

Figure S1. The mRNA expression of IL-10 and TGF- β is not associated with overall survival. (A and B) Kaplan–Meier curves of overall survival according to the mRNA expression of IL-10 (A) and TGF- β (B) in dogs with prostate cancer ($n = 18$). Cases were classified as having a high or low mRNA expression according to the median number ($n = 9$ each). Log-rank test.

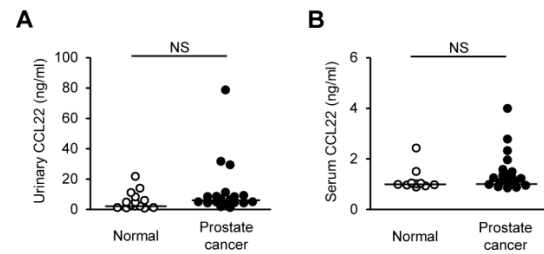


Figure S2. Urinary and serum CCL22 concentration in dogs with prostate cancer.

(A) Urinary CCL22 concentration in normal dogs ($n = 14$) and in dogs with prostate cancer ($n = 19$). Mean values are depicted by horizontal lines. NS, not significant, nonparametric Mann–Whitney U test. (B) Serum CCL22 concentration in normal dogs ($n = 10$) and in dogs with prostate cancer ($n = 19$). NS, not significant, nonparametric Mann–Whitney U test.

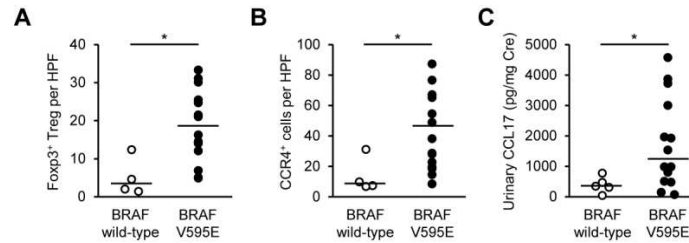


Figure S3. BRAF^{V595E} mutation is associated with intratumoral Foxp3⁺ Tregs, CCR4⁺ cells, and urinary CCL17 concentration in dogs with prostate cancer. (A–C) The number of intratumoral Foxp3⁺ Tregs (A), CCR4⁺ cells (B), and urinary CCL17 concentrations (C) in canine prostate cancer cases with wild-type BRAF and BRAF^{V595E} mutation. * $P < 0.05$, nonparametric Mann–Whitney U test.

