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Supporting Information Figures S1–S5

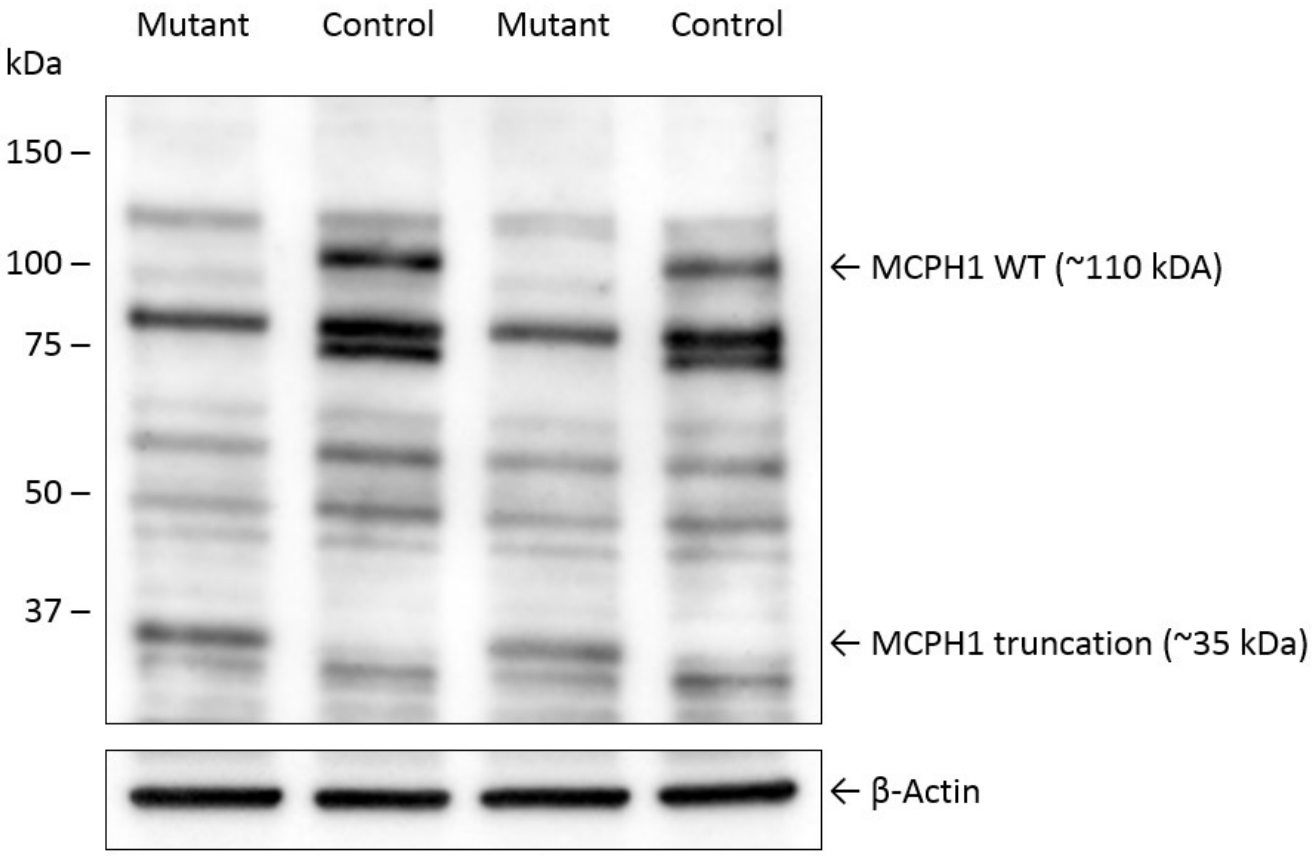

Fig. S1. Immunoblot of CRISPR/Cas9-edited *MCPH1* mutant and control MCF10A cell lines. Mutant cell line shows absence of wild type (~110 kDa) and presence of truncated (~35 kDa) MCPH1 protein.

