Supplementary figures

Suppl. figure 1. Statistical power to detect associations between HLA alleles and immunotherapy responses.

a, A statistical power analysis was performed to determine the required sample size to detect a significant survival difference between patients with and without a certain MHC class I or class II HLA allele. **b**, The minimal sample size to detect a significant difference ($P < 0.05$) with 0.8 statistical power was determined as a function of different allele frequencies and hazard ratio's as indicated. Sample sizes calculated using the *ssizeCT.default* function from the R *powerSurvEpi* package. **c**, Bar plots indicating the population proportion of MHC class I/II for different allele frequencies. Data derived from a Caucasian American population from Allele Frequency Net.

Suppl. figure 2. Survival analysis using different percentiles cut-offs.

Survival analysis of a set of previously published melanoma patients that were treated with nivolumab (n=144). Patients were stratified in 3 groups based on the different percentiles of TMB, MGBS-I, MGBS-II and MGBS-d as indicated. *P* values calculated using log rank test.

Suppl. figure 3. Correlation analysis between TMB, MGBS-I and MGBS-II.

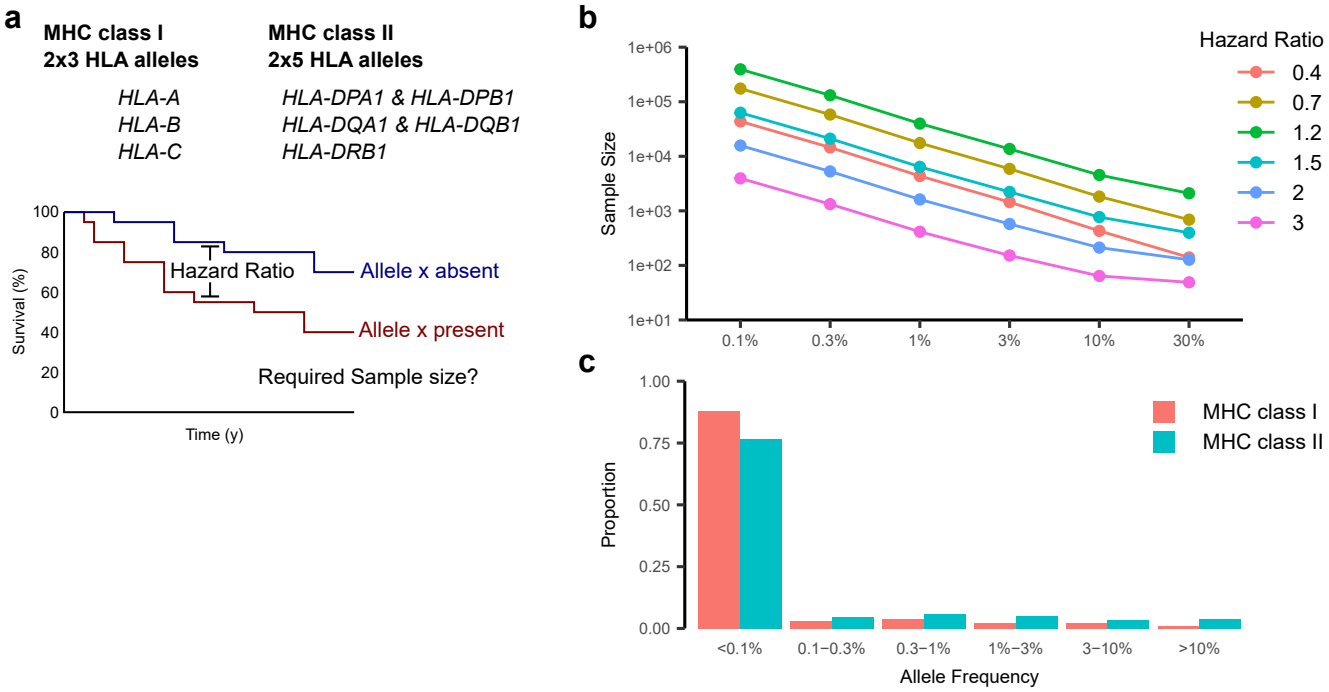
a-c, Nivolumab treated melanoma patients (n=144) were stratified in 2 groups based on the median TMB, MGBS-I and MGBS-II. Bar plots showing percentages of patients with high (hi) MGBS-I/II for 2 groups of patients as indicated. *P* values calculated using two-sided Fisher's exact test. **d-e**, Correlation analysis between TMB (log10 scale) and MGBS-I/II values as indicated. Linear regression line in blue and Pearson correlation coefficient and *P* value indicated on top of each plot.

