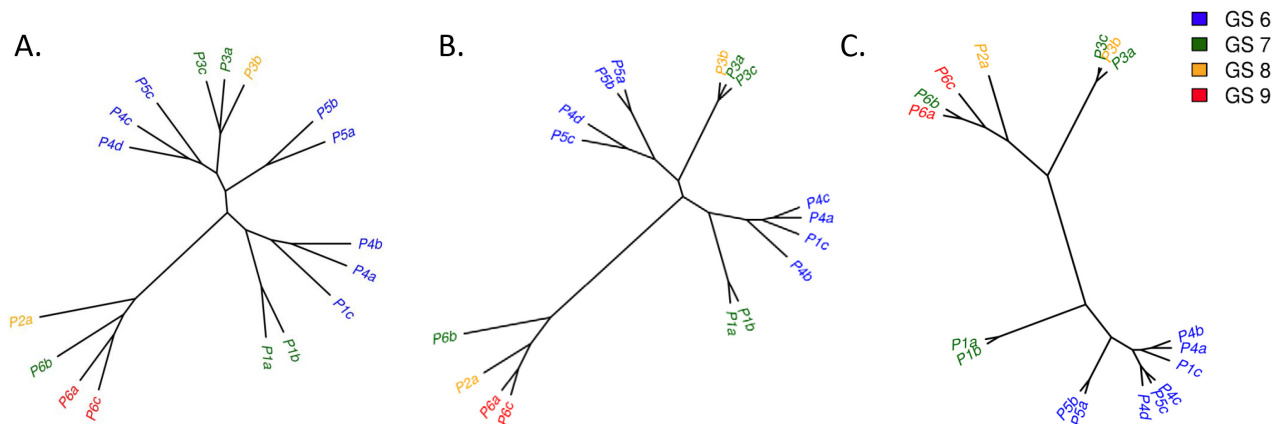
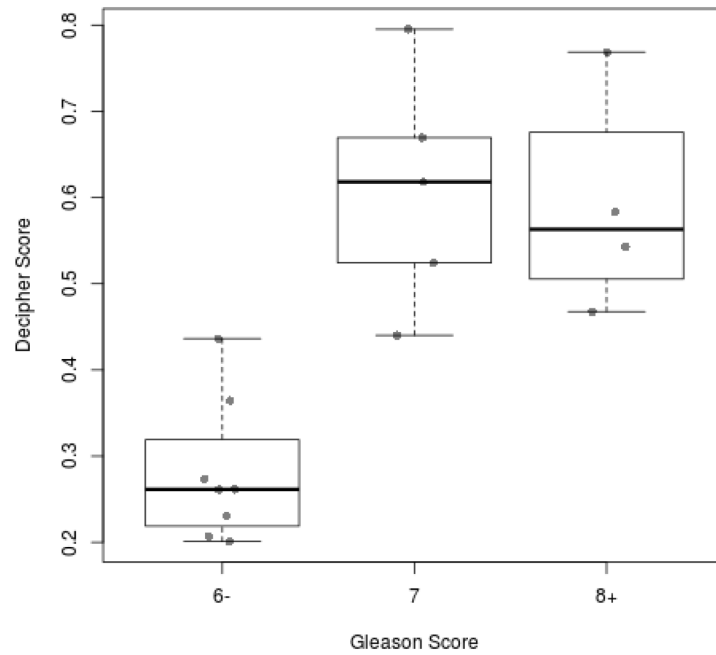


Association of multiparametric MRI quantitative imaging features with prostate cancer gene expression in MRI-targeted prostate biopsies

