

**Table S5.** List of primers for RT-qPCR to verify candidate depletion.

<b>Target</b>	<b>Primer ID</b>	<b>Target sequence</b>	<b>Source</b>
DCLRE1B	JM013F	TGGAACCATCCTCTACACAGGT	This study*
	JM014R	GGATCTGTTTCCCCAGTGTCA	
GAPDH	JM051F	AGCCACATCGCTCAGACAC	(Feretzaki & Lingner, 2017)
	JM052R	GCCAATACGACCAAATCC	
NPAT	JM077F	TCCCAGTATCTGTGGTTGGAC	This study*
	JM078R	CAGGTGCTGTCAAAGGCATA	
PARP9	JM065F	GGCAAAGAGGTCCAAGATGCTG	(Bachmann et al, 2014)
	JM066R	GCCTCACACATCTCTTCCACGT	
PNUTS	JM069F	AAAACGAGCACAGAACCAA	(Kavela et al, 2013)
	JM070R	GGCTCCAAAGAGGCTGTAT	
SAMHD1	JM019F	GAGTCTCGTTTTGAAAATCTTGGA	This study*
	JM020R	CCAATCGCTGGATATAACTAAGCA	
SMCHD1	JM057F	TAACAACGGGCGTGTATAGG	(Tang et al, 2014)
	JM058R	TGGTACTGGACGAACATATCCTG	
TMPO	JM039F	CGGAGTGAATCCTGGTCCTATT	This study*
	JM040R	CCATTCTGCCTTGTATTTTCTGC	

\*Primers were designed using ProbeFinder for the Human Universal ProbeLibrary ([www.universalprobelibrary.com](http://www.universalprobelibrary.com)) from Roche. Primers were designed to recognize common regions of genes that comprise multiple transcript variants.