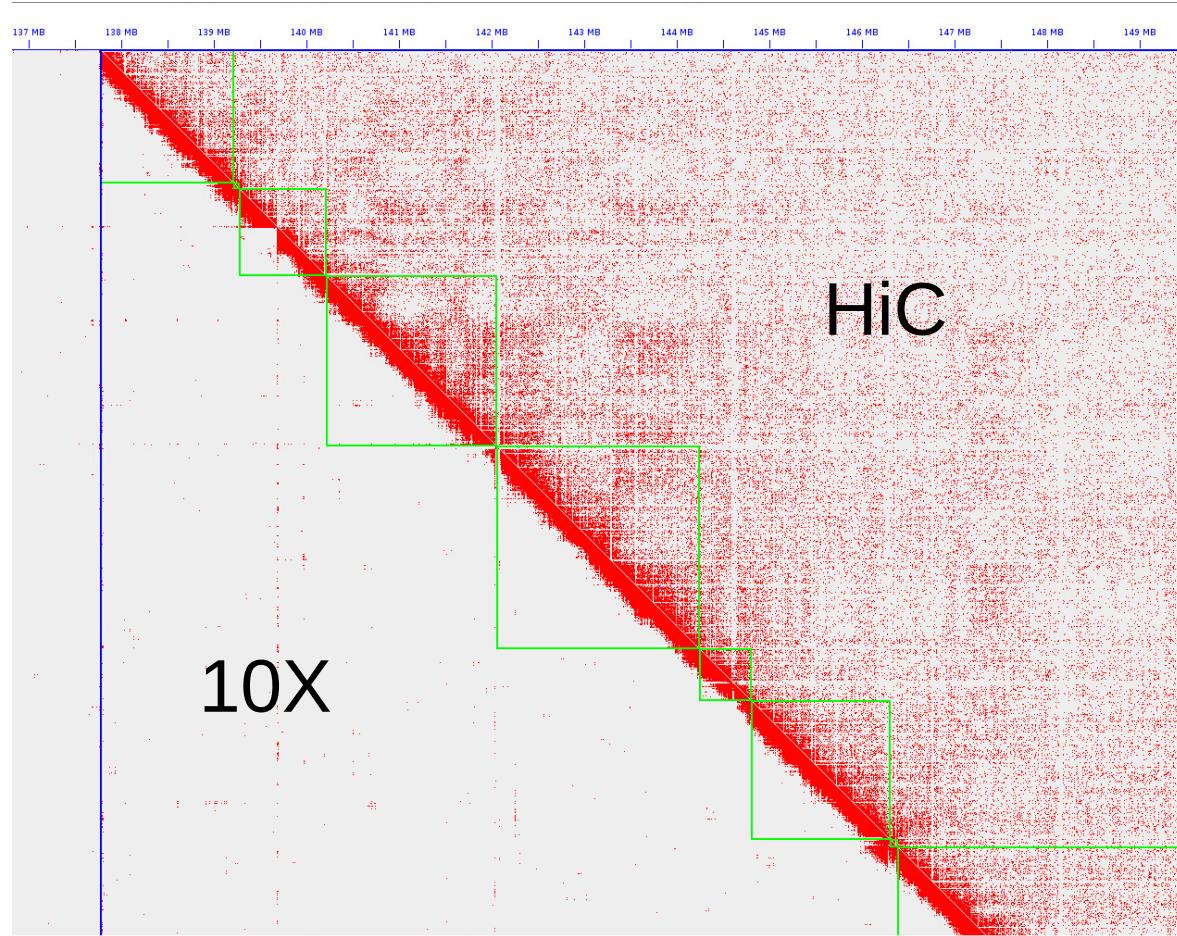


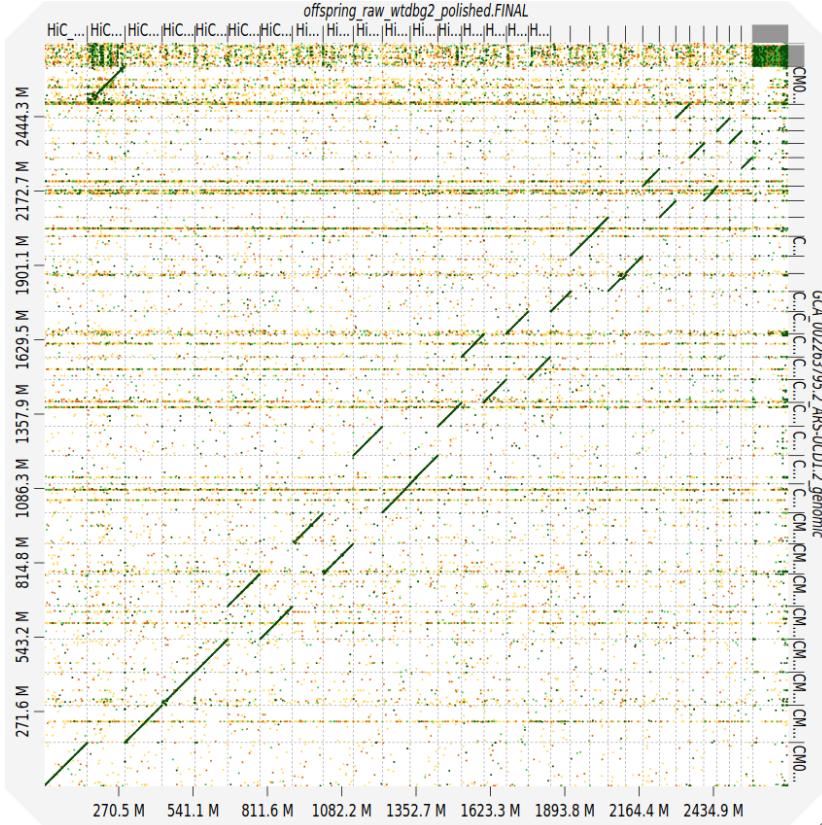
