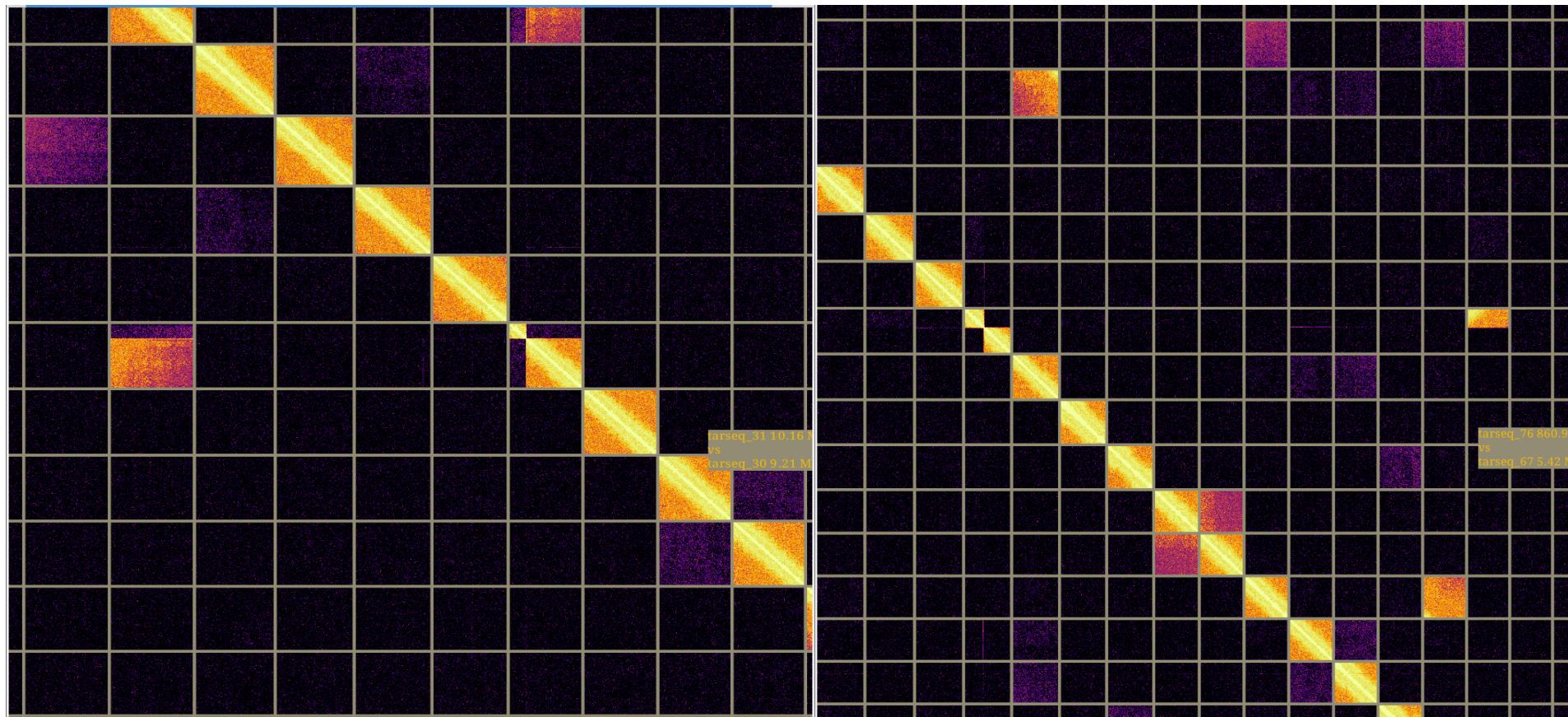


# *BreakHiC - Identification of Assembly Breakpoints by Screening Paired HiC Reads*

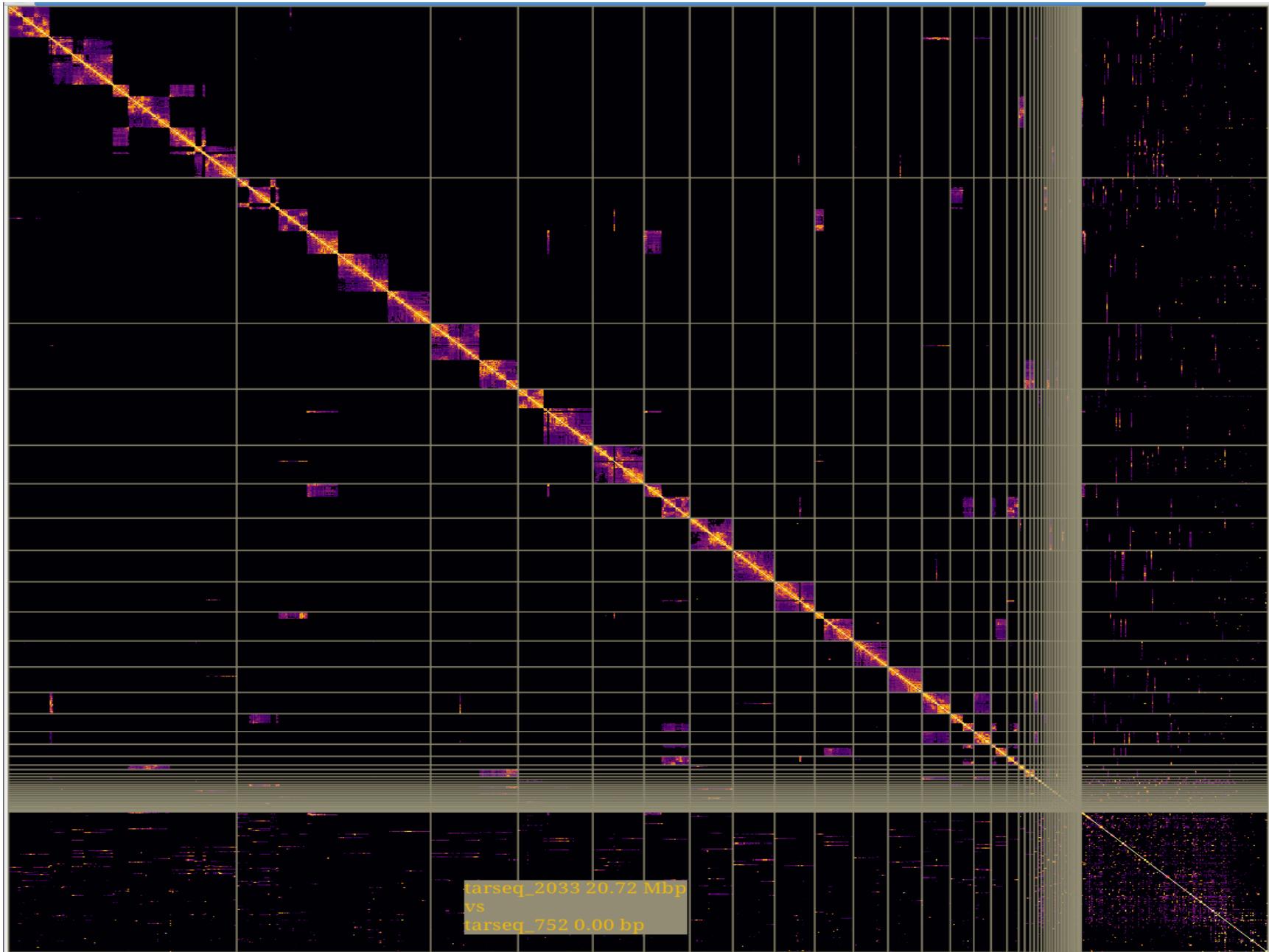
Zemin Ning  
The Wellcome Sanger Institute  
UK



