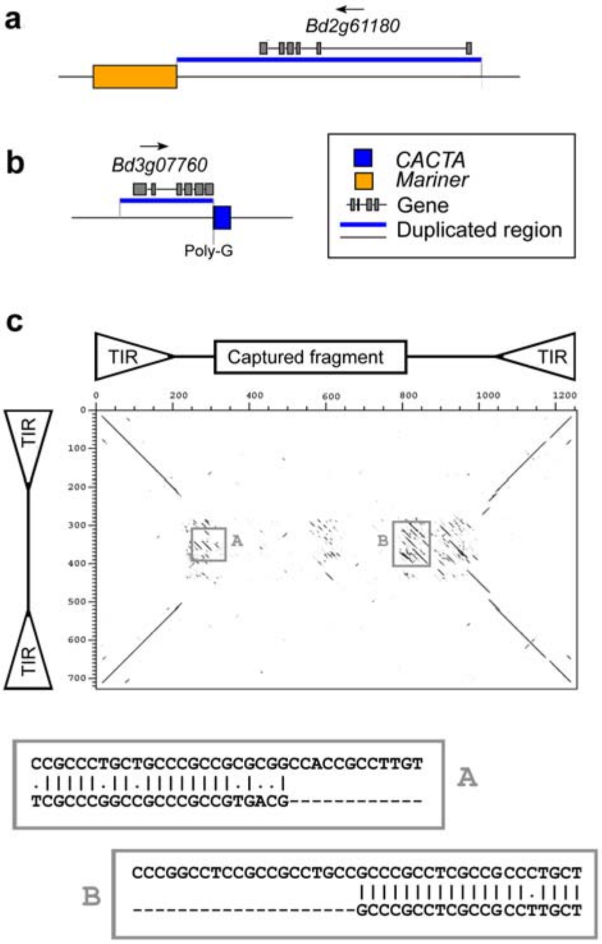
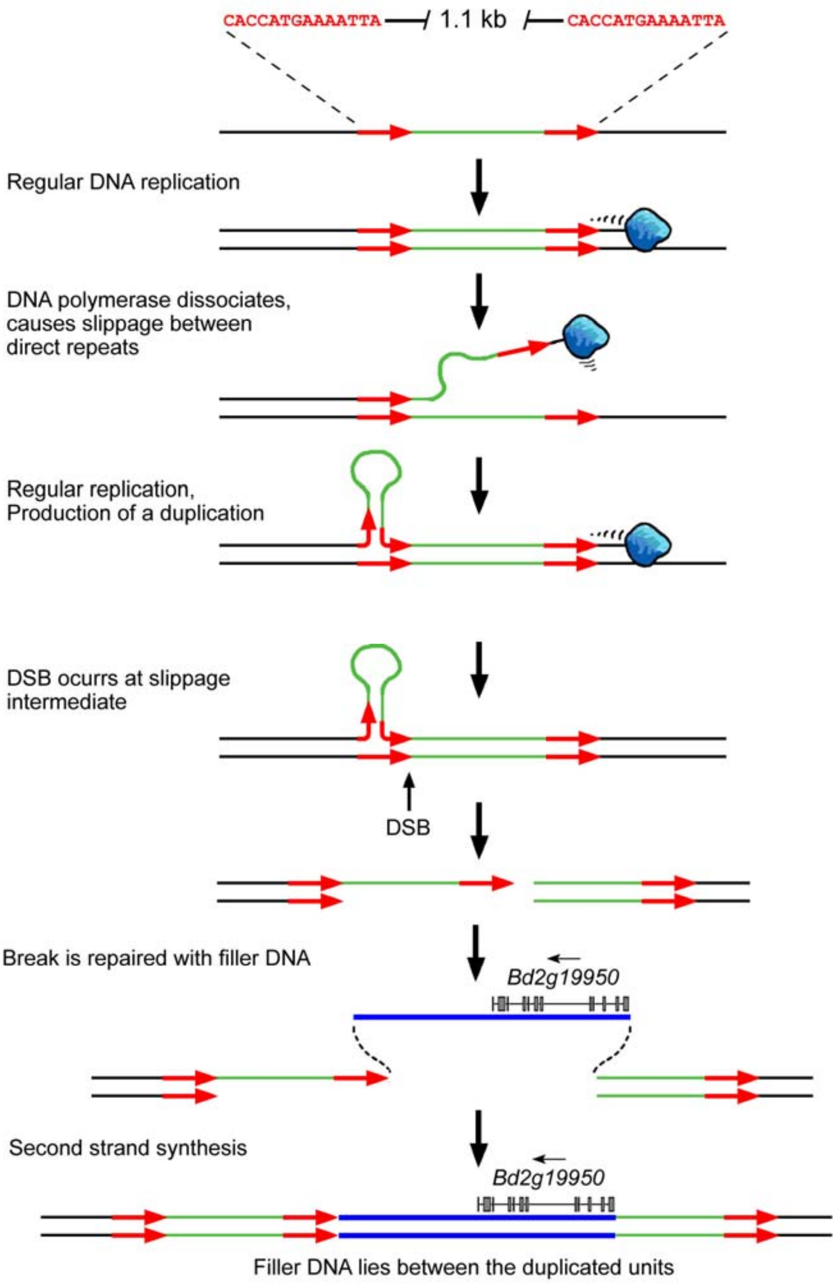


```
CCGCCCTGCTGCCCGCCGCGCGGCCACCGCCTTGT
.|||||.||.||||||||.|..|
TCGCCCGGCCGCCCGCCGTGACG------------
```

```
CCCGGCCTCCGCCGCCTGCCGCCCGCCTCGCCGCCCTGCT
                    |||||||||||||||.||||
--------------------GCCCGCCTCGCCGCCTTGCT
```