Suppl. figure 4. Survival and clinical response analysis based on risk groups defined by TMB and MGBS-d.

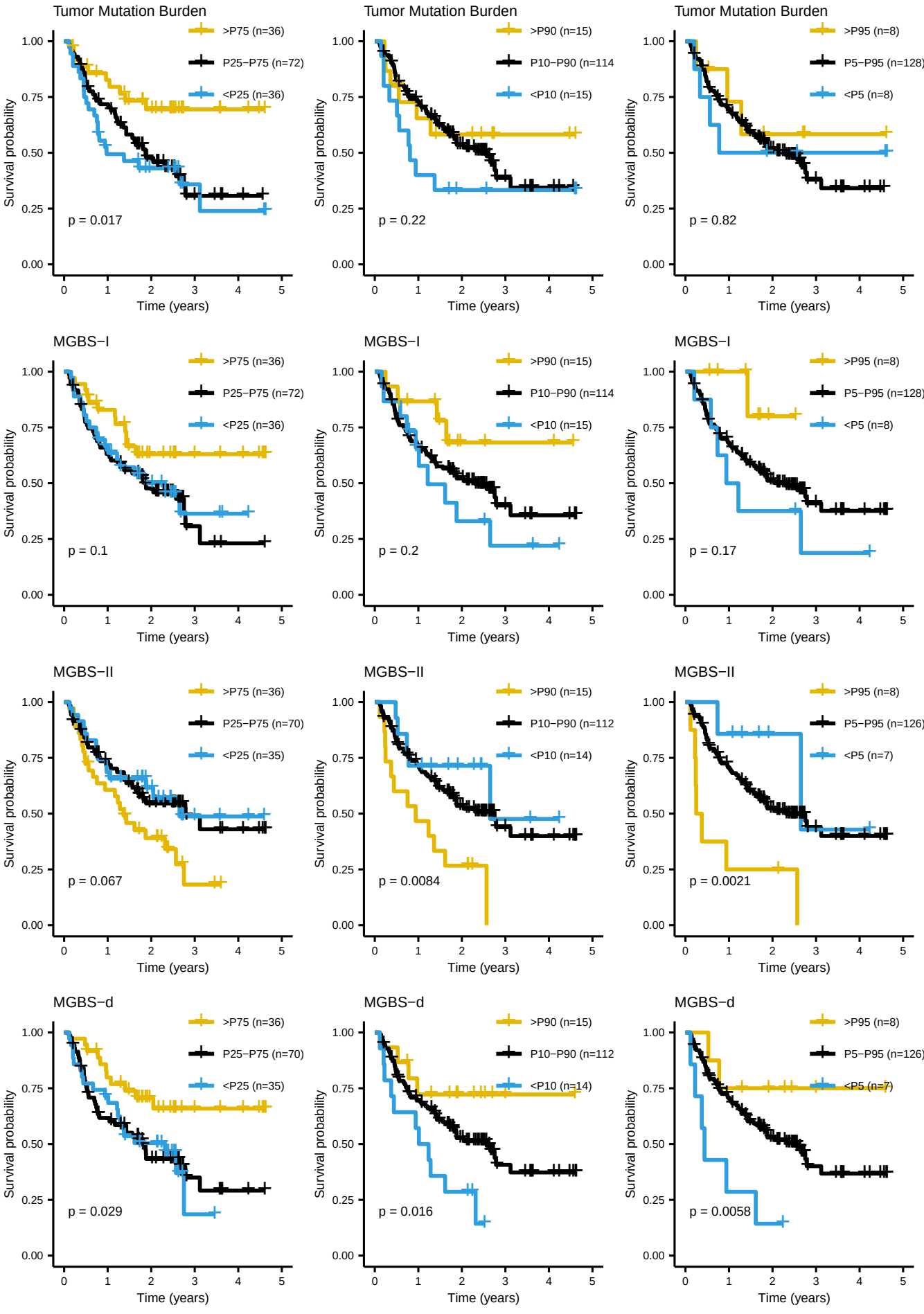
Nivolumab treated melanoma patients (n=144) were stratified in 3 risk groups: high (TMB low and MGBS-d low), intermediate (TMB low and MGBS-d high or vise versa) and low (TMB high and MGBS-d high). Low/high defined based in median values. **a**, Kaplan-Meier analysis with indication of log rank test *P* value. **b**, Stacked bar plots indicating clinical response (RECIST criteria) for the 4 variables as indicated. *P* value calculated using Chi-squared test.

