

## S1 Table

**S1A Table** Details of ANOVA statistical analysis for data collected from repeated batch cultivations. Methylation level in % 5mC was the input variable.

Effect	One-dimensional results for each variable. Sigma-restricted parameterization. Decomposition of effective hypotheses				
	Degrees of Freedom	Methylation			
		SS	MS	F	p
<b>Constant Term</b>	1	307,1237	307,1237	435,4845	0
<b>HS vs control</b>	1	0,4376	0,4376	0,6204	0,434758
<b>Cycle number</b>	<b>2</b>	<b>11,6161</b>	<b>5,8081</b>	<b>8,2355</b>	<b>0,000841</b>
Time after HS	2	2,614	1,307	1,8533	0,167761
<b>Error</b>	48	33,8518	0,7052		
<b>Total</b>	53	48,5195			

**S1B Table** Details of Tukey multiple comparison test for data collected from repeated batch cultivations. Methylation level in % 5mC was the input variable.

No	Tukey HSD Test; Variable: Methylation; Approximate probabilities for post hoc tests				
	<b>Cycle Number</b>	{1}	{2}	{3}	
1	1		0,005678	0,001603	
2	2	0,005678		0,895592	
3	3	0,001603	0,895592		
No	Tukey HSD Test; Variable: Methylation; Approximate probabilities for post hoc tests				
	<b>Time after HS</b>	{1}	{2}	{3}	
1	0		0,255197	0,205908	
2	A	0,255197		0,991399	
3	B	0,205908	0,991399		
No	Tukey HSD Test; Variable: Methylation; Approximate probabilities for post hoc tests				
	<b>HS vs C</b>	{1}	{2}		
1	C		0,434900		
2	HS	0,434900			