

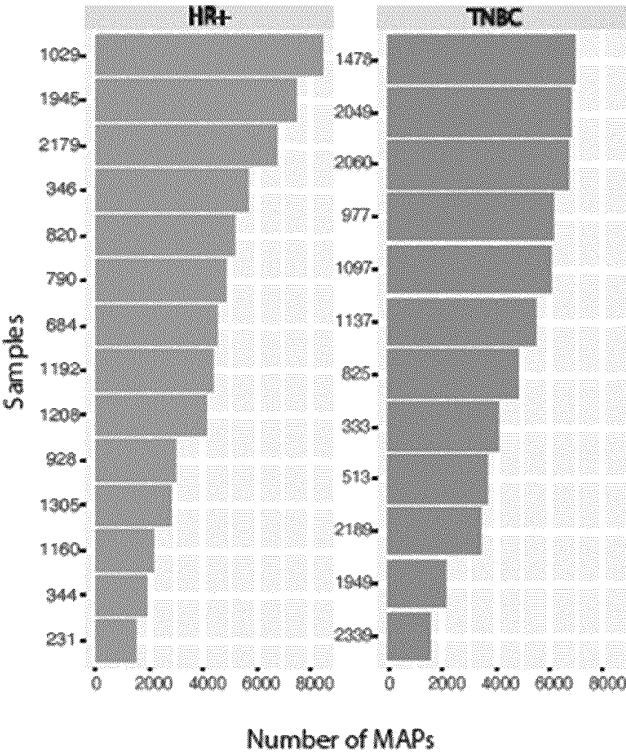


FIG. 1A

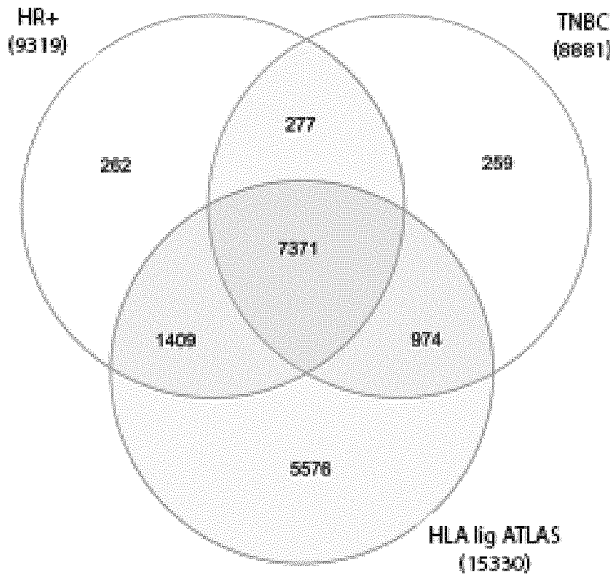


FIG. 1B

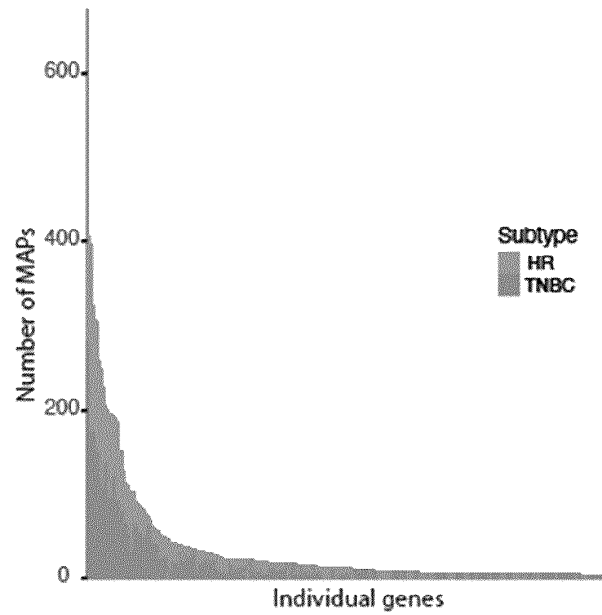