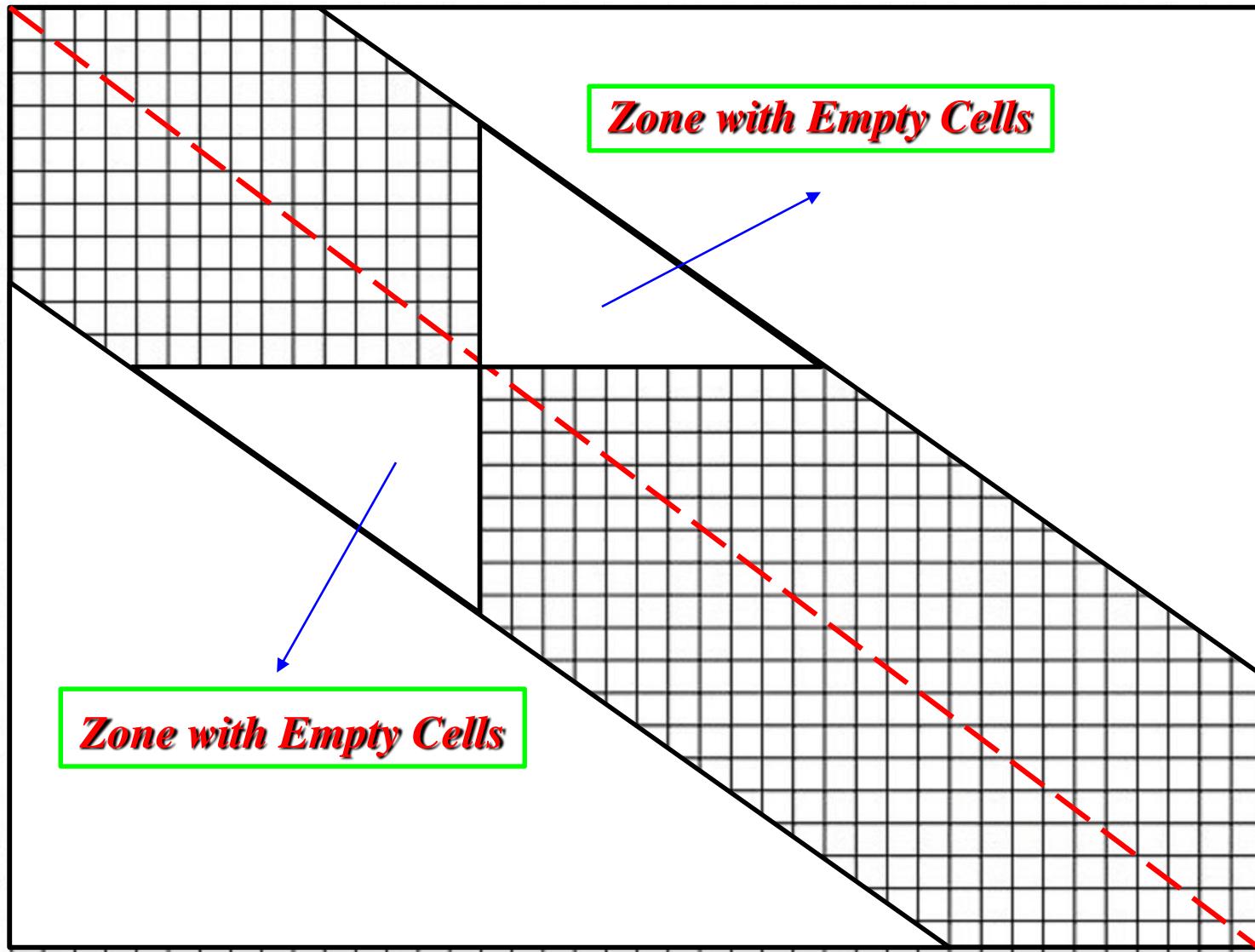
## *Mis-assembly Errors at Contigs*



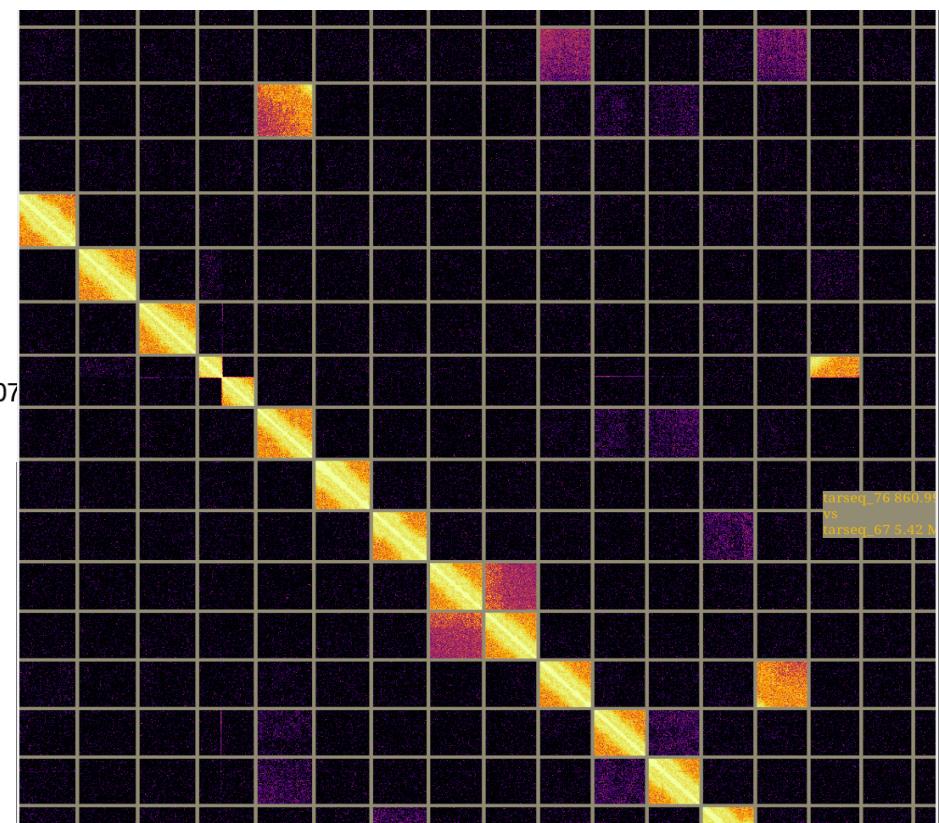
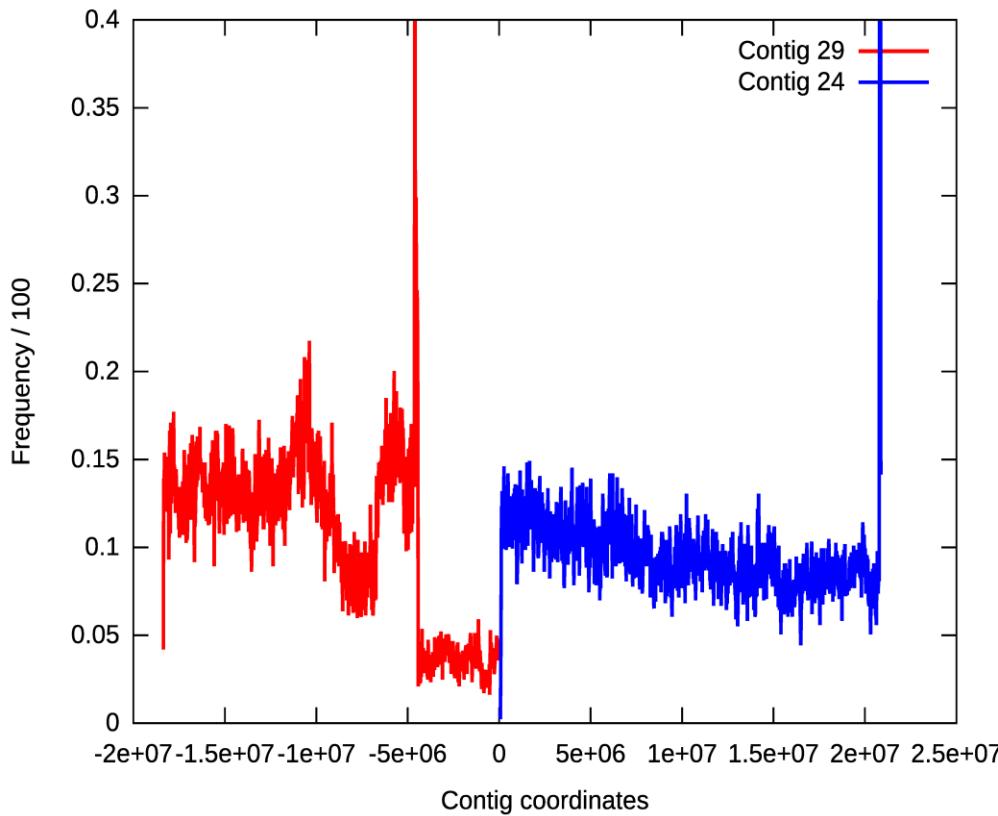
# *Mis-assembly Errors at Scaffolds*



