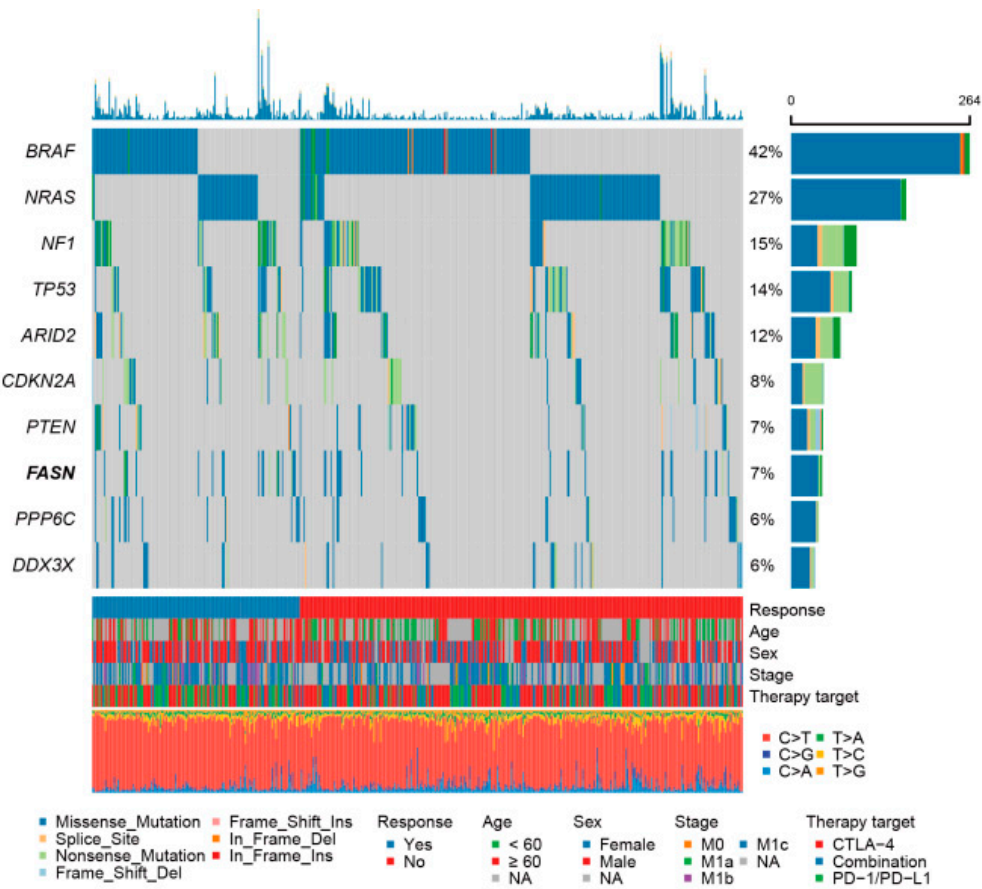
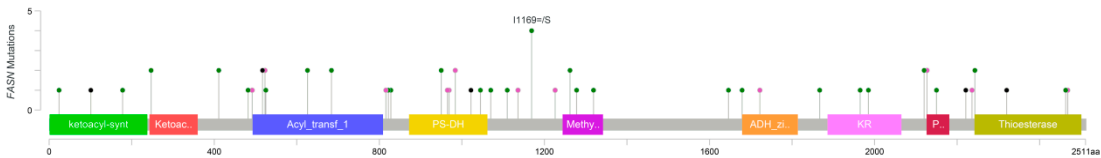