FIG. 1C

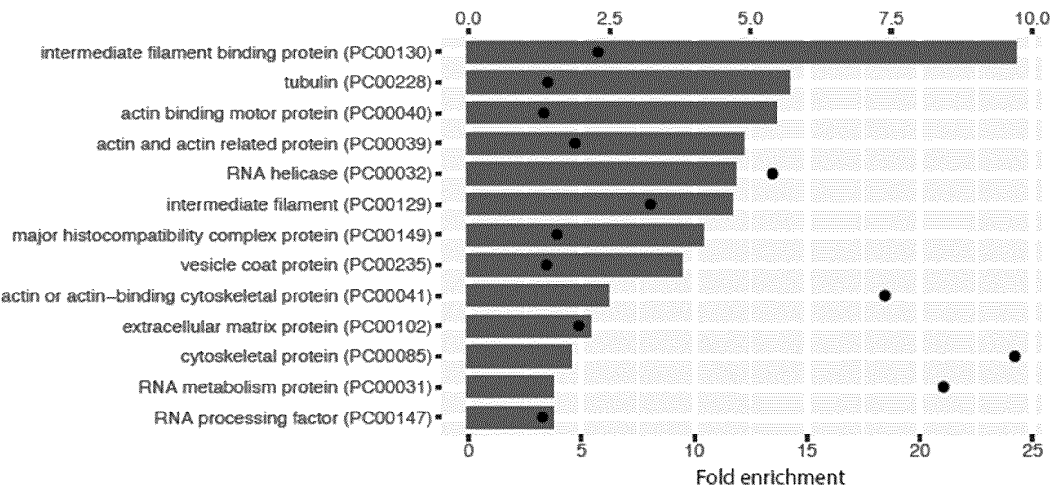


FIG. 1D

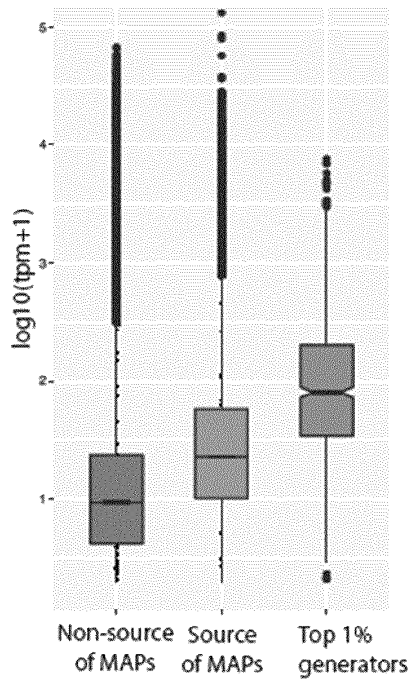


FIG. 1E

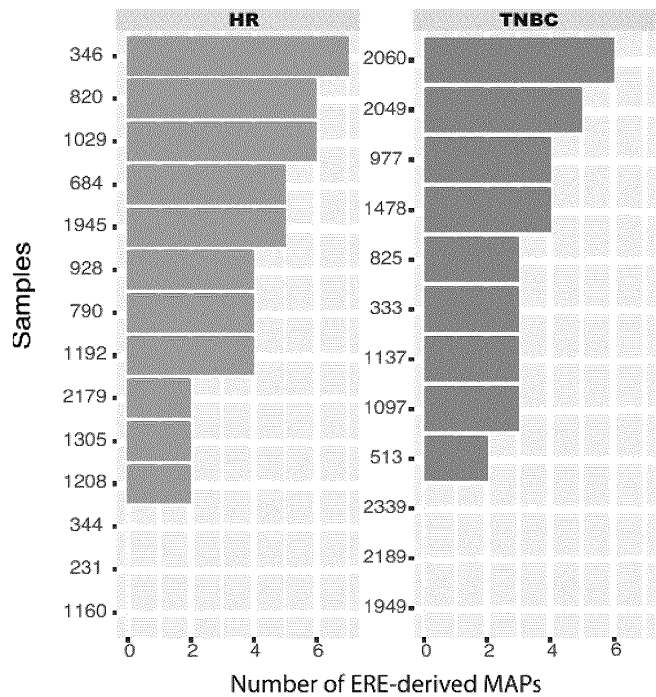


