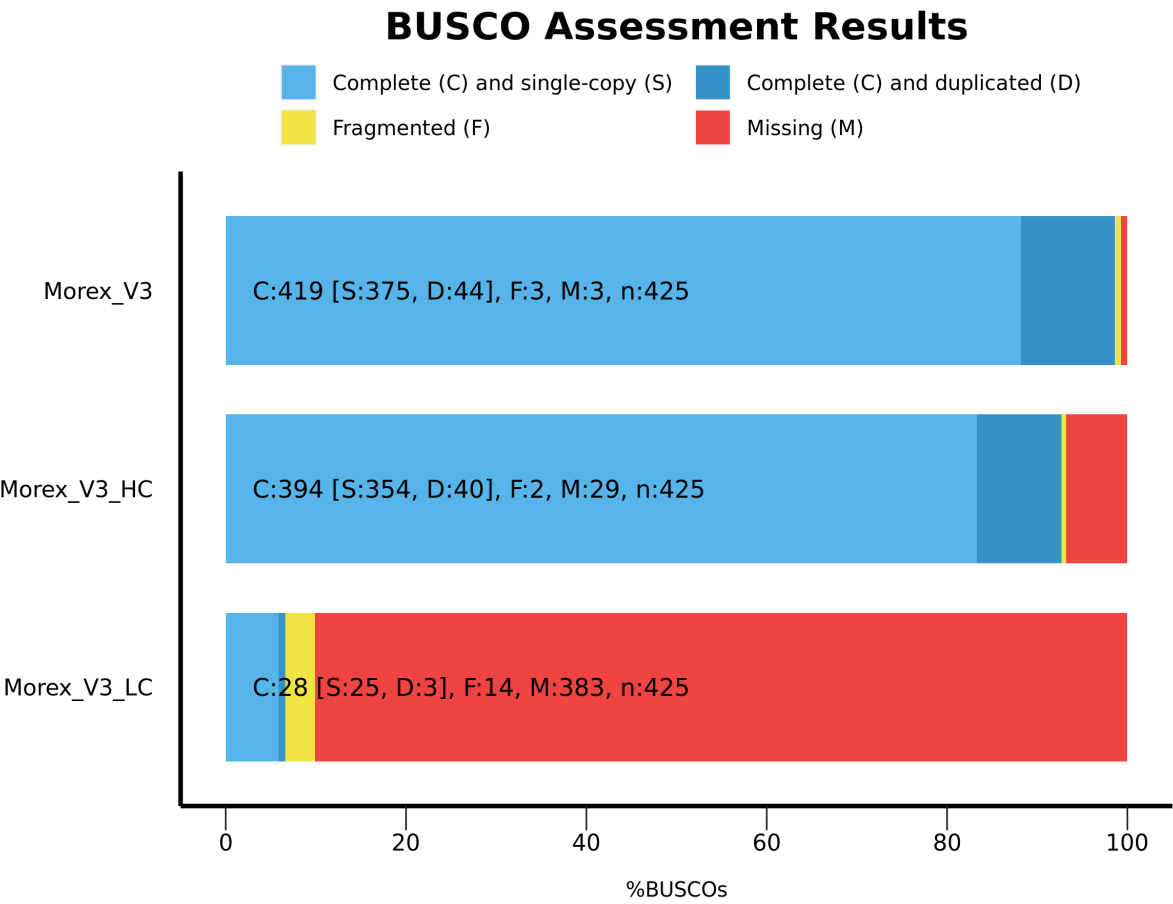
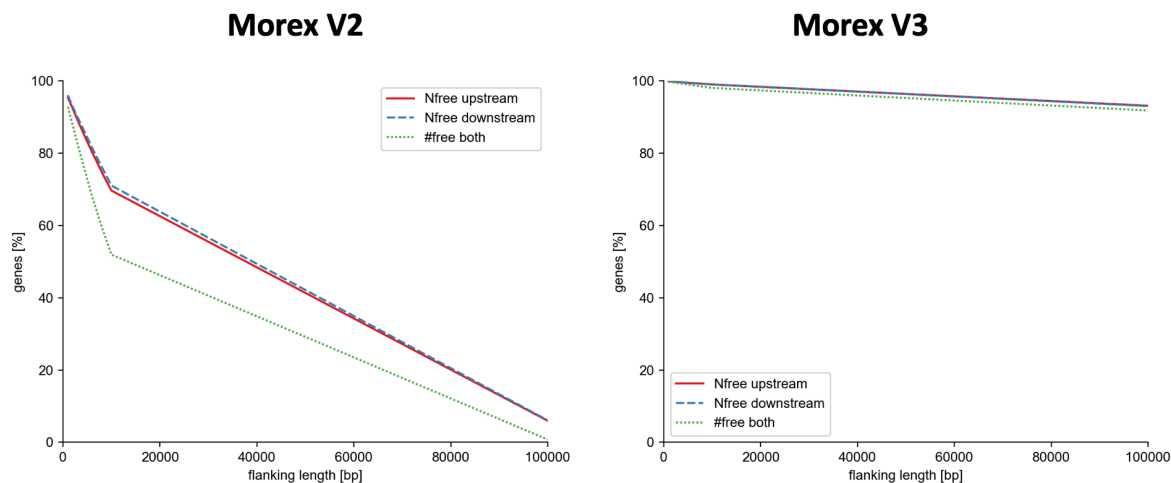


