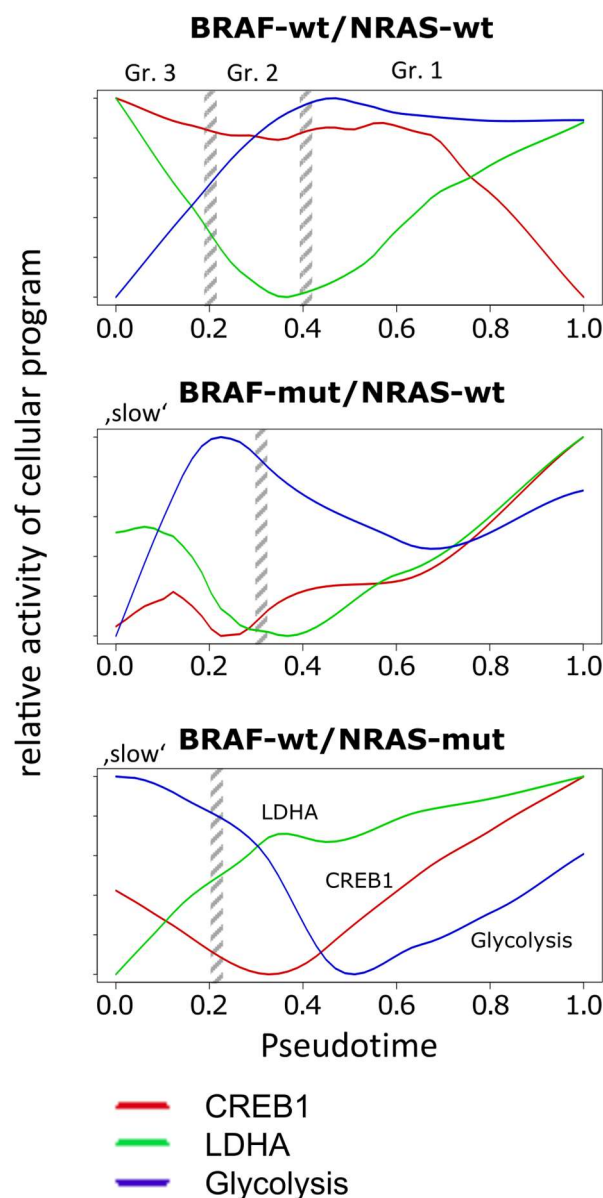


Article

Pseudotime Dynamics in Melanoma Single-Cell Transcriptomes Reveals Different Mechanisms of Tumor Progression

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Supplementary Figure 1. Relative activity of cellular programs of CREB, LDH and glycolysis along PT. Melanoma short-term cultures were analyzed by single-cell RNA-seq and subjected to PT analysis using the Wanderlust algorithm and analysis of relative reactivity profiles of CREB1, LDH and glycolysis. Vertical streaked bars indicate the boundaries of the three different cell subpopulations in wt/wt cells or the two different cell populations in BRAF-mut/NRAS-wt and BRAF-wt/NRAS-mut cells as indicated in Figure 1C.