Additional file 1

SOX2 as a novel contributor of oxidative metabolism in melanoma cells.

Elena Andreucci*1, Silvia Pietrobono*, Silvia Peppicelli1, Jessica Ruzzolini1, Francesca Bianchini1, Alessio Biagioni1, Barbara Stecca2 and Lido Calorini1,3.

1Department of Clinical and Experimental Biomedical Sciences “Mario Serio”, Section of Experimental Pathology and Oncology, University of Florence, Florence, Italy. 2Core Research Laboratory, Institute for Cancer Research and Prevention (ISPRO), Florence, Italy. 3Center of Excellence for Research, Transfer and High Education DenoTHE University of Florence, Florence, Italy.

* These authors contributed equally to this work.

Figure S1 Growth curves of melanoma cells with SOX2 depletion or over-expression under standard and acidic condition. Proliferation of SOX2-depleted A375-M6 (a) and SSM2c (b), and SOX2-overexpressed 501-Mel (c) grown for 24, 48 and 72 hours at pH 7.4 and 6.7. GraphPad Prism software, Two-way ANOVA, N=3.
Figure S2 Western blotting of a panel of glycolysis- and OxPhos-related proteins after SOX2 silencing and over-expression in melanoma cells. a) Western blot of GLUT-1 (p<0.01), GLUT-3 (p<0.05), MCT-1 (p<0.01), MCT-4 (ns) and PGC1a (p<0.05) in A375-M6 siCTRL and siSOX2 at pH 7.4. T-test, N=3. b) Western blot of GLUT-1, GLUT-3, MCT-1, MCT-4 and PGC1a in SSM2c LV-c and LV-shSOX2 at pH 7.4. p<0.05, T-test, N=3. c) Western blot of GLUT-1 (p<0.01), GLUT-3 (p<0.05), MCT-1 (p<0.01), and MCT-4 (ns) in 501-Mel pBABE-c and pBABE-SOX2 at pH 7.4. T-test, N=3. Quantification of protein expression is shown in italic.