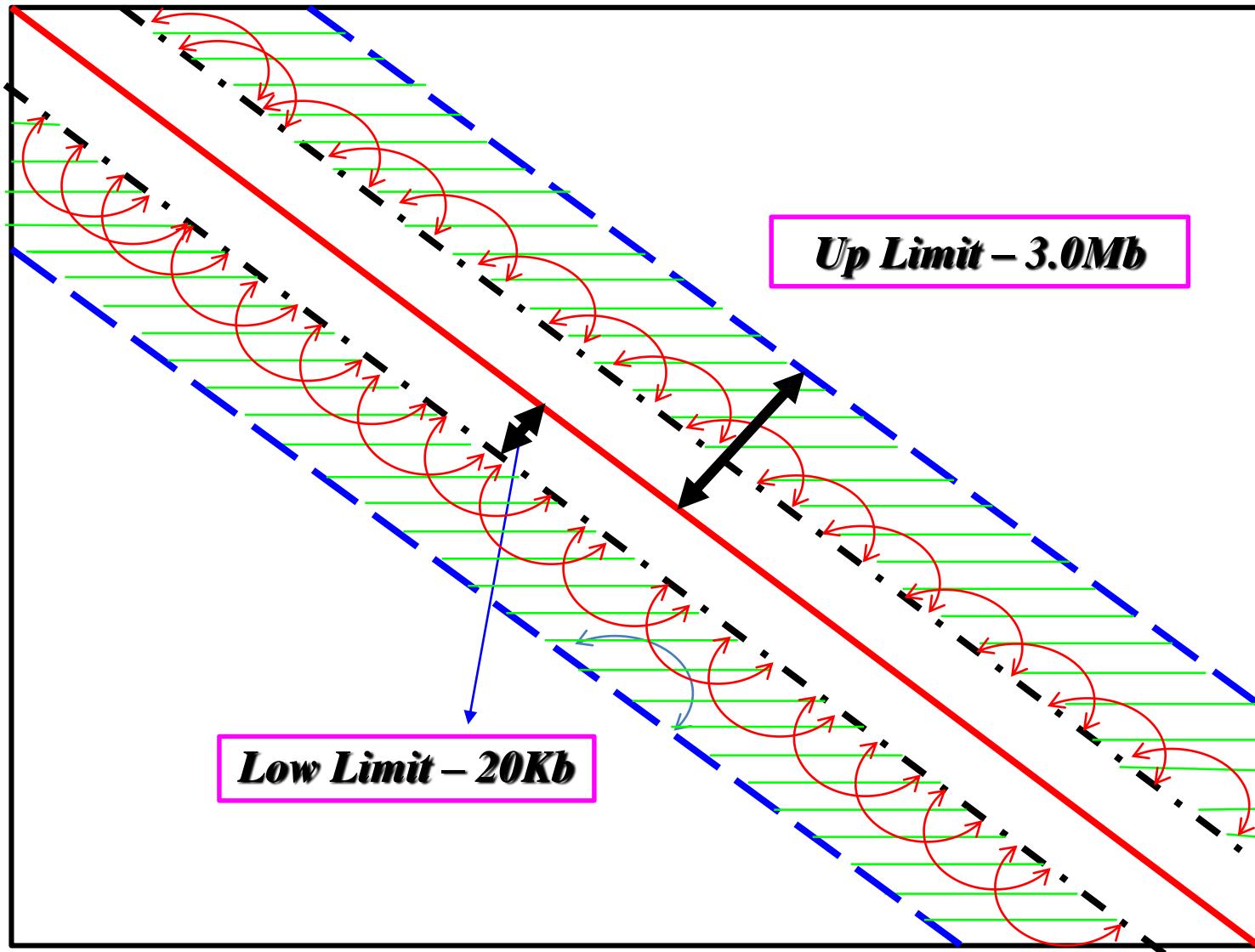
# *Grid Method to Check Empty Cells*



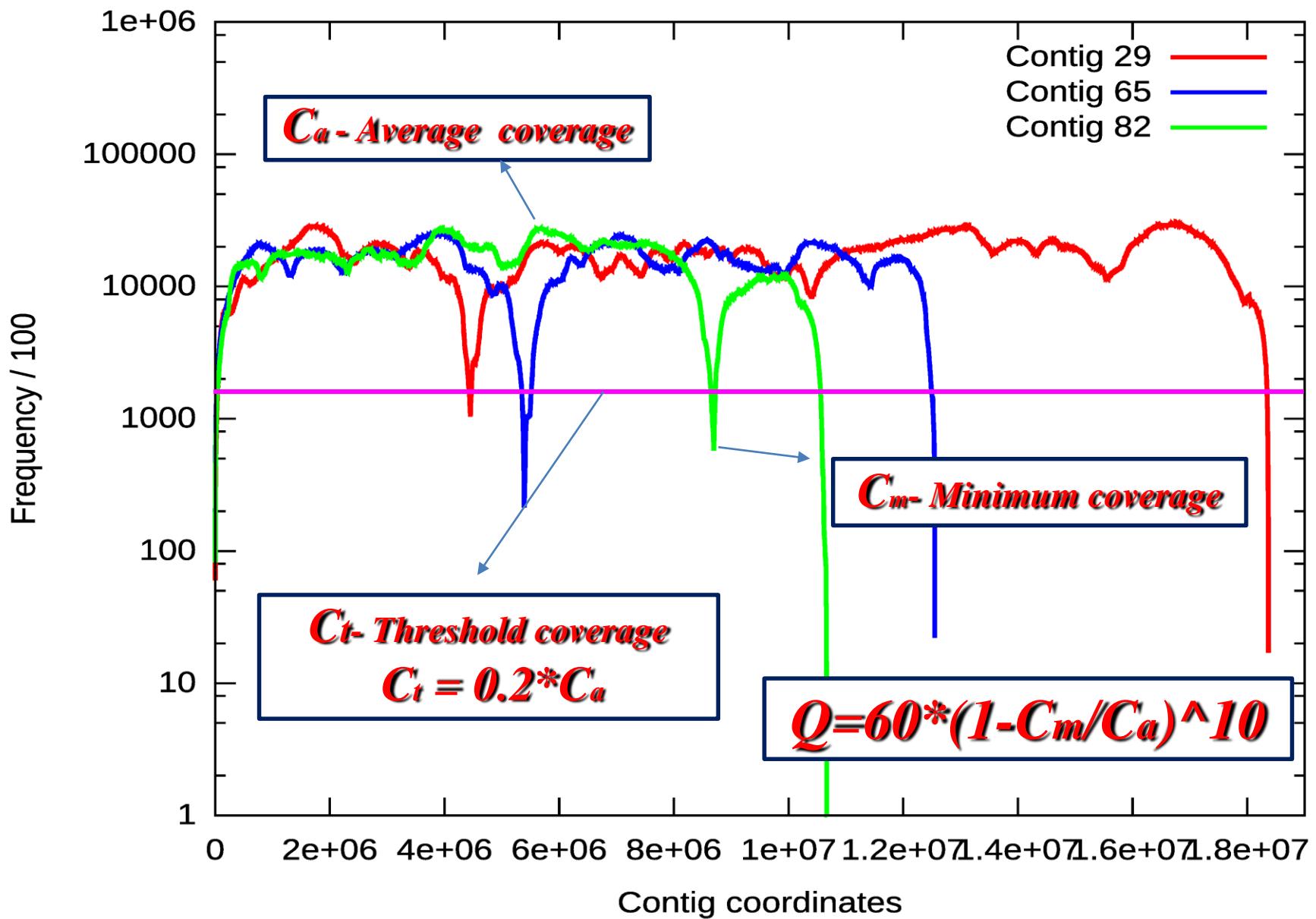
# *Number of Reads in Paired Contigs*



# *HiC Pair Link Coverage*



## Coverage of HiC Pair Links within Contigs



```
Break1: 70 547700 217464711 3156 5 0
Break1: 70 854600 217464711 3447 5 0
Break1: 70 1155600 217464711 2736 6 0
Break2: 70 119259859 217464711 3431 5 200
Break2: 117 1340007 72126970 389 38 200
Break2: 117 4228188 72126970 1157 12 200
Break2: 117 28301466 72126970 556 26 200
Break1: 118 46043000 76603601 1388 9 0
Break2: 118 60007606 76603601 179 60 200
