AncesBin – A Pipeline to Bin 10X, HiC, PacBio and ONT reads Based on Ancestry Assemblies

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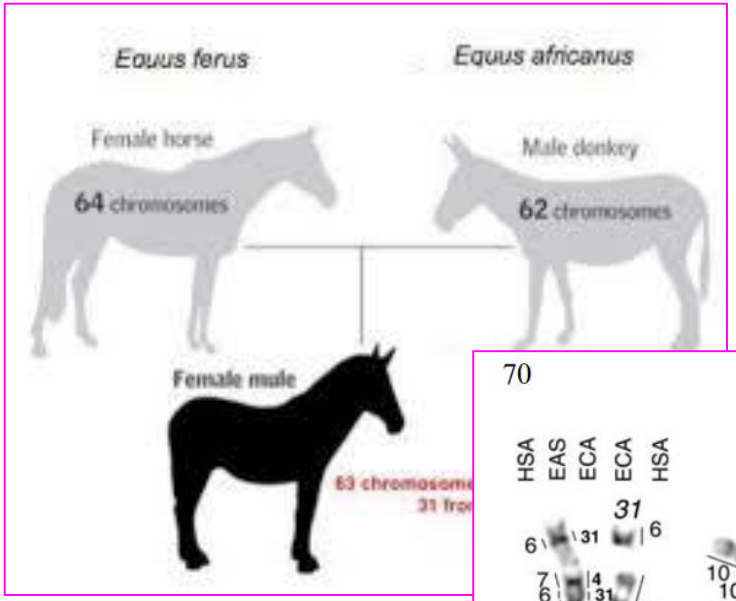
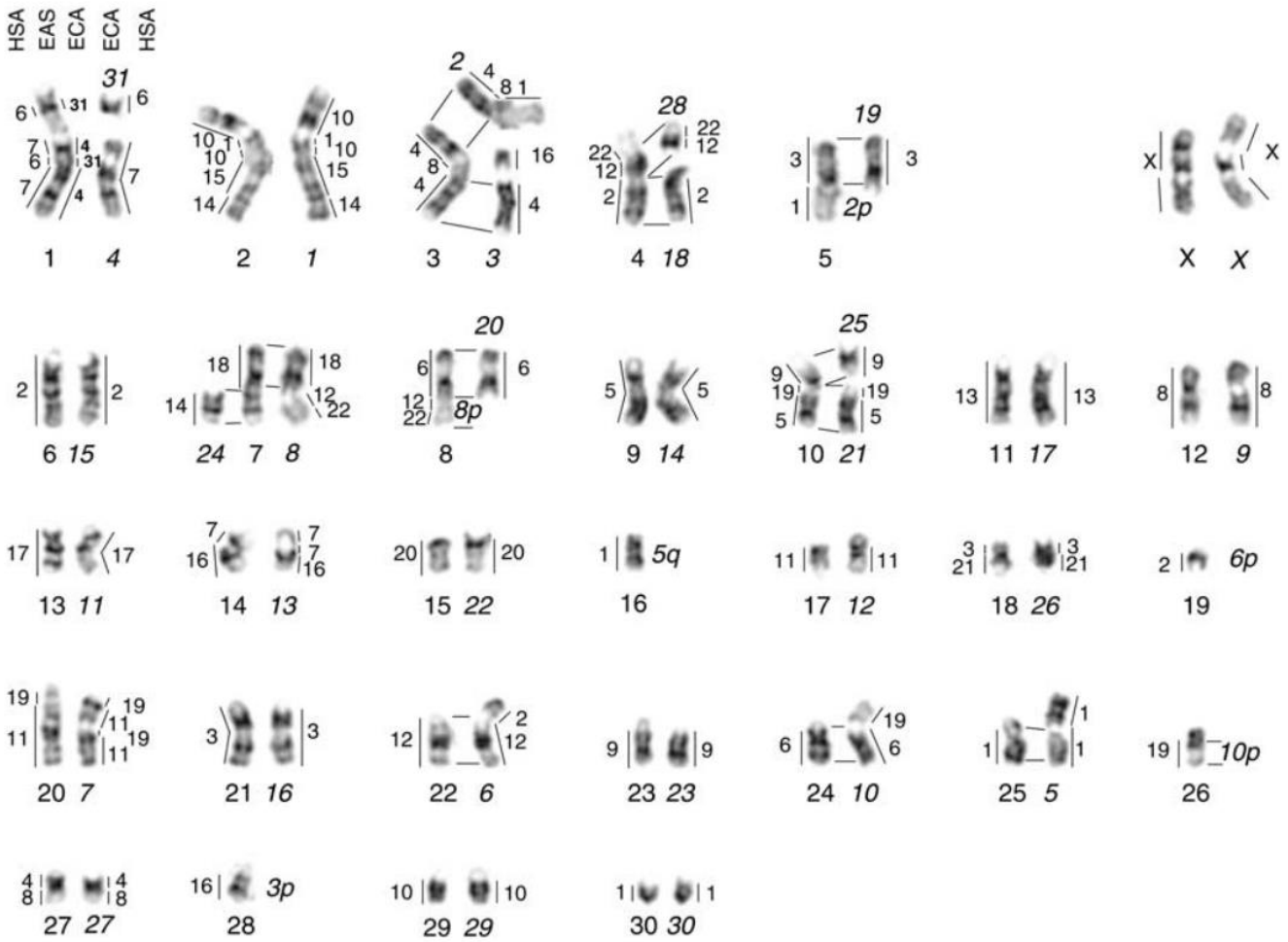
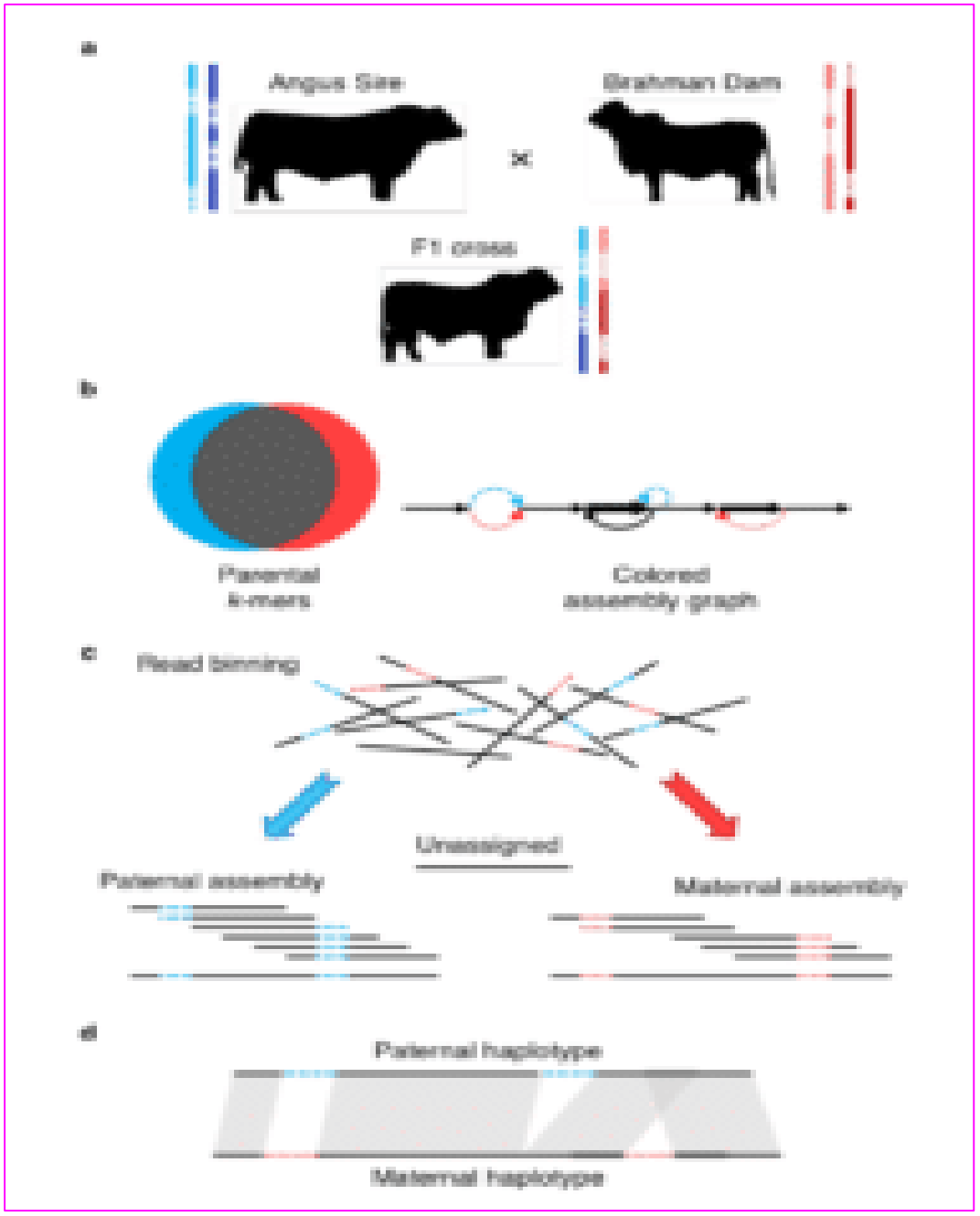


