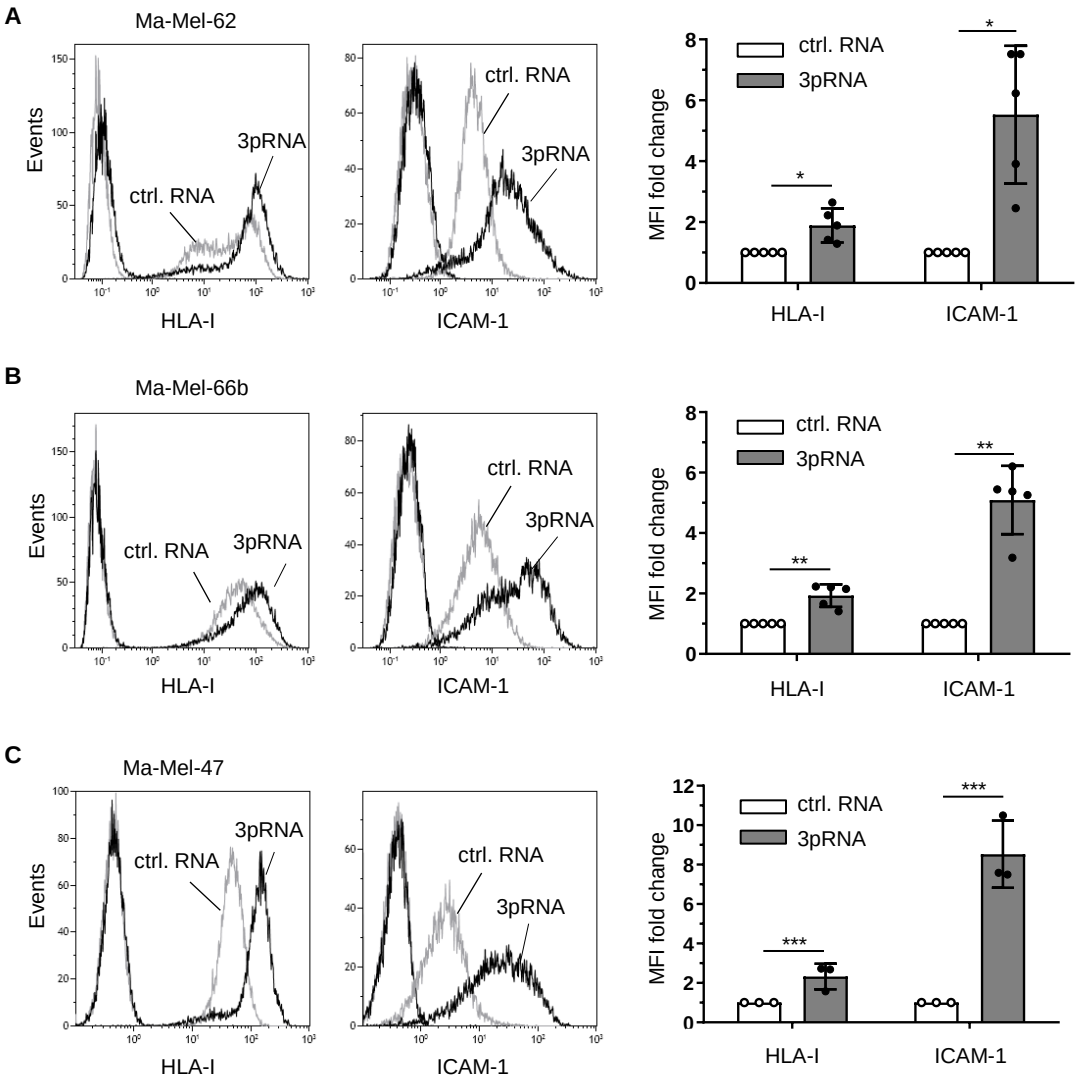
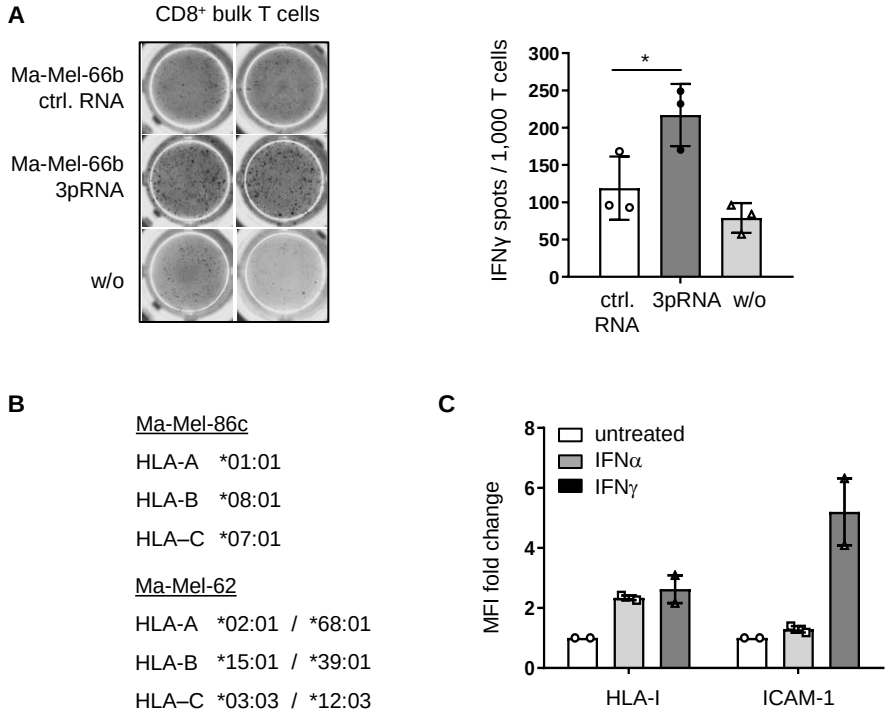
