



# Bos taurus Axis1 - Assembly

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# **Assembly production**

### <u>- 2 Trio :</u>

- 6 Sequenced
- 6 Assembled and scaffolded
- 6 Available assemblies

### - 154 GABILR :

- 154 Sequenced
- 154 Assembled

### - 9 AC-Bovin:

- 9 Sequenced
- 9 Assembled
- 9 Available assemblies

### - 2 Hybrid Trio:

- 2 Sequenced
- 2 Assembled
- Phasing validation

### - 2 Trio GABILR:

- 2 Sequenced
- Phasing validation











## SeqOccin Q20+ Assembly

	Flye Q20+	Hifiasm Q20+	Flye CLR	Wtdbg2 CLR	Flye ONT	Wtdbg2 ONT	Flye Hifi	Hifiasm HiFi
Coverage	30X	30X	33X	33X	58X	58X	41X	41X
Number of scaffolds	2 398	17150	3 466	2 857	2 744	7 226	18159	905
Total size (Gb)	2.70	2.22	2.66	2.63	2.68	2.70	3.44	3.21
Longest contig (Mb)	76.9	4.8	70.5	56.6	95.23	70.7	11.5	167.7
N50 scaffold length (Mb)	28.5	0.17	19.6	16.5	31.4	23.7	0.75	86.9
L50 scaffold count	30	3570	38	46	26	35	948	15
BUSCO	95.8%	56.9%	95.0%	90.0%	85.7%	70.2%	93.5%	96.0%

- Q20+ hifiasm : No good results so far

- Q20+ flye: Results as good as CLR flye + correction CLR

ONT flye + correction short reads

Q20+: Good consensus sequences quality with flye (HiFi equivalent)
 Missing repeated parts (ONT / CLR equivalent)

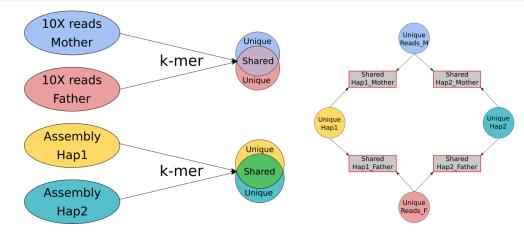






# Seqoccin Phased assembly

	ARS- UCD1.2	Hifiasm consensus	Parent-HiFi Hap1	Parent-HiFi Hap2	HiC-HiFi Hap1	HiC-HiFi Hap2
Number of contigs	3 077	1 444	2 871	2 300	2 658	2 136
Total size (Gb)	2.7	3.2	3.2	3.1	3.1	3.2
N50 contigs length (Mb)	12	84.1	71.6	69.2	80.1	71.6
BUSCO	95.7 %	95.9 %	95.8 %	95.3 %	95.8 %	95.7 %
Phasing ratio			97.3 %	96.7 %	62.6 %	60.5 %
Contigs phasing ratio			97.5 %	96.9 %	84.6 %	85.6 %













# **Phasing assemblies from SNPs**

- Use hapcut2 (&LongShot + WhatsHap) to phase assemblies
- No additional sequencing data
- Work with CLR, CCS, Nanopore

	ARS-UCD1.2	Hifiasm consensus	Hap1	Hap2
Number of contigs	3 077	1 444	3 773	3 009
Total size (Gb)	2.7	3.2	3.5	3.6
N50 contigs length (Mb)	12	84.1	63.2	68.5
BUSCO	95.7 %	95.9 %	95.8 %	95.7 %
Phasing ratio			51.3 %	51.7 %
Number of contigs  Total size (Gb)  N50 contigs length (Mb)  BUSCO  Phasing ratio  Contigs phasing ratio			60.6 %	59.4 %

- First results (from Arnaud) give good metrics but bad phasing
- Test on new Hapcut2 version











# Partenaires du projet

#### Coordination

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### **Axe1 Génomique**

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