

Supplementary Material for

**Clinical interest of combining transcriptomic and genomic signatures
in high-grade serous ovarian cancer**

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SUPPLEMENTARY INFORMATION LEGENDS**Supplementary Figure 1: The Fibrosis subgroup of high-grade serous ovarian cancers exhibits conserved functional pathways across studies**

A. Pathway enrichment analysis showing top significant and non-redundant Gene Ontology (GO) terms in the C1, Fibrosis, Angiogenic and Mesenchymal signatures. **B.** Venn diagram showing overlapping genes between the C1, Fibrosis, Angiogenic and Mesenchymal signatures. **C.** Pathway enrichment analysis showing top significant and non-redundant GO terms in non-fibrosis signatures, such as C2-C6, stress, M2-M4 and D-I-P. Abbreviations are as follows: reg: regulation; loc: localization; pos: positive; neg: negative. **D.** Venn diagram showing overlapping genes between non-Fibrosis Fibrosis signatures.

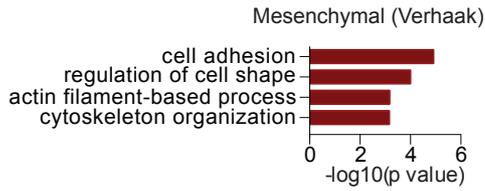
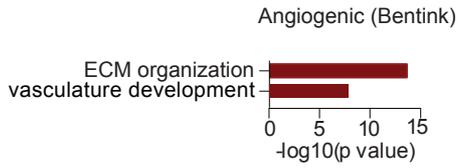
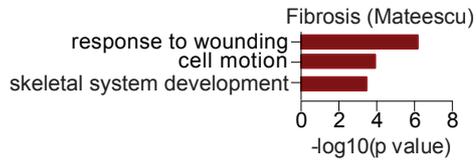
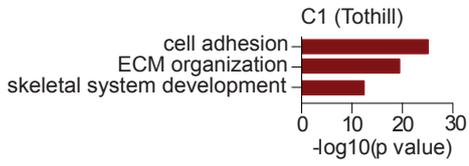
Supplementary Figure 2: High-grade serous ovarian cancer patients classified as Fibrosis/non-Mesenchymal and Fibrosis/Mesenchymal show a similar poor prognosis

A. Kaplan-Meier curves showing 10-year overall survival (OS, **Left**) and disease-free survival (DFS, **Right**) of patients with ovarian tumors classified as Fibrosis/Mesenchymal (red, N=108), Fibrosis/non-Mesenchymal (purple, N=108) or non-Fibrosis/non-Mesenchymal (black, N=307), according to the Mateescu and Verhaak classifications. These analyses were performed on the TCGA cohort, as indicated. P-values were calculated using the Log-rank test.

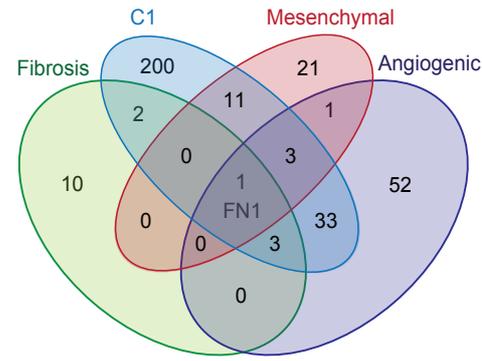
Supplementary Figure 3: miR-200 family members are not prognostic for ovarian cancer patient survival

A. Kaplan-Meier curves showing 10-year overall survival of patients suffering from high-grade serous ovarian cancer with either high expression (red, N=242) or low expression (black, N=241) of miR-200 family members. The threshold between low and high microRNA expression subclasses is based on the median expression of each microRNA individually, as indicated, or on the median of the expression average of all miR-200 family members (**Bottom right**). These analyses were performed on the TCGA cohort and p-values were calculated using the Log-rank test.