Break2: 118 69709038 76603601 116 60 200
```

```
2 - Contig/scaffold index;
3 - Breakpoint offset;
4 - Contig/scaffold length;
5 - Average HiC coverage;
6 - Breakpoint likelihood value QV;
7 - Breakpoint nature: contig break (0); scaffold break or break at a gap (200)
```

```
=====
https://github.com/wtsi-hpag/scaffHiC
=====
```

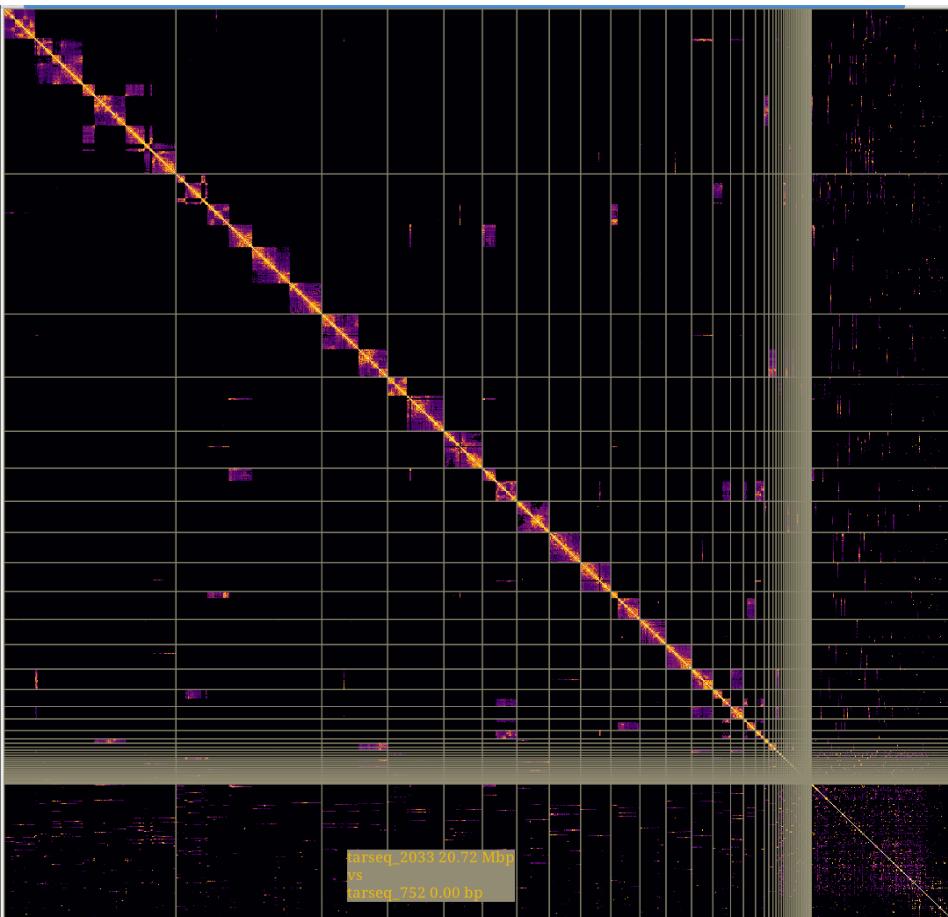
```
$ git clone https://github.com/wtsi-hpag/scaffhic.git
$ cd scaffhic
$ ./install.sh
```

```
/full/path/breakhic -nodes 30 -grid 100 -fq1 GM12878-HiC_1.fastq.gz -fq2 GM12878-HiC_2.fastq.gz
    genome_assembly.fasta genome-break.fasta > try.out
```

