Supplementary Tables

Table S1: Characteristics of six retrospective cohorts

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Variables | JHMI | Mayo | TJU | Durham | Kaiser | BWH | TCGA |
| Tissue type | Radical prostatectomy | Radical prostatectomy | Radical prostatectomy | Radical prostatectomy | Radical prostatectomy | biopsy | Radical prostatectomy |
| Total N= | 355 | 235 | 139 | 117 | 224 | 100 | 333 |
| Age (years) | 59(56-64) | 63(58,69) | 60(56,64) | 61(57,64) | 57(46,64) | 67(47,85) | 61(56-66) |
| PSA at diagnosis (ng/mL) | 8.6(5.8-13.3) | 9.3(6.2,15.6) | 6.9(4.9,12.2) | 7.6(5.3,10.8) | 6.1 (4.7,8.9) | 7.3(1.5,103) | 7.4(5.1-11.9) |
| Gleason Grade group |  |  |  |  |  |  |  |
| Group 1-2 | 157 (44.2) | 96 (40.9 ) | 61(44.2) | 82 (68.3) | 143 (63.8) | 30 (30) | 167 (50) |
| Group 3 | 66 (18.5) | 41 (17.4) | 37 (26.8) | 20 (16.7) | 45 (20.1) | 36 (36) | 78 (23) |
| Group 4-5 | 132 (37.1) | 98 (41.7) | 38 (27.3) | 15 (12.5) | 36 (16.1) | 34 (34) | 88 (26) |
| ADT treatment | 0 | 136 (57.9) | 29 (21) | 25 (21.2) | 30 (13.4) | 100 |  |
| Patients with metastatic outcome/ or recurrence for TCGA | 127 | 76 | 10 | 5 | 12 | 18 | 55 |
| Median follow-up (months) | 108 | 84 | 80 | 105 | 106 | 61 | 28 |

Table S2: p-values of tested genes after fdr multiple test adjustment

|  |  |
| --- | --- |
| Gene/signature | adjusted pvalue |
| DNArepair | 1.97E-115 |
| Treg | 5.82E-75 |
| PMS2 | 1.76E-62 |
| MDSC | 1.93E-61 |
| PORTOS | 2.18E-61 |
| Decipher | 5.00E-58 |
| NCAM1 | 5.79E-58 |
| FGFRactivity | 7.84E-55 |
| MSH3 | 1.05E-54 |
| FGF9 | 3.67E-50 |
| PGR | 3.89E-49 |
| DSBR | 5.34E-45 |
| PMS1 | 7.74E-42 |
| MMRactivity | 7.09E-41 |
| MIAT | 2.96E-38 |
| CDC25B | 3.33E-37 |
| SNAP25 | 4.33E-37 |
| ENO2 | 5.96E-35 |
| MLH1 | 1.02E-34 |
| CD3G | 1.37E-31 |
| MSH2 | 2.18E-31 |
| TUBB2B | 3.49E-31 |
| CCDC88A | 3.73E-31 |
| ESR1 | 5.08E-30 |
| RNF183 | 6.28E-28 |
| ELAVL4 | 3.19E-21 |
| SCG2 | 5.99E-21 |
| PCSK2 | 8.54E-21 |
| HRactivity | 6.13E-19 |
| PCNA | 1.42E-18 |
| NR3C1 | 2.68E-17 |
| PHF19 | 5.31E-17 |
| CD4 | 3.23E-16 |
| FANCL | 1.85E-15 |
| AP3B2 | 3.27E-15 |
| TOX | 1.83E-14 |
| ELAVL3 | 3.69E-13 |
| CD8A | 1.84E-12 |
| NPTX1 | 1.69E-11 |
| UNC13A | 1.77E-11 |
| SRRM4 | 2.81E-11 |
| IGFBPL1 | 3.10E-11 |
| SYP | 6.03E-10 |
| SOX2 | 3.23E-08 |
| NPPA | 1.21E-07 |
| MLH3 | 2.37E-07 |
| APLP1 | 2.05E-04 |
| CRMP1 | 3.36E-04 |
| MSH6 | 1.92E-03 |
| INA | 2.97E-03 |
| KCNC1 | 7.54E-03 |
| RUNDC3A | 1.17E-02 |
| PCSK1 | 1.98E-02 |
| NKX2-1 | 2.35E-02 |
| TMEM145 | 4.18E-02 |
| SH3GL2 | 1.05E-01 |
| INSM1 | 1.64E-01 |
| STMN1 | 1.84E-01 |
| DNMT1 | 2.73E-01 |
| DLL3 | 5.39E-01 |
| FAM161A | 5.44E-01 |
| ASCL1 | 5.91E-01 |
| SEZ6 | 6.69E-01 |

Table S3: Batch-stratified competing risks regression for the pooled retrospective cohort

|  |  |  |
| --- | --- | --- |
| Term | HR (95% CI) | p-value |
| AR-A Low (vs. High) | **2.69 (1.21-5.96)** | **0.02** |
| Gleason Grade ≥ 8 | 2.45(1.12-5.35) | 0.03 |
| SM + | 0.55(0.26-1.14) | 0.1 |
| Log2(PSA) | 1.11(0.84-1.44) | 0.5 |
| Age at RP | 0.97(0.93-1.01) | 0.2 |
| Salvage ADT (vs. Adjuvant) | 0.81(0.34-1.93) | 0.6 |
| ECE | 1.1(0.51-2.37) | 0.8 |
| SVI | 1.15(0.54-2.39) | 0.7 |
| LNI | 1.49(0.52-4.24) | 0.5 |