

Supplementary material

Title

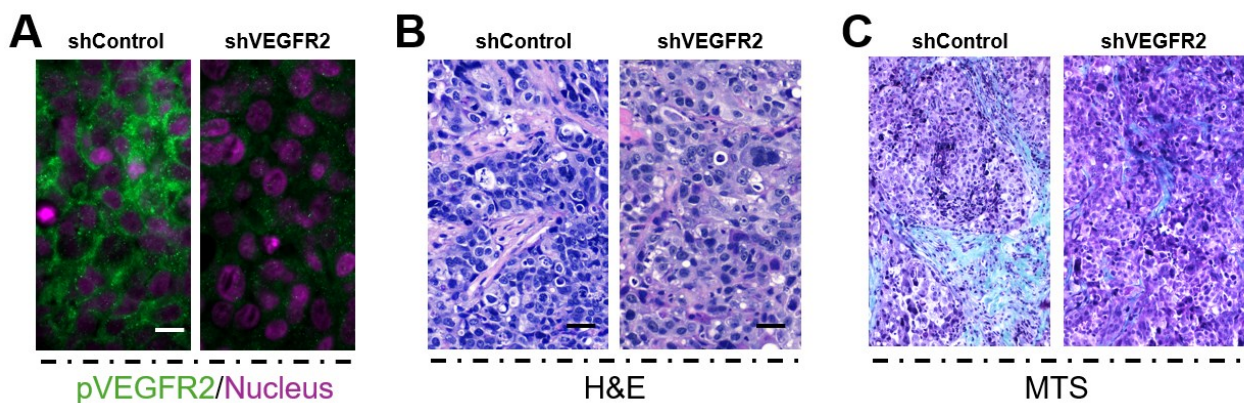
Aberrant VEGFR2 supports tumor growth by extracellular matrix remodeling