FIG. 2A

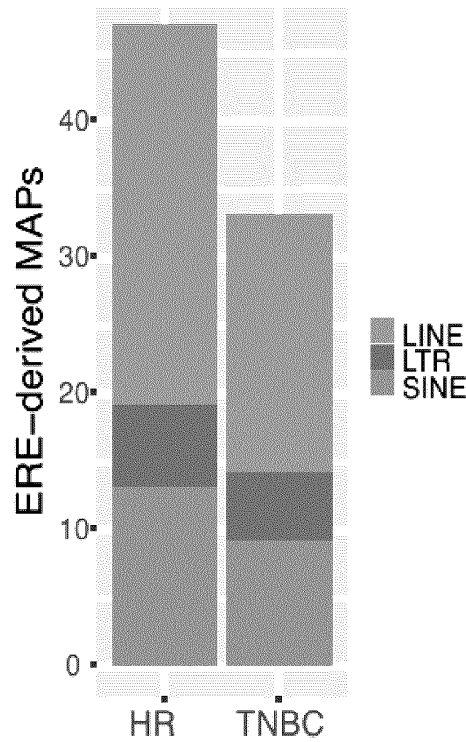


FIG. 2B

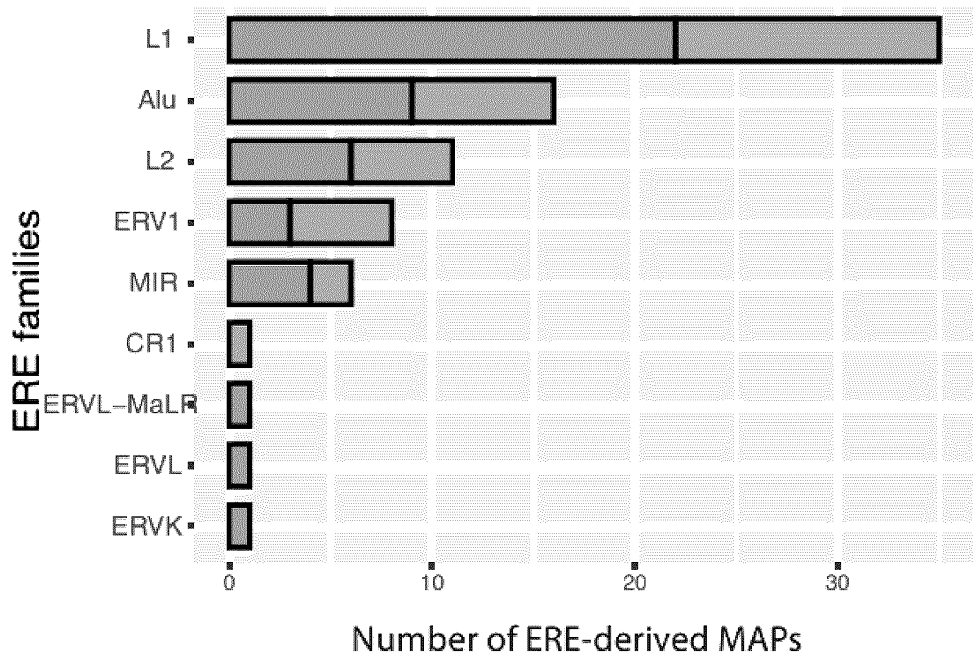
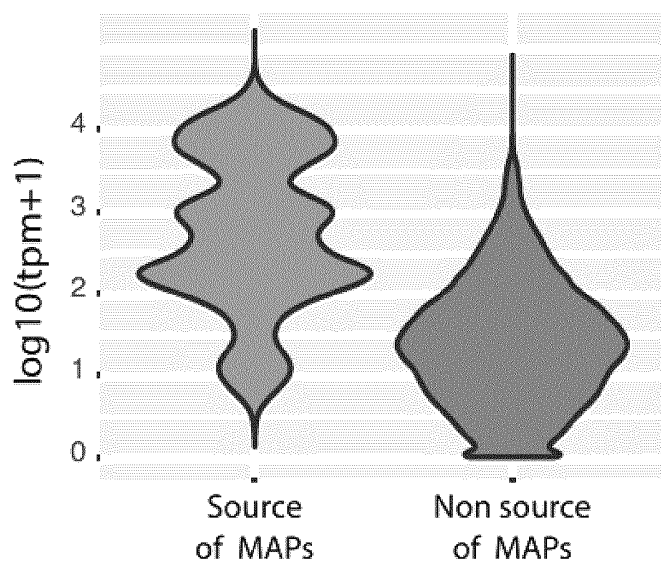


