

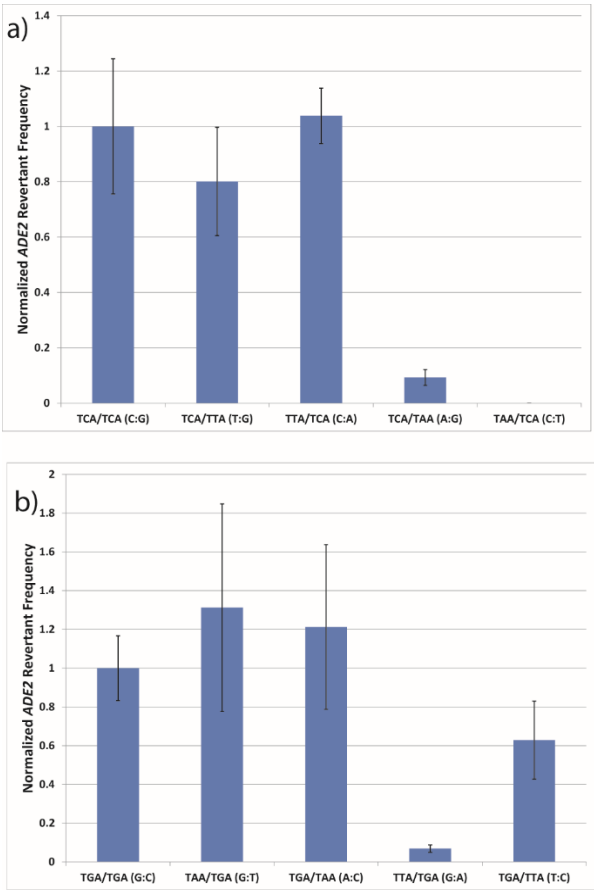
Precise repair of *mPing* excision sites is facilitated by target site duplication derived microhomology

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Additional file 4

Additional non-matching *mPing* TIRs

Charts comparing the frequency of *ADE2* revertant colonies produced for *mPing* elements with matching (i.e. TCA/TCA) and non-matching TSD sequences (i.e. TAA/TCA) in the JIM17 strain. Combinations using TCA TSDs (a) and combinations using TGA TSDs (b) are shown. The TSD sequence is represented as 5'TSD/3'TSD and the proposed middle base pairing that results from 5' overhangs associated with each combination is shown in parenthesis. Results were normalized to matching TSDs (i.e. TCA/TCA) and error bars represent standard error. Sequences of the excision sites recovered from selected *ADE2* revertant colonies produced by *mPing* element with non-homologous TSDs (c). * indicates a recovered excision site sequence that includes a frame shift.



c) *mPing* Excision Sites

ADE2			
CACTAAACCGT TAA		CAGACCTCACAA	
5' TSD/3' TSD			#/Total
TAA/TGA			
CACTAAACCGT TAA		CAGACCTCACAA	5/10
CACTAAACCGT TGA		CAGACCTCACAA	2/10
CACTAAACCGT TAATGA		CAGACCTCACAA	2/10
CACTAAACCGT A TGA		CAGACCTCACAA	1/10*
TGA/TAA			
CACTAAACCGT TAA		CAGACCTCACAA	3/6
CACTAAACCGT TGA		CAGACCTCACAA	3/6
TTA/TCA			
CACTAAACCGT TCA		CAGACCTCACAA	22/27
CACTAAACCGT TTA		CAGACCTCACAA	2/27
CACTAAACCGT TTATCA		CAGACCTCACAA	2/27
CAATAAACCGT TCA		CAGACCTCACAA	1/27
TCA/TTA			
CACTAAACCGT TTA		CAGACCTCACAA	15/22
CACTAAACCGT TCATTA		CAGACCTCACAA	5/22
CACTAAACCGT TCA		CAGACCTCACAA	2/22