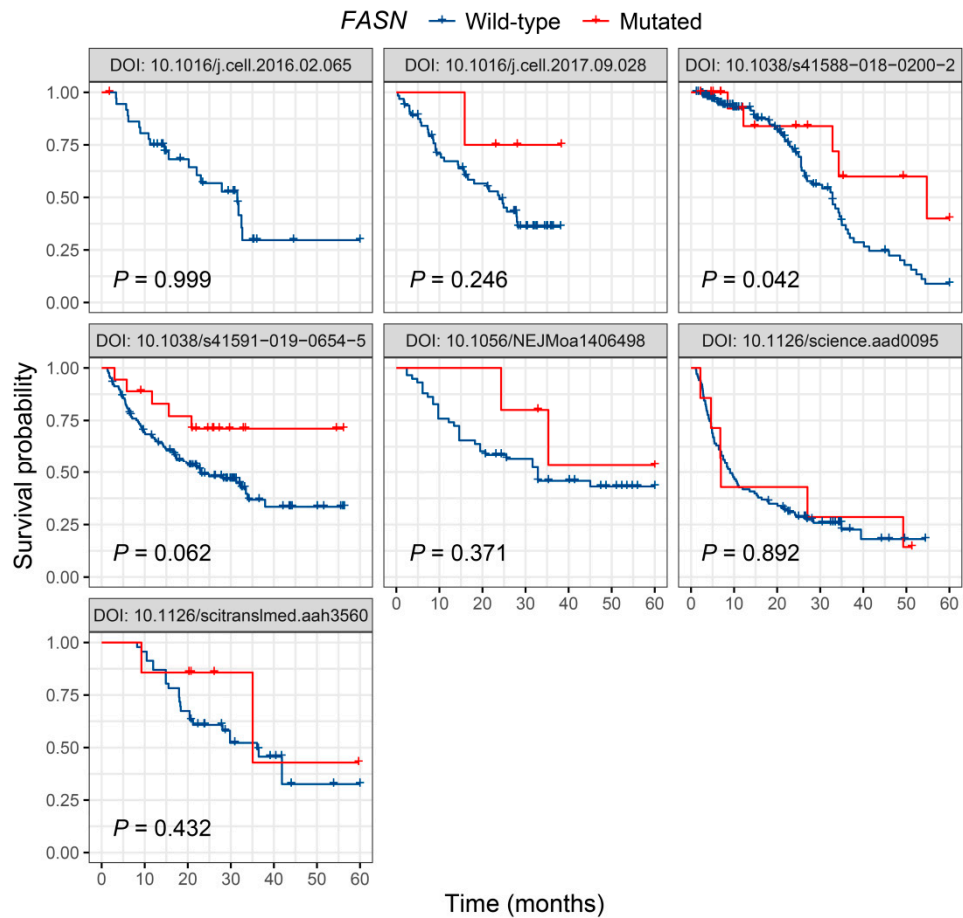
# Supplementary Figures



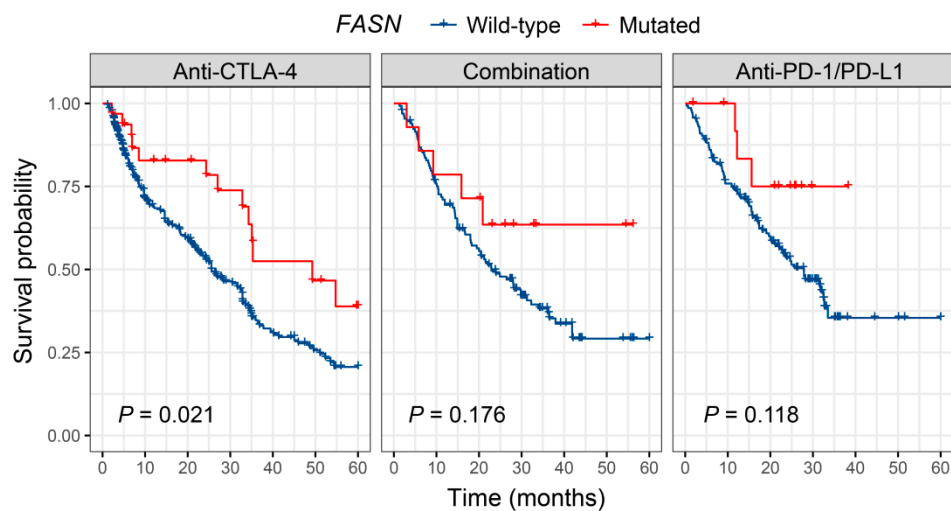
**Figure S1.** Waterfall plot representation of mutation information of *FASN* and specific genes in melanoma.