FIG. 2C

**FIG. 2D**

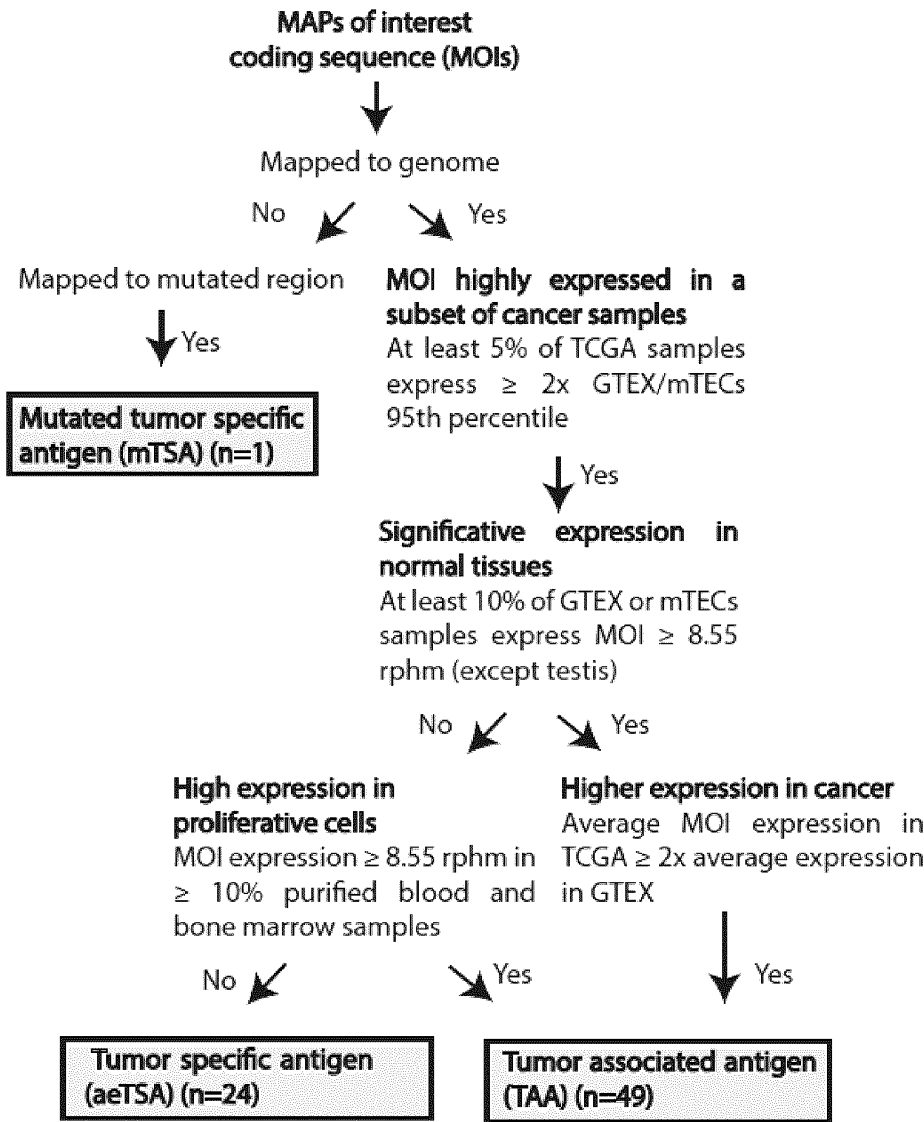


FIG. 3A

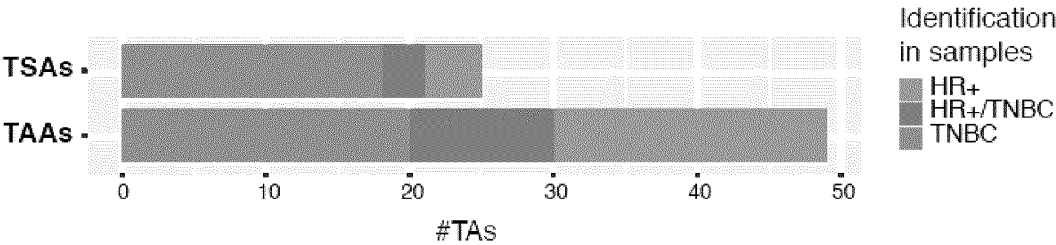


