

Supplementary Material



Supplementary Figure 1. QC analysis. (A) Correlation analysis between replicates for all the BC360 controls shows a good correlation between replicates and low technical variability. **(B)** RNA from all 54 samples included in the FMRP cohort were isolated and sequenced using the NanoString BC360 panel. nSolver's data quality assessment requires a threshold of 202 counts for housekeeping genes in each sample for analysis. Therefore, we removed samples 42 and 43, and only samples above the minimum threshold were used for downstream analysis (n = 51).



Supplementary Figure 2. Summary workflow. We conducted digital transcriptomic with BC360 NanoString panel in Formalin-Fixed Paraffin-Embedded (FFPE) tissues from Faculty of Medicine of Ribeirao Preto (FMRP) cohort (n=53). Two samples were removed from downstream analysis because failure quality control (QC) check. Signatures and differential analysis were perfomed in using our inhouse pipeline (see methods).



Supplementary Figure 3. Venn's Diagram shows the intersection of the DEGs from the NanoString BC360 panel analysis comparing FMRP and TCGA-PRAD cohorts. The genes present in all panels were highlighted. Log2FC > 0.5, P-adjusted < 0.05 (FDR).



Supplementary Figure 4. Expression of hormonal receptors in prostate cancer – Box plot of the normalized log2 transformed gene counts for the androgen receptor (*AR*), estrogen receptor 1 (*ESR1*), estrogen receptor 2 (*ESR2*), and progesterone receptor (*PGR*). a) shows the expression pattern for the markers in the BC360 cohort, while b) shows the results for the TCGA-PRAD cohort. The analysis used no biochemical recurrence as a control. (Mann–Whitney U test, *, p < 0.05).



Supplementary Figure 5. Expression of *TGFB1* in prostate cancer – Box plot of the normalized log2 transformed gene counts for the Transforming Growth Factor Beta 1 (*TGFβ1*). a) shows the expression pattern for the BCR, while b) shows the results for the CAPRA-S score in the FMRP cohort. The normalized log2 transformed transcript counts show a significant increase in *TGFβ1* gene counts for BCR patients (p = 0.018). The analysis used no biochemical recurrence as a control. (Mann-Whitney U test).

Supplementary Material



Supplementary Figure 6. Kaplen-Maier curves illustrate biochemical recurrence free-survival for *INHBA*, *BBC3*, *CDKN2B*, *ORC6*, *THBS4*, *LEFTY2*, *AR*, *LPL*, and *PIP* in the FMRP cohort. Results using the progression-free survival interval for BCR. Median 50% progression probability (a) *INHBA* High 9.14 vs. *INHBA* Low NA, (b) *BBC3* High 7.77 vs. *BBC3* Low 10.34, (c) *CDKN2B* High 7.77 vs. *CDKN2B* Low 10.34, (d) *ORC6* High 7.77 vs. *ORC6* Low NA, (e) *THBS4* High 7.43 vs. *THBS4* Low NA, (f) *LEFTY2* High 8.46 vs. *LEFTY2* Low 10.34, (g) *AR* High 9.14 vs. *AR* Low 9.79, (h) *LPL* High 9.79 vs. *LPL* Low 10.34, (i) *PIP* High 9.14 vs. *PIP* Low 10.34. Log-Rank Test.



Supplementary Figure 7. Kapler-Maier curves illustrate biochemical recurrence free-survival for VCAN, SFRP2, INHBA, BBC3, CDKN2B, ORC6, THBS4, and LEFTY2 in the TCGA-PRAD cohort. Results using the progression-free interval (PFI) for BCR from TCGA. Median 50% progression probability (a) VCAN High 6.86 vs. VCAN Low NA, (b) SFRP2 High NA vs. SFRP2 Low NA, (c) INHBA High 6.78 vs. INHBA Low NA, (d) BBC3 High 6.86 vs. BBC3 Low NA, (e) CDKN2B High 6.78 vs. CDKN2B Low NA, (f) ORC6 High 6.12 vs. ORC6 Low NA, (g) THBS4 High NA vs. THBS4 Low NA, (h) LEFTY2 High 6.78 vs. LEFTY2 Low NA. Log-Rank test.

Supplementary Material



Supplementary Figure 8. Kapler-Maier curves illustrate biochemical recurrence free-survival for VCAN, SFRP2, INHBA, BBC3, CDKN2B, ORC6, THBS4, and LEFTY2 in the GSE54460 cohort. Results using the progression-free interval (PFI) for BCR from TCGA. Median 50% progression probability (a) VCAN High 1.65 vs. VCAN Low 0.8, (b) SFRP2 High 0.7 vs. SFRP2 Low 2.1, (c) INHBA High 1.52 vs. INHBA Low 1.65, (d) BBC3 High 0.45 vs. BBC3 Low 1.92, (e) CDKN2B High 1.16 vs. CDKN2B Low 1.78, (f) ORC6 High 1.53 vs. ORC6 Low 1.65, (g) THBS4 High 0.29 vs. THBS4 Low 2.2, (h) LEFTY2 High 1.92 vs. LEFTY2 Low 1.52. Log-Rank test.