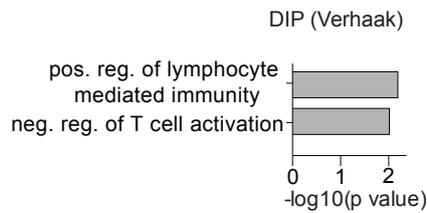
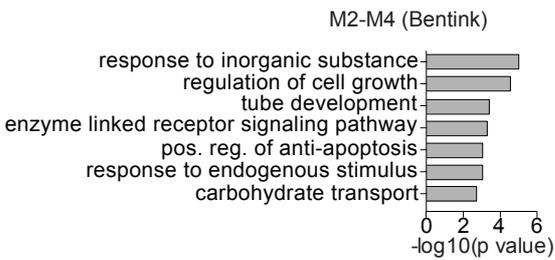
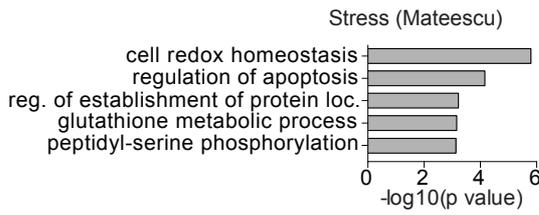
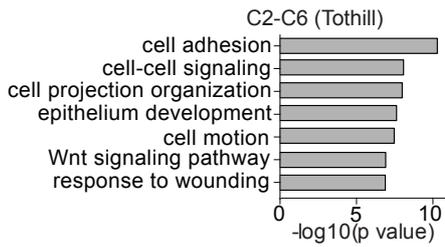
A



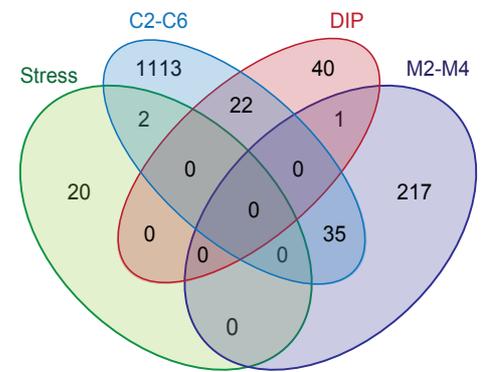
B



C

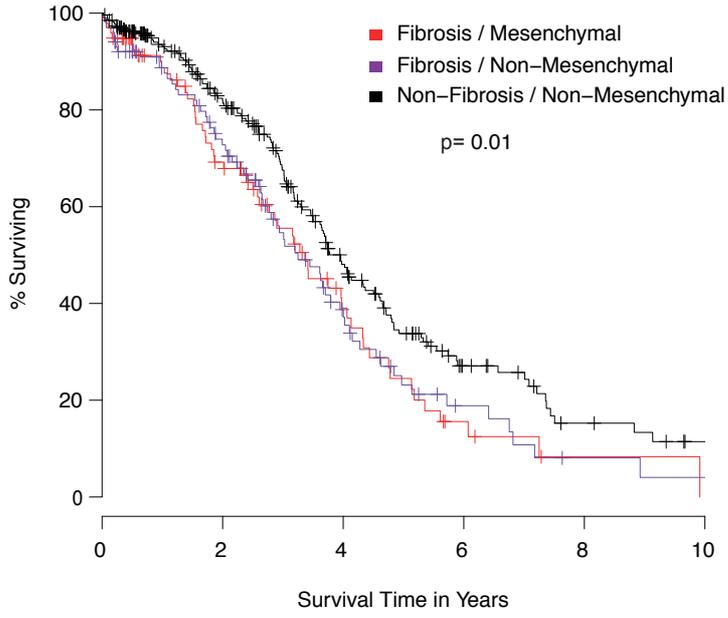


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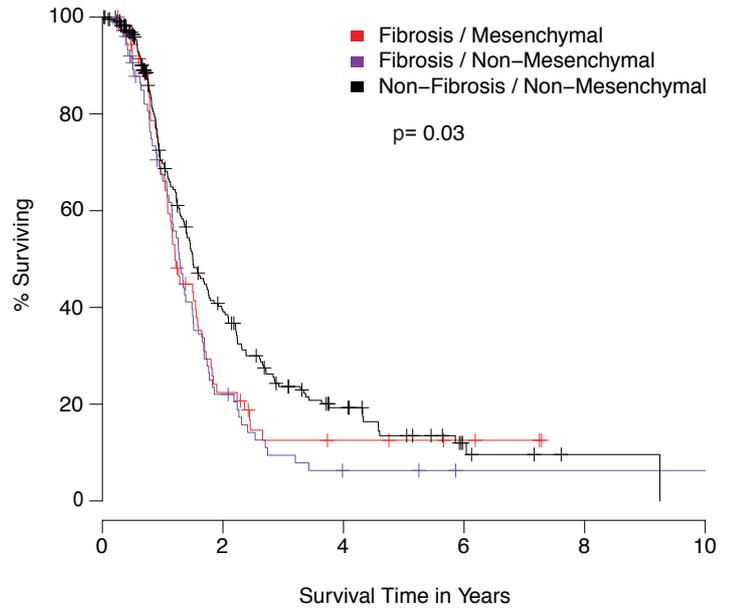


