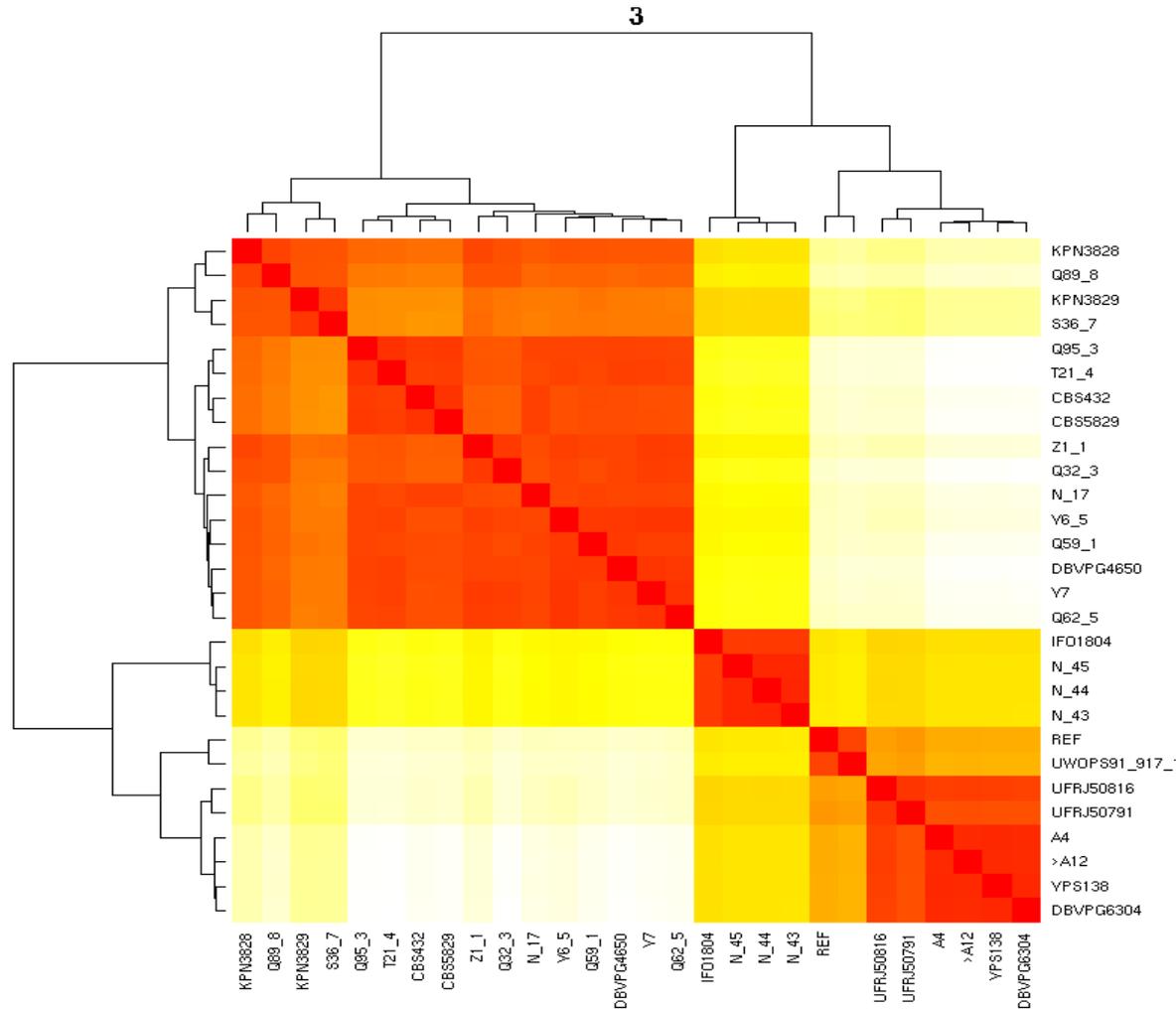
