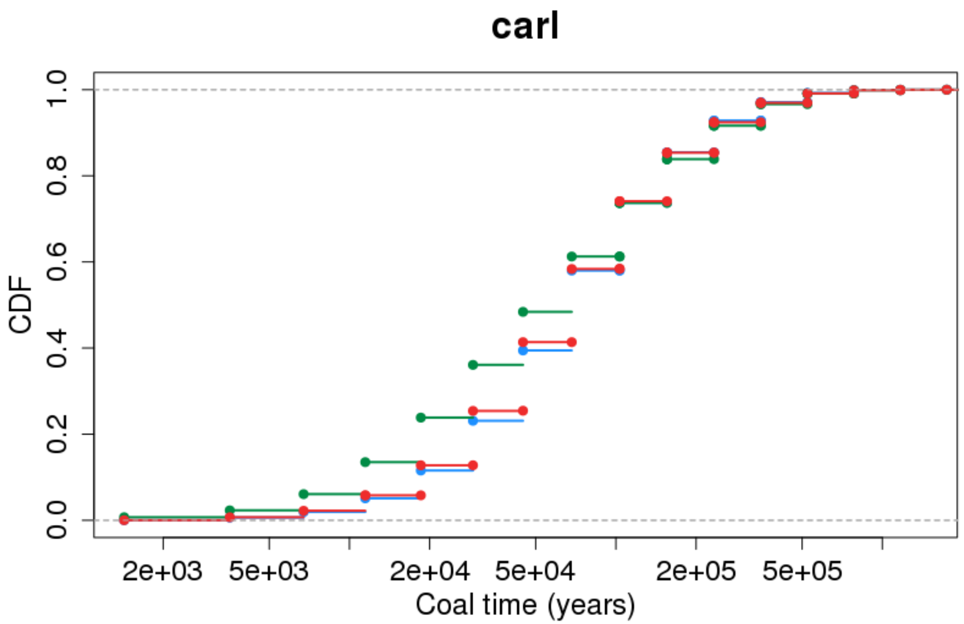
Overview

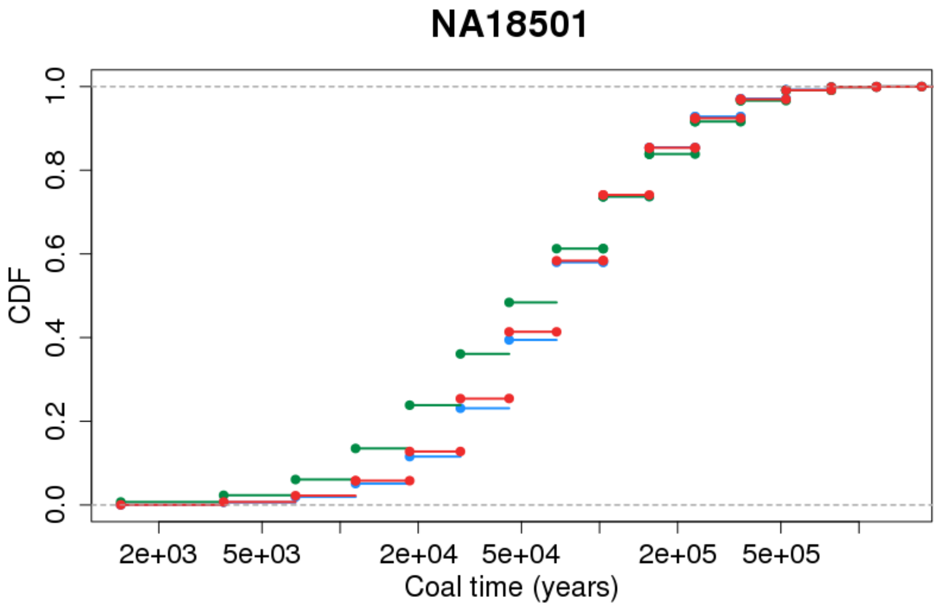
- Ran ARGweaver with these genomes:
    - Altai Neanderthal
    - Denisova
    - Carl
    - 4 Europeans from Complete Genomics public data set (CG)
    - 4 Asians from CG (3 Chinese, 1 Japanese)
    - 4 African from CG (2 Yoruban, 1 Maasai, 1 Luhya)
    - Chimpanzee sequence
- Initialized ARGweaver with previous run which used all individuals except Carl
- Ran 3000 iterations, discarded first 1000, sampled every 20, yielding 100 sampled ARGs
- Most results are averages across these 100
- Roughly 2 years of compute time