Suppl. figure 5. Hallmark gene set enrichment analysis.

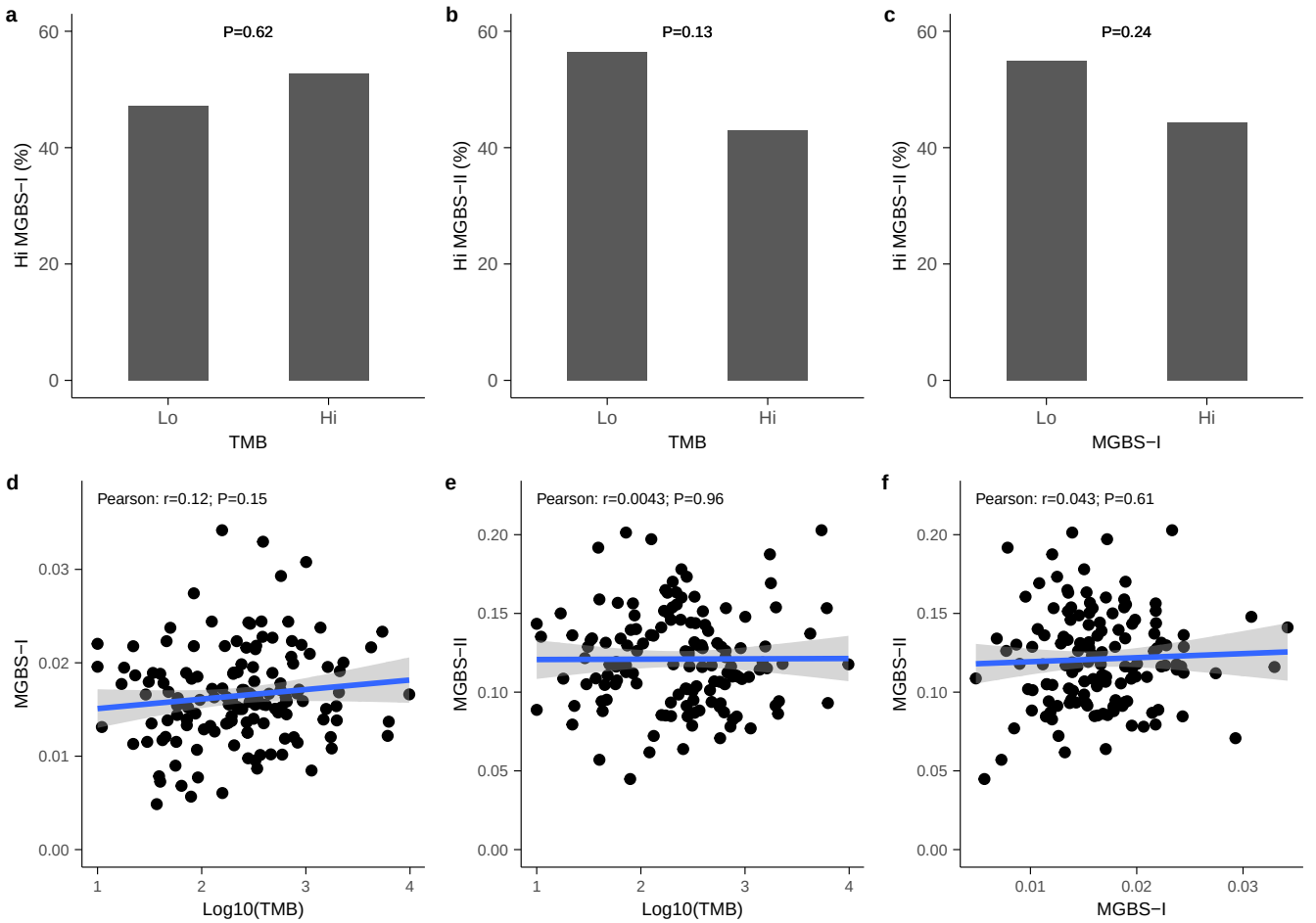
Differential gene expression was determined between patients with low and high TMB/MGBS-I/MGBS-II/MGBS-d (median value cut-offs) and a preranked Hallmark gene set enrichment analysis (GSEA) was performed for different groups of patients as indicated by panel names. Size of circles correlate with significance (-log10(*P* value)) and color indicates size of enrichment as indicated by the color legend on top. Gene sets ranked based on significance for MGBS-II for all patients. NES, Normalized Enrichment Score.