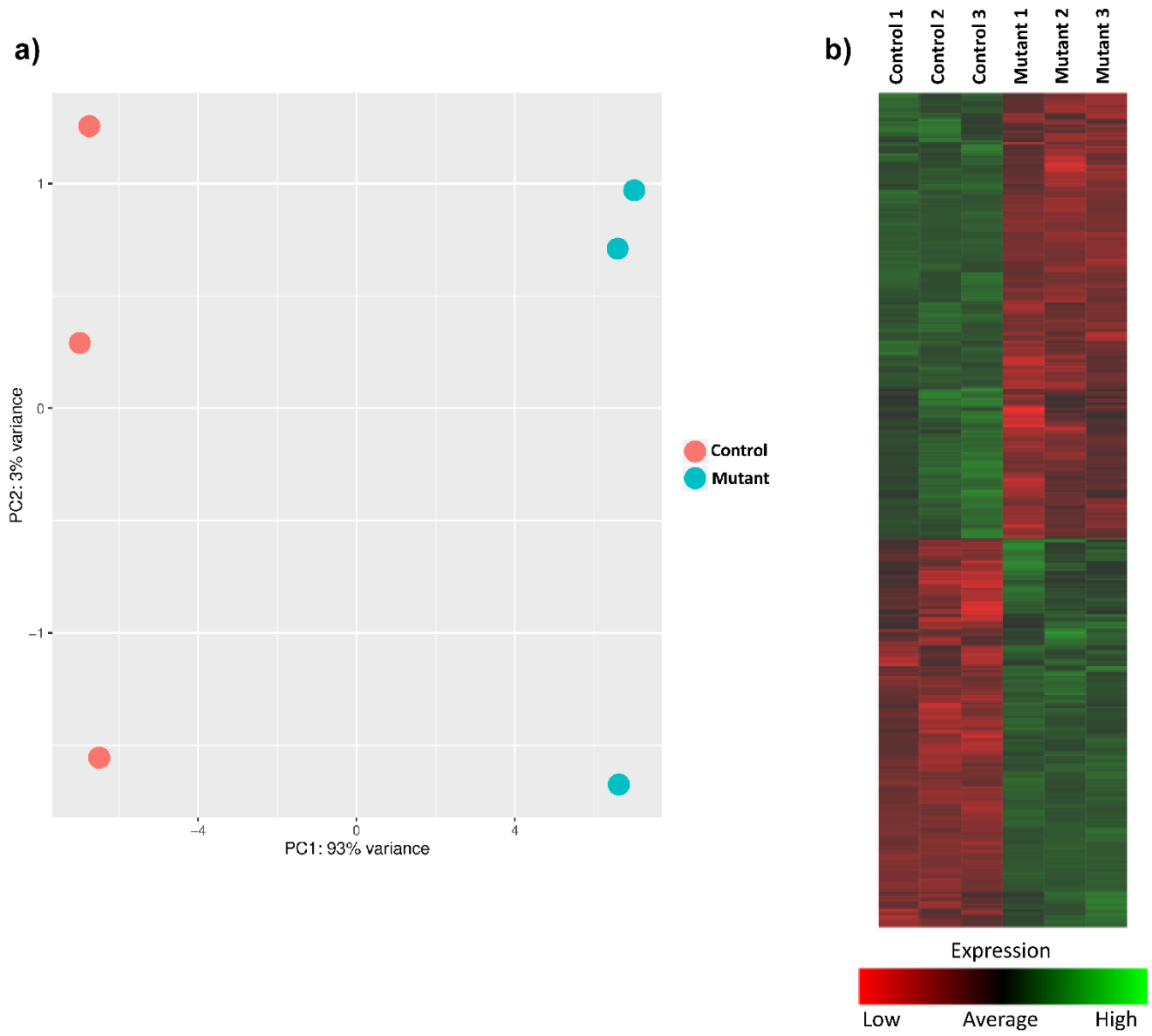

Fig. S2. *MCPH1* mutant and control cells have distinct gene expression profiles. a) Principal component analysis (PCA) shows gene expression patterns of *MCPH1* mutant and control cell lines being distinct from each other, principal component 1 explaining 93% of the variation between the samples. **b)** Differential gene expression patterns presented as a heatmap based on DESeq2 results. Red indicates decreased gene expression and green increased expression.

