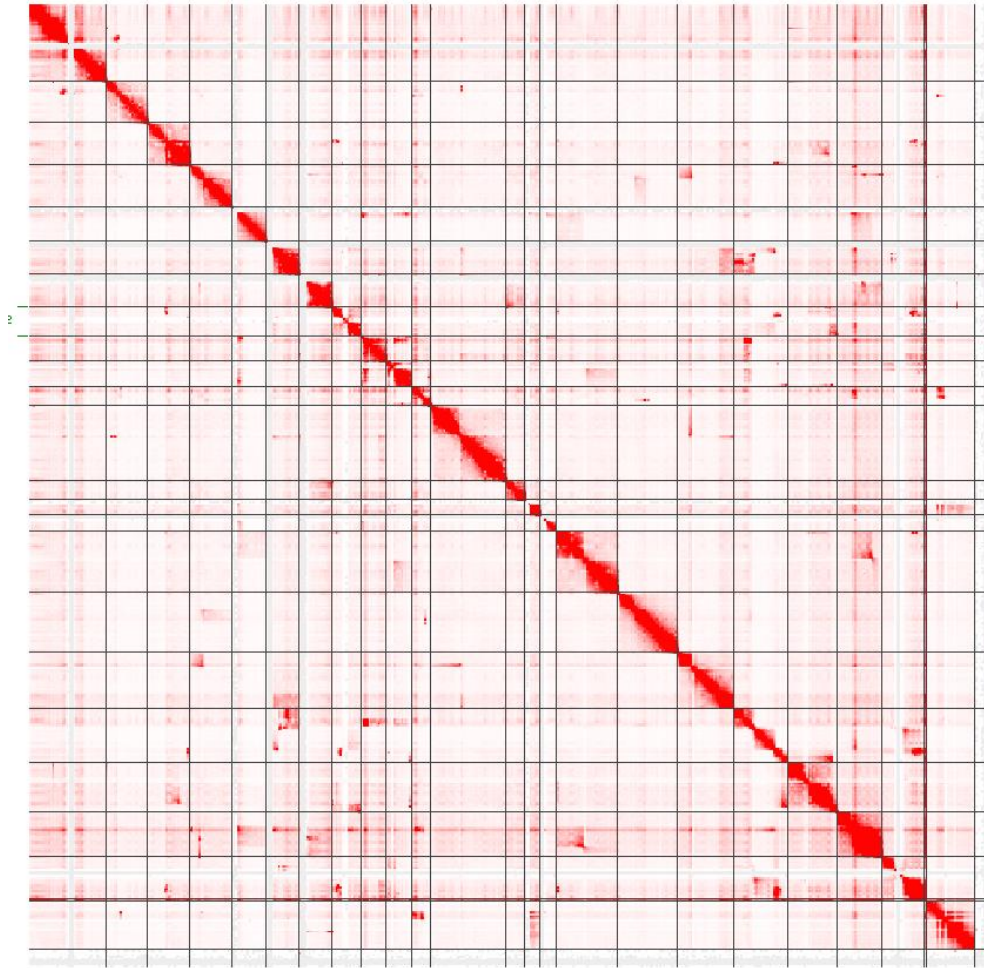


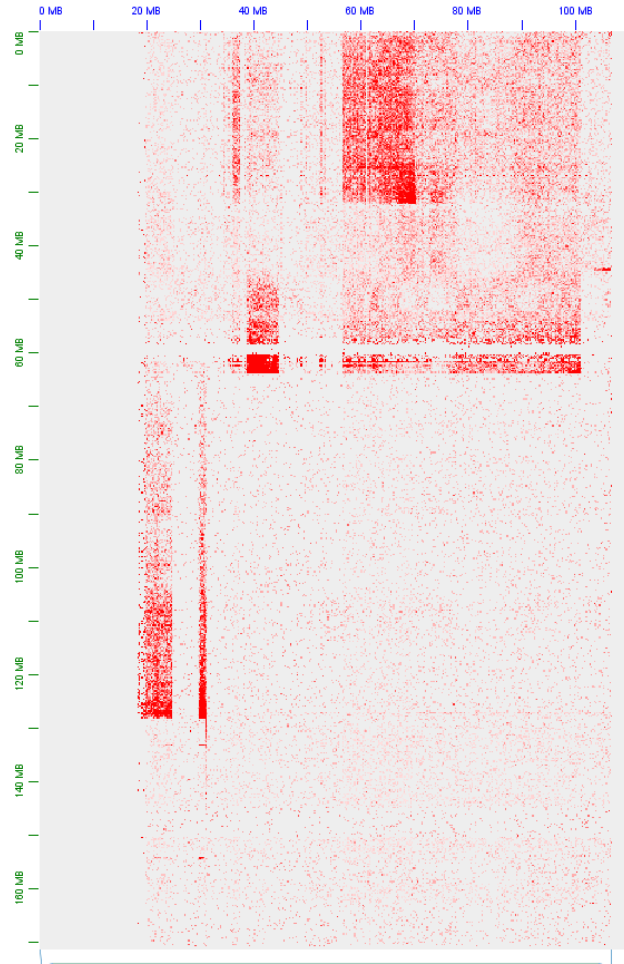
Dataset stats

Species	Read Length	Library	Raw fragments	Unique Reads	Library Complexity Estimate	Hi-C Contacts	L-I-O-R
<i>Homo sapiens</i>	2x38	L1885-OS89_Hi-C	367,693,842	56.76%	345,398,214	111,204,037	25% - 25% - 25% - 25%
<i>Homo sapiens</i> hg38	2x38	L1983-OS08_Hi-C	129,450,366	72.78%	1,713,768,388	65,905,963	25% - 25% - 25% - 25%
<i>Homo sapiens</i> hg38	2x36	L2059+L2062-PSS085_Hi-C	533,120,873	60.00%	691,043,866	174,347,810	25% - 25% - 25% - 25%
<i>Homo sapiens</i> hg38	2x38	L2117-PSS0141-Hi-C	103,493,938	78.92%	626,320,315	37,766,914	25% - 25% - 25% - 25%
<i>Homo sapiens</i> hg38	2x38	L2118-PSS0141-Hi-C	240,646,783	62.61%	2,626,270,953	87,814,368	25% - 25% - 25% - 25%