FIG. 3B

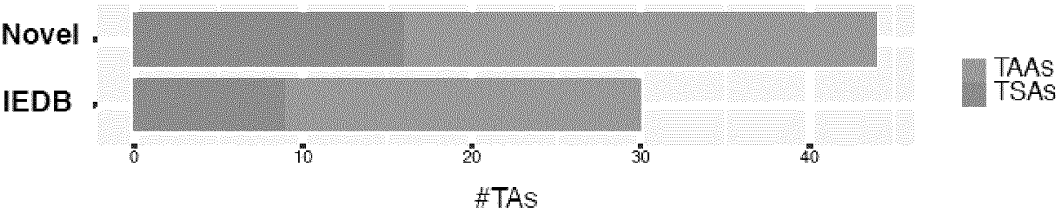


FIG. 3C

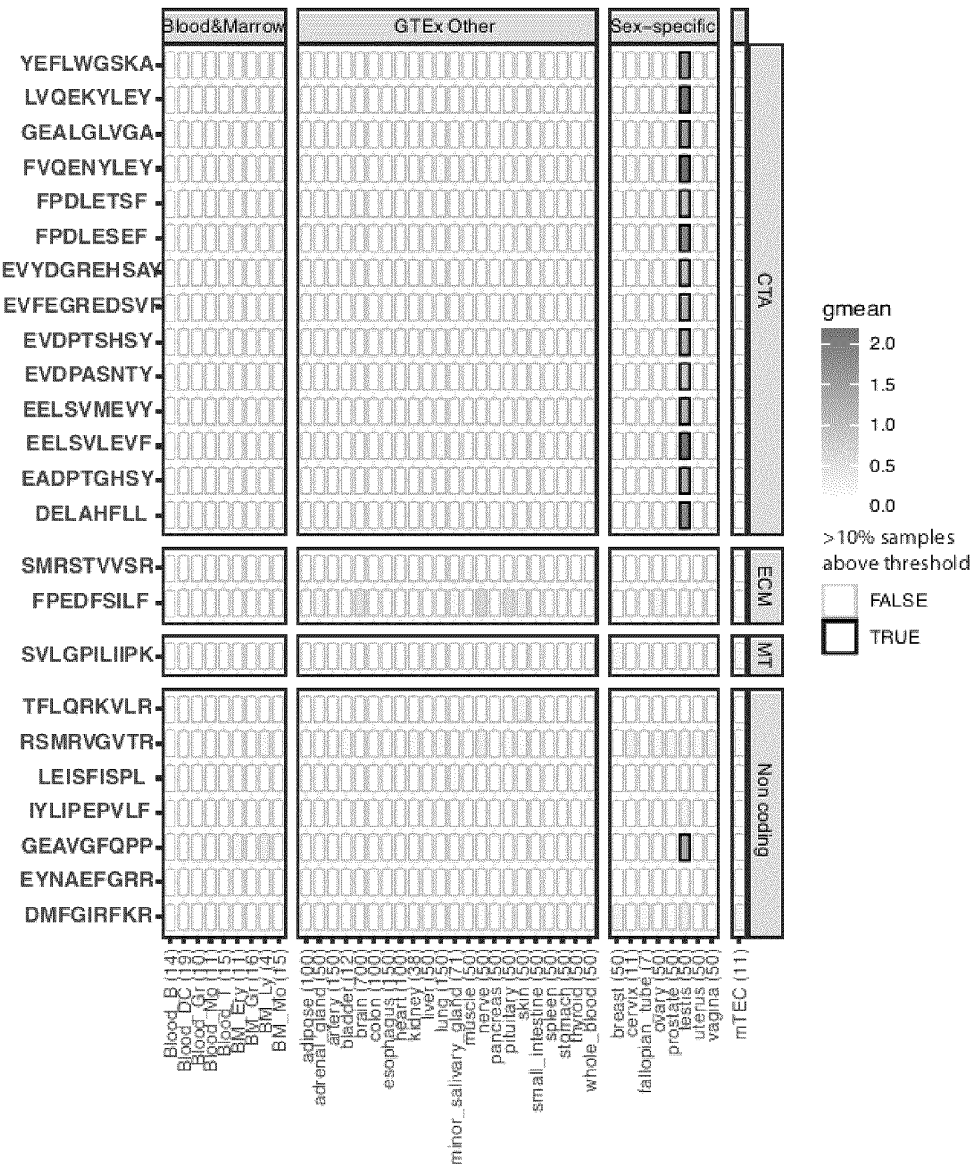