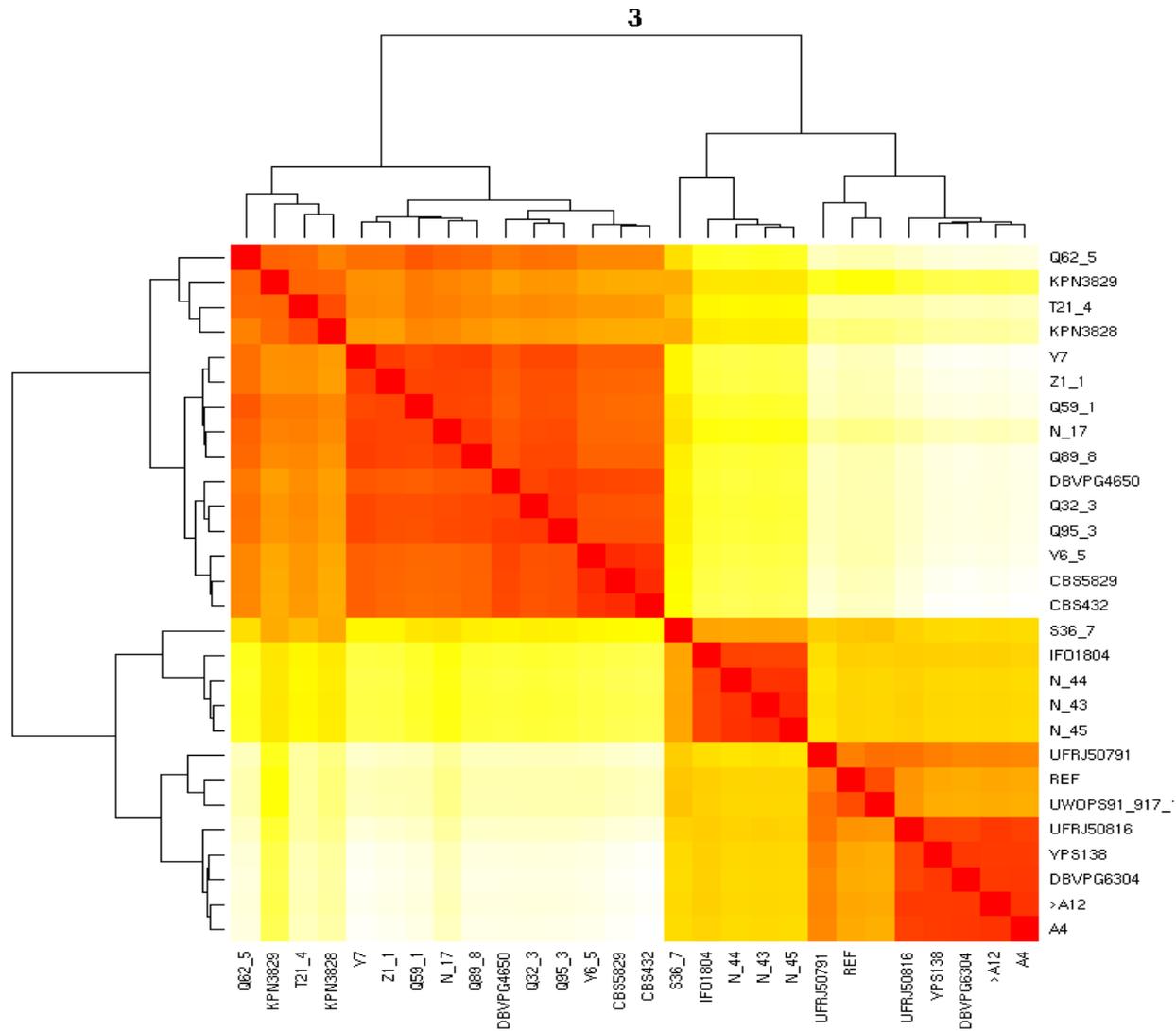


