

S1 Table. Summary of the parent-of-origin genotypes and the corresponding parental *TTG2* dosages.

Cross combinations ^a	<i>TTG2</i> level in		Relative <i>TTG2</i> ^d	Seed phenotype
	Antipodal cells ^b	Sperm ^c		
WT x WT	/	/	balance	Normal
WT x <i>top1α-10</i>	/	↑	A<S	Small
<i>top1α-10</i> x WT	↑↑↑	/	A>S	Large
<i>top1α-10</i> x <i>top1α-10</i>	↑↑↑	↑	A>S	Large
WT x <i>ttg2-6</i>	/	↓	A>S	Large
<i>ttg2-6</i> x WT	↓↓↓	/	A<S	Small
<i>ttg2-6</i> x <i>ttg2-6</i>	↓↓↓	↓	A<S	Small

^a: Since *UPF1* acts similarly as *TOP1α*, only the phenotypes of *TOP1α* and *TTG2* are listed.

^b: Maternal *TTG2* is contributed by three antipodal cells, and its upregulation, downregulation and unchanged status are indicated as “↑↑↑”, “↓↓↓” and “/”, respectively.

^c: Paternal *TTG2* is contributed by the sperm cell, and its upregulation, downregulation and unchanged status are indicated as “↑”, “↓” and “/”, respectively.

^d: “A” indicates relative *TTG2* level in antipodal cells, while “S” indicates relative *TTG2* level in sperms.