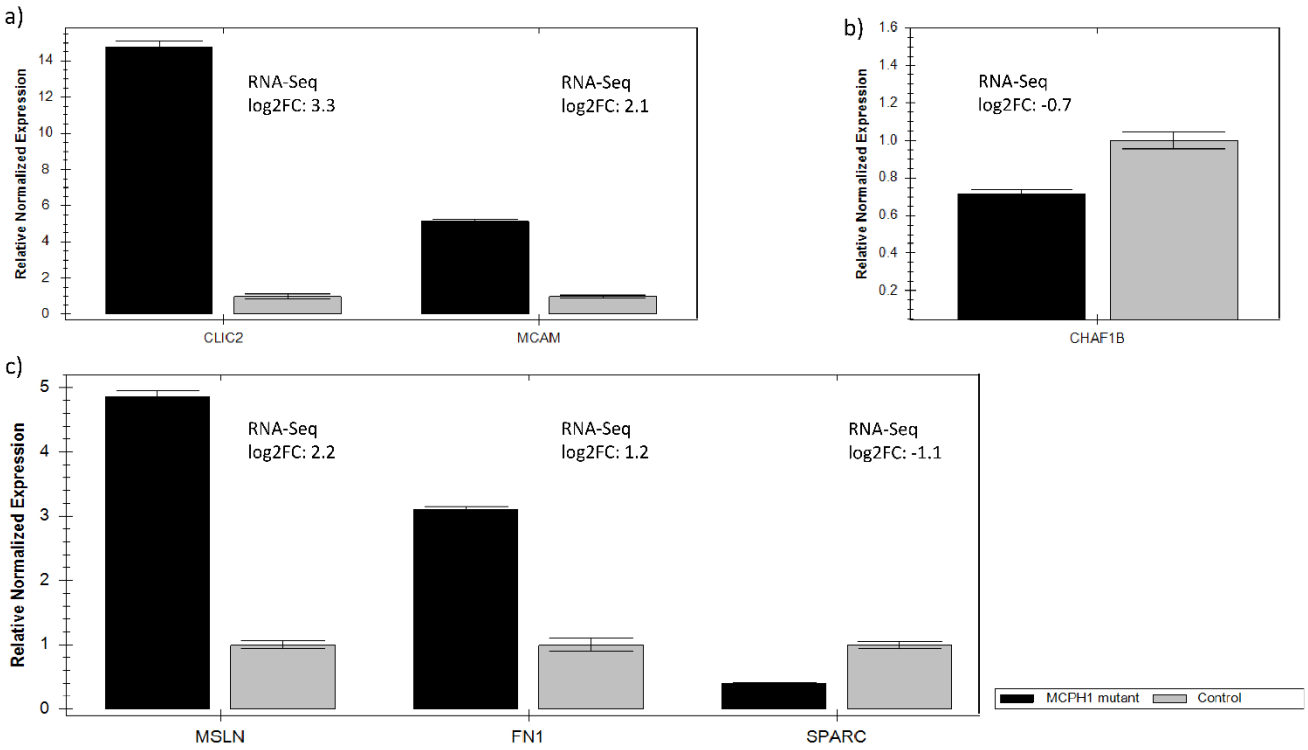

Fig. S3. Six of the differentially expressed genes in RNA-Seq were analyzed with RT-PCR. a) *CLIC2* and *MCAM*, **b)** *CHAF1B* and **c)** *MSLN*, *FN1* and *SPARC*. All analyzed genes showed similar differential expression in the cell lines with both methods. Results are mean (±SE) expression of 3 replicates.