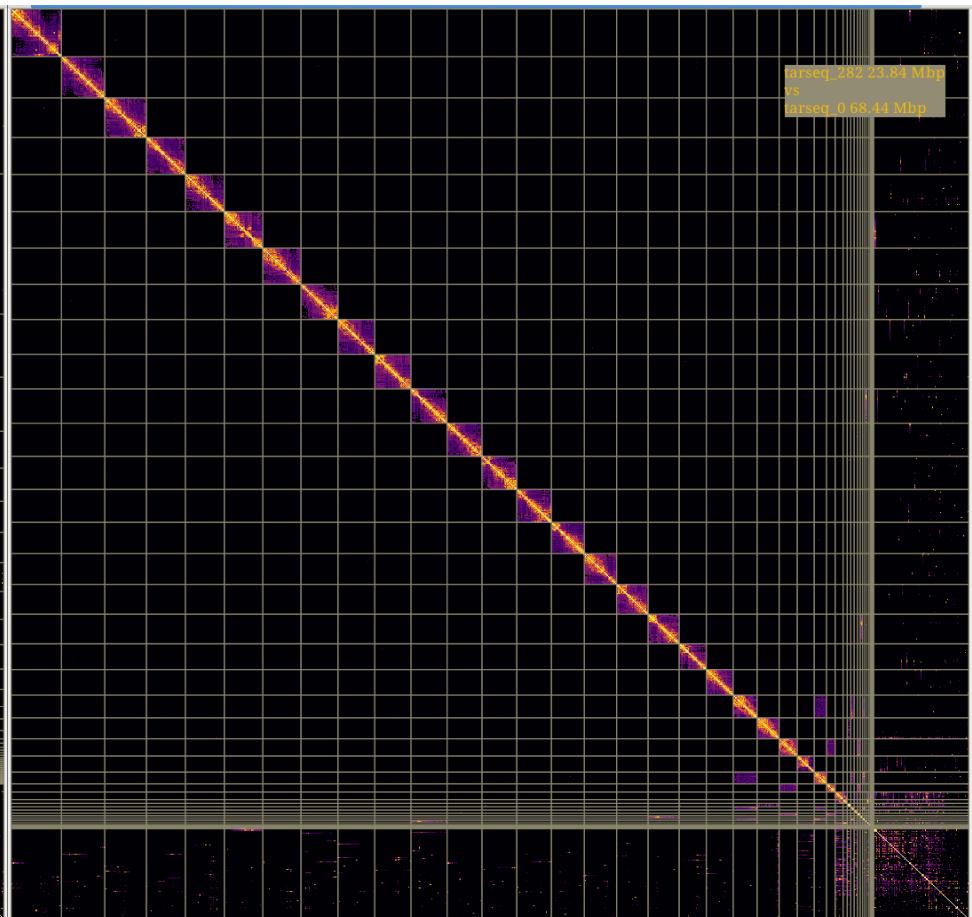
```
/full/path/breakhic -nodes 2 -grid 100 -data /full/path/to/tmp_rununik_27152/align.dat
    genome_assembly.fasta genome-break.fasta > try.out
```

