DDSA traces interpretation			
Site	**Position**	**DDSA type of trace**	**Deduction of the neo-synthesized copy**
1	5838	Tandem repeat	Proximal copy (46o6)
2	5949	Micro-homology traces	Proximal copy (46o6)
3	6198	Tandem repeat	Distal copy (58j14)
4	6992	Micro-homology traces	Proximal copy (46o6)
5	8787	Micro-homology traces	Proximal copy (46o6)

Legends:
tandem repeat
micro-homology traces

Site 1: Position: 5838 bp

```
XSR6d-58j14  CCGGCATTTATCAAAACGGCAATGTCG---------GTGGAATCTTTAACTAGAAACAAC
XSR6p-46o6   CCGGCATTTATCAAAACGGCAATGTCGTGGAATCGTGTGGAATCTTTAACTAGAAACAAC
             ***************************         ************************

Dsim         CCGGCATTTATCAAAACGGCAATGTCG---------GTGGAATCTTTAACTAGAAACAAC
Dsec         CCGGCATTTATCAAAACGGCAATGTCG---------GTGGAATCTTTAACTAGAAACAAC
Dmel         GAGGCATTTATCAAATCGGCAATGTCG---------GGGGAATCTTCAACTAGAAACAAC
```

Site 2: Position: 5949 bp

```
XSR6d-58j14  ATAGATCTCTTTGGCATTAAAT------GAGTGAAGCTCCTAAATGTACATATGCAATAT
XSR6p-46o6   ATAGATCTCTTTGGC----------------------TCCTAAATGTACATATGCAATAT
             ***************                      ************************

Dsim         ATAGATCTCTTTGGCATTAAAT------GAGTGAAGCTCCTAAATGTACATATGCAATAT
Dsec         ATAGATCTCTTTGGCATTAAATTAAAATGAGTGAAGCTCTTAAATGTACATATGCAATAT
Dmel         ATAGATCTTTTTGGCATTAAAT------GAGTGAAGCTCCTAAACATACATATGCAATAT
Dyak         ATAGACCTTTTTGGTATTAAAT------GAGAGAAGCTCCTAAATGTACATTTGAAATAT
```

Site 3: Position: 6198 bp

```
XSR6d-58j14  TCGATGTTGGTGCATAACTGTTGTTGTTGCATAACTGTTGTTGTTGCTGTTGCTCGATTT
XSR6p-46o6   TCGATGTTGGTGCATAACTGTTGTTGTTGC------------------TGTTGCTCGATTT
             ****************************                    ************

Dsec         TCGATGTTGGTGCATAACTGTTGTTGTTGC------------------TGTTGCTCGATTT
Dsim         TCGATGTTGGTGCATAACTGTTGTTGTTGC------------------TGTTGCTCGATTT
Dmel         TCGATGTTGGTGCATAACTGTTGTTGTTG--------------------TTGCTTGATTT
```

Site 4: Position: 6992 bp

```
XSR6d-58j14  AATTTGCGTGTTCTTATTTTCCCAAATGTCAACTTTTCCAATTATTTATTTACTTTTTAT
XSR6p-46o6   AATTTACGTGTTCTTATTTTCCCAA----------------TTATTTATTTACTTTTTAT
             ***** ******************                  ******************

Dsim-a       AATTTGCGTGTTCTTATTTTCCCAAATTTCAACTTTTCCAATTATTTATTTACTTTTTAT
Dsim-b       AATTTGCGTGTTCTTATTTTCCCAAATGTCAACTTTTCTAATTATTTATTTACTTTTTAT
Dsec         AATTTGCATGTTCTTATTTTCCCAAATGTCAACTTTTCCGATTATTTATTTACTTTTGAT
Dmel         AATTTGCATGTTTTCATTTTCCCAAATGTCAACTTTACGA-----TTATTAACTTTTATT
```

Site 5: Position: 8787 bp

```
XSR6d-58j14  GAGTACCAGGATTCAAATCACGAGTACCAGGACTTGAATCACGAGTATCAGGACTCAACA
XSR6p-46o6   GAGTACCAGGATTCAA----------------ATCACGAGTATCAGGACTCAACA
             ****************                ************************

Dsim         GAGTACCAGGATTCAAATCACGAGTACCAGGACTTGAATCACGAGTATCAGGACTCAACA
```

Figure S3 Signatures of the DDSA model. Several traces of the DDSA model have been detected when aligning the duplicated fragments according to Fiston-Lavier *et al* (2007): XSR6d-58j14 = distal copy on X^{SR6}, XSR6p-58j14 = proximal copy on X^{SR6}. The stars show the position identical between the copies. Homologous sequences in other species were found in flybase. Dsim: *D. simulans*, Dsec: *D. sechellia*, Dmel: *D. melanogaster*, and *Dyak*: *D. yakuba.* The positions of sites correspond to those in abscissa of Figure 2.