## **Supplementary Figures**

#### Title: G9a-dependent histone methylation can be induced in G1 phase of cell

#### cycle

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### Supplementary Figure 1. Phenotypic analysis of G9a KO iMEFs.

a) Contents of G9a and GLP in *G9a* KO iMEFs were examined by western blot analysis.
b) H3K9me3 level was determined by western blot using Odyssey CLs. N=5, independet experiments. c) Expression of G9a target genes, *Magea, XIr5* and *Wfdc15a* were measured by quantitative RT-PCR. The mean values show the relative expression level to *Hprt*. N=3, technical replicates. N.D., not detected. d) Chip analysis for H3K9me2. Upstream of *Magea2* was measured by quantitative PCR. N=3, independet experiments. Error bars indicate ±SD.



### Supplementary Figure 2. The amount of G9a protein in the cell cycle.

The cells were stained by Hoechst33342 and sorted by FACSAria SORP (Left). G9a was detected by western blot analysis using Odyssey CLs. The relative fluorescence intensity of G9a to Tubulin is showed in the graphs (Right). Experiments were performed 2 times.





Fig.5a left



## Fig.5a right



### Supplementary Figure 3. Images of the immunoblotting in Fig.2f and Fig.5a.

Histones were immunoblotted by anti-H3K9me1 or me2 and anti-H3 antibodies as primary antibodies and detected by IRDye secondary antibodies. Three (Fig.2f and Fig.5a left) and four (Fig.5a right) independent experiments were performed. Fig.2f, (-): total cells, A: AmCyan (+) sorted cells, C: mCherry (+) sorted cells.



**Supplementary Figure 4. Al662270 expression profile in WT and G9a KO ESCs.** *Al662270* mRNA was mesuered by quantitative RT-PCR. WT: TT2, *G9a* KO: 22-10, *Jmjd1a* KO: 31-1<sup>28</sup> and *Jmjd1b* KO: D4-1<sup>27</sup>. All KO ES lines are derived from TT2. N=3, technical replicates. Error bars indicate ±SD.



G9a

Tubulin



Supplementary Figure 5. Images of the immunoblotting used in Fig.S1b and Fig.S2. Histones were immunoblotted by anti-H3K9me3 and anti-H3 antibodies (Fig.S1b) and G9a and Tubulin were immunoblotted (Fig.S2) as primary antibodies and detected by IRDye secondary antibodies. Five (Fig.S1b) and two (Fig.S2) independent experiments were performed.









Fig.S1a



Supplementary Figure 6. Uncropped images of the immunoblotting in Fig.2e, Fig.4e, Fig.S1a, Fig.S3 and Fig.S5.

Each graph picked selection area.

# Fig.S3 (Fig.2f)







Fig.S3 (Fig.5a left)



Fig.S3 (Fig.5a Right)









# Fig.S5 (Fig.S1b)



# Fig.S5 (Fig.S2 Right)