FIG. 4A

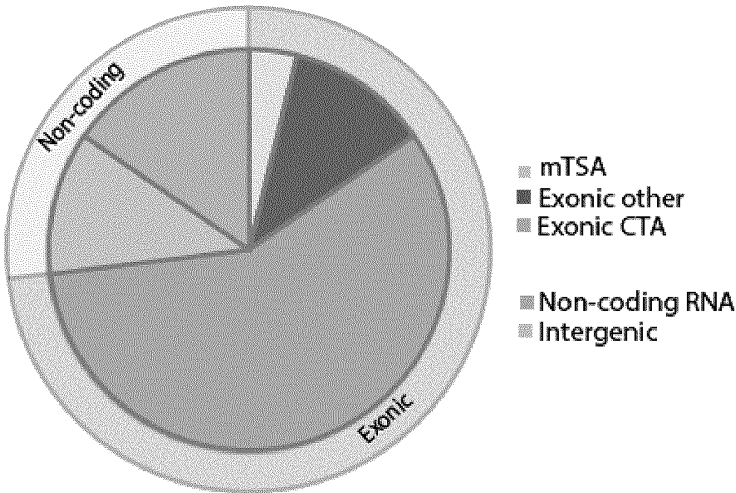
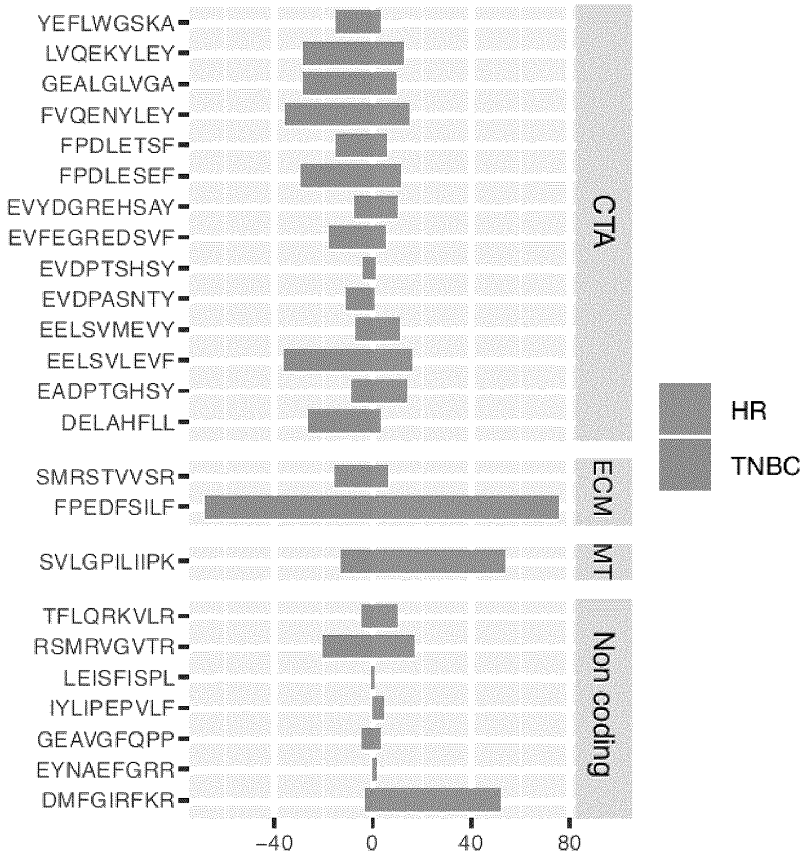