***Output File .brk  
and  
Pipeline Download***

# Zfish – MAT-DHAB

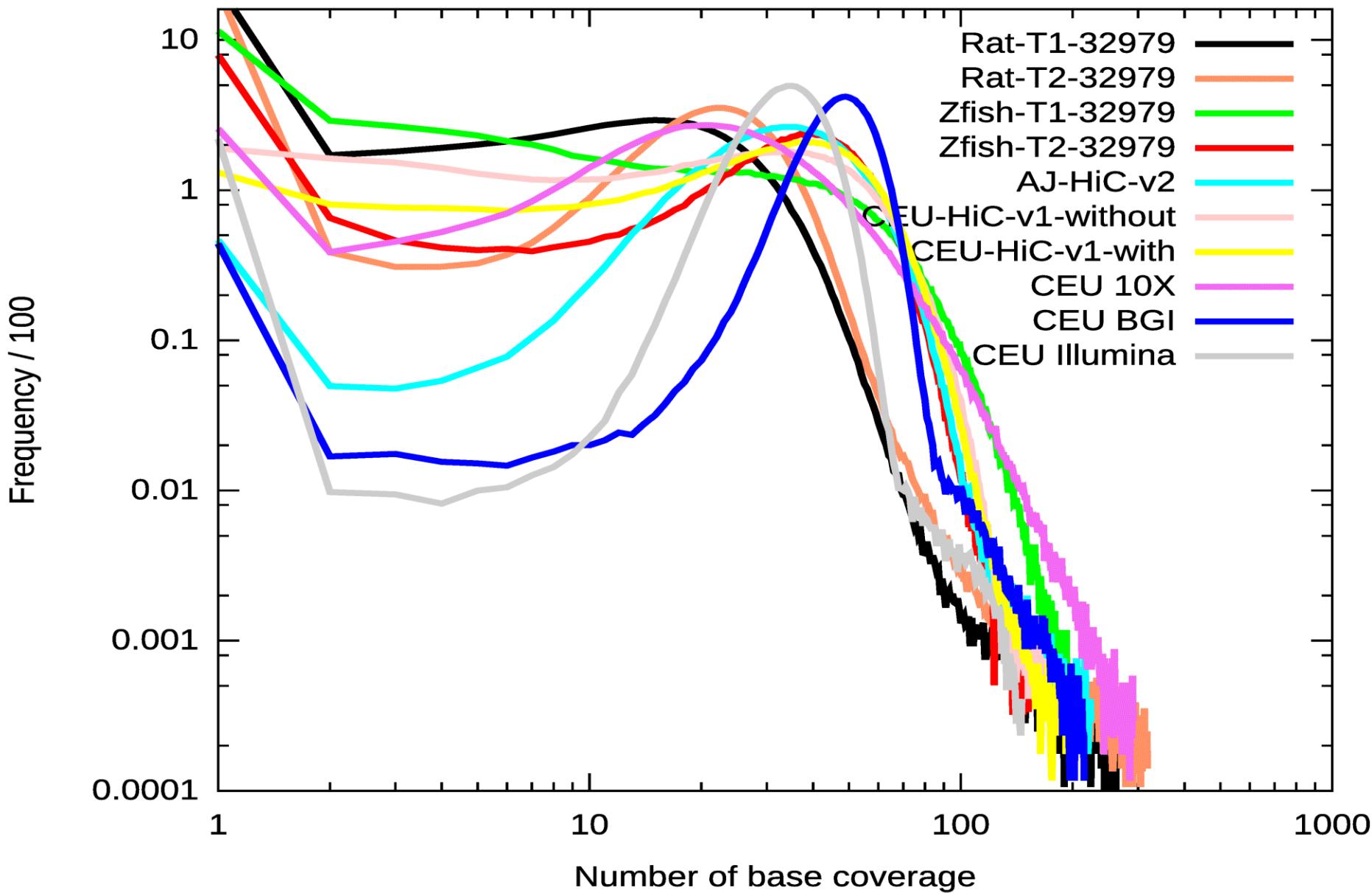


**Without breakHiC**

