**Supplementary Table S1: Bivariate logistic regression models for the immune- and proliferation-associated gene signatures**

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| --- | --- | --- |
| All patients | OR (95 % CI) | P |
| Prolif-Sig high (vs. low) | 2.348 (0.927-6.211) | 0.077 |
| G6-Sig high (vs. low) | 2.179 (1.327-3.692) | 0.003 |
| Interaction | 0.792 (0.403-1.539) | 0.494 |
|  |  |  |
| Durvalumab arm | OR (95 % CI) | P |
| Prolif-Sig high (vs. low) | 1.607 (0.465-5.752) | 0.455 |
| G6-Sig high (vs. low) | 2.535 (1.273-5.509) | 0.012 |
| Interaction | 0.710 (0.268-1.817) | 0.479 |
|  |  |  |
| Placebo arm | OR (95 % CI) | P |
| Prolif-Sig high (vs. low) | 4.091 (0.966-21.849) | 0.069 |
| G6-Sig high (vs. low) | 2.092 (0.970-5.000) | 0.071 |
| Interaction | 0.793 (0.279-2.132) | 0.651 |
|  |  |  |

Bivariate logistic regression models with interaction term in all patients and within the two treatment arms for prediction of treatment response (pCR vs. no pCR) using the proliferation (Prolif-Sig) and lymphocyte-associated GeparSixto signature (G6-Sig.) as covariates.