

Table S2. Groups with more than five sequences.

Group n°		49	44	103	54	99	19	117	20	110	106
No. of sequences		6	6	6	7	7	8	13	21	27	32
mean size (bp)		950	1061	6266	441	6207	785	793	4436	6641	936
min size / max size (bp)		607/ 1121	919/1141	649/33754	441/441	513/30617	367/1199	787/829	434/8124	459/65477	576/3253
identity (%)		95.98	88.20	90.20	96.61	91.53	98.71	98,98	99.80	91.19	89,45
Sequence coverage (%)	Gene	0.33	83.26	3.31	0.00	1.74	0.00	66.37	0.00	9.90	0.00
	TE	85.08	0.00	0.02	79.12	0.91	96.96	0.00	98.22	0.34	0.00
	Satellite	15.17	4.43	9.73	9.44	9.76	13.80	6.23	10.52	8.23	9.92
Chromosomal location of all sequences		2/3	X/2R/3	X	2R/3R	X	X/2L/3R/4	X	X/2/3	X (only one on 3R)	X (only one on 2L)
Particularity		1360 *	Actin	XDMR & SAR_DM	Invader4 *	gt,CG32797,CG32733, SAR_DM	Jockey*	Stellate cluster	297,1731,rover	XDMR & SAR_DM	XDMR & SAR_DM

* TE flanked by repeated regions greater than 20 bp which do not correspond to TE or satellite regions.