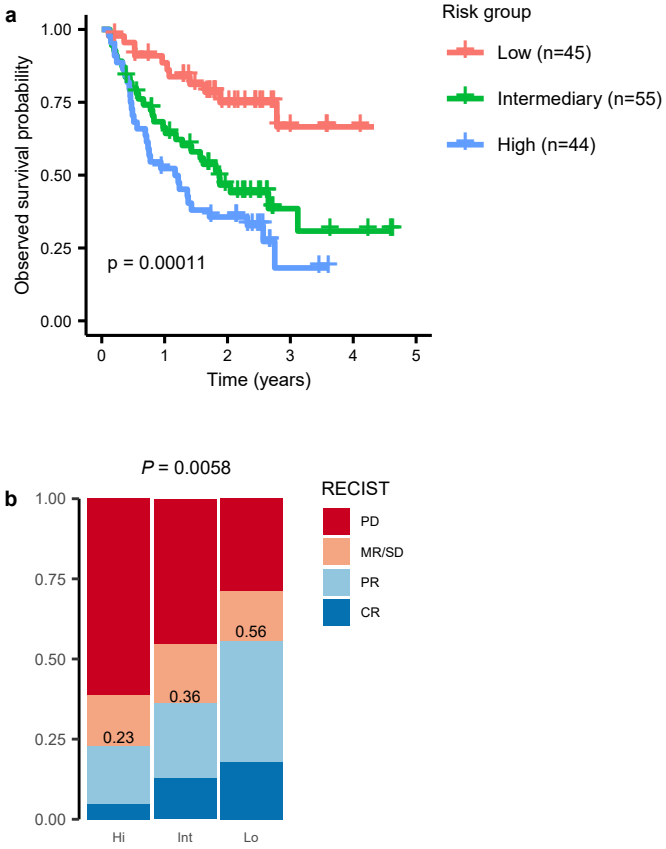
Claeys et al. 2023 − Supplementary Figure 1



