**Supplementary figure legends**

**Supplementary Figure 1**

**Abundance of immune markers across melanoma subtypes and correlation of immune cells and TMB in cutaneous melanoma** A, Mean proportion of CD103+ CD8+ Trm in in cutaneous (n=151), acral (n=30) and mucosal (n=5) melanoma, B, Mean percentage of PD-L1 positive cells in the tumors of cutaneous (n=151), acral (n=30) and mucosal (n=5) melanoma. C, The mean number of CD4+ T cells per mm2 of tumor in cutaneous (n=151), acral (n=30) and mucosal (n=5) melanomas. D, The mean number of CD20+ cells per mm2 of tumor in cutaneous (n=151), acral (n=30) and mucosal (n=5) melanomas. E, The mean number of CD68+ cells per mm2 of tumor in cutaneous (n=151), acral (n=30) and mucosal (n=5) melanomas. F, The mean number of CD11c+ cells per mm2 of tumor in cutaneous (n=151), acral (n=30) and mucosal (n=5) melanomas. G, Spearman correlation (r) between single nucleotide variant (SNV) counts and percentage of PD-L1 positive cells in (n=97) cutaneous melanoma tumors. H, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD45RO positive lymphocytes per mm2 of tumor in (n=97) cutaneous melanoma tumors. I, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD4+ T cells per mm2 of tumor in (n=97) cutaneous melanoma tumors. J, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD20+ cells per mm2 of tumor in (n=97) cutaneous melanoma tumors. K, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD68+ cells per mm2 of tumor in (n=97) cutaneous melanoma tumors. L, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD11c+ cells per mm2 of tumor in (n=97) cutaneous melanoma tumors. PD-L1 positivity was determined as the percentage of cells (total) in the tumor microenvironment (tumor cells and immune cells) positive for PD-L1 using a continuum scale from 0-100%. All error bars are displayed as ±1 standard error of the mean (SEM).

**Supplementary Figure 2**

**Correlation of single nucleotide variant counts and CD8 T cells in whole slide sections of cutaneous melanoma.** A, Spearman correlation (r) between single nucleotide variant (SNV) counts and CD8 positive lymphocytes (left) or PD-L1 positive staining (right) in n=17 cutaneous samples from seventeen patients. B, Multiplex fluorescence staining of marked cutaneous samples (1-4) from (A) with relatively high single nucleotide variant counts (top) and relatively low single nucleotide variant counts (bottom).

**Supplementary Figure 3**

**Correlation between immune cells and single nucleotide variant counts in acral and mucosal melanoma**s. A, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD8 positive lymphocytes per mm2 of tumor in (n=32) acral and mucosal melanoma tumors. B, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD8+ CD103+ tumor resident cells per mm2 of tumor in (n=32) acral and mucosal melanoma tumors. C, Spearman correlation (r) between single nucleotide variant (SNV) counts and percentage of PD-L1 positive cells in (n=32) acral and mucosal melanoma tumors. D, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD45RO positive lymphocytes per mm2 of tumor in (n=32) acral and mucosal melanoma tumors. E, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD4+ T cells per mm2 of tumor in (n=32) acral and mucosal melanoma tumors. F, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD20+ cells per mm2 of tumor in (n=32) acral and mucosal melanoma tumors. G, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD68+ cells per mm2 of tumor in (n=32) acral and mucosal melanoma tumors. H, Spearman correlation (r) between single nucleotide variant (SNV) counts and number of CD11c+ cells per mm2 of tumor in (n=32) acral and mucosal melanoma tumors. PD-L1 positivity was determined as the percentage of cells (total) in the tumor microenvironment (tumor cells and immune cells) positive for PD-L1 using a continuum scale from 0-100%. All error bars are displayed as ±1 standard error of the mean (SEM).

**Supplementary Figure 4**

**Immune infiltration in cutaneous and acral/ mucosal melanoma of different melanoma molecular subtypes.** A) Meannumber of CD8+ T cells, CD103+ CD8+ tumor resident T cells, percentage of PD-L1 cells in tumor, CD45RO+ cells, CD4+ T cells, CD20+ cells, CD68+ cells, CD11c+ cells, and SNV counts in cutaneous melanoma (n=97) of different molecular subtypes (*BRAF, NF1, NRAS*, and wild-type). B) Meannumber of CD8+ T cells, CD103+ CD8+ tumor resident T cells, percentage of PD-L1 cells in tumor, CD45RO+ cells, CD4+ T cells, CD20+ cells, CD68+ cells, and CD11c+ cells in acral/mucosal melanoma (n=32) of different molecular subtypes (*BRAF, NF1, NRAS*, and wild-type). All error bars are displayed as ±1 standard error of the mean (SEM).

**Supplementary Figure 5**

**Correlation between immune cells and structural variant counts in acral and mucosal melanoma**s. A, Spearman correlation (r) between SVs counts and percentage of tumor positive for PD-L1 in acral and mucosal melanoma tumors (n=32). B, Spearman correlation (r) between SVs counts and number of CD45RO+ cells of tumor per mm2 in acral and mucosal melanoma tumors (n=32). C, Spearman correlation (r) between SVs counts and number of CD4+ T cells of tumor per mm2 in acral and mucosal melanoma tumors (n=32). D, Spearman correlation (r) between SVs counts and number of CD20+ cells of tumor per mm2 in acral and mucosal melanoma tumors (n=32). E, Spearman correlation (r) between SVs counts and number of CD68+ cells of tumor per mm2 in acral and mucosal melanoma tumors (n=32). E, Spearman correlation (r) between SVs counts and number of CD11c+ cells of tumor per mm2 in acral and mucosal melanoma tumors (n=32).

**Supplementary Figure 6**

**Correlation between structural variant counts and CD8+ T cells in whole slide sections of acral and mucosal melanomas.** A, Spearman correlation (r) between structural variant (SVs) counts and CD8 positive lymphocytes (left) or PD-L1 positive staining (right) in n=21 acral and n=8 mucosal melanoma samples from twenty-nine patients. B, Multiplex fluorescence staining of marked cutaneous samples (1-4) from (A) with relatively high structural variant counts (top) and relatively low structural variant counts (bottom).

**Supplementary Figure 7**

**Correlation between TMB, structural variant counts, and PD-L1 expression in validation cohort for cutaneous and acral/mucosal melanomas.** A, Spearman correlation (r) between single nucleotide variant counts and PD-L1 positivity of tumor in n=56 cutaneous melanoma tumors. B, Spearman correlation (r) between neoantigen counts and PD-L1 positivity of tumor in n=56 cutaneous melanoma tumors. C, Spearman correlation (r) between structural variant counts and PD-L1 positivity of tumor in acral (n=8) and mucosal (n=3) melanoma (total n=11). PD-L1 positivity was determined as the percentage of cells (total) in the tumor microenvironment (tumor cells and immune cells) positive for PD-L1 using a continuum scale from 0-100%.

**Supplementary Figure 8**

**Prognostic effect of PD-L1 expression in treatment-naïve melanoma patients.** A, Kaplan-Meier curve for n= 43 stage III cutaneous melanoma patients with high PD-L1 expression (greater than the median (1%); red) and low PD-L1 expression (lower than median; black). The average TMB is given for PD-L1 high and PD-L1 low groups. PD-L1 positivity was determined as the percentage of cells (total) in the tumor microenvironment (tumor cells and immune cells) positive for PD-L1 using a continuum scale from 0-100%.