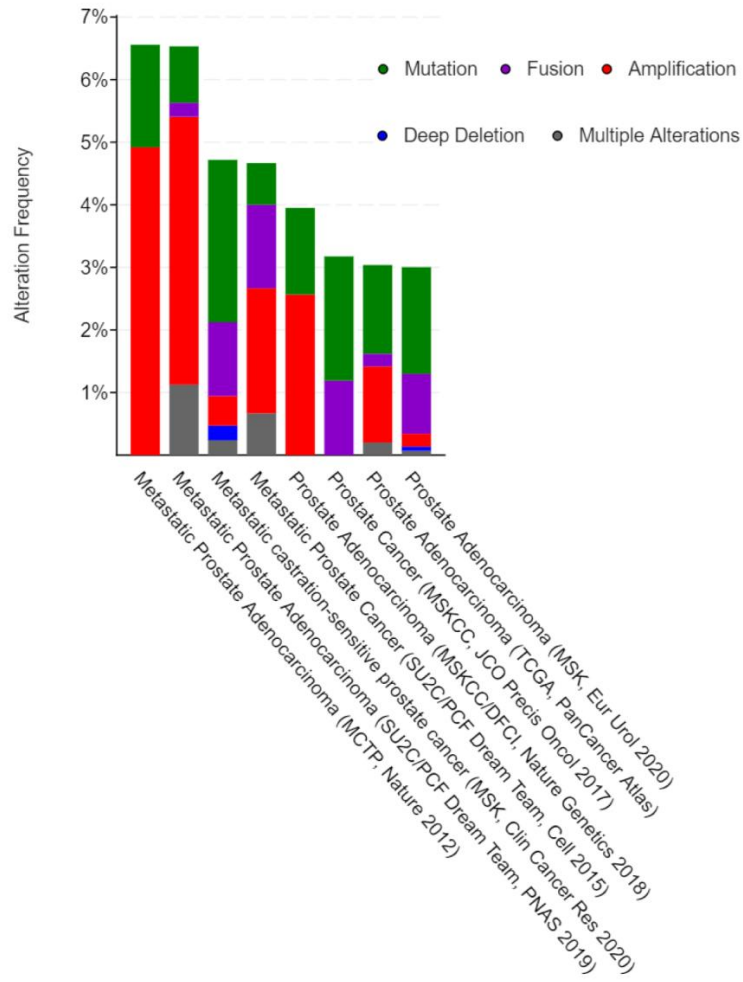


Figure S4. BRAF gene alterations in human prostate cancer. Histogram displaying frequency of BRAF gene somatic mutation, fusion, copy-number amplification, deletion, and multiple alterations across eight human prostate cancer genomic datasets.

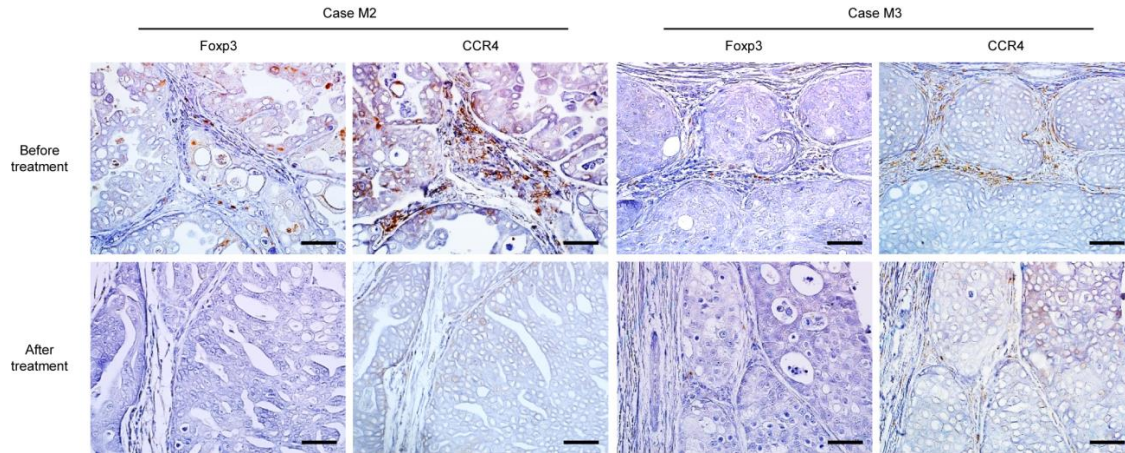


Figure S5. Intratumoral Foxp3⁺ and CCR4⁺ cells in two dogs with prostate cancer before and after mogamulizumab treatment. Before treatment, a number of Foxp3⁺ and CCR4⁺ cells were observed in the tumor tissue. After three (Case M2) and 33 cycles (Case M3) of mogamulizumab treatment, both Foxp3⁺ and CCR4⁺ cells were clearly decreased when compared with the pre-treatment tissue.

