**Supplementary Table II**. Overall and event-free survival in relation to SNP distributions in the Training set (Cox regression for adjusted estimates)

| | | | | | | OS | | | | | EFS | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Gene** | **dbSNP ID** | **Genotype** | **N[a]** | **Events** | **Expected** | **HR (95% CI)[b]** | **p-value** | **N[a]** | **Events** | **Expected** | **HR (95% CI)[b]** | **p-value** |
| *SMUG1* | | | | | | | | | | | | |
| | rs2233921 | GG | 205 | 94 | 85.3 | Ref | | 199 | 89 | 88.2 | | |
| | | GT | 392 | 181 | 171.9 | 1.24 (0.90-1.71) | 0.19 | 381 | 182 | 169.1 | 1.19 (0.86-1.63) | 0.29 |
| | | TT | 121 | 38 | 55.8 | 0.62 (0.39-1.00) | **0.05** | 119 | 46 | 59.6 | 0.89 (0.58-1.36) | 0.60 |
| | rs971 | GG | 262 | 102 | 117.2 | Ref | | 254 | 105 | 120.7 | Ref | |
| | | GA | 368 | 173 | 153.5 | 1.38 (1.02-1.86) | **0.04** | 360 | 173 | 154.0 | 1.28 (0.96-1.72) | 0.10 |
| | | AA | 92 | 35 | 39.3 | 1.92 (0.57-1.50) | 0.75 | 89 | 36 | 39.3 | 0.99 (0.62-1.56) | 0.91 |
| *MBD4* | | | | | | | | | | | | |
| | rs2307285 | AA | 231 | 98 | 104.2 | Ref | | 226 | 110 | 102.2 | | |
| | | GA | 364 | 155 | 156.0 | 0.91 (0.66-1.24) | 0.53 | 354 | 159 | 160.5 | 0.88 (0.65-1.19) | 0.42 |
| | | GG | 126 | 59 | 51.8 | 0.97 (0.65-1.45) | 0.88 | 123 | 50 | 56.3 | 0.77 (0.51-1.16) | 0.21 |
| | rs2307294 | GG | 621 | 264 | 268.6 | Ref | | 607 | 263 | 272.4 | | |
| | | GC | 98 | 46 | 41.4 | 1.09 (0.74-1.59) | 0.66 | 93 | 49 | 39.6 | 1.21 (0.82-1.76) | 0.33 |
| | | CC | - | - | | - | - | - | - | - | - | |
| *NEIL2* | | | | | | | | | | | | |
| | rs1534862 | CC | 457 | 201 | 195.0 | Ref | | 445 | 210 | 193.2 | | |
| | | CT | 230 | 96 | 101.0 | 0.88 (0.65-1.19) | 0.41 | 225 | 91 | 107.6 | 0.73 (0.54-0.98) | **0.04** |
| | | TT | 32 | 13 | 14.0 | 0.86 (0.45-1.64) | 0.64 | 30 | 14 | 14.2 | 0.79 (0.42-1.48) | 0.46 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | rs6997097 | TT | 618 | 258 | 266.8 | Ref | | 600 | 264 | 270.3 | | |
| | | TC | 106 | 54 | 43.3 | **1.77 (1.23-2.53)** | **≥0.01** | 105 | 53 | 44.5 | 1.21 (0.83-1.75) | 0.32 |
| | | CC | 5 | 1 | 2.9 | 0.87 (0.12-6.37) | 0.89 | 5 | 1 | 3.2 | 0.43 (0.06-3.18) | 0.41 |
| | rs8191670 | TT | 461 | 209 | 199.5 | Ref | | 449 | 199 | 201.7 | | |
| | | TC | 227 | 90 | 98.6 | 0.95 (0.70-1.27) | 0.72 | 221 | 99 | 100.6 | 1.11 (0.83-1.48) | 0.48 |
| | | CC | 40 | 16 | 16.9 | 0.82 (0.42-1.57) | 0.54 | 39 | 21 | 16.7 | 1.51 (0.89-2.58) | 0.13 |
| | rs2740439 | GG | 702 | 302 | 301.5 | Ref | | 684 | 303 | 304.6 | | |
| | | GC | 16 | 6 | 6.5 | 0.65 (0.21-2.07) | 0.47 | 15 | 8 | 6.4 | 0.49 (0.15-1.54) | 0.22 |
| | | CC | - | - | - | - | - | | | | | |
| | rs4639 | AA | 194 | 82 | 83.1 | Ref | | 189 | 80 | 84.5 | | |
| | | AG | 360 | 158 | 153.5 | 0.83 (0.59-1.15) | 0.25 | 353 | 156 | 156.2.3 | 1.02 (0.73-1.42) | 0.92 |
| | | GG | 165 | 66 | 69.4 | 0.72 (0.48-1.07) | 0.11 | 159 | 75 | 70.3 | 1.15 (0.78-1.68) | 0.48 |
| | rs1043180 | CC | 524 | 222 | 226.7 | Ref | | 509 | 230 | 225.0 | | |
| | | CT | 178 | 84 | 75.8 | 1.07 (0.78-1.48) | 0.66 | 175 | 74 | 77.1 | 0.92 (0.66-1.28) | 0.62 |
| | | TT | 15 | 4 | 7.5 | 0.17 (0.02-1.23) | 0.08 | 14 | 6 | 7.9 | 0.52 (0.17-1.66) | 0.27 |
| *NEIL3* | | | | | | | | | | | | |
| | rs1055678 | CC | 637 | 277 | 275.5 | Ref | | 622 | 277 | 281.4 | | |
| | | CT | 79 | 32 | 34.6 | 1.00 (0.64-1.58) | 0.99 | 75 | 36 | 32.9 | 1.15 (0.75-1.75) | 0.53 |
| | | TT | 5 | 3 | 1.9 | 3.50 (0.46-26.63) | 0.23 | 5 | 3 | 1.7 | 7.98 (1.04-61.34) | **0.05** |
| *LIG3* | | | | | | | | | | | | |
| | rs1052536 | CC | 193 | 75 | 85.6 | Ref | | 186 | 76 | 86.7 | | |
| | | CT | 369 | 168 | 154.3 | 1.07 (0.77-1.50) | 0.68 | 362 | 171 | 160.0 | 1.24 (0.89-1.72) | 0.20 |
| | | TT | 168 | 72 | 75.1 | 0.88 (0.59-1.31) | 0.53 | 163 | 73 | 73.3 | 0.99 (0.67-1.47) | 0.97 |

HR, hazard ratio; 95% CI, confidence interval. Significant results in bold.

[a] Numbers may not add up to 100% of available subjects because of genotyping failure. All samples that did not give a reliable result in the first round of genotyping were resubmitted to up to two additional rounds of genotyping. Data points that were still not filled after this procedure had been left blank.

[b] Adjusted for sex, age, TNM and chemotherapy.