

1 **Supplementary figure legends**

2 **Supplementary Figure 1.** Carboxypeptidase A6 (*CPA6*) mRNA Gene Expression in Taylor's prostate cancer data
3 set across various visualization tools: *CANCERTOOL* (**A**), *Oncomine* (**B**, www.oncomine.org), *cBioportal* (**C**,
4 www.cbioportal.org) and *GEO2R* (**D**, <https://www.ncbi.nlm.nih.gov/geo/geo2r/>).

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6 **Supplementary Figure 2.** Kaplan-Meier curves representing the disease-free survival (DFS) of patient groups
7 selected according to the mean expression of *MITF* in three prostate cancer datasets. Statistical analysis: Mantel-
8 Cox test.

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10 **Supplementary Figure 3.** Violin plots depicting the expression of the Long intergenic non-coding RNA LINC00116
11 between non-tumoral (N) and cancer specimen in (**A**) Breast Cancer (BCa), (**B**) Colon Cancer (CRC), (**C**) Lung
12 Cancer (LUAD) and (**D**) Prostate Cancer (PCa). The Y-axis represents the Log2-normalized gene expression.
13 Statistical analysis: Student's T-Test.

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15 **Supplementary Figure 4.** Correlation of *MITF* and *CRYAB* expression in prostate cancer datasets. Correlation
16 and linear regressions (red line) with Spearman correlation coefficient and p-value in non-tumoral prostate tissue
17 (**A**), all tumors (**B**), primary tumors (**C**) and metastatic specimens (**D**). Plotted values correspond to the log2-
18 normalized gene expression values (fluorescence intensity or RSEM-UQ) for each pair of genes (in X and Y-axis)
19 for each patient in the indicated dataset.

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21 **Supplementary Table 1.** Databases available in the gene enrichment analysis in *CANCERTOOL*.

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23 **Supplementary Table 2.** Resulting table from custom correlation analysis in all prostate tumors among the
24 indicated genes in *CANCERTOOL*.

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