FIG. 4B



% TCGA samples with rphm > 2

FIG. 4C

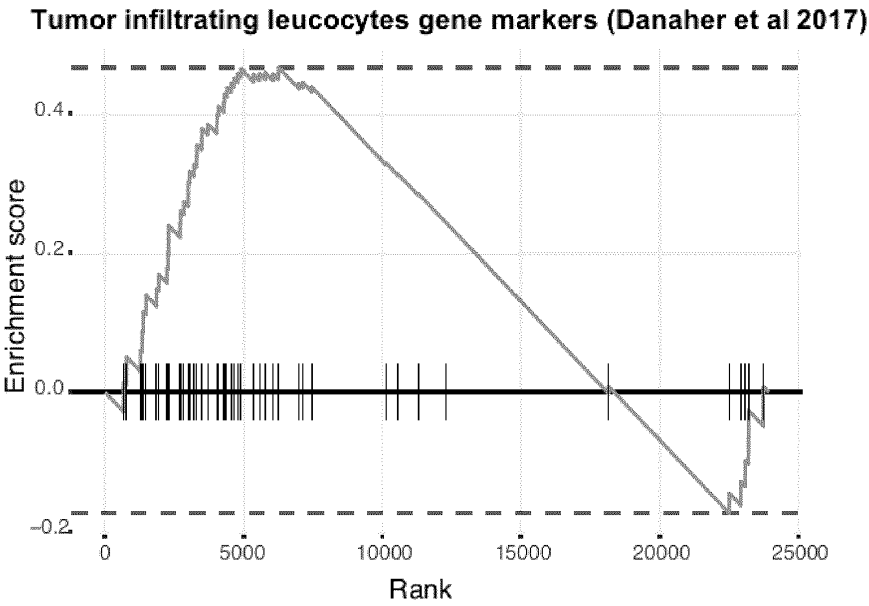