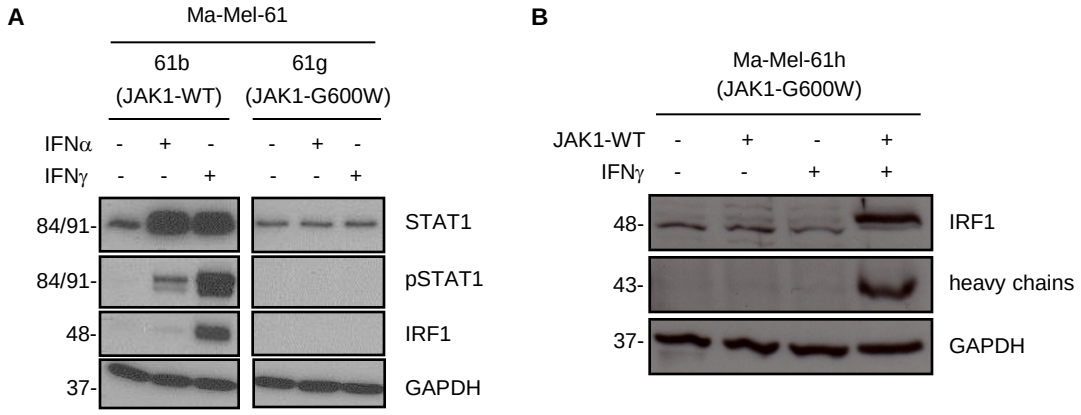


