**Supplementary Tables:**

|  |  |  |
| --- | --- | --- |
|  |   |   |
|  | UW mCRPC TAN TMA | FDA normal organ TMA |
| Patients | 34 prostate cancer | 69 Healthy |
| No. tissue samples (total) | 108 | 117 |
| No. tissue samples per patient | 2-4 | N/A |
| Replicates of each sample | 1-3 | 1 |
| No. sample sites (total) | 26 (Visceral and bone) | 24 (Visceral and bone) |

**Supplemental Table 1. Overview of TMA composition.**

|  |  |  |  |
| --- | --- | --- | --- |
| Bone | No. samples | Visceral | No. samples |
| L1 | 7 | Liver | 20 |
| T11 | 8 | Lymph node | 16 |
| Iliac | 8 | Mediastinal mass | 1 |
| L5 | 3 | Lung | 8 |
| T12 | 4 | Bladder | 1 |
| Sacrum | 5 | Pleural metastasis | 1 |
| L2 | 3 | Retroperitoneal | 1 |
| T9 | 3 | Adrenal | 1 |
| L4 | 3 | Periaortic | 1 |
| Humerus | 3 | Spleen | 1 |
| Rib | 2 | Diaphragm | 1 |
| L3 | 3 | Omentum | 1 |
| T8 | 1 |  |  |
| T10 | 2 |   |   |
| Sum | 55 | Sum | 53 |

**Supplemental Table 2. Metastatic disease sites represented in the UW mCRPC TAN TMA.**

|  |  |
| --- | --- |
| Tissue type | No. samples |
| Adrenal gland | 6 |
| Breast | 4 |
| Cervix | 3 |
| Colon | 6 |
| Esophagus | 5 |
| Heart | 3 |
| Hypophysis | 3 |
| Kidney | 6 |
| Liver | 3 |
| Lung | 5 |
| Lymph node | 3 |
| Nerve | 1 |
| Ovary | 5 |
| Pancreas | 5 |
| Prostate | 6 |
| Salivary gland | 6 |
| Small intestine | 5 |
| Spleen | 7 |
| Stomach | 5 |
| Striated muscle | 4 |
| Testis | 6 |
| Thymus gland | 11 |
| Tonsil | 4 |
| Uterus | 5 |
| Sum | 117 |

**Supplemental Table 3. FDA normal organ TMA sample composition.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |   |   |   |   |   |   |
| *Gene* | Copy Number Amplification (%) | Copy Number Deletion (%) | Mutation (%) |
| CEACAM5+ | CEACAM5- | CEACAM5+ | CEACAM5- | CEACAM5+ | CEACAM5- |
| *RB1* | 0.0 | 0.0 | 64.7 | 61.9 | 5.9 | 4.8 |
| *TP53* | 5.9 | 0.0 | 35.3 | 47.6 | 41.2 | 52.4 |
| *PTEN* | 0.0 | 0.0 | 64.7 | 52.4 | 0 | 0 |
| *PIK3CA*  | 29.4 | 14.3 | 0.0 | 4.8 | 0 | 0 |
| *PIK3C2B*  | 41.2 | 28.6 | 0.0 | 0.0 | 0 | 0 |
| *PDPK1*  | 0.0 | 0.0 | 5.9 | 14.3 | 0 | 0 |
| *SGK3* | 41.2 | 38.1 | 0.0 | 4.8 | 0 | 0 |
| *DEPTOR* | 52.9 | 66.7 | 0.0 | 0.0 | 0 | 0 |
| *FOXO1* | 0.0 | 0.0 | 47.1 | 42.9 | 0 | 0 |
| *FOXO3* | 11.8 | 9.5 | 35.3 | 14.3 | 0 | 0 |
| *MAP3K7* | 0.0 | 14.3 | 47.1 | 23.8 | 0 | 0 |
| *SESN1* | 5.9 | 9.5 | 29.4 | 28.6 | 0 | 0 |
| *RRAGD* | 5.9 | 0.0 | 35.3 | 9.5 | 0 | 0 |

**Supplemental Table 4. Frequency of common prostate cancer genetic alterations in CEACAM5+ and CEACAM5- samples in the UW mCRPC TAN TMA.** Deletion percentage represents both monoallelic and biallelic loss. CEACAM5+ (n = 17 tissues); CEACAM5- (n = 21 tissues).