**Code Functionality Overview**

This codebase provides a high-level description of the functionality of each custom R script used in the manuscript. Each section below outlines the purpose, input, procedure, and output of one script.

**Script 1: mRNAsi Stemness Index Quantification**

* Computes the mRNAsi score using Spearman correlation with stemness weights from Malta et al. (Cell 2018).
* Supports Ensembl gene IDs with version (e.g., ENSG00000123456.10).
* Outputs normalized mRNAsi scores and optional boxplot by group using metadata file.

**Script 2: PCa-Stem Signature Enrichment via ssGSEA**

* Performs single-sample GSEA (ssGSEA) for a curated 12-gene prostate stemness signature.
* Supports three gene ID formats (gene symbols, Ensembl IDs, and Ensembl IDs with version).
* Visualizes group-wise enrichment using optional metadata.

**Script 3: Jonckheere–Terpstra Trend Testing**

* Evaluates monotonic trends across ordered clinical groups (e.g., Gleason score).
* Outputs statistical significance and optional visual summary.

**Script 4: Multivariable Cox Regression**

* Fits Cox models for survival analysis integrating molecular features and clinical variables.
* Outputs HRs, p-values, and forest plots using survminer.

**Script 5: Linear Regression with Interaction Term**

* Tests interaction effect between stemness and clinical variables (e.g., Gleason score) on response (e.g., AR activity).
* Produces regression summary and an interaction plot.

Each script includes:

* Sample data
* Output CSV and PDF files
* Toggle options for optional visualization

All scripts are intended to run as standalone modules.

**End of Document**