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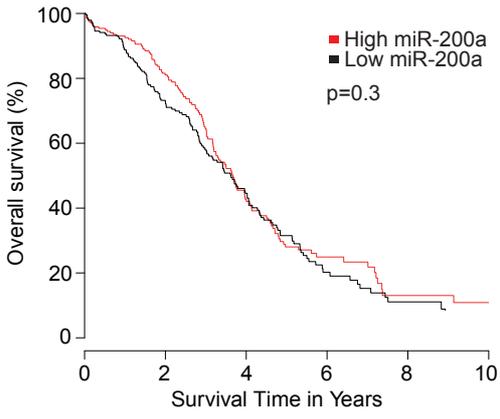
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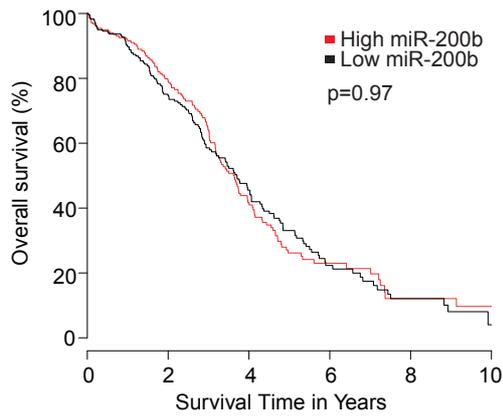
TCGA - DFS



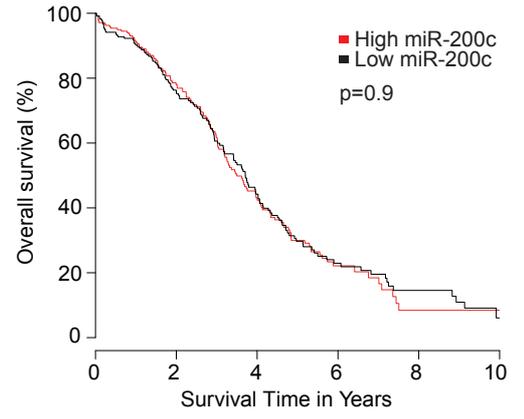
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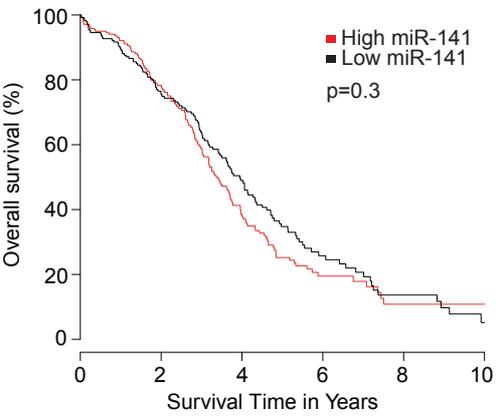
miR-200b



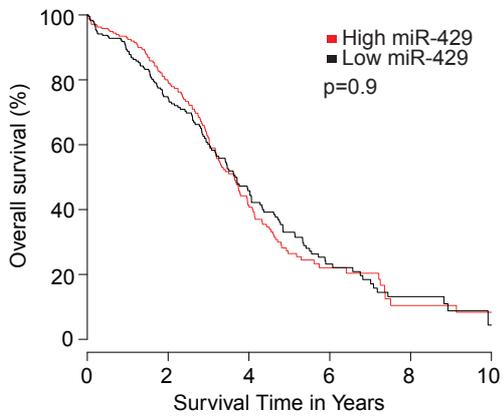
miR-200c



miR-141



miR-429



average miR