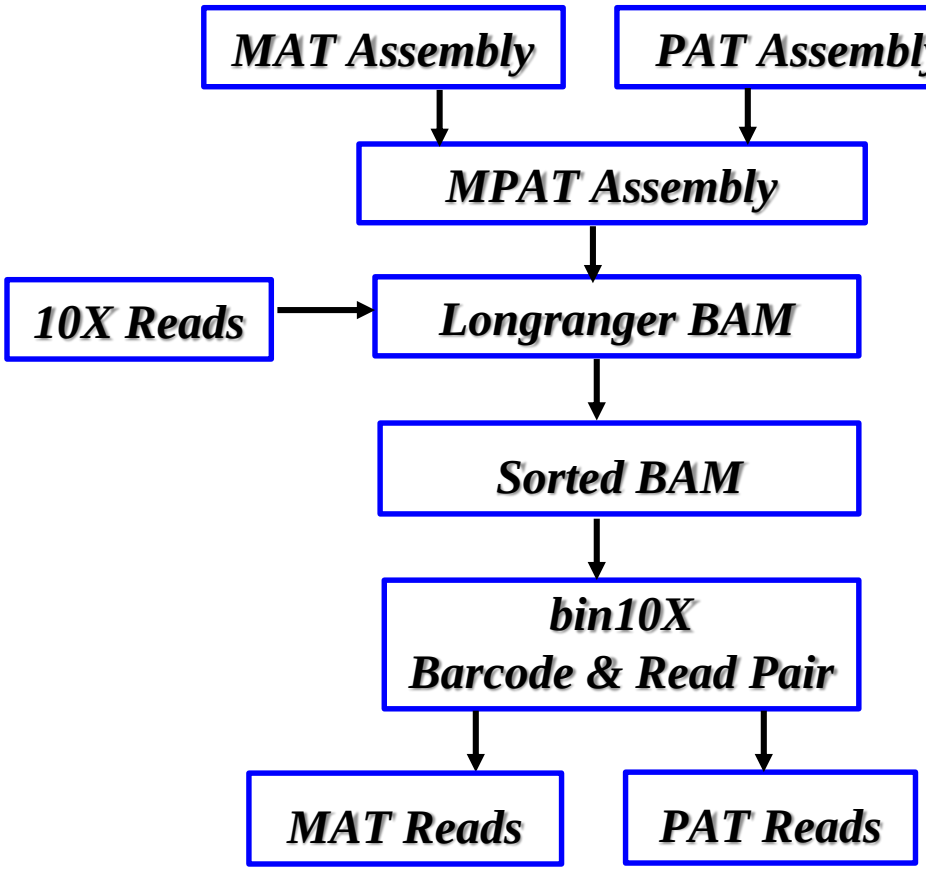
Mule Genome and Chromosome Painting

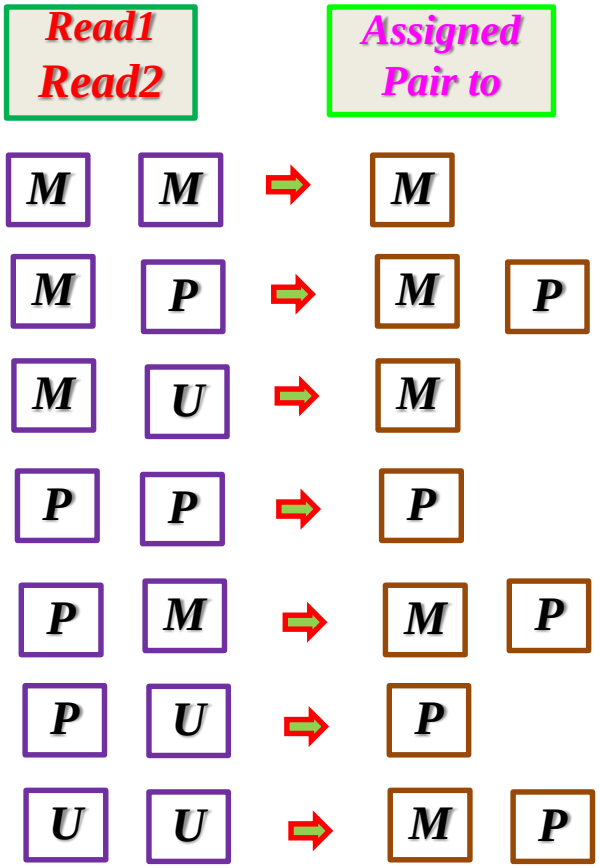


Cattle Genome with triobinning



Flowchart of bin10X

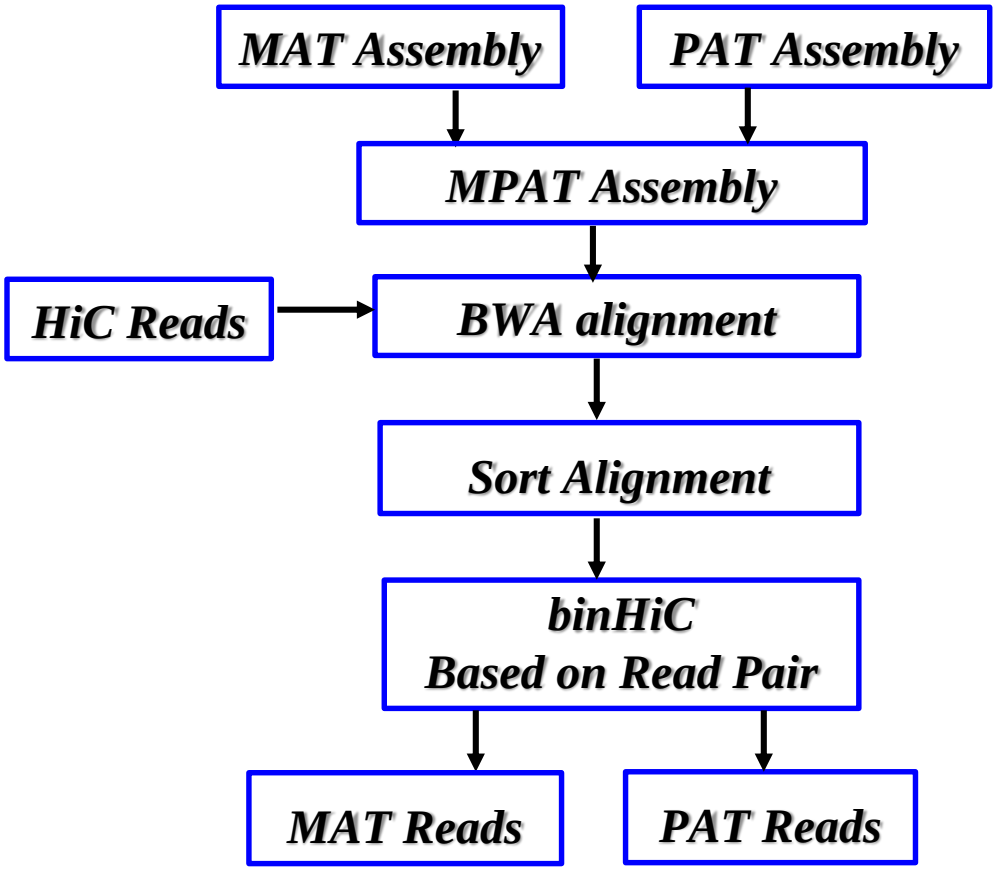




How to run bin10X

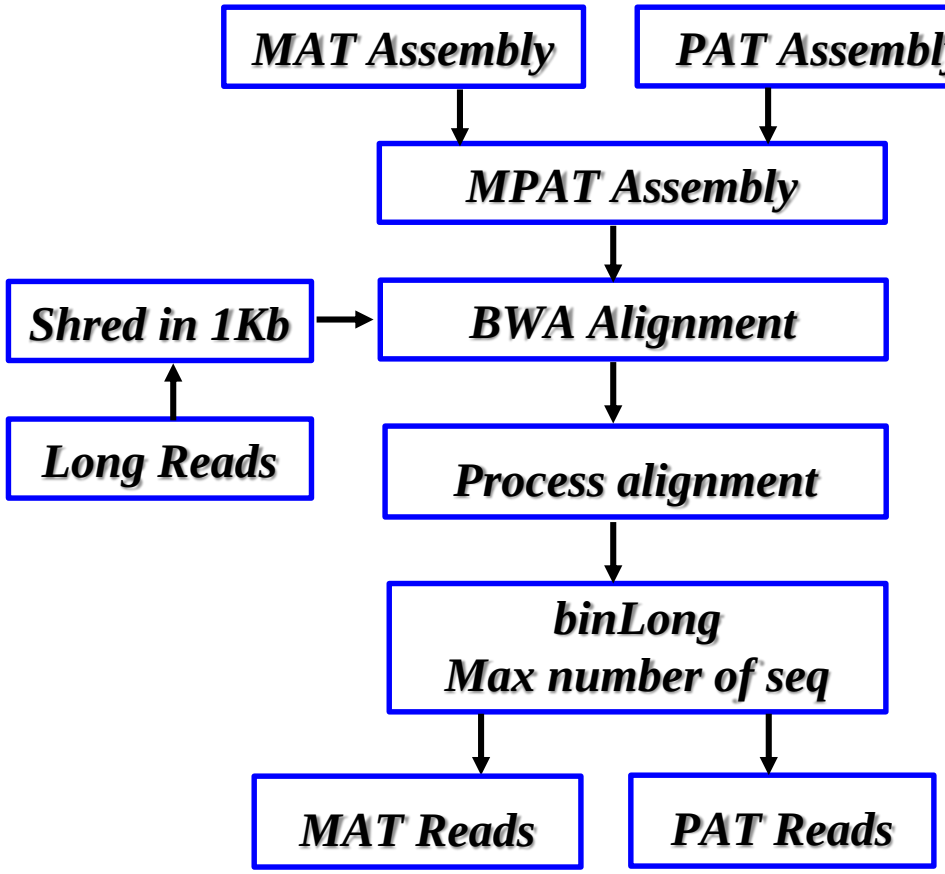
```
#### Run bin10x:
          $ /full/path/to/AncesBin/src/bin10x -nodes <nodes> Input_sorted_bam Input_data_file Output_directory \

          Parameters:
            nodes:            number of CPUs requested  [ default = 30 ]
            Input_sorted_bam: read name sorted longranger BAM file
                              input a bam file which had been produced by using lariat in longranger,
                        (a). rename the assembly file:
                         $ /full/path/to/AncesBin/src/scaff-bin/seqbin_rename -name MAT MAT_assembly.fa MAT_ref.fasta