Running title

VEGFR2-dependent ECM remodeling

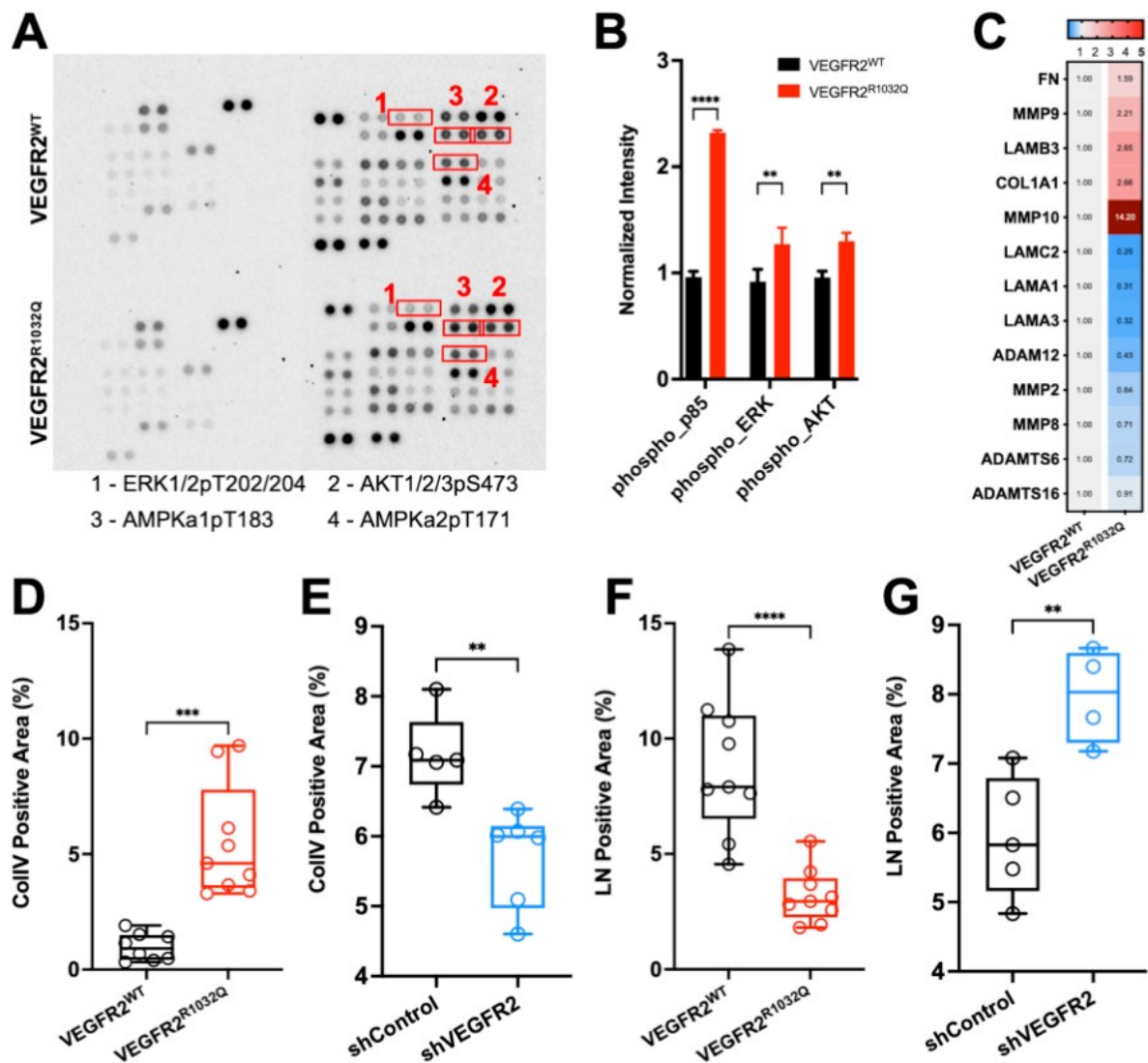
Authors

Michela Corsini^{1,2,*}, Cosetta Ravelli^{1,2}, Mattia Domenichini¹, Anna Ventura¹, Camilla Maggi¹, Elisa Moreschi^{1,2}, Mirko Tamma³, Chiara Romani^{4,5}, Claudia Piccoli³, Elisabetta Grillo^{1,2}, and Stefania Mitola^{1,2,*}.



Supplementary Figure 1: VEGFR2 silencing reduces phosphorylation and ECM deposition (A)

Representative pVEGFR2 staining of FFPE slices from shControl and shVEGFR2 OVCAR-derived tumors. pVEGFR2 signal in green, nuclear staining in magenta (n=4-5). Scale bars, 20 μm. (B-C) Representative H&E and MTS staining of FFPE slices from shControl and shVEGFR2 OVCAR-derived tumors. Scale bars, 50 μm. (n=4-5).



Supplementary Figure 2: Altered Signaling Pathway Modulation and ECM deposition in Sk-Mel-31-VEGFR2^{WT} and Sk-Mel-31-VEGFR2^{R1032Q} cells.

(A) Phospho-protein array of VEGFR2^{R1032Q} Sk-Mel-31 and VEGFR2^{WT} Sk-Mel-31 cells. Differentially phosphorylated proteins are highlighted in red. (B) Spot Quantification of pP85, pERK, and pAKT normalized to total protein levels. Data are presented as mean ± SD from two independent experiments. Statistical significance was determined by two-way ANOVA, **P < 0.01, ****P < 0.0001. (C) Heatmap showing ECM-related gene expression in VEGFR2^{R1032Q} Sk-Mel-31 vs VEGFR2^{WT} Sk-Mel-31. (D) Quantification of ColIV-positive areas in VEGFR2^{R1032Q} Sk-Mel-31 and VEGFR2^{WT} Sk-Mel-31 cells. Single data are represented as empty dots in Min to Max box &

whiskers plot (n=7-9). Statistical significance was determined by two-way ANOVA, ***P < 0.001.

(E) Quantification of ColIV-positive areas in shControl OVCAR3 and shVEGFR2 OVCAR cells. Single data are represented as empty dots in Min to Max box & whiskers plot (n=5-6). Statistical significance was determined by two-way ANOVA, **P < 0.01.

(F) Quantification of LN-positive areas in VEGFR2^{R1032Q} Sk-Mel-31 and VEGFR2^{WT} Sk-Mel-31 cells. Single data are represented as empty dots in Min to Max box & whiskers plot (n=7-9). Statistical significance was determined by two-way ANOVA, ****P < 0.0001.

(G) Quantification of LN-positive areas in shControl OVCAR3 and shVEGFR2 OVCAR cells. Single data are represented as empty dots in Min to Max box & whiskers plot (n=5-6). Statistical significance was determined by two-way ANOVA, **P < 0.01.