

Zea mays ssp. parviglumis sequence

... 20 21 22 23 ... -36 -35 -34 -33 -32 -31 63 64 65 -11 -10 -9 -8 -18 -17 -16 -15 -14 -34 -33 -32 -31 63 64 65 12 13 14 15 16 17 19 20 21 22 ...

Step 1 : find tandem duplication boundaries

* remember syntenic anchor groups for tandem duplication

... 20 21 22 23 ... -36 -35 [-34 -33 -32 -31 63 64 65 -11 -10 -9 -8 -18 -17 -16 -15 -14] [-34 -33 -32 -31 63 64 65 12 13 14 15 16 17] 19 20 21 22 ...

Step 2 : find potential positions for missing syntenic anchors

... [-34 -33 -32 -31 63 64 65 [12 13] -11 -10 -9 -8 -18 -17 -16 -15 -14 [-12 -13] -34 -33 -32 -31 63 64 65 [-11 -10 -9 -8 -18] 12 13 14 15 16 17 [18 8 9 10 11] ...

Step 3 : use syntenic anchor adjacencies to resolve syntenic anchor group position conflicts

* remember syntenic anchors for syntenic anchor losses

... [-34 -33 -32 -31 63 64 65 -11 -10 -9 -8 -18 -17 -16 -15 -14 -12 -13] -34 -33 -32 -31 63 64 65 -11 -10 -9 -8 12 13 14 15 16 17 18 ...

Step 4 : use syntenic anchor adjacencies to choose the ancestral order

* remember rearrangements that appeared after duplication

... [-34 -33 -32 -31 63 64 65 -11 -10 -9 -8 12 13 14 15 16 17 18] -34 -33 -32 -31 63 64 65 -11 -10 -9 -8 12 13 14 15 16 17 18 ...

Step 5 : keep only one of the duplicated groups for further analyses

... [20 21 22] 23 ... -36 -35 [-34 -33 -32 -31 63 64 65 -11 -10 -9 -8 12 13 14 15 16 17 18] 19 [20 21 22] ...

Step 6 : use syntenic anchor adjacencies to identify paralogous syntenic anchors in non tandem duplicates

... [20a 21a 22a] 23 ... -36 -35 [-34 -33 -32 -31 63 64 65 -11 -10 -9 -8 12 13 14 15 16 17 18] 19 [20b 21b 22b] ...