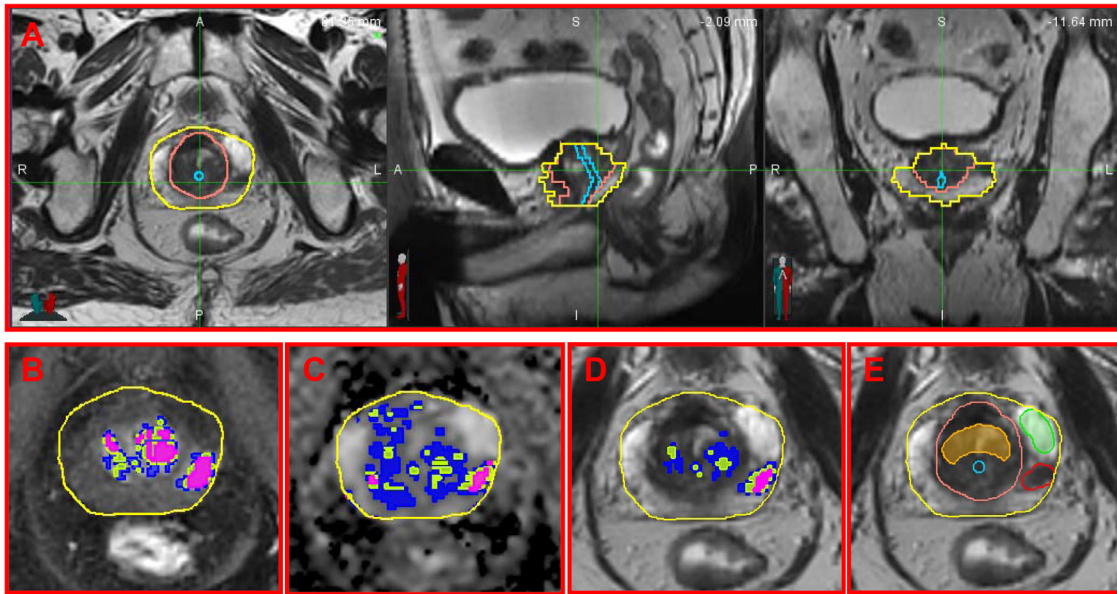
SUPPLEMENTARY FIGURES AND TABLES



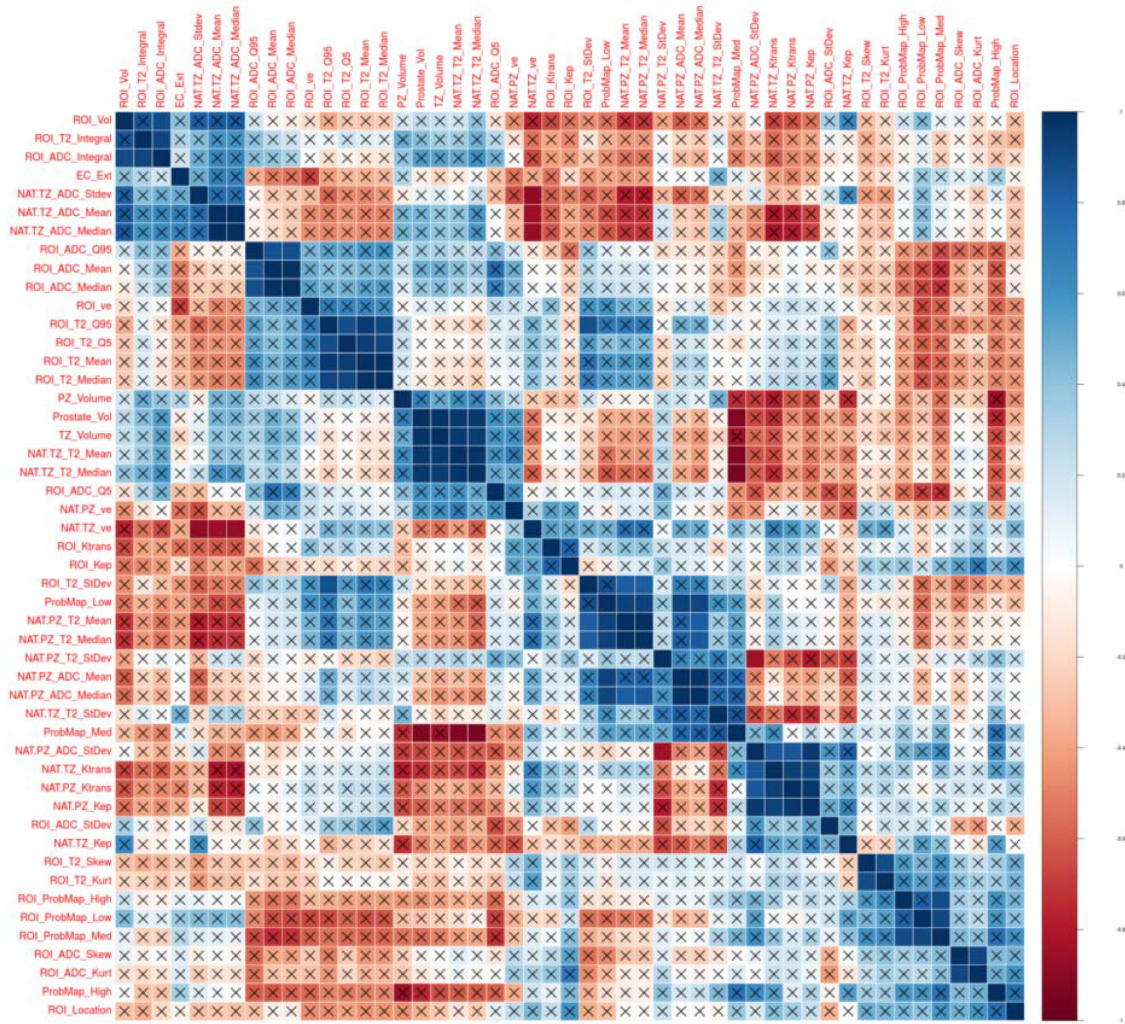
Supplementary Figure S1: Clustering of biopsy samples. A. Unbiased genomic cluster analysis with all genes groups the samples mainly by patient; B. When only prostate related genes are used, the samples tend to cluster and by Gleason Score (GS); and C. Decipher genes separate the samples by tumor aggressiveness.



Supplementary Figure S2: Association of Decipher score with Gleason score. Low Decipher scores are significantly associated with lower Gleason scores. All 8 samples with GS 6 were classified as Decipher low risk (Decipher score < 0.45). The difference in Decipher scores between GS 6 vs. GS7+ was significant with p-value = 8.32e-05.



Supplementary Figure S3: Delineation of prostate habitats. A. Prostate (yellow), Peripheral Zone (PZ) (pink) and urethra (blue) were manually contoured in MIM software in three dimensions. The volumes are presented in three views: axial, sagittal and coronal. Prostate Transition Zone (TZ) is determined by subtracting PZ and Urethra from the prostate volume; B. Perfusion: Areas of high perfusion are presented on three levels (see *Methods*) for risk for tumor aggressiveness: high – pink, mid – green-yellow and low – blue, and overlaid on the early enhancing series from the DCE-MRI; C. Diffusion: Areas of low diffusion are presented on three levels (see *Methods*) for risk for tumor aggressiveness: high – pink, mid – green-yellow and low – blue, and overlaid on the ADC map. D. Volumes of high (pink), mid (green) and blue (low) probabilities for aggressive cancers are determined as intersections of the corresponding areas of high perfusion/low diffusion; E. Biopsy target (ROI), normal appearing tissue - peripheral zone (NAT_PZ) and central region (NAT_TZ) are presented in red, green, and orange.



Supplementary Figure S4: Heatmap of auto-correlation matrix of radiomic features. Positive and negative correlations are shown in blue and red, respectively. Significantly correlated imaging features (p-value (Holm's p-value adjustment) cutoff of 0.05) are not marked with 'X'.

Supplementary Table S1: Pearson's correlation between radiomic and genomic features

See Supplementary Table 1

Supplementary Table S2: Radiomic features, strongly correlated with expression of prostate cancer related genes

See Supplementary Table 2