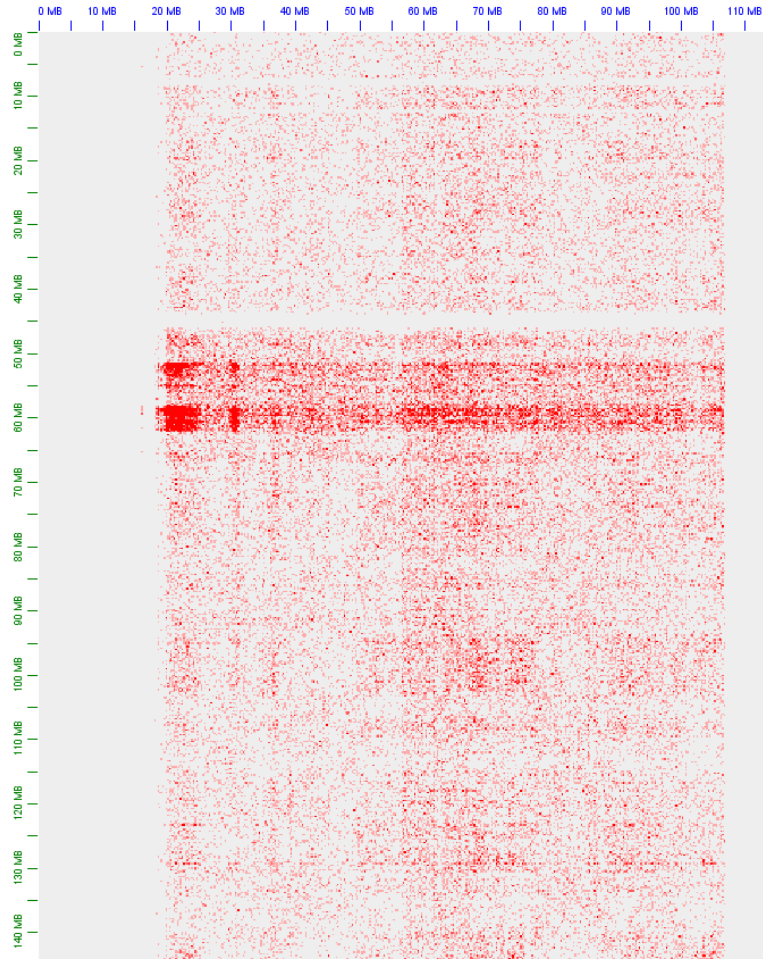
OS08 Global map



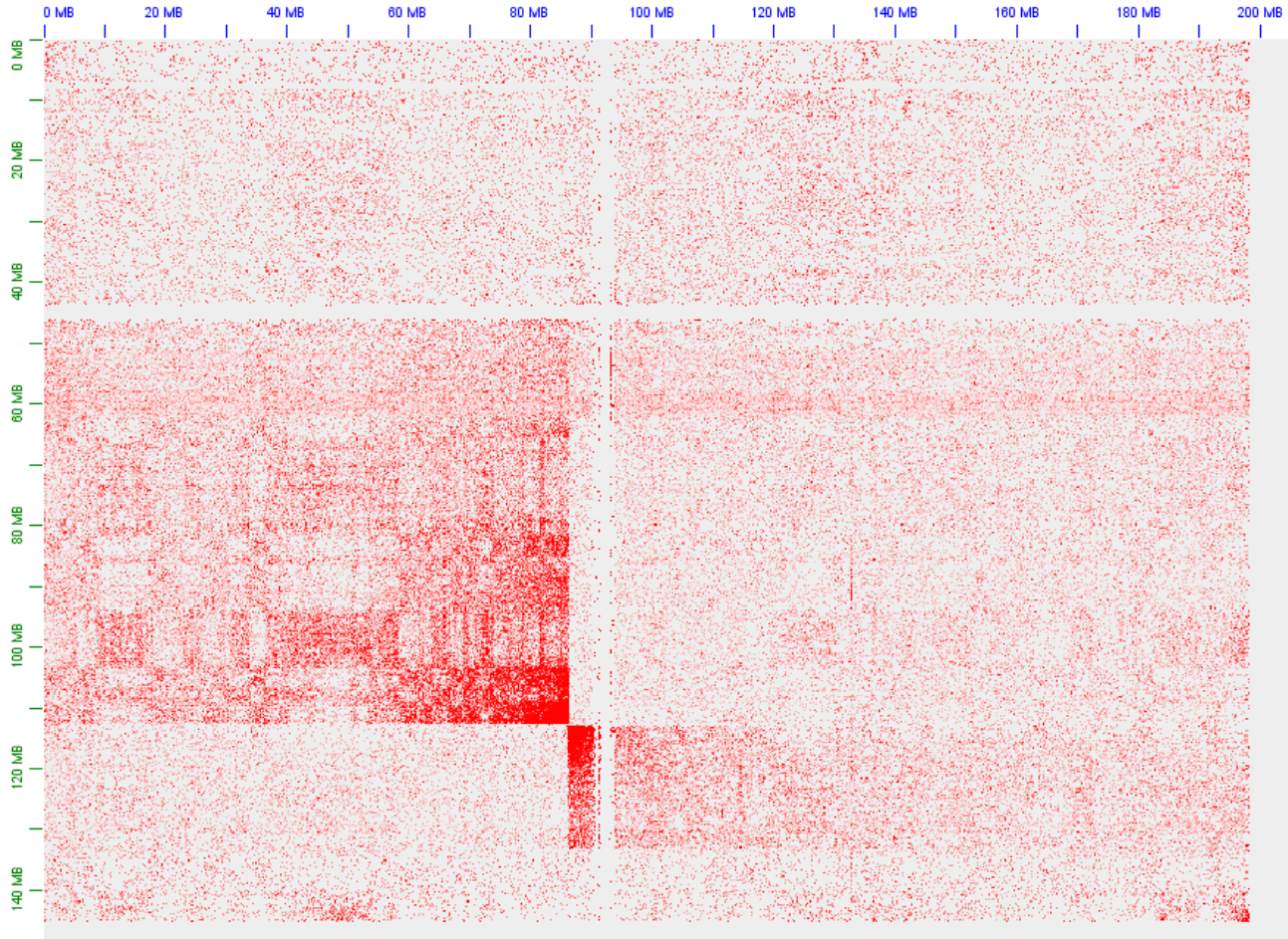
chr6 vs chr14



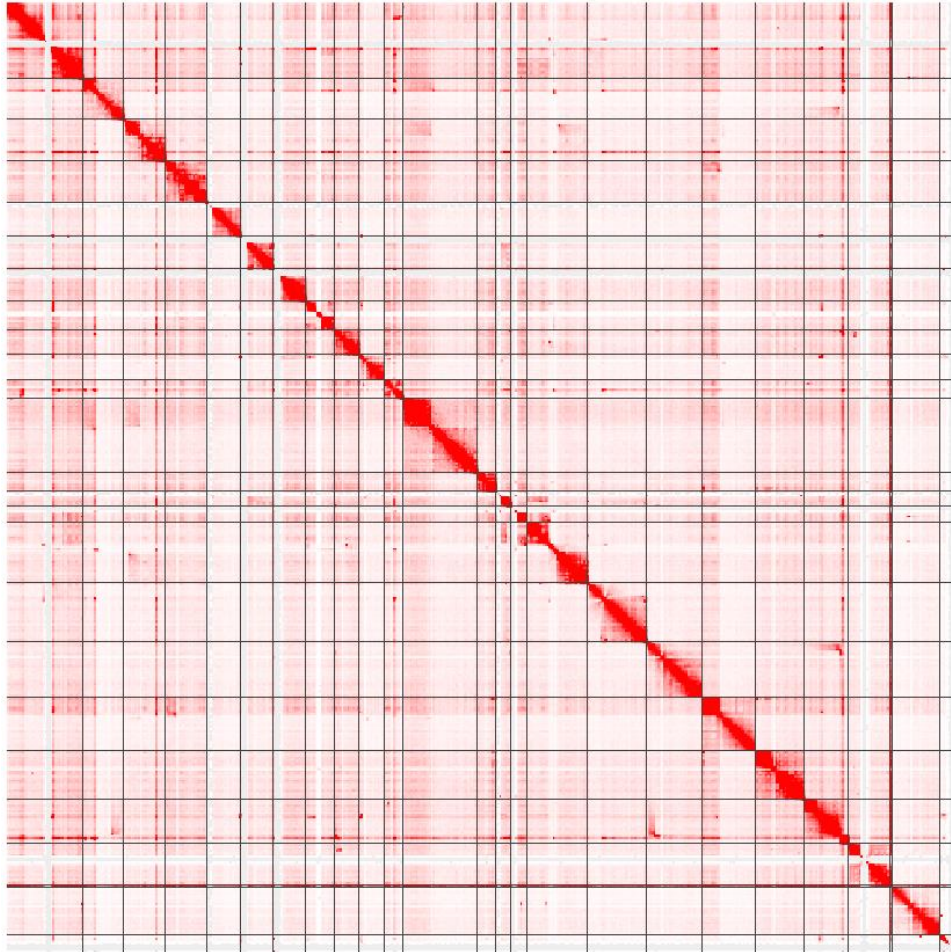