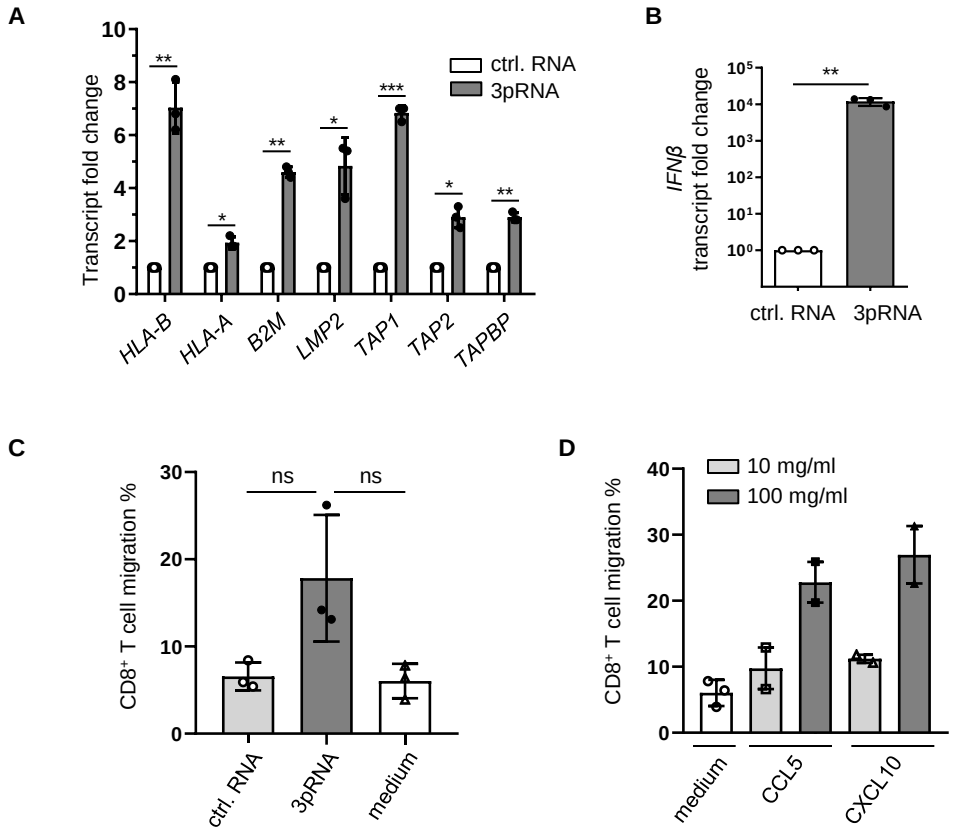

**Supplemental Figure 1. RIG-I activation upregulates HLA-I expression in different melanoma patient models.** (**A-C**) Melanoma cell lines established from metastases of patients Ma-Mel-62 (**A**), Ma-Mel-66b (**B**) and Ma-Mel-47 (**C**) were transfected with 3pRNA or control (ctrl.) RNA. Following an incubation of 20-24 h, cells were analyzed for HLA-I and ICAM-1 surface expression by flow cytometry. Left, representative histograms; right, relative MFI given as mean (+ SEM) of n ≥ 3 independent experiments. Significantly different experimental groups: *p<0.05, **p<0.01, ***p<0.001, 2-tailed paired t-test.



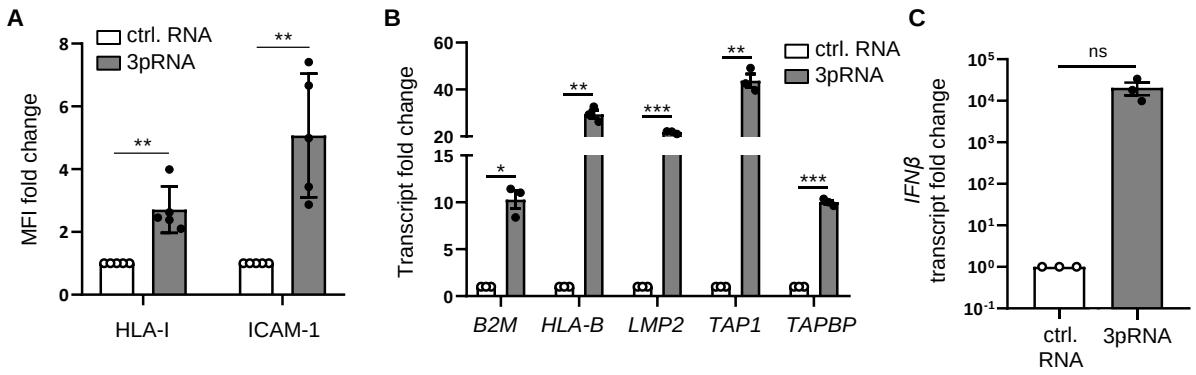

**Supplemental Figure 2. RIG-I activation in melanoma cells enhances recognition by autologous CD8⁺ T cells.** (**A**) Melanoma cells Ma-Mel-66b were transfected with 3pRNA or control (ctrl.) RNA following an incubation of 20-24 h. Activation of bulk CD8⁺ T cells by autologous melanoma cells was determined by IFNγ ELISpot assay. w/o, incubation of T cells without tumor cells. Left, representative IFNγ ELISpot result; right, mean IFNγ spots (+ SEM) of n = 3 independent experiments. Significantly different experimental groups: *p<0.05, 2-tailed paired t-test. (**B**) HLA-I genotypes of indicated cell lines.(**C**) Ma-Mel-86c cells were treated with IFNα or IFNγ for 20-24 h. Controls were left untreated. HLA-I and ICAM-1 surface expression was measured by flow cytometry. Relative MFI given as mean (+ SEM) of n = 2 independent experiments.