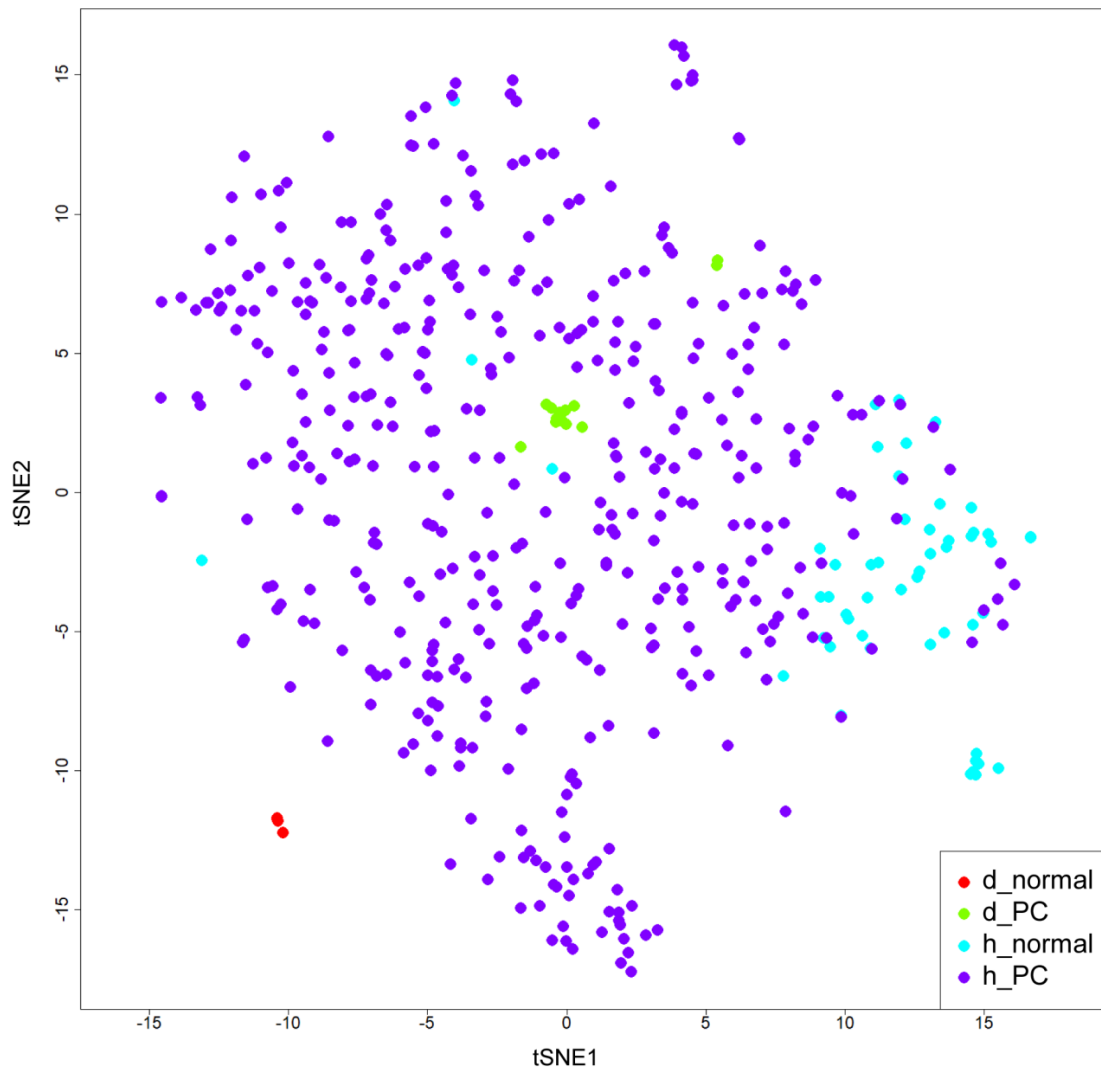


Figure S6. Cross-species t-SNE analysis of canine and human prostate tissues. Differentially expressed genes ($q < 0.01$) between canine prostate cancer and normal prostate were selected and extracted concordant genes in the expression data of humans. The expression patterns of 2,297 differentially expressed genes in the cross-species tissues were visualized with t-SNE. Color-coded sphere showed each type of prostate tissue as following; red: canine normal prostate, green: canine prostate cancer, blue: human normal prostate, purple: human prostate cancer.