Extra material in paradoxus
strains

Paradoxus population structure

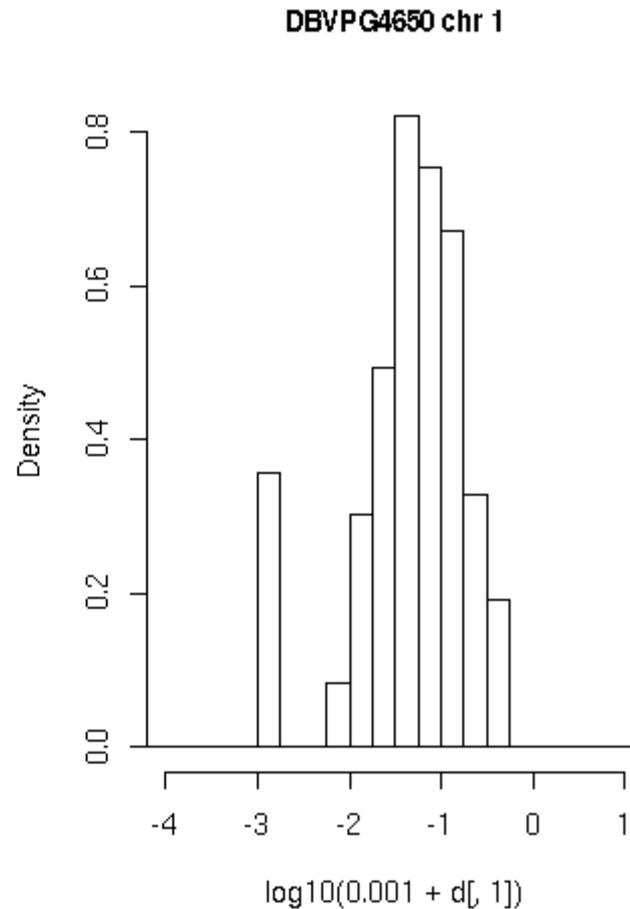
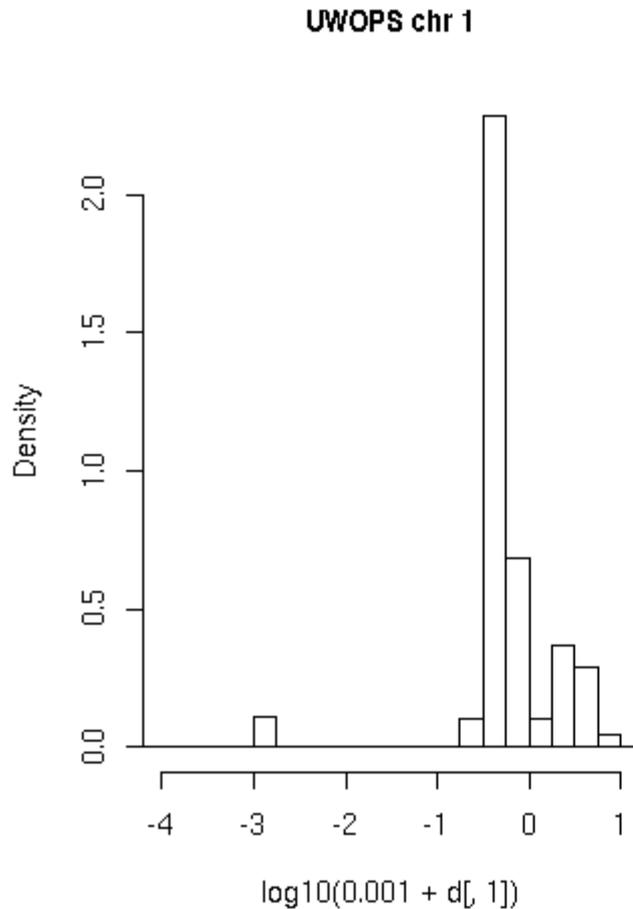