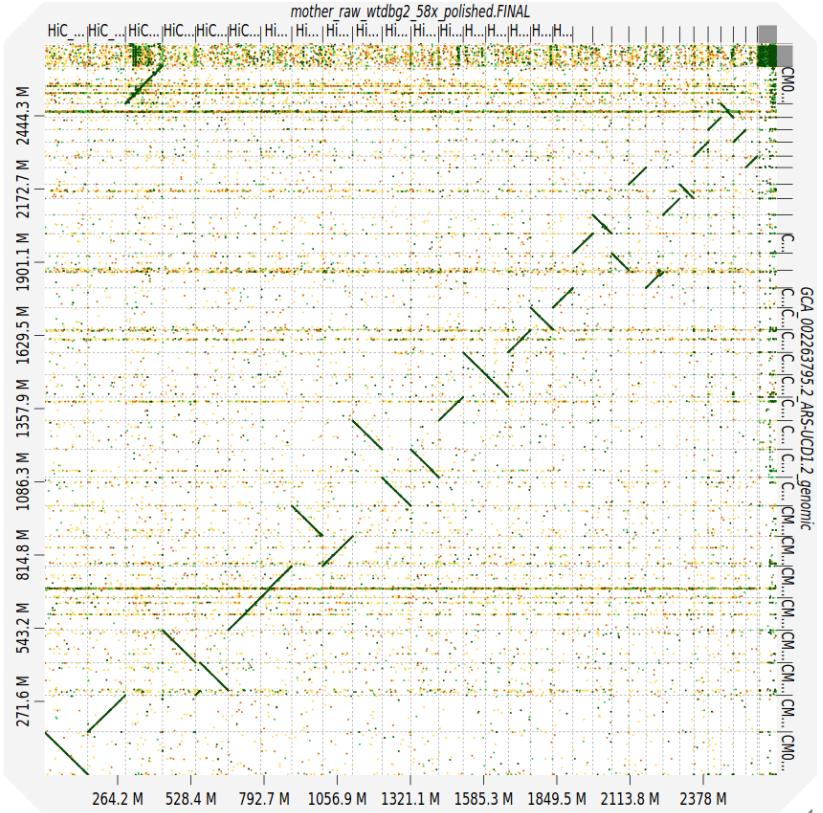
Avancée générale