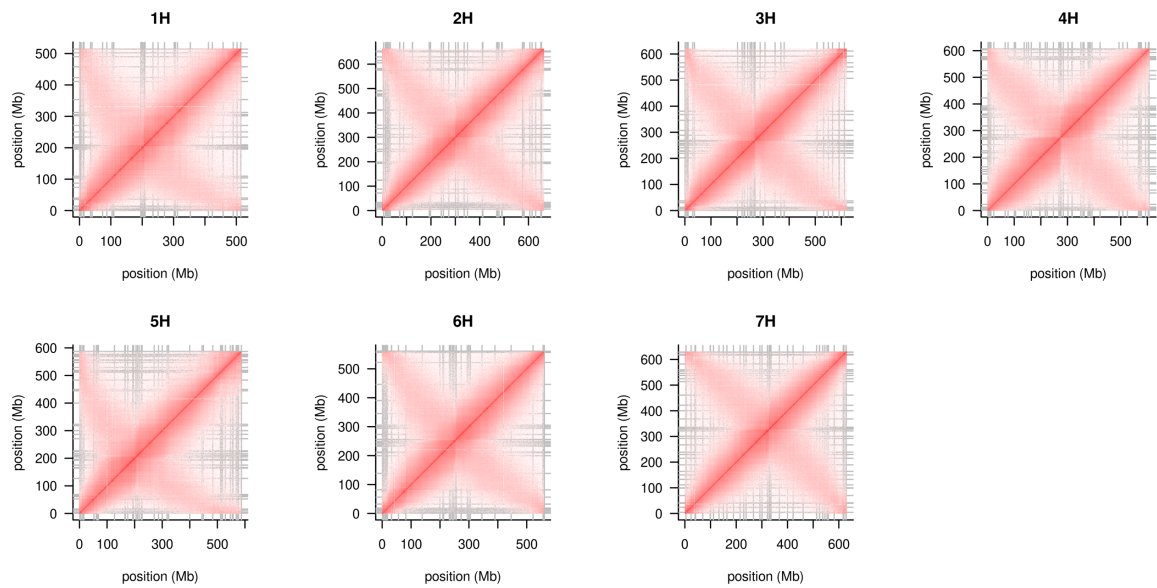
Supplemental Figure S1: BUSCO assessment of different sequence assemblies.



Supplemental Figure S2: BUSCO assessment of the structural gene annotation of the Morex V3 pseudomolecules. Note that multiple isoforms were annotated for some genes so that a higher proportion of duplicates is found. HC: high-confidence; LC: low-confidence.



Supplemental Figure S3: Gap-free sequence in upstream and downstream regions of genes in Morex V2 and Morex V3.



Supplemental Figure S4: Hi-C contact matrices for pseudomolecules constructed from the CCS_Canu assembly (without Bionano scaffolding). Grey lines indicate contig boundaries. The absence of off-(anti)-diagonal signals supports the accuracy of the assembly.

Supplemental Table S4: Gene annotation statistics.

	Complete		High-confidence (HC)		Low-confidence (LC)	
	Total	Average	Total	Average	Total	Average
Number of genes	81687	NA	35827	NA	45860	NA
Number of monoexonic genes	46175	NA	11537	NA	34638	NA
Transcripts per gene	83990	1.03	37963	1.06	46027	1
Coding transcripts per gene	83990	1.03	37963	1.06	46027	1
CDNA lengths	81400273	969.17	53654543	1,413.34	27745730	602.81
CDNA lengths (mRNAs)	81400273	969.17	53654543	1,413.34	27745730	602.81
CDS lengths	71837620	855.31	45079806	1,187.47	26757814	581.35
CDS lengths (mRNAs)	NA	855.31	NA	1,187.47	NA	581.35
CDS/cDNA ratio	NA	92.96	NA	86.24	NA	98.5
Monoexonic transcripts	46175	634.6	11537	963.96	34638	524.9
MonoCDS transcripts	47011	618.84	12246	905.33	34765	517.93
Exons per transcript	240677	2.87	169194	4.46	71483	1.55
Exons per transcript (mRNAs)	3164	2.87	3027	4.46	2010	1.55
Exon lengths	NA	338.21	NA	317.12	NA	388.14
Exon lengths (mRNAs)	NA	338.21	NA	317.12	NA	388.14
Intron lengths	NA	564.07	NA	577.67	NA	493.98
Intron lengths (mRNAs)	NA	564.07	NA	577.67	NA	493.98
CDS exons per transcript	2775	2.8	2648	4.32	1781	1.54
CDS exons per transcript (mRNAs)	2775	2.8	2648	4.32	1781	1.54
CDS exon lengths	71837620	305.88	45079806	274.8	26757814	377.88
CDS Intron lengths	83014426	550.25	70971472	562.89	12042954	485.92
5'UTR exon number	83990	0.26	37963	0.54	46027	0.04
3'UTR exon number	83990	0.26	37963	0.53	46027	0.04
5'UTR length	3166948	37.71	2816553	74.19	350395	7.61
3'UTR length	6395705	76.15	5758184	151.68	637521	13.85
Stop distance from junction	NA	3.6	NA	5.13	NA	2.35
Intergenic distances	NA	49,823.15	NA	114,705.99	NA	91,228.58
Intergenic distances (coding)	NA	49,823.15	NA	114,705.99	NA	91,228.58