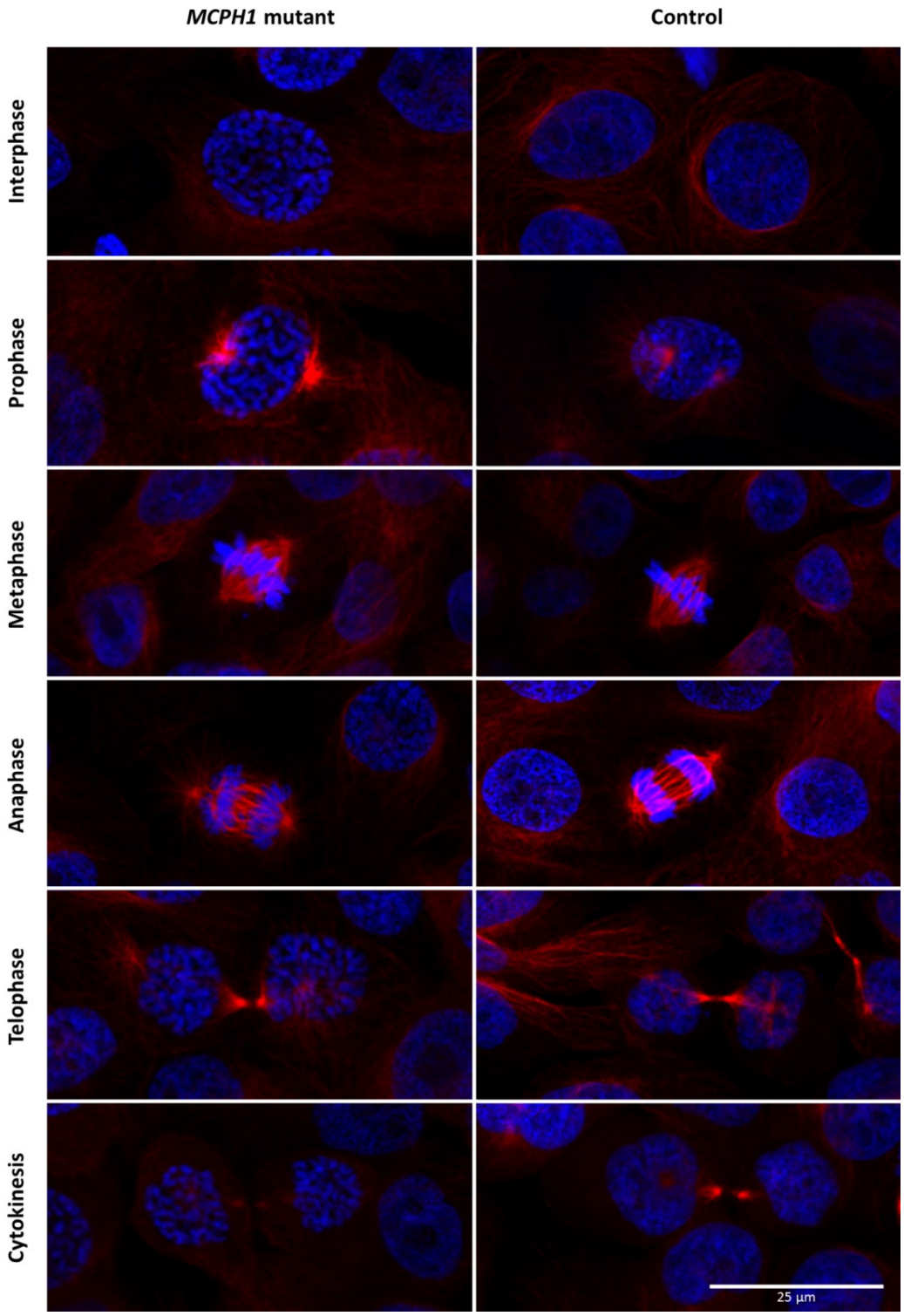

Fig. S4. Representative images of mitotic phases of *MCPH1* mutated and control MCF10 cells. Mutant cells show PCC phenotype and prolonged chromatin condensation during telophase and cytokinesis. Fixed cells were stained with DAPI (blue) and anti-tubulin (red). Scale bar 25 µm.