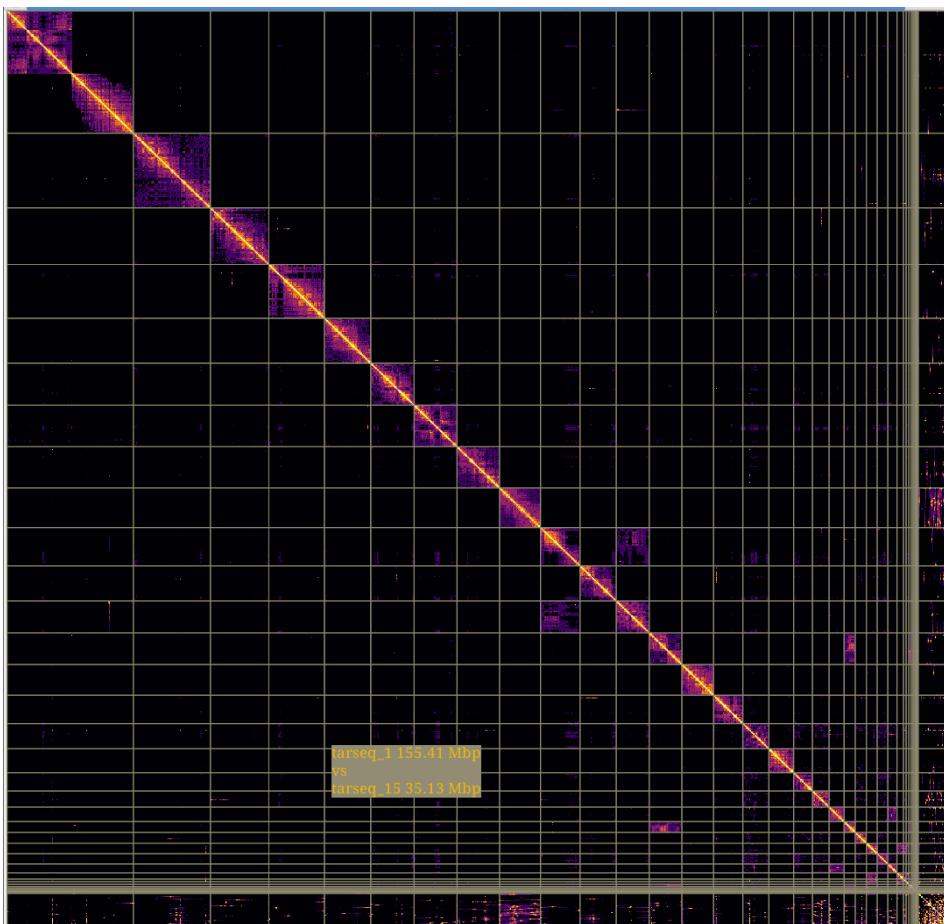


**With breakHiC**

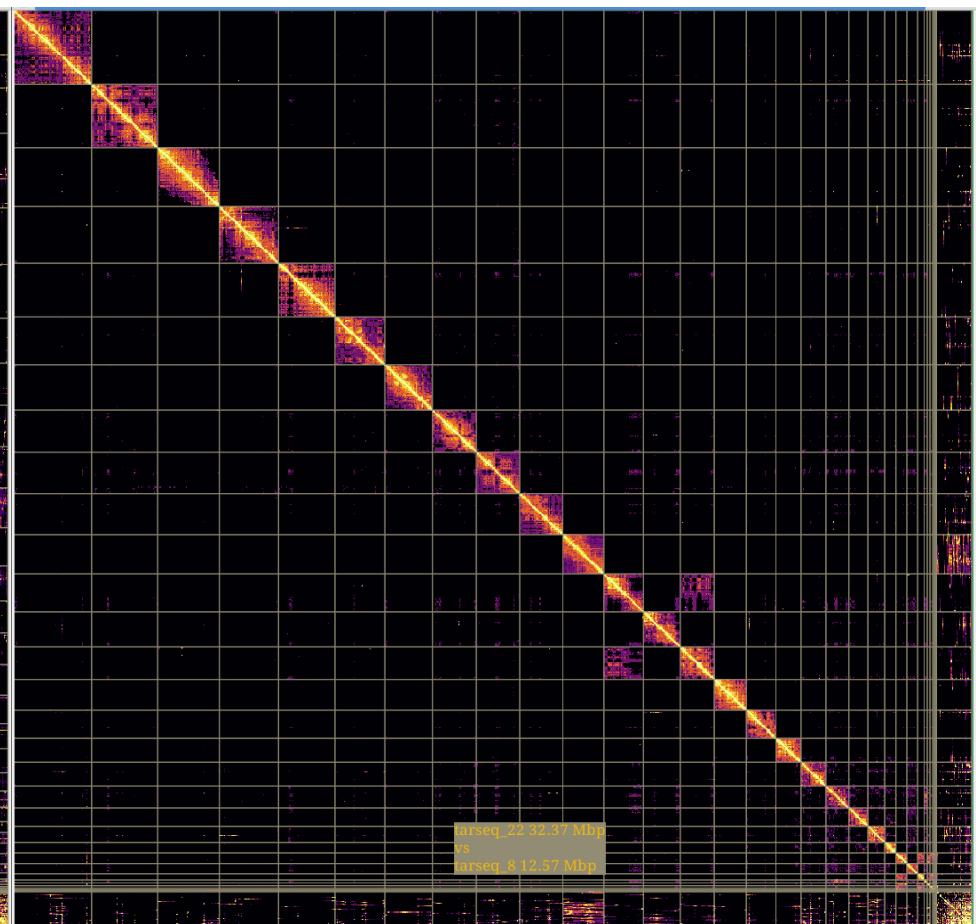
# *Recently Sequenced Arima V2 on Rat and Zfish*