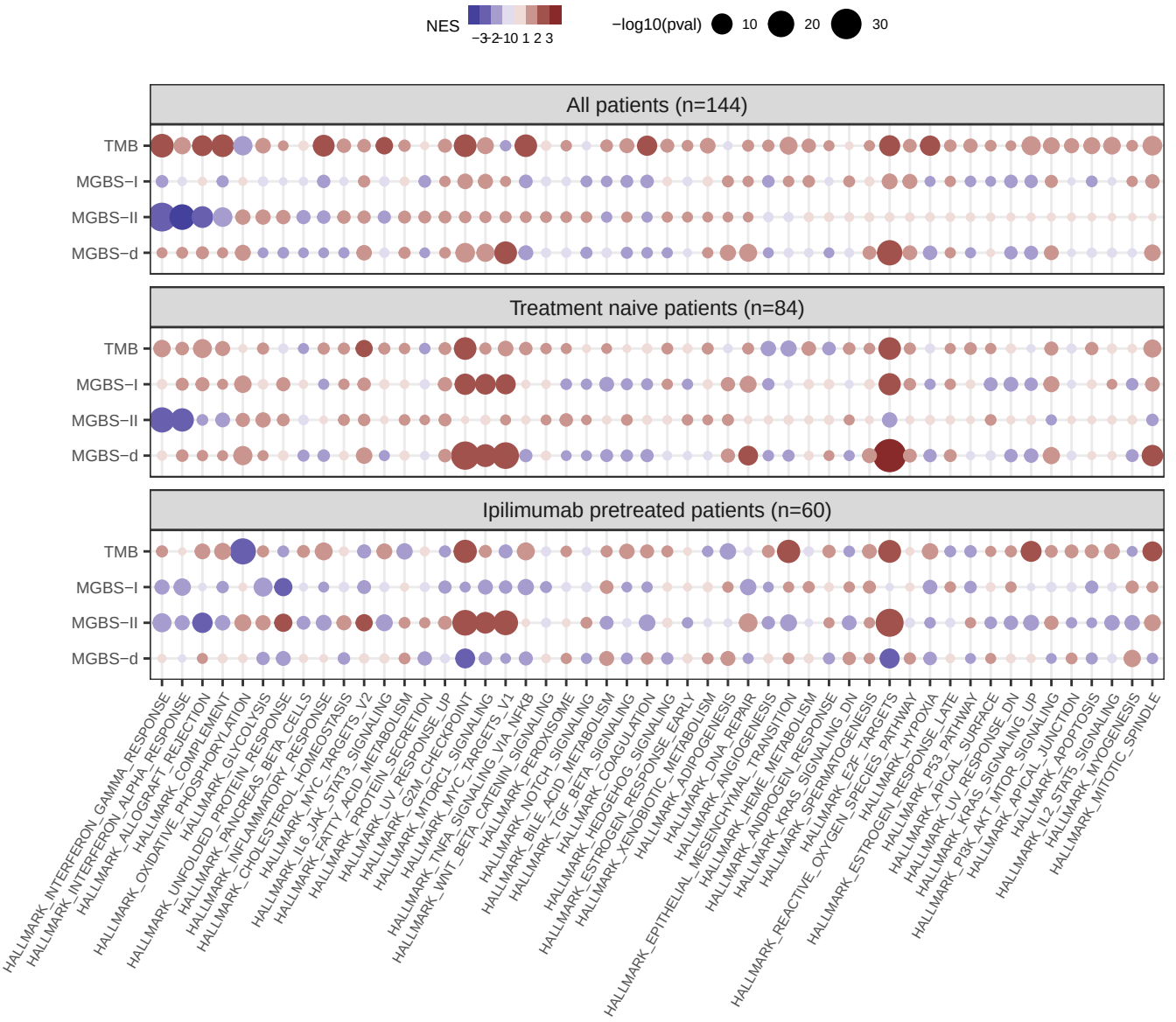
Claeys et al. 2023 − Supplementary Figure 2



Claeys et al. 2023 − Supplementary Figure 3



Claeys et al. 2023 − Supplementary Figure 4



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