

Table S1. Repeat content of the subset draft assembly. We used RepeatModeler to detect repeats and the Dfam_3.1 Combined Database with RepeatClassifier to classify them [33,50], then used RepeatMasker to locate repeats in the assembly [35]. 1: Most repeats fragmented by insertions or deletions have been counted as one element.

| | Number of elements ¹ | Length | Percentage occupied of sequence |
|------------------------------------|---------------------------------|--------------|---------------------------------|
| Retroelements | 208423 | 102784249 bp | 9.24 % |
| SINEs: | 0 | 0 bp | 0.00 % |
| Penelope | 36938 | 13813895 bp | 1.24 % |
| LINEs: | 191930 | 88657653 bp | 7.97 % |
| CRE/SLACS | 0 | 0 bp | 0.00 % |
| L2/CR1/Rex | 63334 | 24555690 bp | 2.21 % |
| R1/LOA/Jockey | 4526 | 2934064 bp | 0.26 % |
| R2/R4/NeSL | 1736 | 1662589 bp | 0.15 % |
| RTE/Bov-B | 13972 | 4650200 bp | 0.42 % |
| L1/CIN4 | 0 | 0 bp | 0.00 % |
| LTR elements: | 16493 | 14126596 bp | 1.27 % |
| BEL/Pao | 3775 | 2519145 bp | 0.23 % |
| Ty1/Copia | 344 | 270624 bp | 0.02 % |
| Gypsy/DIRS1 | 12155 | 11090256 bp | 1.00 % |
| Retroviral | 0 | 0 bp | 0.00 % |
| DNA transposons | 259238 | 83605564 bp | 7.52 % |
| hobo-Activator | 35507 | 7694409 bp | 0.69 % |
| Tc1-IS630-Pogo | 151555 | 51159902 bp | 4.60 % |
| En-Spm | 0 | 0 bp | 0.00 % |
| MuDR-IS905 | 0 | 0 bp | 0.00 % |
| PiggyBac | 4495 | 1270461 bp | 0.11 % |
| Tourist/Harbinger | 9472 | 1631942 bp | 0.15 % |
| Other (Mirage, P-element, Transib) | 2578 | 1135450 bp | 0.10 % |
| Rolling-circles | 64570 | 11870671 bp | 1.07 % |
| Unclassified: | 2562568 | 583055017 bp | 52.41 % |
| Total interspersed repeats: | | 769444830 bp | 69.17 % |
| Small RNA: | 17929 | 2803112 bp | 0.25 % |
| Satellites: | 0 | 0 bp | 0.00 % |
| Simple repeats: | 135224 | 7066969 bp | 0.64 % |
| Low complexity: | 29913 | 1422099 bp | 0.13 % |

Table S2. Number of SNPs under selection using BayeScan [44] ($Q < 0.01$) or cross-population extended haplotype homozygosity (XPEHH) analysis [51,52] ($-\log_{10} p > 4$). α is BayeScan's locus-specific component of F_{ST} coefficient [44]. Positive values suggest diversifying selection. Positive XPEHH scores suggest selection in the South group, and negative scores suggest selection in the North group.

| Contig | Total SNPs | BayeScan SNPs | BayeScan region | α | XPEHH SNPs | XPEHH region | XPEHH |
|--------|------------|---------------|-----------------|----------|------------|--------------|-------|
|--------|------------|---------------|-----------------|----------|------------|--------------|-------|

| | | | | | | | |
|----------------|----|---|----------------------|-------------------|---|--------------------|-------------------|
| contig_40523 | 26 | 5 | 103,989 – 111,755 | 1.93 – 2.14 | 0 | | |
| contig_11164 | 23 | 4 | 60,487 – 179,797 | 1.84 – 2.05 | 0 | | |
| scaffold_43207 | 11 | 4 | 102,783 – 102,811 | 1.70 – 2.14 | 0 | | |
| contig_12006 | 10 | 3 | 46,975 – 47,031 | 2.09 – 2.15 | 0 | | |
| contig_13287 | 10 | 3 | 58,727 – 58,738 | 1.68 – 1.98 | 0 | | |
| contig_18336 | 20 | 3 | 233,287 – 342,618 | 1.90 – 1.99 | 0 | | |
| contig_2677 | 22 | 3 | 109,260 – 110,069 | 1.79 – 1.99 | 0 | | |
| contig_39072 | 10 | 3 | 55,060 – 55,126 | 2.06 – 2.14 | 0 | | |
| contig_23638 | 6 | 2 | 118,602 – 118,616 | 2.08 – 2.15 | 0 | | |
| contig_37676 | 17 | 2 | 47,912 – 47,954 | 2.01 – 2.03 | 0 | | |
| contig_4080 | 13 | 2 | 26,024 – 26,027 | 1.78 – 1.79 | 0 | | |
| contig_1196 | 24 | 1 | 393,177 | 1.68 | 0 | | |
| contig_12091 | 3 | 1 | 43,431 | 2.02 | 0 | | |
| contig_14933 | 7 | 1 | 80,478 | 1.98 | 0 | | |
| contig_19450 | 6 | 1 | 37,951 | 2.39 | 0 | | |
| contig_202 | 8 | 1 | 80,251 | 2.03 | 0 | | |
| contig_20252 | 20 | 1 | 34,278 | 1.87 | 0 | | |
| contig_205 | 6 | 1 | 28,713 | 2.13 | 0 | | |
| contig_21253 | 6 | 1 | 43,048 | 1.76 | 0 | | |
| contig_23312 | 12 | 1 | 171,714 | 1.95 | 0 | | |
| contig_27115 | 20 | 1 | 111,838 | 1.94 | 0 | | |
| contig_28985 | 6 | 1 | 22,034 | 2.01 | 0 | | |
| contig_3057 | 13 | 1 | 272,534 | 1.91 | 0 | | |
| contig_8456 | 36 | 1 | 88,819 | 1.92 | 0 | | |
| contig_2544 | 65 | 0 | | | 3 | 83,144 – 83,595 | -6.46 – – 5.23 |