**Supplementary Table 1. Clinical Characteristics of the Whole Genome Sequencing Cohort**

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| --- | --- | --- | --- |
|  | **Overall Patient Cohort**  **(N = 101)** | **t-SCNC Subgroup**  **(N = 5)** | **Adenocarcinoma Subgroup**  **(N = 96)** |
| **Median Age (range)** | 71 (45-90) | 68 (57-74) | 72 (45-90) |
| **Race/Ethnicity (%)**  **White**  **Black**  **Asian**  **Unknown** | 85 (84)  5 (5)  4 (4)  7 (7) | 5 (100)  0  0  0 | 80 (83)  5 (5)  4 (4)  7 (7) |
| **Gleason Grade at Diagnosis (%)**  **6**  **7**  **≥ 8**  **Unknown** | 11 (11)  28 (28)  52 (51)  10 (10) | 0  0  3 (60)  2 (40) | 11 (11)  28 (29)  49 (51)  8 (8) |
| **Site of Biopsy (%)**  **Bone**  **Lymph Node**  **Liver**  **Other Soft Tissue** | 42 (42)  40 (40)  11 (11)  8 (8) | 0  3 (60)  2 (40)  0 | 42 (44)  37 (39)  9 (9)  8 (8) |
| **Prior Therapy (%)**  ***Second Generation AR Antagonist***  **Abiraterone**  **Enzalutamide**  **Both**  **Neither**  ***Chemotherapy***  **Docetaxel**  **Cabazitaxel** | 27 (27)  17 (17)  20 (20)  37 (37)  17 (17)  4 (4) | 1 (20)  1 (20)  0  3 (60)  0  0 | 26 (27)  16 (17)  20 (21)  34 (35)  17 (18)  4 (4) |
| **Visceral Metastases (%)**  **Yes**  **No** | 31 (31)  70 (69) | 3 (60)  2 (40) | 28 (29)  68 (71) |