**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.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Samplea** | **Origin** | **Main phase** | **Primary particle sizeb** | **Main impurities**  **(wt %)c** | **BET SSA (m2/g)d** | **DLSe** | |
| Z-average diameter in water (nm) | Polydispersity index |
| **NM-203** | Pyrogenic | Amorphous | 24.7 ± 17.7 nm | Al (0.43) | 204 | 318.7 ± 4.9 | 0.420 ± 0.026 |
| **Min-U-Sil 5** | Natural; US Silica Co. (Berkeley) | Crystalline | 1.33 ± 0.85 µm | Al (0.16)d | 5 | 1385.7 ± 377.0 | 0.380 ± 0.130 |

a 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);

b Determined by transmission electron microscopy;

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

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

e 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.**

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

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

|  |  |  |
| --- | --- | --- |
| **Target gene** | **Forward and reverse sequences** | **Amplicon size** |
| ***β-actin*** | F: GGCCAACCGTGAAAAGATGA  R: TACGACCAGAGGCATACAGG | 104 |
| ***α-tubulin*** | F: CACTACACCATTGGCAAGGA  R: GCTGTGGAAAACCAAGAAGC | 102 |
| ***Gapdh*** | F: CTGCACCACCAACTGCTTAG  R: GTCTTCTGGGTGGCAGTGAT | 108 |
| ***Tbp*** | F: ACGGACAACTGCGTTGATTTT  R: ACTTAGCTGGGAAGCCCAAC | 128 |
| ***c-myc*** | F : CCCTAGTGCTGCATGAGGA  R : TGCCTCTTCTCCACAGACAC | 103 |
| ***Col1A2*** | F: TTGCAATCGGGATCAGTACG  R : TGGGACCATCAACACCATCT | 103 |
| **P1** | F: CGCCCTTTATATTCCGGGGG  R: GAGCTGAGTGAGGCGAGTC | 96 |
| **P2** | F: AGGGATCCTGAGTCGCAGT  R: CGCTCACTCCCTCTGTCTCT | 92 |
| **e2** | F: GAGGAGACATGGTGAACCAGA  R: AACCGCTCCACATACAGTCC | 93 |
| **neg** | F: CAGTCTTCACCCGACCATCT  R: CTGACAGAGCTTTCCCCAAA | 92 |