chr14 vs chr 8



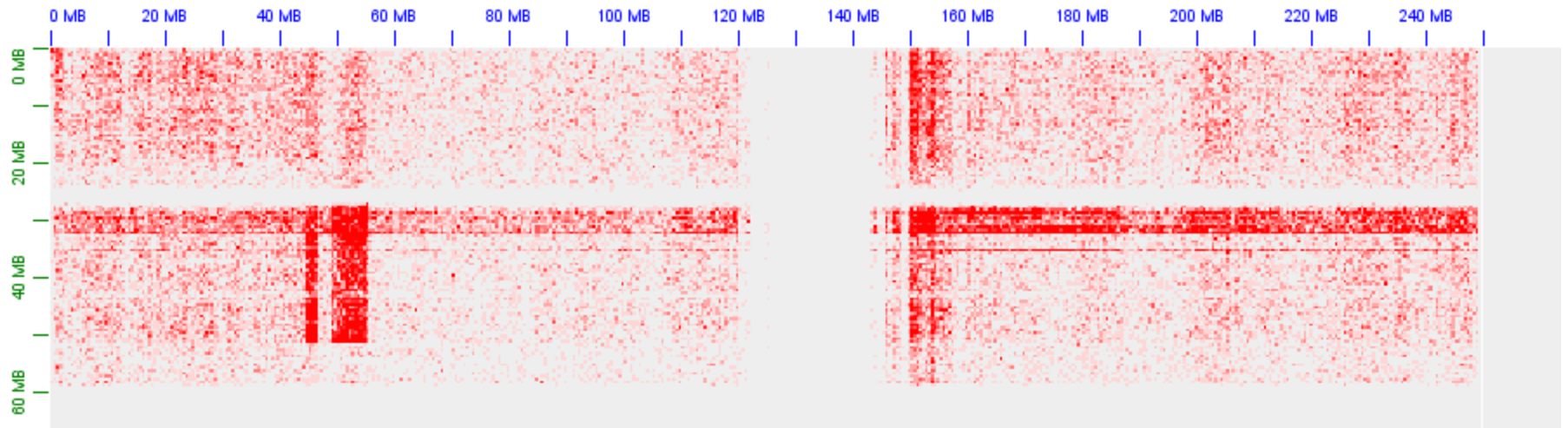
chr3 vs chr8



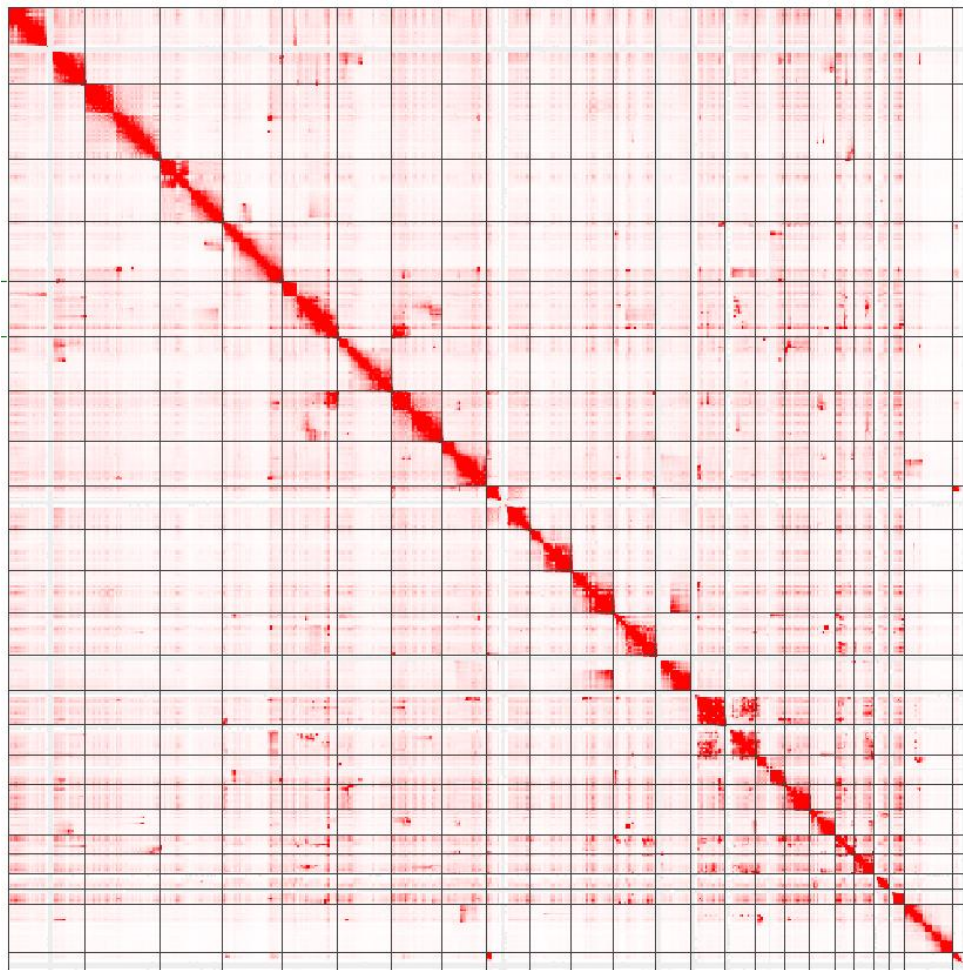
OS89 Global map