**Supplemental Figure 3. Mutant JAK1-G600W abrogates IFN signaling in Ma-Mel-61g and Ma-Mel-61h melanoma cells.** (**A**) Ma-Mel-61b and Ma-Mel-61g cells, treated with IFNα-2b or IFNγ for 48 h, were analyzed for (p)STAT1 and IRF1 expression by immunoblot; GAPDH, loading control. Representative data of n = 3 independent experiments. (**B**) Mutant JAK1-G600W Ma-Mel-61h cells, transfected with an expression plasmid encoding wild-type JAK1 followed by treatment with IFNγ for 48 h, were analyzed for expression of the indicated proteins. Representative data from n = 3 independent experiments.




**Supplemental Figure 4. RIG-I activation enhances HLA-I antigen presentation in IFN-resistant Ma-Mel-61g melanoma cells.** (**A-C**) Ma-Mel-61g cells were transfected with 3pRNA or control (ctrl.) RNA and subjected to further analyses following an incubation of 20-24 h. (**A** and **B**) HLA-I APM (**A**) and *IFNβ* (**B**) mRNA expression analyzed by qPCR. Relative expression given as mean (+ SEM) of n = 3 independent experiments. Significantly different experimental groups: *p<0.05, **p<0.01, ***p<0.001, 2-tailed paired t-test. (**C**) Migration of $CD8^+$ T cells towards conditioned medium from 3pRNA- or ctrl. RNA-transfected Ma-Mel-61g cells measured in transwell-assays after an incubation of 4 h. Representative results of n = 3 independent experiments. ns, not significant; 2-tailed paired t-test. (**D**) Chemokine-induced $CD8^+$ T cell migration. Migration of $CD8^+$ T cells towards medium supplemented with recombinant CCL5 or CXCL10 was determined in transwell-assays after 4 h of incubation. Representative results of n = 2 independent experiments.




**Supplemental Figure 5. RIG-I activation enhances HLA-I antigen presentation in 3pRNA-treated UKE-Mel-154c cells.** (**A**-**C**) UKE-Mel-154c cells were transfected with 3pRNA or control (ctrl.) RNA and subjected to further analyses following an incubation of 20-24 h. (**A**) HLA-I and ICAM-1 surface expression measured by flow cytometry. Relative MFI given as mean (+ SEM) of n ≥ 3 independent experiments. (**B** and **C**) HLA-I APM component (**B**) and *IFNβ* (**C**) mRNA expression was quantified by qPCR. Relative expression given as mean (+ SEM) of n = 3 independent experiments. Significantly different experimental groups: *p<0.05, **p<0.01, ***p<0.001; ns, not significant; 2-tailed paired t-test.

**Supplemental Table 1:** Differential expression analysis results for HLA-I APM genes in the anti-CTLA-4-treated cohort. Mann-Whitney U test p-values and FDR-corrected q-values are shown for the comparison of individual HLA-I APM gene expression in clinical responders vs. non-responders.

| Gene | P-value | Q-value |
|---|---|---|
| *HLA-A* | 0.284 | 0.365 |
| *HLA-B* | 0.231 | 0.347 |
| *HLA-C* | 0.344 | 0.387 |
| *TAP1* | 0.036 | 0.148 |
| *TAP2* | 0.231 | 0.347 |
| *TAPBP* | 0.486 | 0.486 |
| *B2M* | 0.020 | 0.148 |
| *PSMB9* | 0.049 | 0.148 |
| *PSMB8* | 0.082 | 0.185 |

**Supplemental Table 2:** Differential expression analysis results for HLA-I APM genes in the anti-PD-1-treated cohort. Mann-Whitney U test p-values and FDR-corrected q-values are shown for the comparison of individual HLA-I APM gene expression in clinical responders vs. non-responders.

| Gene | P-value | Q-value |
|---|---|---|
| *HLA-A* | 0.038 | 0.172 |
| *HLA-B* | 0.195 | 0.339 |
| *HLA-C* | 0.111 | 0.333 |
| *TAP1* | 0.458 | 0.515 |
| *TAP2* | 0.186 | 0.339 |
| *TAPBP* | 0.226 | 0.339 |
| *B2M* | 0.034 | 0.172 |
| *PSMB9* | 0.441 | 0.515 |
| *PSMB8* | 0.604 | 0.604 |