Paradoxus population structure

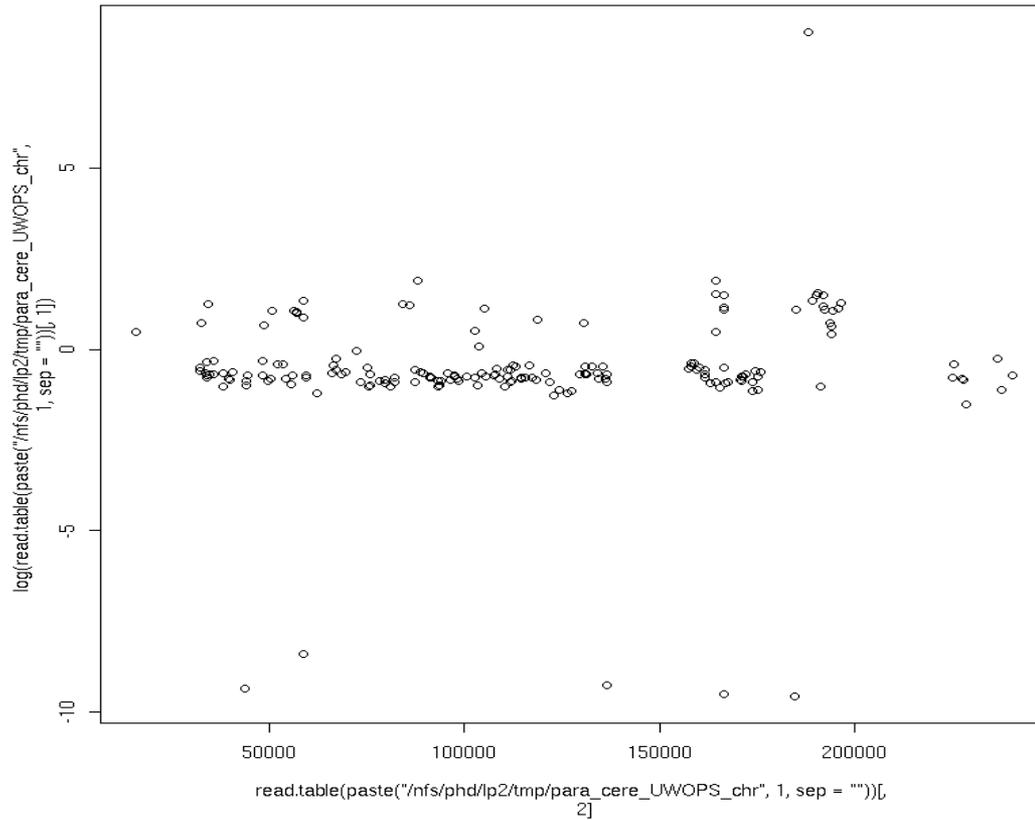


Hawaiian paradoxus

- $\log(\text{differences to para}/\text{differences to cere})$