# *Human Genome - Assembly*

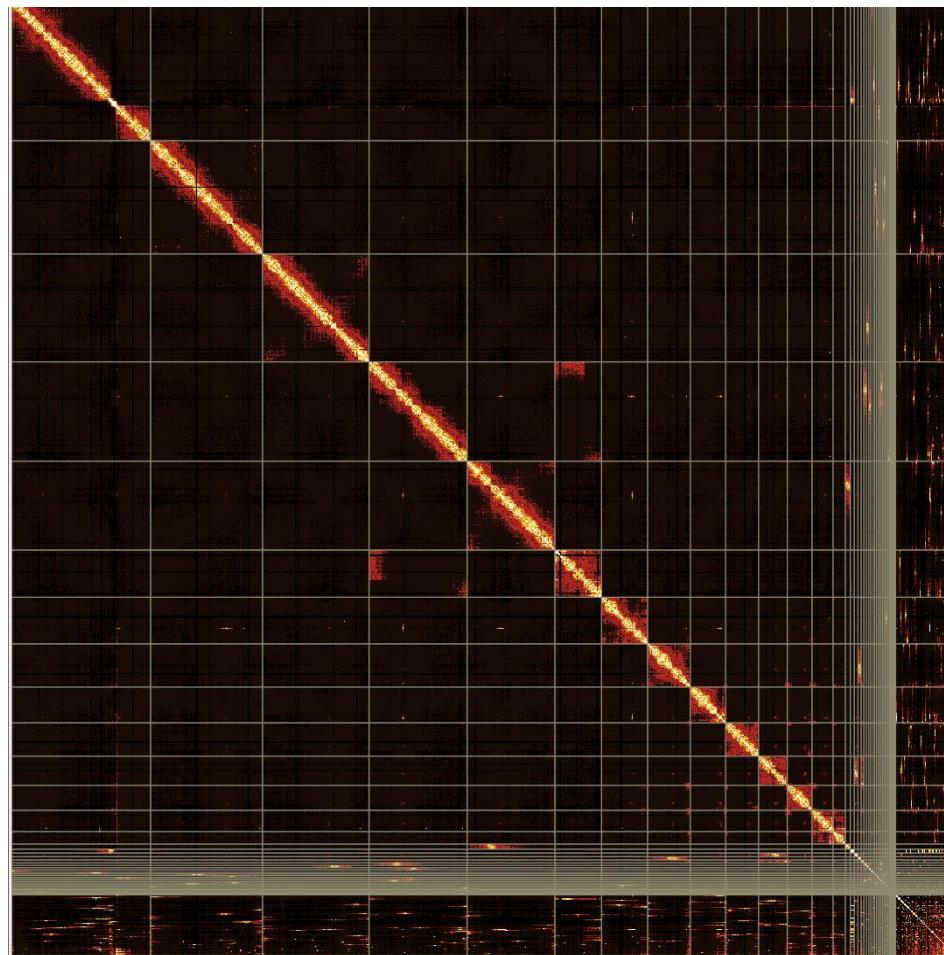


*Without breakHiC*

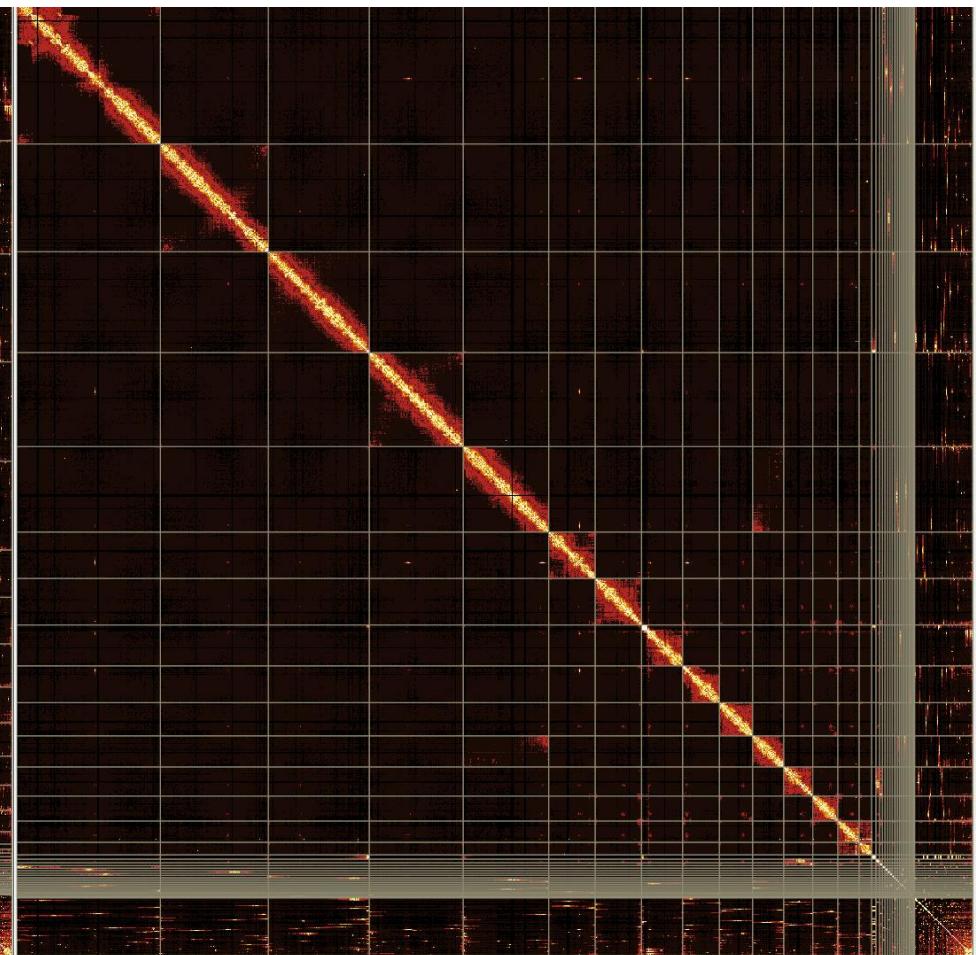


*With breakHiC*

# *Genome Assembly of Frog aRanTem1*



*Run 1*



*Run 2*

# Summary

- *Reviewed three methods to identify assembly breakpoints*
- *Grid method and distribution of reads in paired contigs have issues in finding exact breakpoints*
- *HiC pair link coverage within contigs offers the best detection results*
- *ScaffHiC with breakhic are working well for the assemblies with errors*
- *More work is need to insert small contigs into established scaffolds to increase the ratio of chromosome assignment.*

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- Mike Quail***
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- Edward Harry***
- Shane McCarthy***



*Phase Genomics*