

Supplementary Table 7. Two-tailed paired Student's t-tests comparing the integrated areas between unamplified %G+C bias curve of unamplified and each amplified treatment for H105/1. Significant ($p < 0.05$) values are yellow; highly significant ($p < 0.001$) values are orange. "n.a." indicates not enough data to test, as the 20-cycle treatment was dropped from the analysis due to failed sequencing.

(a) Probability that differences between cycle numbers and starting DNA amounts is due to chance.

(b) Probability that differences between reconditioned and non-reconditioned samples is due to chance. All reconditioned samples are compared to all non-reconditioned ("all treatments"); reconditioning is also tested within replicates of each cycle number.

(a) All data: %G+C range 0.31-0.55						(b) All data: %G+C range 0.31-0.55	
All treatments (n = 6 for all)						Non-recond. vs. Reconditioned	
cycles	15	18	20	25	30	all treatments (n = 14)	
15						15 cycles, 10 ng (n = 3)	0.314
18	0.279					18 cycles, 1 ng (n = 3)	0.057
20	n.a.	n.a.				20 cycles, 0.1 ng (n = 3)	n.a.
25	0.641	0.151	n.a.			25 cycles, 10 pg (n = 3)	0.010
30	0.954	0.037	n.a.	0.444		30 cycles, 1 ng (n = 3)	0.019
Non-reconditioned (n = 3 for all)							
cycles	15	18	20	25	30		
15							
18	0.001						
20	n.a.	n.a.					
25	0.211	0.102	n.a.	n.a.			
30	0.101	0.175	n.a.	0.460			
Reconditioned (n = 3 for all)							
cycles	15	18	20	25	30		
15							
18	0.986						
20	n.a.	n.a.					
25	0.726	0.706	n.a.				
30	0.312	0.204	n.a.	0.021			