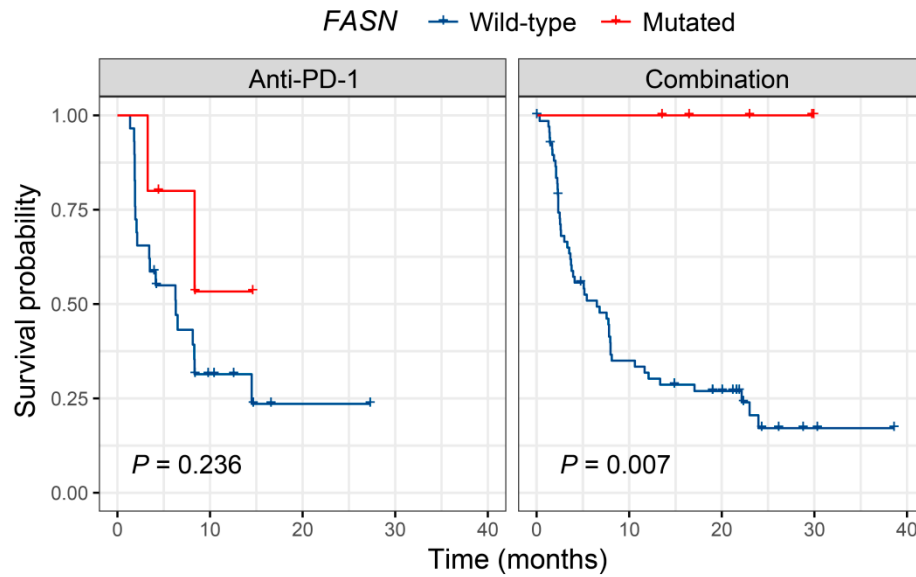
**Figure S2.** Amino acid changes associated with *FASN* alterations in melanoma patients.



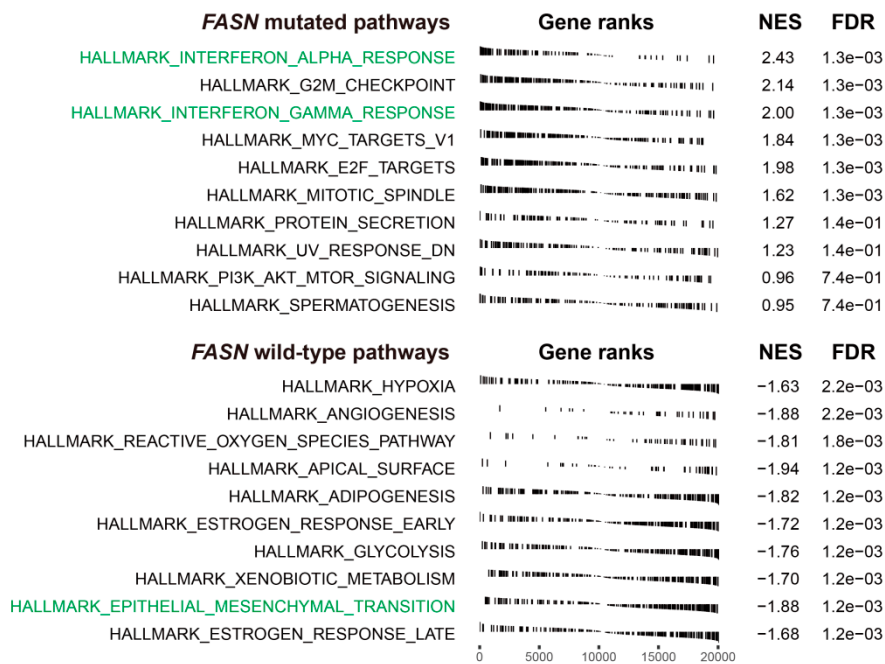
**Figure S3.** Survival predictive capacities of *FASN* mutations in single melanoma datasets.