                         $ /full/path/to/AncesBin/src/scaff-bin/seqbin_rename -name PAT PAT_assembly.fa PAT_ref.fasta

                        (b). cat assemblies
                         $ cat MAT_ref.fasta PAT_ref.fasta > MPAT_ref.fasta

                        (b). generate reference assembly file using longranger
                         $ longranger mkref MPAT_ref.fasta

                        (c). align 10x reads using lariat longranger
                         $ longranger align --fastq="reads_10x" --sample=fTakRub1 --reference="refdata-MPAT_ref" --localcores=50 --id=10x-align
                         Note: for reads_10x please provide full path
                               10x-align is an output directory

                        (d). sort the longranger bam
                         $ samtools sort -n -@ 30 -O BAM -o possorted_sort.bam possorted_bam.bam

            Input_data_file:  a text file to point the locations of the reads in paired files\n");

q1=/lustre/scratch116/vr/projects/Tes1_S1_L008_R1_001.fastq.gz \
q2=/lustre/scratch116/vr/projects/Tes1_S1_L008_R2_001.fastq.gz \
q1=/lustre/scratch116/vr/projects/Tes1_S2_L008_R1_001.fastq.gz \
q2=/lustre/scratch116/vr/projects/Tes1_S2_L008_R2_001.fastq.gz \
q1=/lustre/scratch116/vr/projects/Tes1_S3_L008_R1_001.fastq.gz \
q2=/lustre/scratch116/vr/projects/Tes1_S3_L008_R2_001.fastq.gz \
q1=/lustre/scratch116/vr/projects/Tes1_S4_L008_R1_001.fastq.gz \
q2=/lustre/scratch116/vr/projects/Tes1_S4_L008_R2_001.fastq.gz \

            Output_directory: a director contained all the binned 10X reads\n");
:
```