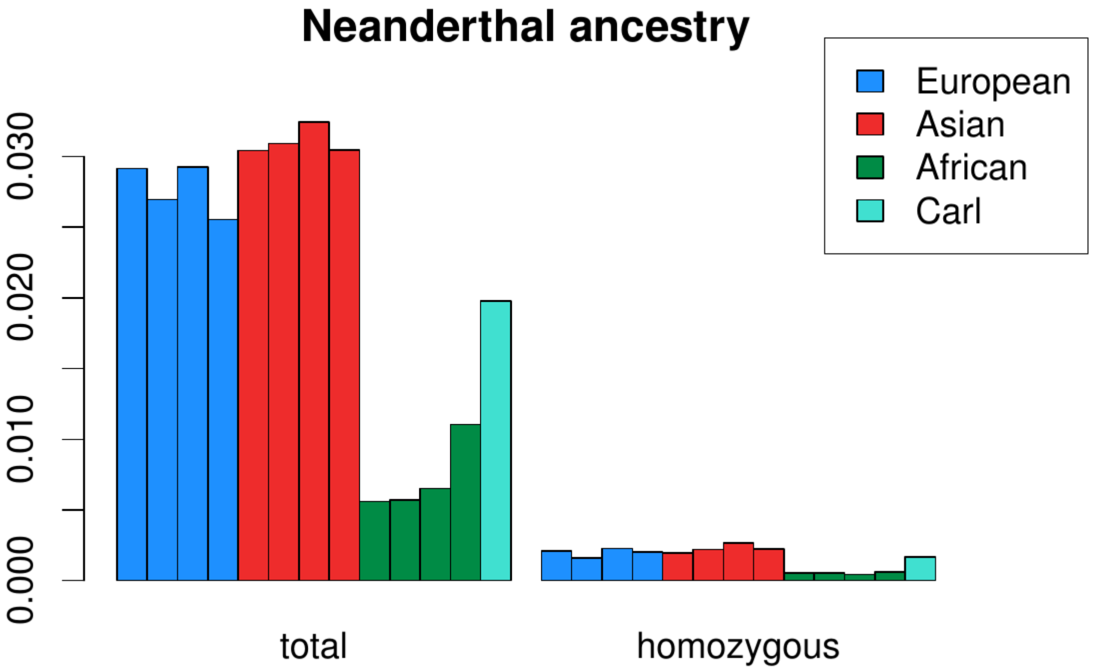
pop assignments

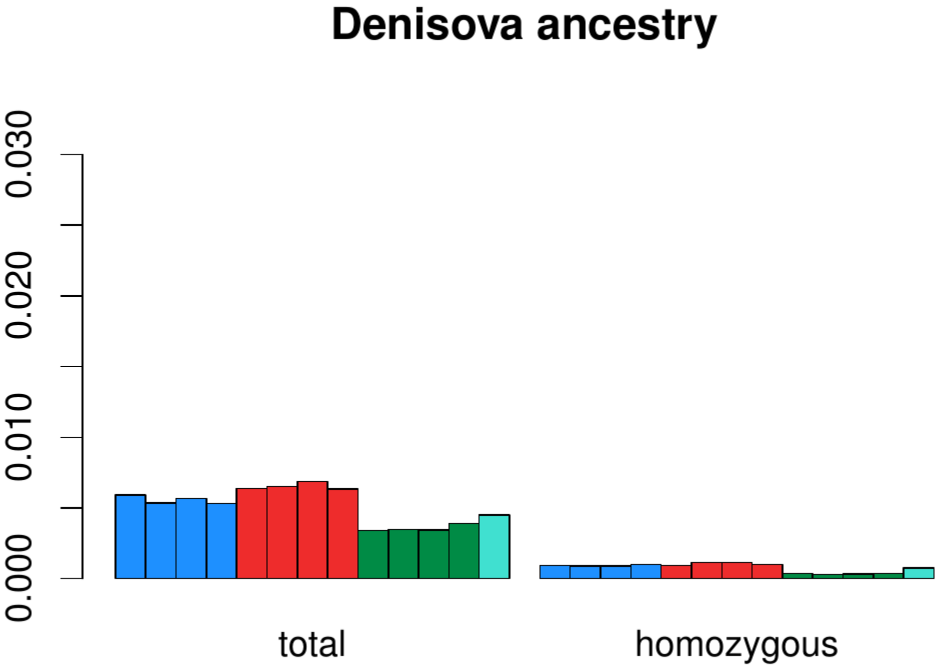
- 🟦 Europe
- 🟥 Asia
- 🟩 Africa





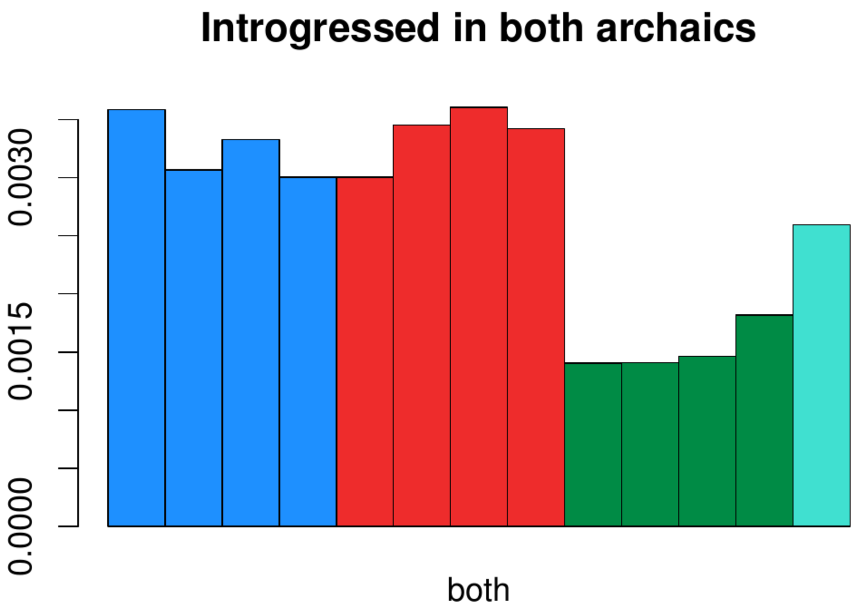



Neanderthal ancestry


Denisova ancestry

Error rate ~ 0.6%
Carl: 2.0%

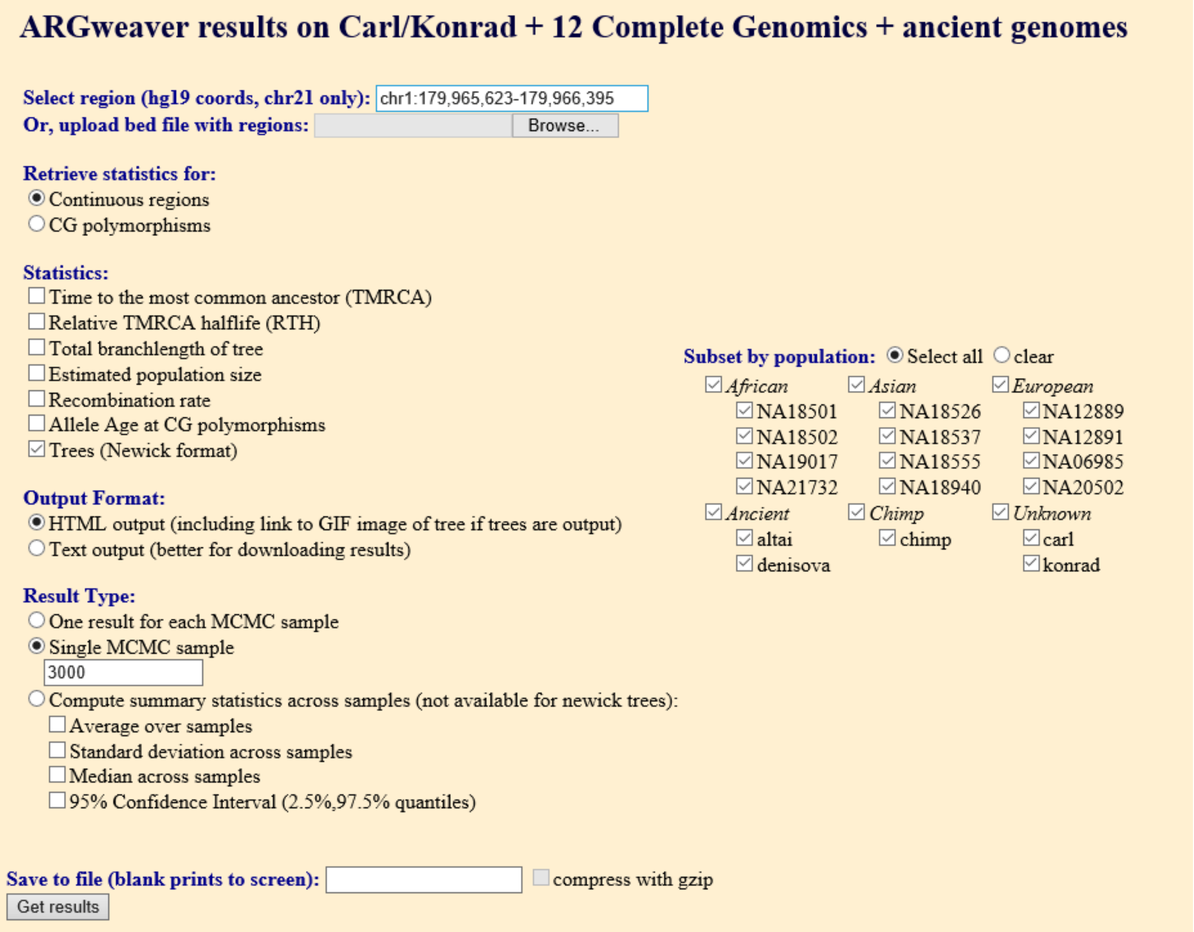
Error rate ~ 0.35%
Carl: 0.46%


Introgressed in both archaics

Resources: Launchers

- Neanderthal introgressed: http://compgen.cshl.edu/~mhubisz/carlZimmer/carl.altai.introgressed.html
- Denisovan introgressed: http://compgen.cshl.edu/~mhubisz/carlZimmer/carl.denisova.introgressed.html

ARG browser: http://compgen.cshl.edu/~mhubisz/carlZimmer/



ARGweaver results on Carl/Konrad + 12 Complete Genomics + ancient genomes

Select region (hg19 coords, chr21 only): chr1:179,965,623-179,966,395

Or, upload bed file with regions: Browse...

Retrieve statistics for:
● Continuous regions
○ CG polymorphisms

Statistics:
☐ Time to the most common ancestor (TMRCA)
☐ Relative TMRCA halflife (RTH)
☐ Total branchlength of tree
☐ Estimated population size
☐ Recombination rate
☐ Allele Age at CG polymorphisms
☑ Trees (Newick format)

Output Format:
● HTML output (including link to GIF image of tree if trees are output)
○ Text output (better for downloading results)

Result Type:
○ One result for each MCMC sample
● Single MCMC sample
3000
○ Compute summary statistics across samples (not available for newick trees):
☐ Average over samples
☐ Standard deviation across samples
☐ Median across samples
☐ 95% Confidence Interval (2.5%,97.5% quantiles)