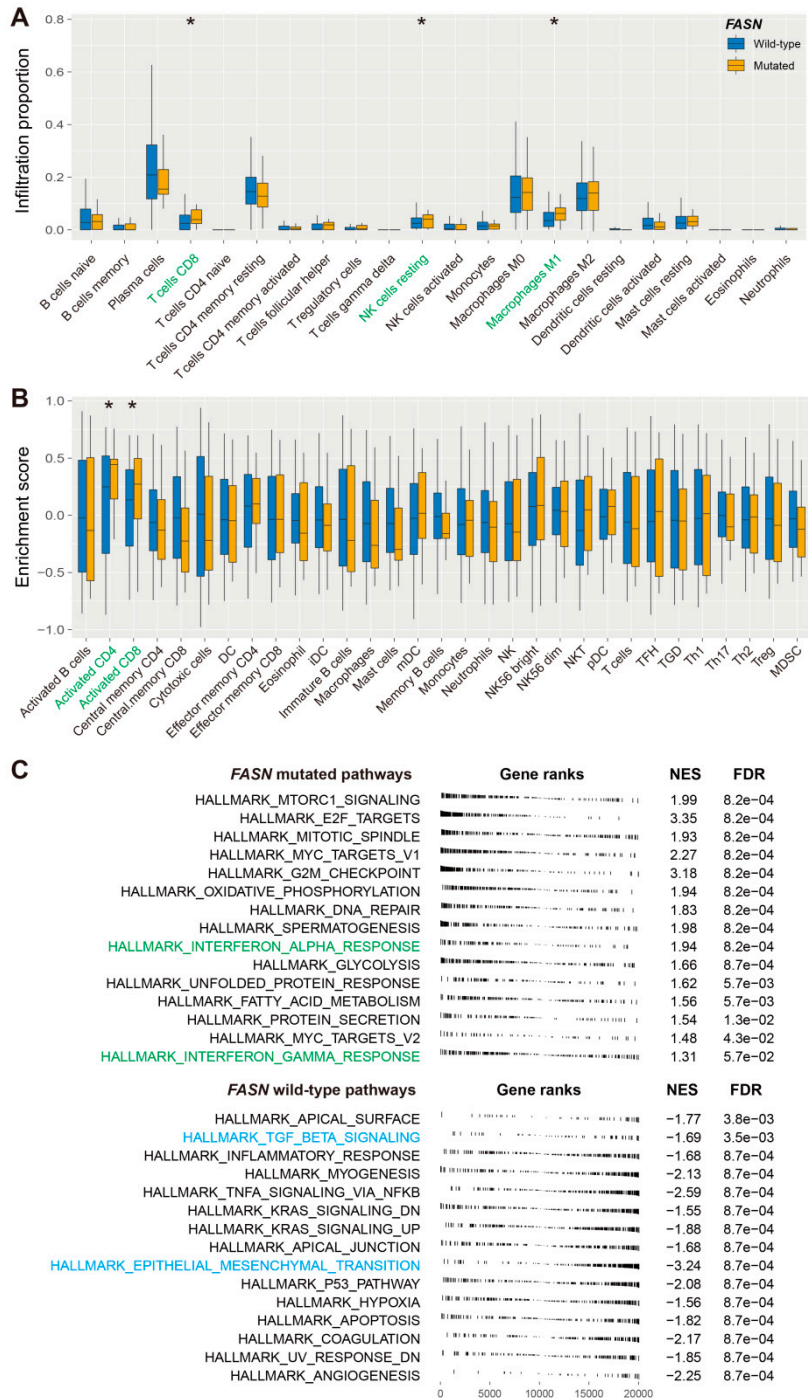
**Figure S4.** Survival predictive capacities of *FASN* mutations in different melanoma ICI treatments.