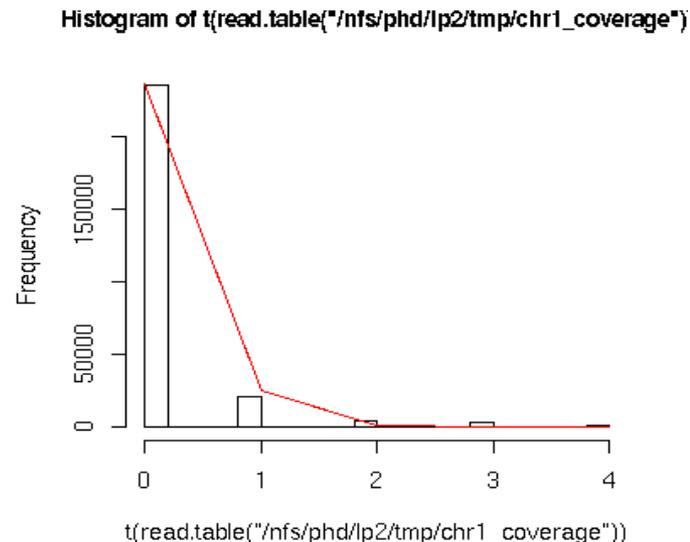


Hawaiian paradoxus

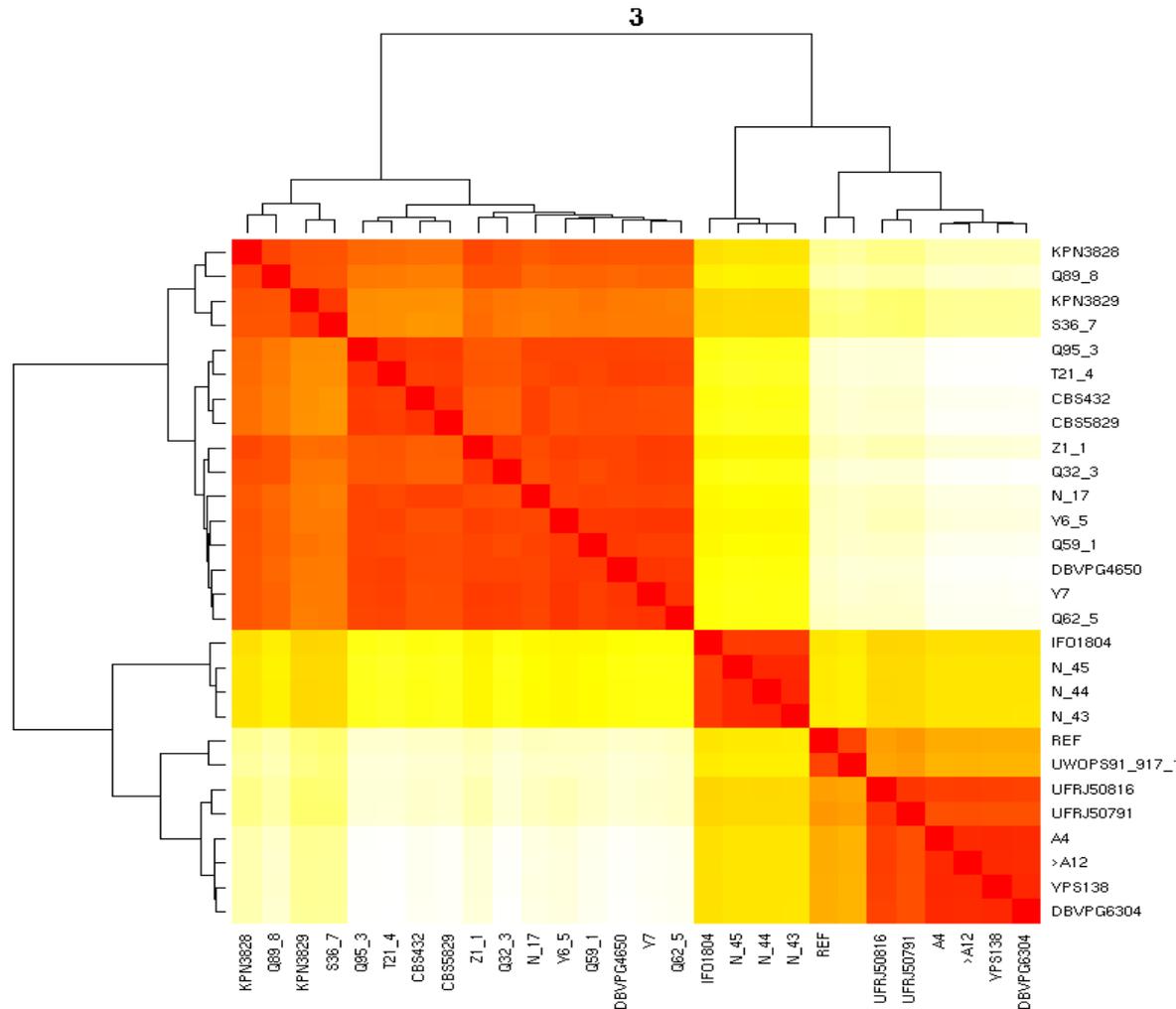


Hawaiian paradoxus

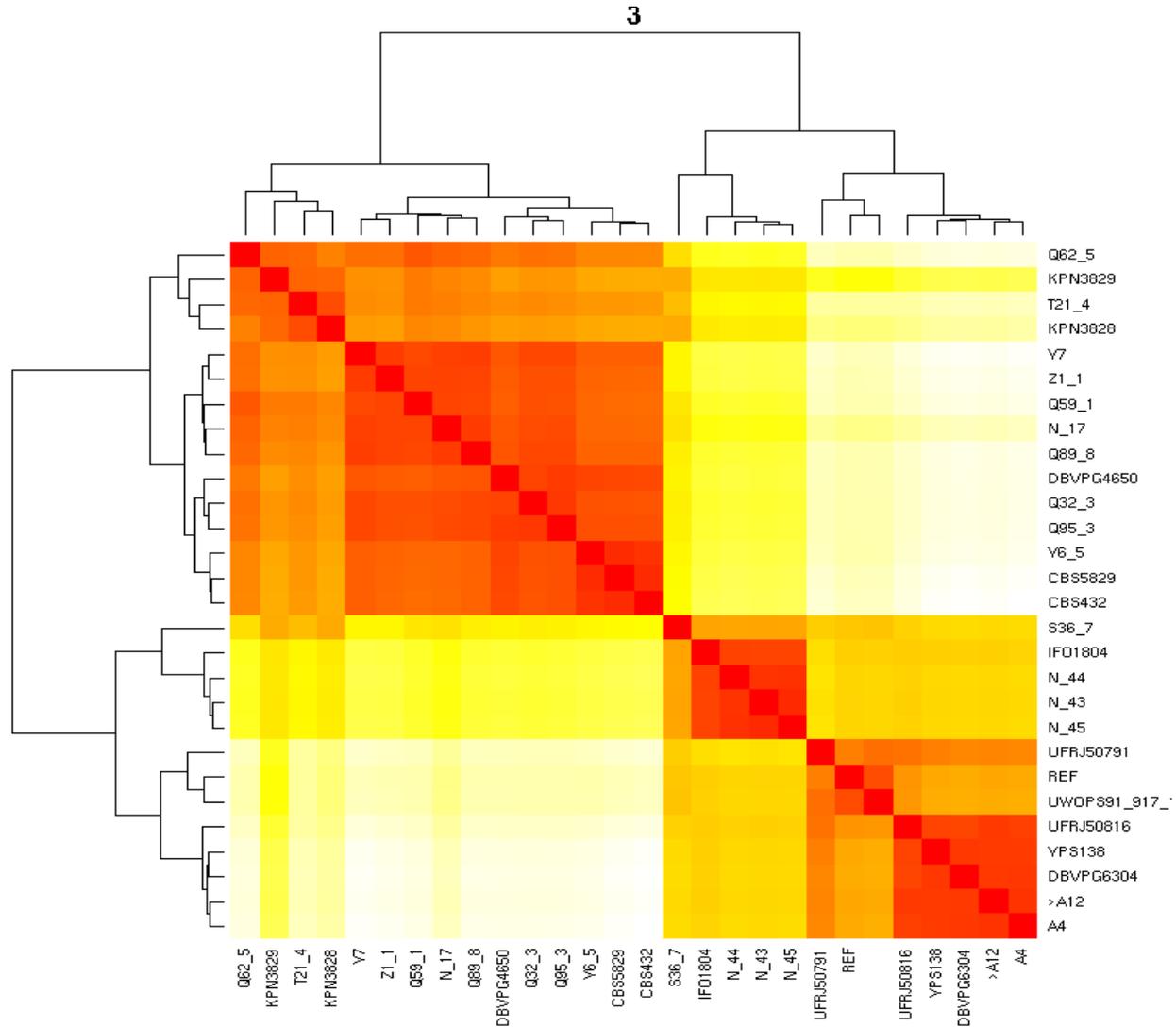
- But – numbers (chr1)
 - 263.8 kb total length
 - 27.9 kb high divergence (~10 % of total)
 - 98.1 kb low divergence (~37% of total)
 - 15.8 kb both (~53 % of high divergence)
 - No evidence of closeness