Individu	Assembly	Polishing LR	Splitting	Polishing SR	Scaffolding	10X Validation	Gap Filling	Final Polishing	Reformatting
Mother1 37165	ONT				HiC				
Father1 37164	ONT				HiC				
Offspring1 37163	ONT				HiC				
Mother2 37162	ONT				HiC				
Father2 37161	ONT				HiC				
Offspring2 37160	ONT					10X			
<i>Sus scrofa</i>	ONT					10X			
<i>Coturnix japonica</i>	ONT				HiC	10X			
Mais F2	HiFi				HiC				
Mais MBS847	HiFi				HiC	10X			
Mais F252	HiFi				HiC				
Zea Mais F4	HiFi				HiC				

10X Validation



Dgenies bovin vs reference

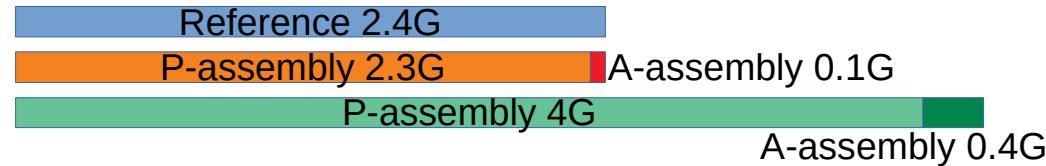


- Reformatting for Mother1 and Offspring2
 - Need 10X validation

Assemblage maïs HiFiasm

Primary assembly = main assembly

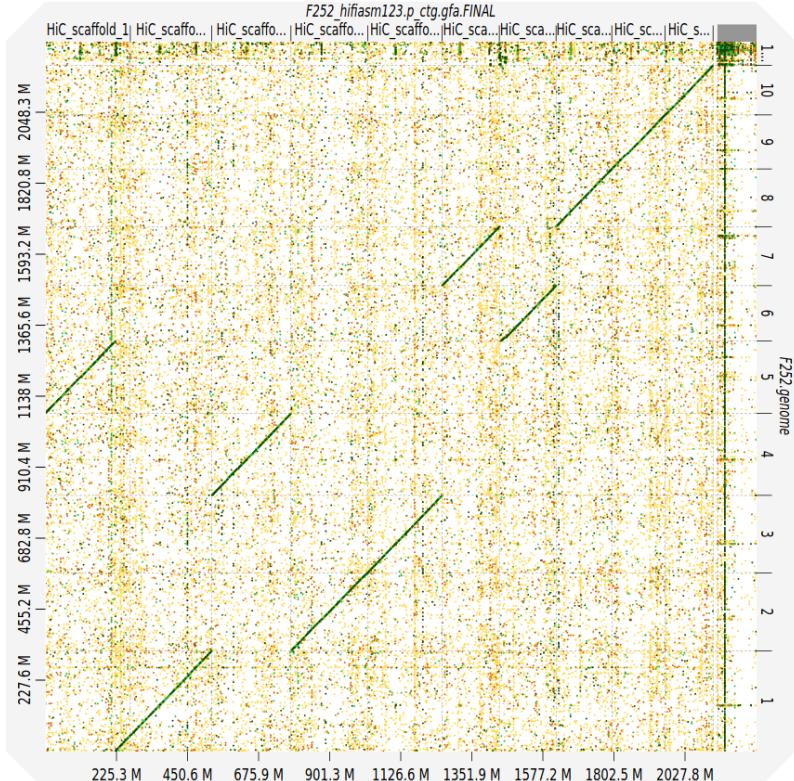
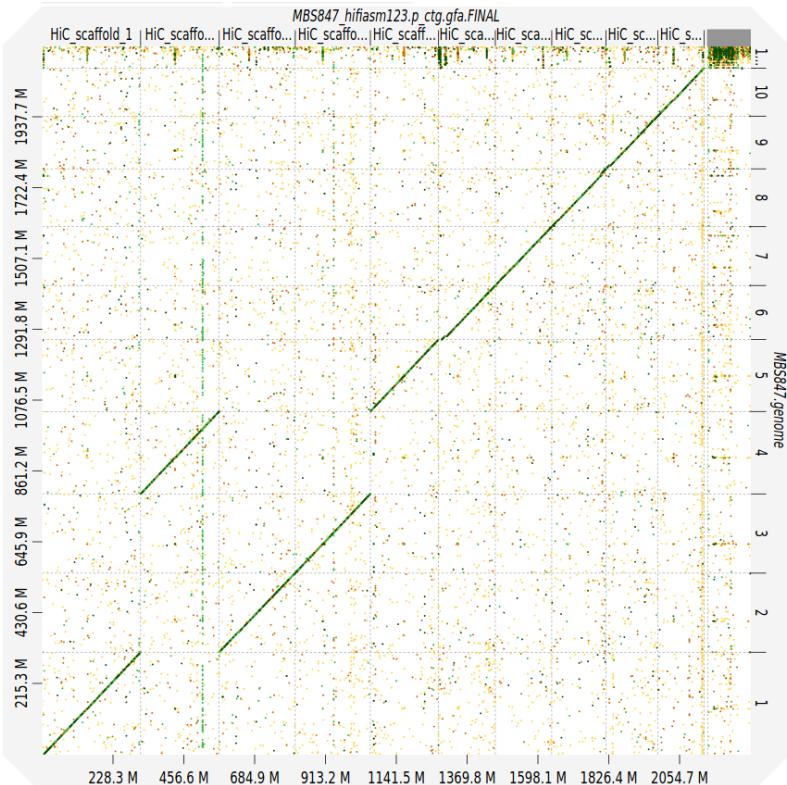
Alternative assembly = alternative locus



	3 SmrtCell			2 SmrtCell			1 SmrtCell		
	Coverage	Assembly size	N50	Coverage	Assembly size	N50	Coverage	Assembly size	N50
MBS	28X	2.282.760.051 105.167.175	57.102.315 37.153						