Flowchart of binHiC



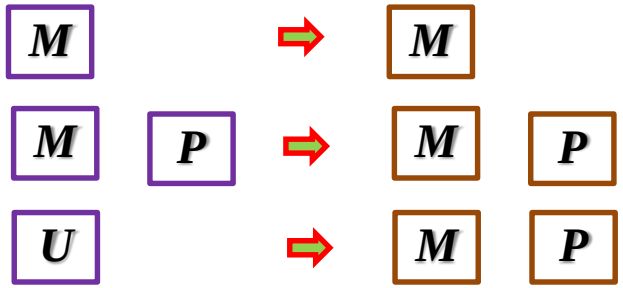
Read1	Read2	Assign the Pair to	
M	M	M	
M	P	M	P
M	U	M	
P	P	P	
P	M	M	P
P	U	P	
U	U	M	P

Flowchart of binLong



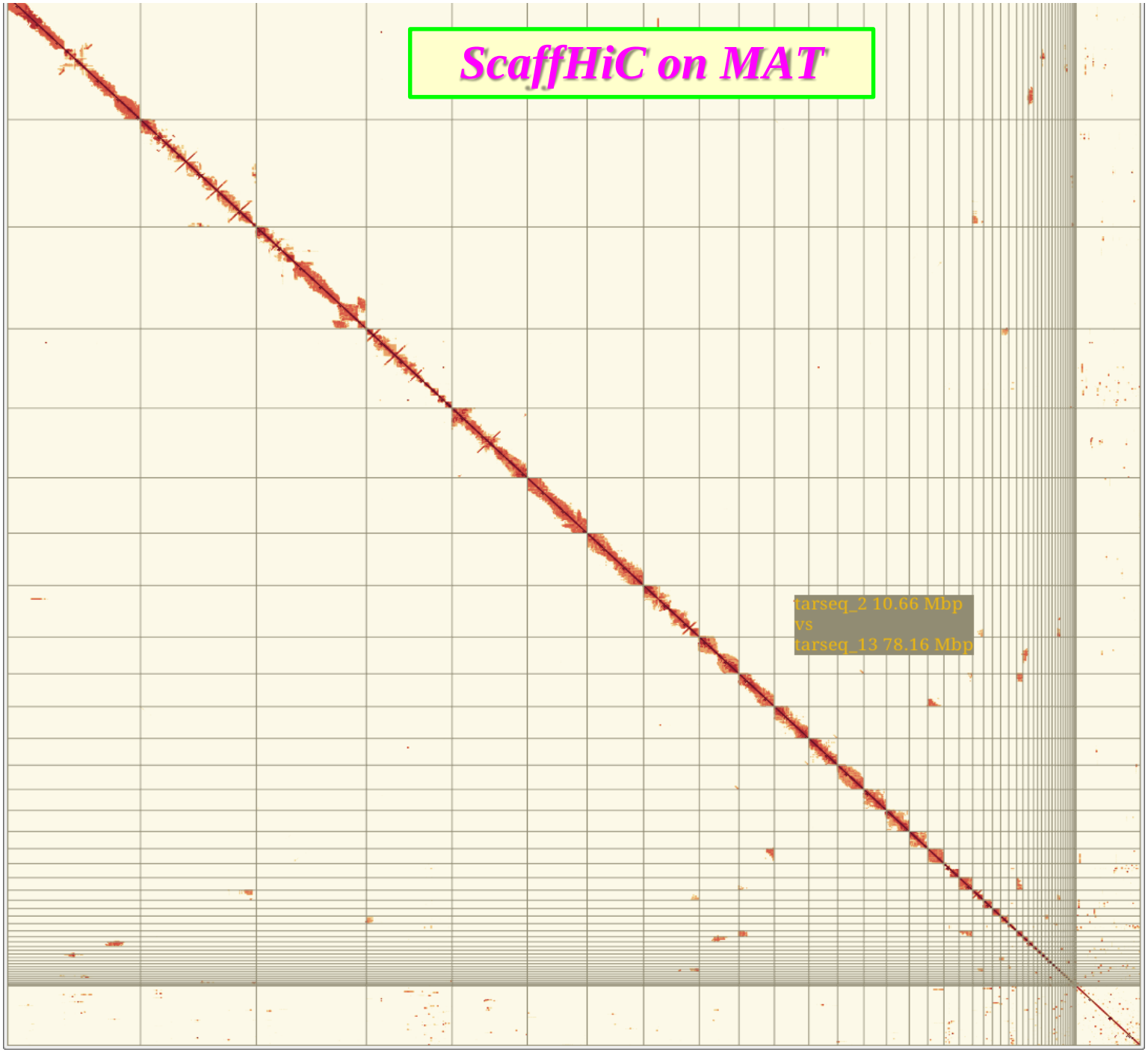
Seq1
Seq2
…
SeqN

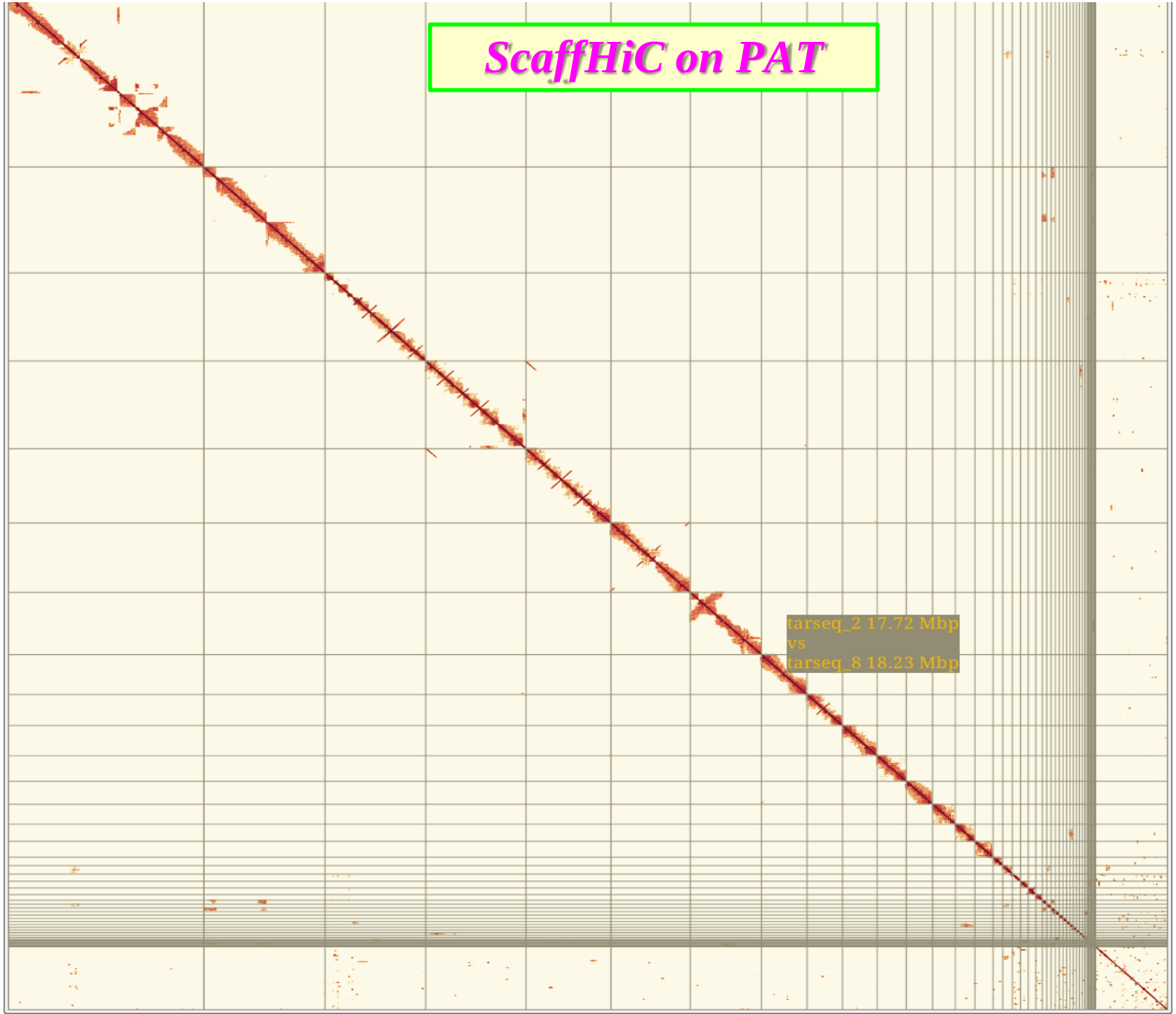
Assign the Read to



How to run binHiC and binLong

```
#### Run binHiC:

          $ /full/path/to/AncesBin/src/binHiC -nodes 30 MAT_ref.fasta PAT_ref.fasta Input_read_1.fq.gz Input_read_2.fq.gz Output_directory

          Parameters:
            nodes:              number of CPUs requested  [ default = 30 ]
            MAT_ref.fasta:      ancestry MAT assembly
            PAT_ref.fasta:      ancestry PAT assembly
               Note:            you need to rename the assembly file:
                                $ /full/path/to/AncesBin/src/scaff-bin/seqbin_rename -name MAT MAT_assembly.fa MAT_ref.fasta
