Table S3. Density of *S. japonicum* retrotransposable elements found in EBRs (Evolutionary Breakpoint Regions) and non-EBR intervals (determined from homologous synteny blocks at 10 kb resolution).

Element type[1]	Density EBRs[2]	Density non-EBRs[3]	*p*-value[4]
LTR	0.53	0.48	0.0002
non-LTR	1.04	0.97	0.0004
Penelope-like	0.14	0.16	0.01

---

[1] Twenty-five retrotransposable elements detected in the *S. japonicum* genome were used (SjCHGCS1 to SjCHGCS22, and Sj-penelope1 to Sj-penelope3). Of these, 18 were classified as LTR, 4 as non-LTR, and 3 as Penelope-like. Positions of the retrotransposable elements were identified in the *S. japonicum* genome using the RepeatMasker (http://www.repeatmasker.org/) program with the –s option.

[2] Average no. of retrotransposable elements found in the 10 kb intervals overlapping with EBRs.

[3] Average no. of retrotransposable elements found in the non-EBR regions.

[4] Statistically significant differences in retrotransposable elements in the EBR regions as compared to the rest of *S. japonicum* genome were calculated using the Student's *t-test* with uneven variances.