F4	36X	2.282.760.051 145.339.070	65.799.919 27.086	22X	2.198.673.730 90.941.154	39.835.685 26.192	10X	2.174.819.662 31.842.783	3.427.745 23.047
F4									
F2	31X	2.179.294.636 116.801.547	54.714.342 27.335	20X	2.161.160.622 66.349.646	45.430.689 26.405	14X	2.185.759.644 46.958.077	16.743.894 25.425
F252	33X	2.252.981.446 107.364.903	51.617.720 33.547				8X	2.127.690.102 26.829.327	1.149.281 22.663
F252_MBS847	32X (19X MBS)	3.540.903.366 968.062.301	14.603.842 962.690	23X	3.786.662.434 616.827.159	4.906.073 220.241			
F2_MBS847	30X (19X MBS)	4.097.378.060 428.479.388	12.739.816 875.422	21X	4.056.599.338 390.399.163	3.869.964 475.861			
F4_F2				25X	3.060.188.015 1.355.772.902	13.851.688 522.879			
F4_MBS847	32X (19X MBS)	3.327.549.475 1.256.965.660	20.943.429 1.211.178	23X	3.934.108.867 560.667.118	4.881.412 383.711			
F2_F252				25X	3.515.567.684 909.642.923	10.299.412 1.185.202			
F4_F252				27X	3.306.543.201 1.171.676.556	14.787.673 1.137.896			

