**Table S2. Antigen presentation pathway mutations in TCGA *POLE* proofreading-mutant ECs**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| TCGA ID | *POLE* mutation | No. exonic mutations | CD8A expression\* | Antigen presentation pathway mutations | Variant allele frequency | Predicted functional effect | |
|  |  |  |  |  |  | Mutation assessor | SIFT |
| TCGA-B5-A0JY | P286R | 8890 | High | HLA-B E253K  B2M R117\*  PDIA3 R344C  PDIA3 E384D | 0.33  0.59  0.36  0.30 | Medium  N/A  Medium  Neutral | Deleterious (0.00)  N/A  Deleterious (0.00)  Deleterious (0.00) |
| TCGA-BS-A0TC | M444K | 1203 | Low | None |  |  |  |
| TCGA-D1-A103 | A456P | 5965 | High | PDIA3 R344C | 0.30 | Medium | Deleterious (0.00) |
| TCGA-D1-A16X | P286R | 1755 | High | None |  |  |  |
| TCGA-D1-A16Y | V411L | 952 | Low | None |  |  |  |
| TCGA-A5-A0GP | V411L | 1235 | Low | None |  |  |  |
| TCGA-AP-A051 | L424I | 6716 | High | PDIA3 A69T | 0.31 | Low | Deleterious (0.04) |
| TCGA-AP-A056 | V411L | 7226 | High | HLA-C E288K  CALR S300Y | 0.16  0.34 | Low  Neutral | Tolerated (0.06)  Deleterious (0.00) |
| TCGA-AP-A059 | S297F | 9187 | High | None |  |  |  |
| TCGA-AP-A0LM | V411L | 10489 | High | B2M A6V  CANX K182N | 0.13  0.20 | Low  Medium | Tolerated (1.0)  Deleterious (0.00) |
| TCGA-AX-A05Z | P286R | 5677 | High | None |  |  |  |
| TCGA-AX-A0J0 | P286R | 6913 | Low | HLA-B S112R  CALR K62R  TAPBP R383Q | 0.71  0.50  0.57 | High  Medium  Medium | Deleterious (0.00)  Deleterious (0.00)  Tolerated (0.34) |
| TCGA-B5-A11E | V411L | 8210 | High | PDIA3 E384\* | 0.44 | N/A | N/A |
| TCGA-B5-A11N | P286R | 1557 | High | None |  |  |  |
| TCGA-BG-A0VX | L424V | 163 | High | None |  |  |  |
| TCGA-BS-A0UF | P286R | 7391 | High | CANX D37N | 0.33 | Medium | Deleterious (0.00) |
| TCGA-BS-A0UV | P286R | 7801 | High | None |  |  |  |
| TCGA-D1-A17Q | P286R | 5141 | Low | CALR Y128C  CANX Q508H  TAPBP R383Q | 0.13  0.48  0.38 | High  Medium  Medium | Deleterious (0.00) Deleterious (0.00)  Tolerated (0.34) |

\* relative to median CD8A expression in all TCGA ECs