Supplementary Figure 1. Duplicated fragments are often flanked on one side by a TE fragment. Often the borders between duplicated fragment and acceptor sites contain G/C-rich motifs. These can form strong secondary structures such as DNA-quadruplexes which can induce DSBs. **a.** and **b.** show examples where fragments of TEs are adjacent to the duplicated fragment. **b.** A poly-G motif forms the border between the fragment containing *Bradi3g07760* and a *CACTA* transposon. **c.** Gene fragments captured by TEs are often bordering G/C-rich motifs. The DotPlot alignment shows a comparison of two *Mutator* element copies one with, and one without a captured fragment. All members of the analysed *Mutator* families have a very GC-rich internal domain with many low-complexity motifs at the border of the captured fragment. Additionally, almost all captured fragments terminate on one or both ends in G/C rich motifs.



Supplementary Figure 2. Gene movement following a DSB caused by a replication slippage event. We propose that the DSB was introduced at the border of the slippage intermediate, leading to the duplicated fragment containing gene *Bradi2g19950* lying precisely at one end of the direct repeat.

Supplementary Table 1. Ancestor chromosome index. The fused chromosomes of *Brachypodium* and sorghum are assigned index numbers (ancestor chromosome index) describing which chromosomal segments correspond to the hypothetical ancestor chromosomes as proposed by Salse et al. (2009). The ancestral chromosomal organisation is still preserved in rice. Bd: *Brachypodium distachyon*, Sb: *Sorghum bicolor*.

Chromosome	Chromosomal region[a]	Ancestral chromosome index
Bd1	Bradi1g16450 - Bradi1g29120	7
Bd1	Bradi1g29130 - Bradi1g52490	6
Bd1	Bradi1g52500 - Bradi1g59820	7
Bd2	Bradi2g14080 - Bradi2g40140	12
Bd3	Bradi3g12460 - Bradi3g20720	8
Bd3	Bradi3g20730 - Bradi3g34600	10
Bd3	Bradi3g34610 - Bradi3g43080	8
Bd4	Bradi4g08170 - Bradi4g08960	9
Bd4	Bradi4g08970 - Bradi4g26920	11
Bd4	Bradi4g26920 - Bradi4g39010	9
Sb1	Sb01g16880 - Sb01g31280	11
Sb2	Sb02g11385 - Sb02g32810	12

[a] Defined by gene identifier numbers