Table S2. Table with some statistics of additional assemblies that were generated for investigation if it would give a more complete Y chromosome. These are different sets of contigs, extracted reads and assemblies. The first section includes data sets related to the provided O11 NextDenovo assembly, while the other section includes data sets from the provided O11 Canu assembly. ER is data for the extracted Nanopore reads that were aligned to putative Y contigs. GF is some interesting contigs from the gene fishing.

Data type	Nr of contigs	Nr of extracted reads	Tot. length (bp)	N50	Longest fragment (bp)
Provided O11 NextDenovo assembly NDN-Full					
Putative Y-contigs: DCA + GF	54	625 902			
Flye assembler, DCA + GF	352	-	119 147 494	11 970 674	31 709 624
Putative Y-contigs: DCA increased threshold	105	1 366 237	19 354 832 403 (ER)	21 201 (ER)	187 825 (ER)
Flye assembler DCA: DCA increased threshold	835	-	245 896 946	9 368 670	26 209 426
Provided O11 Canu assembly CANU-Full					
Putative Y-contigs: DCA mix 0	492	822 068	11 596 876 230 (ER)	21 128 (ER)	174 779 (ER)
Flye assembler: DCA mix 0	574	-	164 676 450	9 356 346	26 350 732
Putative Y-contigs: DCA mix 0 + GF	496	822 318	11 600 803 035 (ER)	21 129 (ER)	174 779 (ER)
Flye assembler: DCA mix 0 + GF	557	-	164 358 994	7 957 017	16 918 338