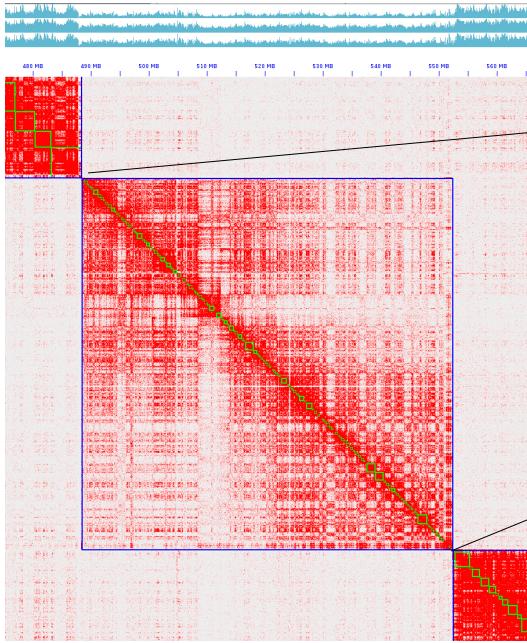
Coverage threshold ≈ 20X for homozygotes
40X for heterozygotes

DGenie maïs HiFi



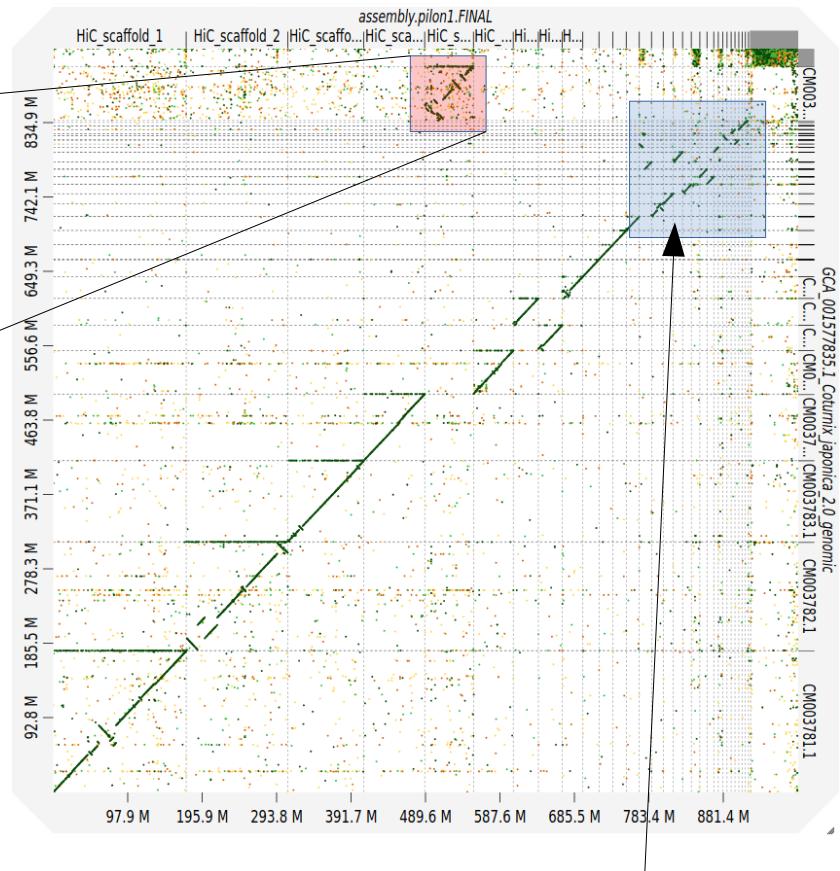
- 10X validation
- Reformatting for MBS847 and F252
- Low error in map with HiFi assembly

