

**Table S1.** Summary of preliminary and filtered G:C to A:T transitions in the whole genome and protein-coding region SNPs in the error-prone SNPs filtering.

Line	WG <sup>a</sup> gcat%	WG N <sup>b</sup>	CDS <sup>c</sup> gcat%	CDS <sup>d</sup> N	- BSWG <sup>e</sup> gcat%	- BSWG <sup>f</sup> N	- BSCDS <sup>g</sup> gcat%	- BSCDS <sup>h</sup> N
10-2	49.70	19,452	45.51	3,032	77.21	10,426	69.16	1,741
10-3	59.60	15,566	59.06	1,876	84.77	9,636	91.07	1,097
10-d	50.43	18,155	44.95	2,605	78.87	9,663	71.95	1,408
12-2	53.94	4,885	57.89	1,033	77.93	2,891	80.84	663
<i>dhr2-1</i>	29.58	13,000	32.19	1,839	65.45	3,184	79.58	524

<sup>a</sup> WG gcat% refers to Percentage of G:C to A:T SNPs in the whole genome prior to filtering.

<sup>b</sup> WG N refers to Number of G:C to A:T SNPs in the whole genome prior to filtering.

<sup>c</sup> CDS gcat% refers to Percentage of G:C to A:T SNPs in the coding sequences prior to filtering.

<sup>d</sup> CDS N refers to Number of G:C to A:T SNPs in the coding sequences prior to filtering.

<sup>e</sup> -BSWG gcat% refers to Percentage of G:C to A:T SNPs in the whole genome after filtering.

<sup>f</sup> -BSWG N refers to Number of G:C to A:T SNPs in the whole genome after filtering.

<sup>g</sup> -BSCDS gcat% refers to Percentage of G:C to A:T SNPs in the coding sequences after filtering.

<sup>h</sup> -BSCDS N refers to Number of G:C to A:T SNPs in the coding sequences after filtering.