Additional file 1

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

Elena Andreucci^{1*}, Silvia Pietrobono^{2*}, Silvia Peppicelli¹, Jessica Ruzzolini¹, Francesca Bianchini¹, Alessio Biagioni¹, Barbara Stecca² and Lido Calorini^{1,3}.

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.

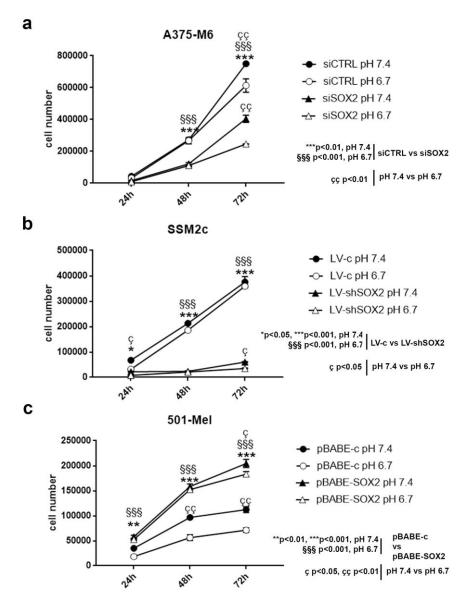


Figure S1 Growth curves of melanoma cells with SOX2 depletion or over-expression under standard and acidic condition. Proliferation of SOX2-depleted A375-M6 (a) and SSM2c (b), and SOX2-overexpressed 501-Mel (c) grown for 24, 48 and 72 hours at pH 7.4 and 6.7. GraphPad Prism software, Two-way ANOVA, N=3.

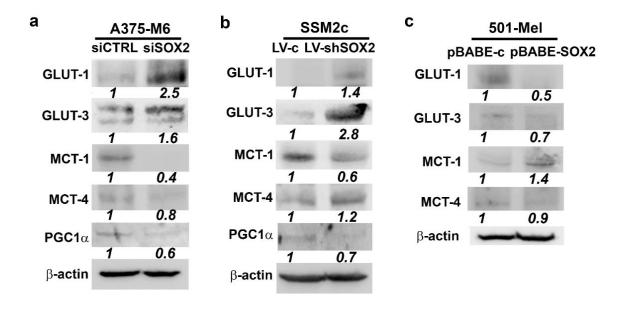


Figure S2 Western blotting of a panel of glycolysis- and OxPhos-related proteins after SOX2 silencing and over-expression in melanoma cells. a) Western blot of GLUT-1 (p<0.01), GLUT-3 (p<0.05), MCT-1 (p<0.01), MCT-4 (ns) and PGC1a (p<0.05) in A375-M6 siCTRL and siSOX2 at pH 7.4. T-test, N=3. b) Western 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.