HiC Caille



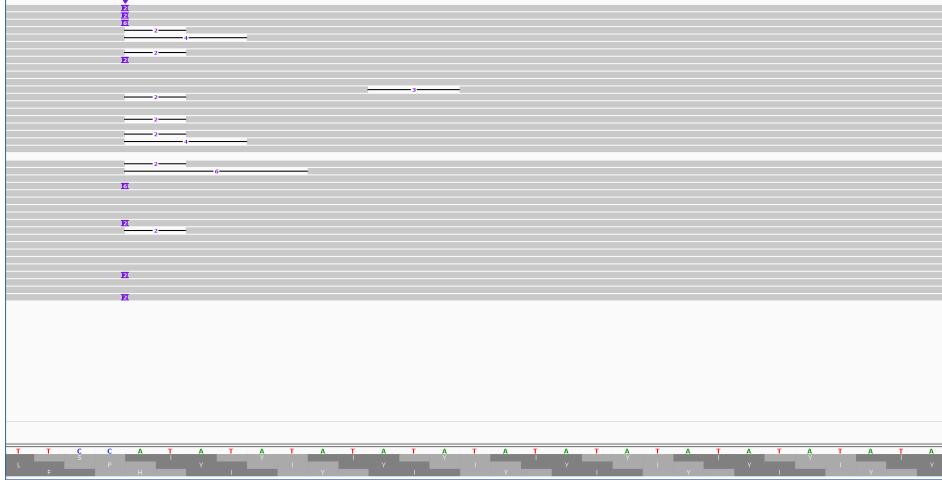
Low coverage area, hard to scaffold

Need to use 10X data to facilitate scaffolding



Micro-chromosome with high inter-HiC contact

Does a HiFi assembly need to be polished?

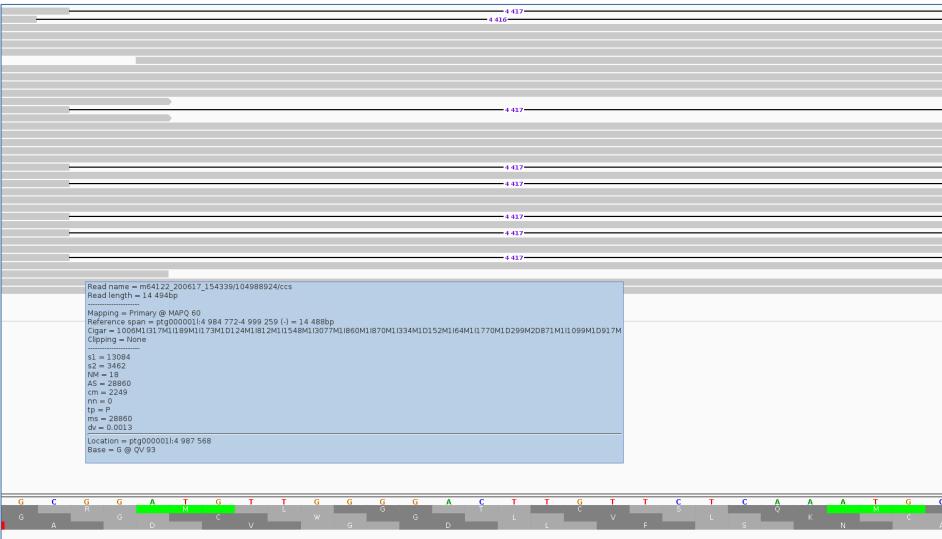


Alignment of reads on assembly

Only 13 000 variations on Maize assembly

2 Types of variations:

- repetitions
- minority of readings with different information (heterozygosity)



Polishing pipeline

News :

Exportable (Conda + Singularity)

Splitting step

6 Runs test on E.coli

1 Run test on Offspring2

Valuation :

Create artifical random assembly and reads

Benchmark pipeline vs others pipeline

Compare polished assembly to reference