Paradoxus population structure

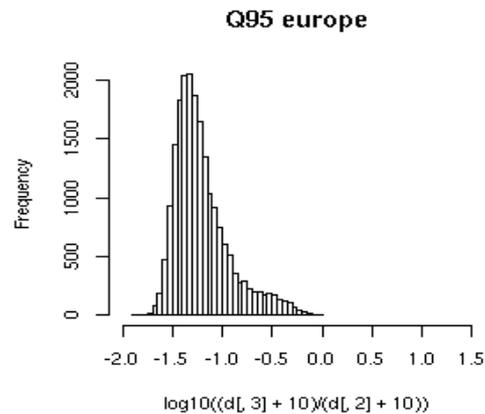
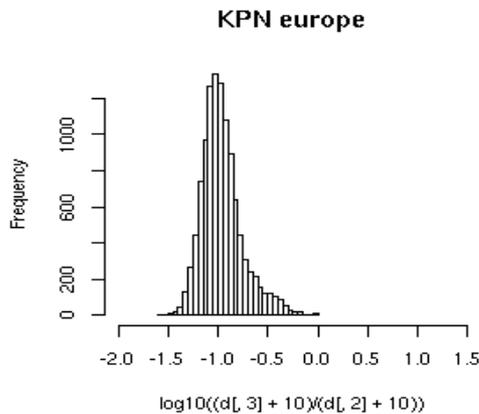
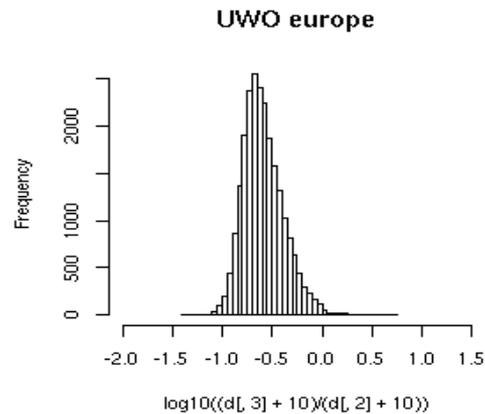
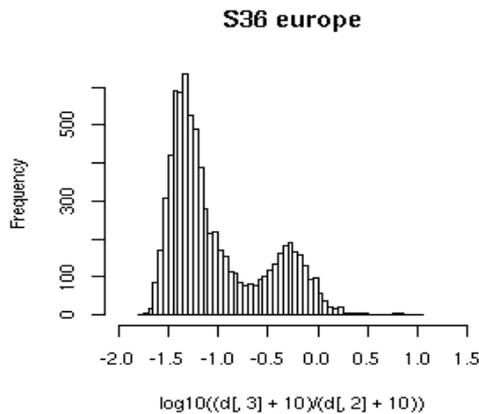


Paradoxus population structure



S36_7

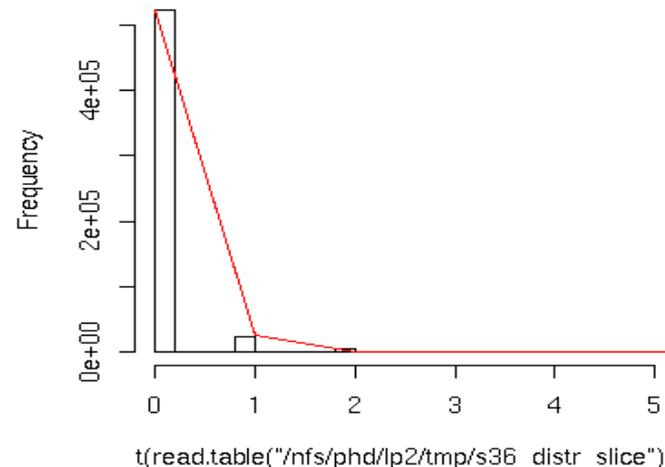
- Differences to European consensus



S36_7

- But – numbers
 - 10,974 kb total length in contigs
 - 508 kb high divergence
 - 4,293 kb low divergence (~40% of total)
 - 222 kb both
(~40 % of high divergence)
 - No evidence of closeness

Histogram of `t(read.table("/nfs/phd/lp2/tmp/s36_distr_slice"))`



Also - A12

- 202 traces closer to *cerevisiae*
- Almost all map to mouse/human reads
- None map to assembled genomes
- Do not share sequence
- AT rich

Verdict

- Does confound analysis
- Hybrid?
- Extra material in sequencing?
- Sequencing another sample/more material?