                                $ /full/path/to/AncesBin/src/scaff-bin/seqbin_rename -name PAT PAT_assembly.fa PAT_ref.fasta
            Input_read_1.fq.gz: gzipped HiC read 1
            Input_read_2.fq.gz: gzipped HiC read 2
            Output_directory:   a director contained all the binned HiC reads\n");



#### Run binLong:

          $ /full/path/to/AncesBin/src/binLong -nodes 30 MAT_ref.fasta PAT_ref.fasta Input_data_file Output_directory  \

          Parameters:
            nodes:            number of CPUs requested  [ default = 30 ]
            MAT_ref.fasta:    ancestry MAT assembly
            PAT_ref.fasta:    ancestry PAT assembly
               Note:          you need to rename the assembly file:
                              $ /full/path/to/AncesBin/src/scaff-bin/seqbin_rename -name MAT MAT_assembly.fa MAT_ref.fasta
                              $ /full/path/to/AncesBin/src/scaff-bin/seqbin_rename -name PAT PAT_assembly.fa PAT_ref.fasta
            Input_data_file:  a text file to point the locations of the reads in gzipped files\n");

/lustre/fTakRub1/PacBio/fasta/m54097_180320_123755.subreads.fasta.gz \
/lustre/fTakRub1/PacBio/fasta/m54097_180321_135512.subreads.fasta.gz \
/lustre/fTakRub1/PacBio/fasta/m54097_180322_133901.subreads.fasta.gz \
/lustre/fTakRub1/PacBio/fasta/m54097_180323_154627.subreads.fasta.gz \

            Output_directory: a director contained all the binned PacBio or ONT long reads\n");

:
```


ScaffHiC on MAT
tarseq_2 10.66 Mbp
vs
tarseq_13 78.16 Mbp


ScaffHiC on PAT
tarseq_2 17.72 Mbp
vs
tarseq_8 18.23 Mbp

Download and Compile

```
# AncesBin v1.0
Pipeline to bin 10X, HiC, PacBio and ONT reads based on ancestry assemblies.

### Download and Compile:
Requirements for compiling: gcc:

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

If everything compiled successfully you must see the final comment:
                "Congrats: installation successful!"
```