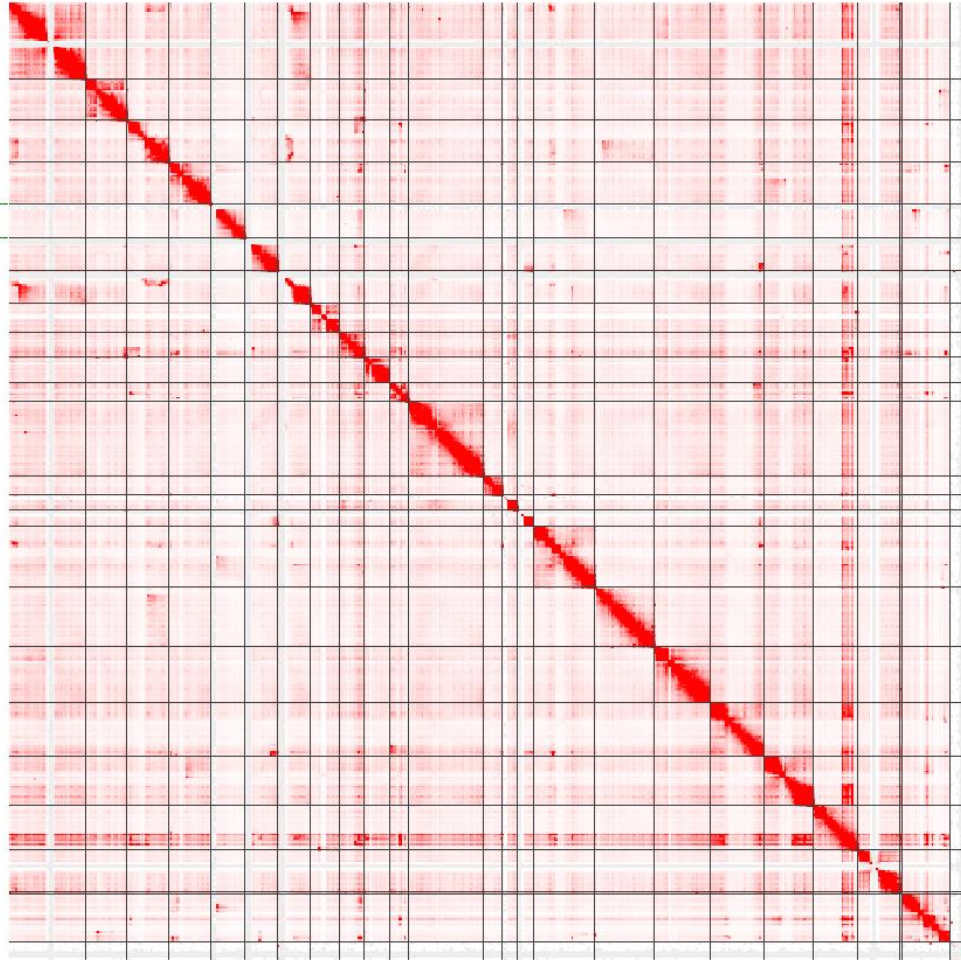
chr1 vs chr 11



PSS0141 Global map



PSS085 Global map



Still running:

- Automated 3D-DNA resc scaffolding
- Manual review and final genome assembly

- CNVs can be called from the Hi-C data

- SNPs will be difficult as we sequenced 2x36mers