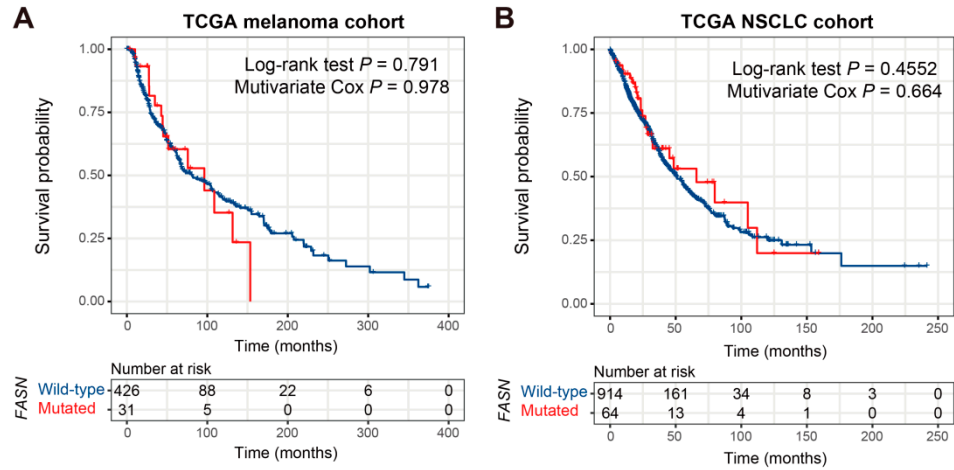
**Figure S5.** Survival predictive capacities of *FASN* mutations in different NSCLC ICI treatments.



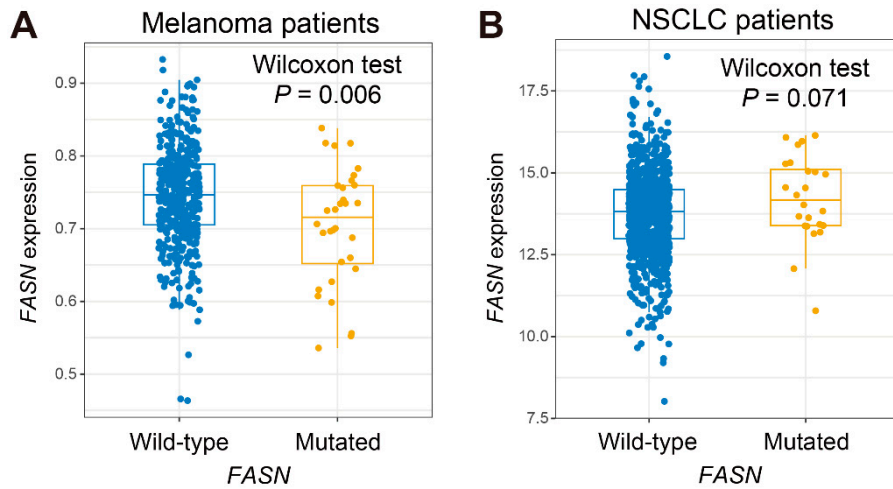
**Figure S6.** Pathway analysis results of *FASN* two subgroups based on the GSEA in melanoma.



**Figure S7.** Immunological features and pathway enrichment behind *FASN* alterations in NSCLC. (A) CIBERSORT algorithm infers distinct infiltrating levels of 22 immune cells in *FASN* two subgroups. (B) Angelova *et al.* method infers distinct infiltrating levels of 31 immune cells in *FASN* two subgroups. (C) Pathway analysis results of *FASN* two subgroups based on the GSEA.



**Figure S8.** Survival predictive capacities of *FASN* mutations in (A) melanoma and (B) NSCLC samples obtained from the TCGA cohort.



**Figure S9.** Association of *FASN* mutations with *FASN* expression in (A) melanoma and (B) NSCLC patients based on the TCGA cohort.