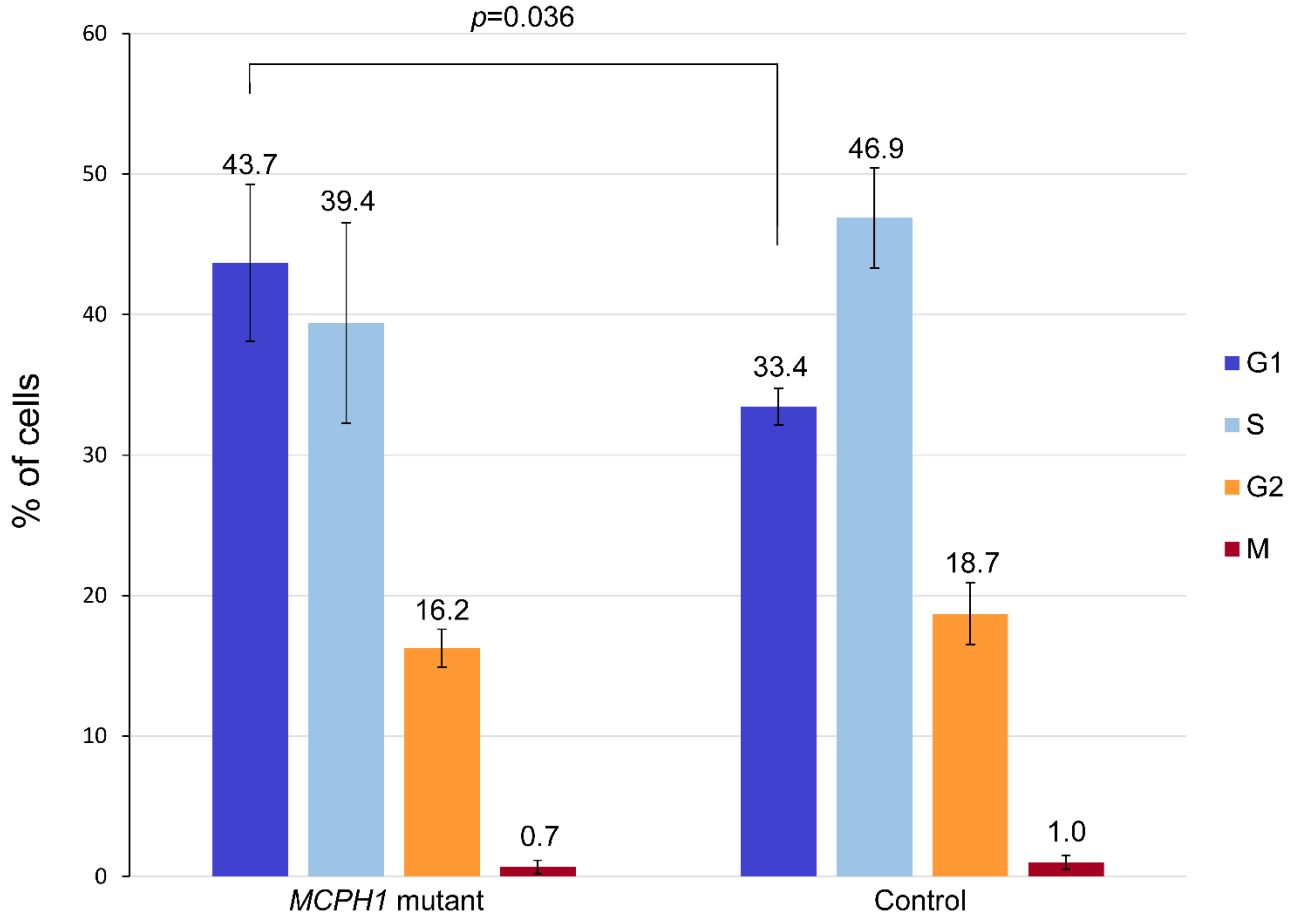

Fig. S5. *MCPH1* mutant cells have larger proportion of G1 phase cells. Cell cycle distribution analysis by flow cytometry shows *MCPH1* mutant cell line having more cells in G1 phase (43.7%) than controls (33.4%), p=0.036. Means of three independent experiments (±SD), Student's t-test.