**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)000 | 80 (83)5 (5)4 (4)7 (7) |
| **Gleason Grade at Diagnosis (%)****6****7****≥ 8****Unknown** | 11 (11)28 (28)52 (51)10 (10) | 003 (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) | 03 (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)03 (60)00 | 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) |