SUPPLEMENTARY MATERIALS

2995 immune-related genes

We obtained these 2995 immune-related genes from 160 immune signatures curated in a previous study [1], which was based on 11 immune relevant studies. Eighty-three of these 160 immune signatures were cancer immune response-related signatures, whereas the remaining 77 signatures are of general validity for immunity. These 83 signatures consisted of 68 gene sets from a earlier study [2], 9 signatures derived from TCGA gene expression data (immune metagene attractors) [3, 4], 3 signatures representing immune contexture function [5–7], and 3 signatures from a recent study [8]. The remaining 77 signatures comprised of 45 immune-cell specific signatures from 2 sources [9, 10], and 32 signatures from the ImmuneSigDB [11, 12].

Main *R* codes used in this study

```
# Nonnegative matrix factorization (NMF)
        library(NMF)
        estim.r <- nmf(gene_expression_matrix, 2:6,
        nrun = 200, method = 'brunet')
        plot(estim.r)
        consensusmap(estim.r)
        fit <- nmf(gene_expression_matrix, 2, nrun =
        200, method = "brunet")
        subtype.result <- predict(fit)
# Gene set enrichment analysis (GSEA)
        library(fgsea)
library(ggplot2)
        fgsea.result <- fgsea(pathways =
        annotation_pathways,
            stats = genes_rank_list,
            minSize = 15,
            maxSize = 500,
            nperm = 1000000)
        plotEnrichment(path[["pathway_name"]],
        genes_rank_list)
# Waterfall plot
        library(GenVisR)
waterfall(mutation_data, plotGenes = genes_to_plot,
        mainDropMut = TRUE, coverageSpace =
        30000000, clinDat = clinical_data)
# Multivariate regression model
        library(forestmodel)
library(survival)
forest_model(coxph(Surv(survival_time,
survival_end) ~ variables, related_data),
factor_separate_line = T)
forest_model(glm(categorical variable ~ variables,
binomial(), related_data), factor_separate_line = T))
```

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