**SUPPLEMENTARY TABLES**

**Table S1**: Characteristics of the full and reduced cohorts of patients

|  |  |  |
| --- | --- | --- |
|  | Full cohort (981) | Reduced cohort (586) |
| Age |  |  |
| Mean | 65.6 | 65.8 |
| Median | 68 | 68 |
| Min | 22 | 22 |
| Max | 80 | 80 |
| Gender |  |  |
| Male | 857 (87%) | 517 (88%) |
| Female | 124 (13%) | 69 (12%) |
| Area |  |  |
| 1 | 222 (23%) | 116 (20%) |
| 2 | 161 (16%) | 97 (17%) |
| 3 | 83 (8%) | 56 (10%) |
| 4 | 150 (15%) | 117 (20%) |
| 5 | 363 (37%) | 199 (34%) |
| TG |  |  |
| 1 (PUNLMP/TaG1) | 424 (43%) | 179 (31%) |
| 2 (TaG2) | 292 (30%) | 214 (37%) |
| 3 (TaG3) | 102 (10%) | 74 (13%) |
| 4 (T1G2) | 28 (3%) | 13 (2%) |
| 5 (T1G3) | 129 (13%) | 102 (17%) |
| 6 (Tis) | 6 (1%) | 4 (1%) |
| Risk |  |  |
| High | 340 (35%) | 250 (43%) |
| Low | 641 (65%) | 336 (57%) |

**Table S2**: Cox regression analysis results displaying association of CD8 infiltration with risk of recurrence in the T1 cohort with 2 spots available (N=67). Reduced number of events (11 recurrences) only allowed adjustment for 3 variables.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | HR | *p*-value |  | lower 95 | upper 95 |
| **Number of CD8** |  |  |  |  |  |
| <35/mm2 | *Ref* |  |  |  |  |
| ≥ 35 /mm2 | 0.36 | 0.13 |  | 0.07 | 1.40 |
| **Multiplicity** |  |  |  |  |  |
| 1 tumor | *Ref* |  |  |  |  |
| ≥ 2 tumors | 3.70 | 0.06 | . | 0.95 | 14.47 |
| Missing | 1.15 | 0.92 |  | 0.11 | 11.79 |
| **Size** |  |  |  |  |  |
| < 3cm | *Ref* |  |  |  |  |
| ≥ 3cm | 4.40 | 0.06 | . | 0.90 | 21.51 |
| Missing | 1.71 | 0.52 |  | 0.33 | 8.95 |

**SUPPLEMENTARY FIGURES**

Figure S1: Correlation between maunal and automated counting of lymphocytes in the tumor compartment

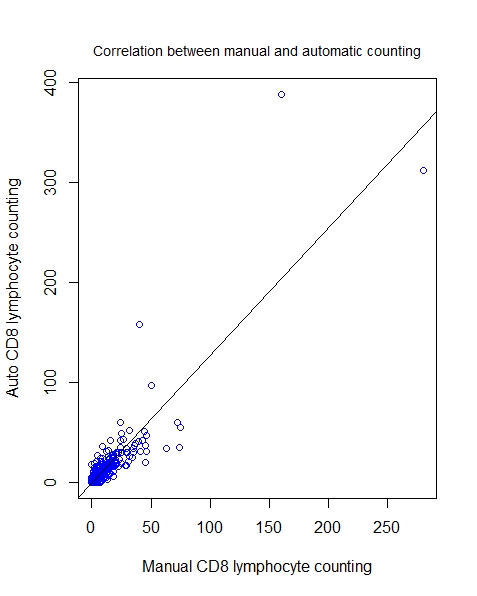


Figure S2 : Boxplots figuring CD8+ count Interquartile range in the stroma compartment in Ta and T1 tumors.

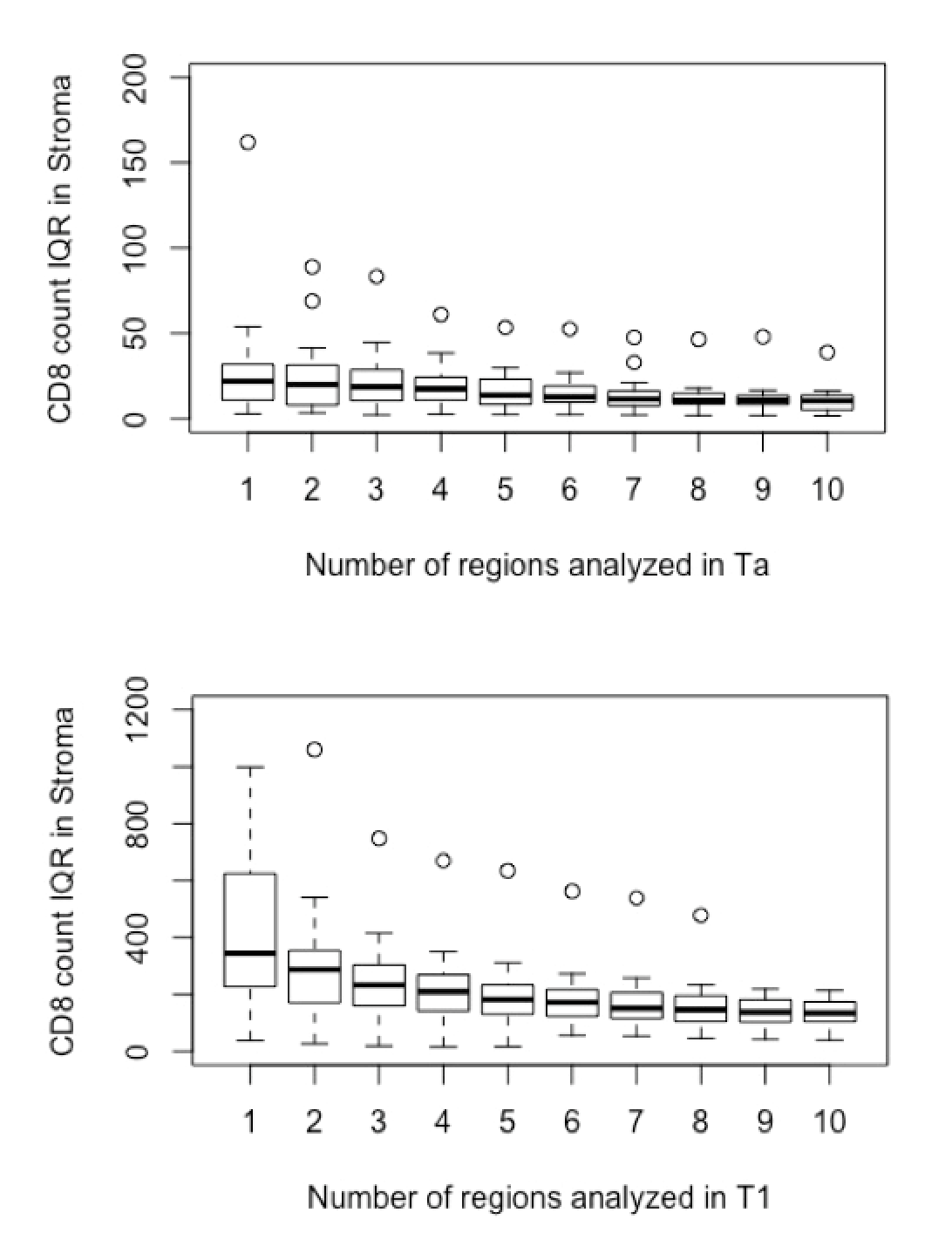


Figure S3 : Histograms showing the distribution of GATA3, FGFR3 and CK5/6 expression in the EPICURO cohort.