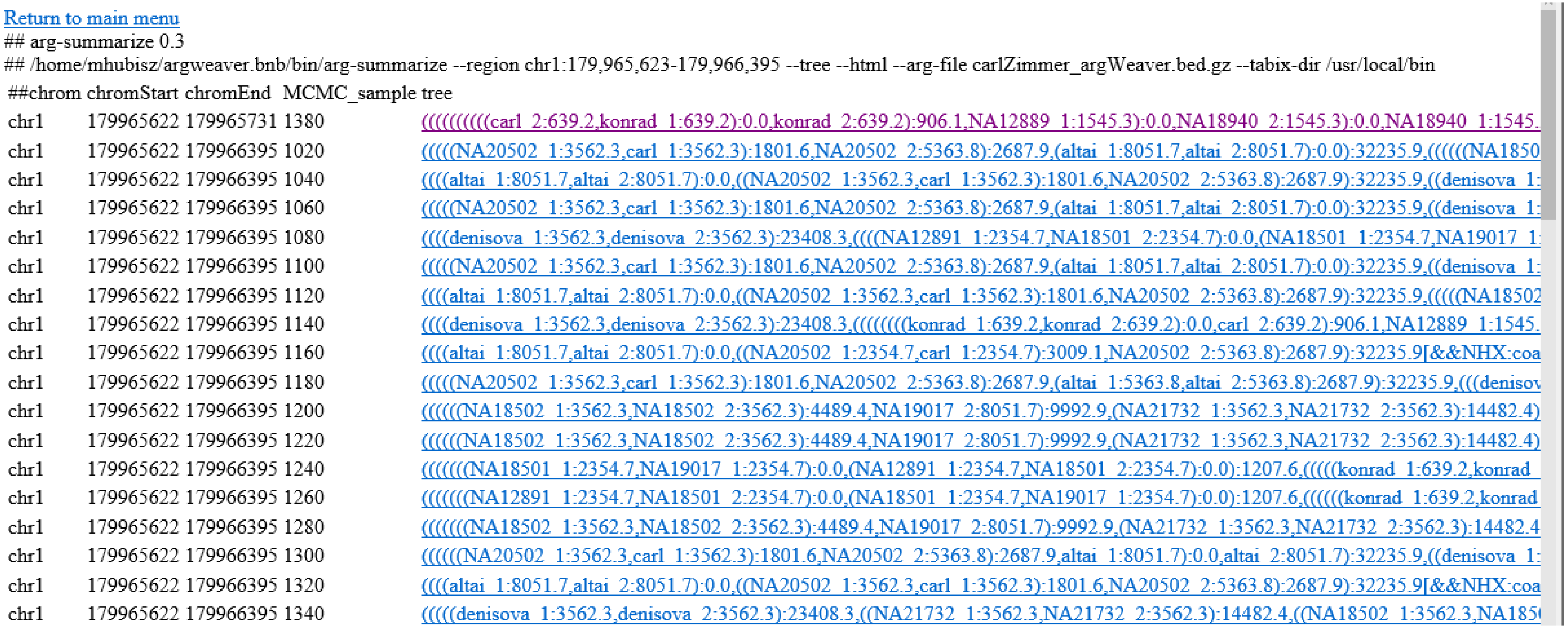
Subset by population: ● Select all ○ clear

☑ *African*	☑ *Asian*	☑ *European*
☑ NA18501	☑ NA18526	☑ NA12889
☑ NA18502	☑ NA18537	☑ NA12891
☑ NA19017	☑ NA18555	☑ NA06985
☑ NA21732	☑ NA18940	☑ NA20502
☑ *Ancient*	☑ *Chimp*	☑ *Unknown*
☑ altai	☑ chimp	☑ carl
☑ denisova		☑ konrad

Save to file (blank prints to screen): ☐ compress with gzip

Get results

ARG browser: http://compgen.cshl.edu/~mhubisz/carlZimmer/



[Return to main menu]()

```
## arg-summarize 0.3
## /home/mhubisz/argweaver.bnb/bin/arg-summarize --region chr1:179,965,623-179,966,395 --tree --html --arg-file carlZimmer_argWeaver.bed.gz --tabix-dir /usr/local/bin
##chrom chromStart chromEnd  MCMC_sample tree
chr1    179965622 179965731 1380    (((((((((carl_2:639.2,konrad_1:639.2):0.0,konrad_2:639.2):906.1,NA12889_1:1545.3):0.0,NA18940_2:1545.3):0.0,NA18940_1:1545.
chr1    179965622 179966395 1020    ((((NA20502_1:3562.3,carl_1:3562.3):1801.6,NA20502_2:5363.8):2687.9,(altai_1:8051.7,altai_2:8051.7):0.0):32235.9,((((((NA1850
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chr1    179965622 179966395 1100    ((((NA20502_1:3562.3,carl_1:3562.3):1801.6,NA20502_2:5363.8):2687.9,(altai_1:8051.7,altai_2:8051.7):0.0):32235.9,((denisova_1:
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chr1    179965622 179966395 1220    (((((NA18502_1:3562.3,NA18502_2:3562.3):4489.4,NA19017_2:8051.7):9992.9,(NA21732_1:3562.3,NA21732_2:3562.3):14482.4)
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chr1    179965622 179966395 1340    (((((denisova_1:3562.3,denisova_2:3562.3):23408.3,((NA21732_1:3562.3,NA21732_2:3562.3):14482.4,((NA18502_1:3562.3,NA185
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