

## **Supplementary material and methods**

### **Epigenetic changes in the early stage of silica-induced cell transformation**

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**Table S1: Physical characteristics of the silica samples.**

Sample <sup>a</sup>	Origin	Main phase	Primary particle size <sup>b</sup>	Main impurities (wt %) <sup>c</sup>	BET SSA (m <sup>2</sup> /g) <sup>d</sup>	DLS <sup>e</sup>	
						Z-average diameter in water (nm)	Polydispersity index
<b>NM-203</b>	Pyrogenic	Amorphous	24.7 ± 17.7 nm	Al (0.43)	204	318.7 ± 4.9	0.420 ± 0.026
<b>Min-U-Sil 5</b>	Natural; US Silica Co. (Berkeley)	Crystalline	1.33 ± 0.85 μm	Al (0.16) <sup>d</sup>	5	1385.7 ± 377.0	0.380 ± 0.130

<sup>a</sup> In-depth physical and chemical characterizations of the samples (except DLS data) are available in Rasmussen *et al*, 2013 (NM-203) and Elias *et al*, 2006 (Min-U-Sil);

<sup>b</sup> Determined by transmission electron microscopy;

<sup>c</sup> Impurities were determined by energy dispersive spectrometry for NM-203 and by inductively coupled plasma spectrometry for Min-U-Sil;

<sup>d</sup> The BET (Brunauer-Emmet-Teller) specific surface area (SSA) was determined by nitrogen adsorption;

<sup>e</sup> Dynamic light scattering (DLS) was performed using a Nanozetasizer (Malvern). Samples were dispersed in water as described in the Materials and methods section. Values represent the mean ± standard deviation of three DLS analyses.

**Table S2: Antibodies used for Western Blot and ChIP analyses.**

<b>Target</b>	<b>Supplier</b>	<b>Reference</b>	<b>Molecular weight (kDa)</b>
<b>DNMT1</b>	Cell Signaling	5119	200
<b>DNMT3a</b>	Cell Signaling	2160	130
<b>DNMT3b</b>	Abcam	ab2851	100
<b>HDAC1</b>	Cell Signaling	2062	63
<b>HDAC2</b>	Cell Signaling	2540	60
<b>HDAC3</b>	Cell Signaling	2632	49
<b>HDAC6</b>	Cell Signaling	7612	140
<b>Total histone H3</b>	Millipore	06-755	17
<b>Acetylated histone H3</b>	Millipore	06-599	17
<b>Total histone H4</b>	Millipore	05-858	10
<b>Acetylated histone H4</b>	Millipore	06-866	10
<b><math>\beta</math>-actin</b>	Cell Signaling	4970	42
<b>c-Myc</b>	Cell Signaling	13987	57
<b>RNA polymerase II</b>	Abcam	ab210527	
<b>Trimethylated histone H3 lysine 4</b>	Abcam	ab8580	
<b>Acetylated histone H3 lysine 4</b>	Abcam	ab113672	
<b>Acetylated histone H3 lysine 9</b>	Millipore	06-942	
<b>Acetylated histone H3 lysine 27</b>	Abcam	ab4729	
<b>5-methylcytosine</b>	Diagenode	C15200081	

**Table S3: Primers used for QRT-PCR and ChIP analyses.**

<b>Target gene</b>	<b>Forward and reverse sequences</b>	<b>Amplicon size</b>
<i><b><math>\beta</math>-actin</b></i>	F: GGCCAACCGTGAAAAGATGA R: TACGACCAGAGGCATACAGG	104
<i><b><math>\alpha</math>-tubulin</b></i>	F: CACTACACCATTGGCAAGGA R: GCTGTGGAAAACCAAGAAGC	102
<i><b>Gapdh</b></i>	F: CTGCACCACCAACTGCTTAG R: GTCTTCTGGGTGGCAGTGAT	108
<i><b>Tbp</b></i>	F: ACGGACAACCTGCGTTGATTTT R: ACTTAGCTGGGAAGCCCAAC	128
<i><b>c-myc</b></i>	F : CCCTAGTGCTGCATGAGGA R : TGCCTCTTCTCCACAGACAC	103
<i><b>Col1A2</b></i>	F: TTGCAATCGGGATCAGTACG R : TGGGACCATCAACACCATCT	103
<b>P1</b>	F: CGCCCTTTATATTCCGGGGG R: GAGCTGAGTGAGGCGAGTC	96
<b>P2</b>	F: AGGGATCCTGAGTCGCAGT R: CGCTCACTCCCTCTGTCTCT	92
<b>e2</b>	F: GAGGAGACATGGTGAACCAGA R: AACCGCTCCACATACAGTCC	93
<b>neg</b>	F: CAGTCTTCACCCGACCATCT R: CTGACAGAGCTTTCCCCAAA	92