



Erratum: Transcription and replication result in distinct epigenetic marks following repression of early gene expression

Barry Milavetz^{1*}, Les Kallestad¹, Emily Woods¹, Kendra Christensen¹, Amanda Gefroh¹ and Lata Balakrishnan²

¹ Department of Biochemistry and Molecular Biology, University of North Dakota School of Medicine and Health Sciences, Grand Forks, ND, USA

² Department of Biochemistry and Biophysics, University of Rochester School of Medicine and Dentistry, Rochester, NY, USA

*Correspondence: barry.milavetz@med.und.edu

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An erratum on

Transcription and replication result in distinct epigenetic marks following repression of early gene expression

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In reviewing our recent publication, “Transcription and replication result in distinct epigenetic marks following

repression of early gene expression” published 30 July 2013, we noted that there was an error in **Figure 3**. Apparently between the original submission and our review of the proofs we did not notice that the correct **Figure 3** graphic had been replaced by a copy of the graphic in Figure 2B. We regret the error.

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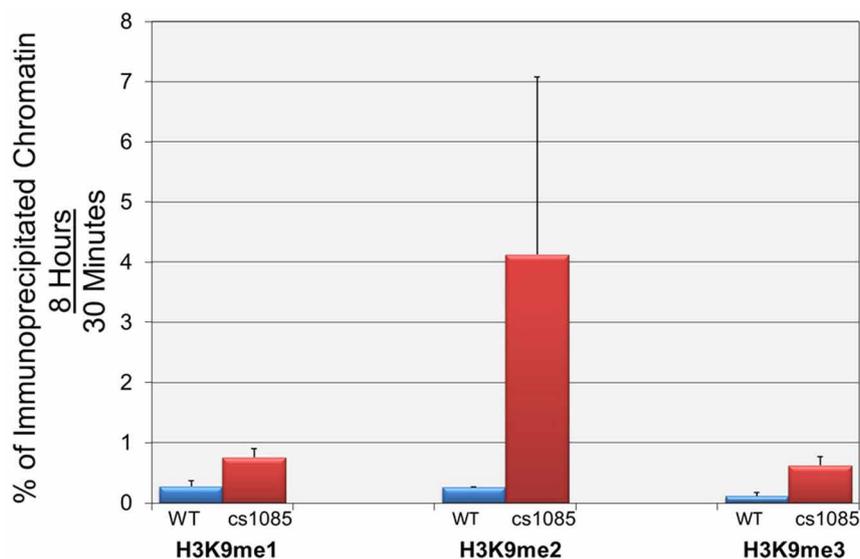


FIGURE 3 | H3K9me2 is significantly increased during active early transcription in the site I deletion mutant cs1085. Wild-type and cs1085 SV40 minichromosomes were isolated from appropriately infected cells at 30 min and 8 h post-infection. Isolated minichromosomes were subjected to ChIP analyses with antibodies against H3K9me1, H3K9me2, and H3K9me3, and the percentage of input minichromosomes containing each form of methylated H3 determined by real-time PCR. The results are displayed as the ratio

of the percentage of minichromosomes isolated at 8 h which contain a particular modification divided by the percentage of minichromosomes isolated at 30 min which contain the same modification. Ratios greater than 1 indicate that a modification is increasing during the period from 30 min to 8 h, while a ratio less than 1 indicates that the modification is decreasing during this period of infection. All analyses were performed a minimum of three times using different preparations of SV40 minichromosomes.