FIG. 4D

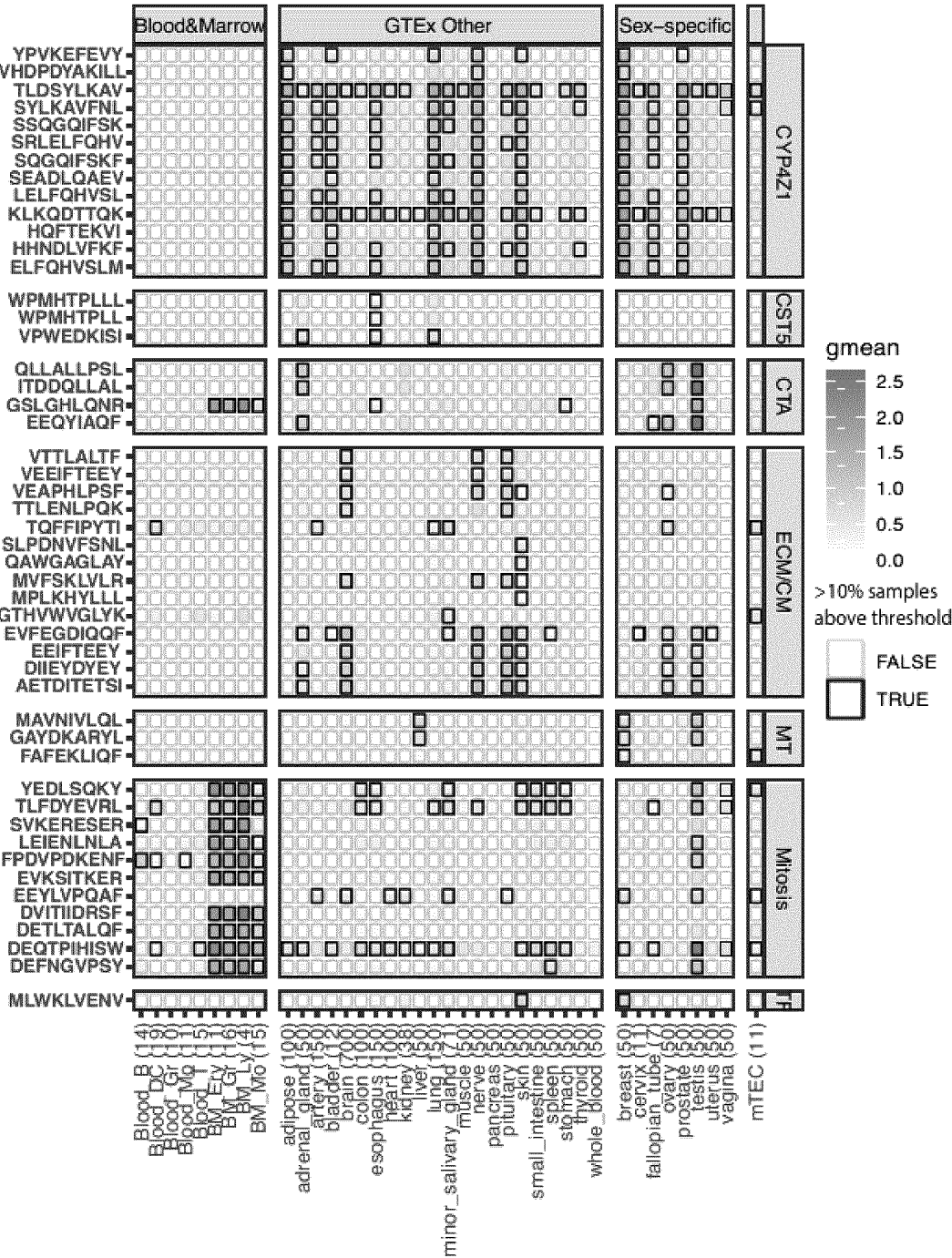


FIG. 5A

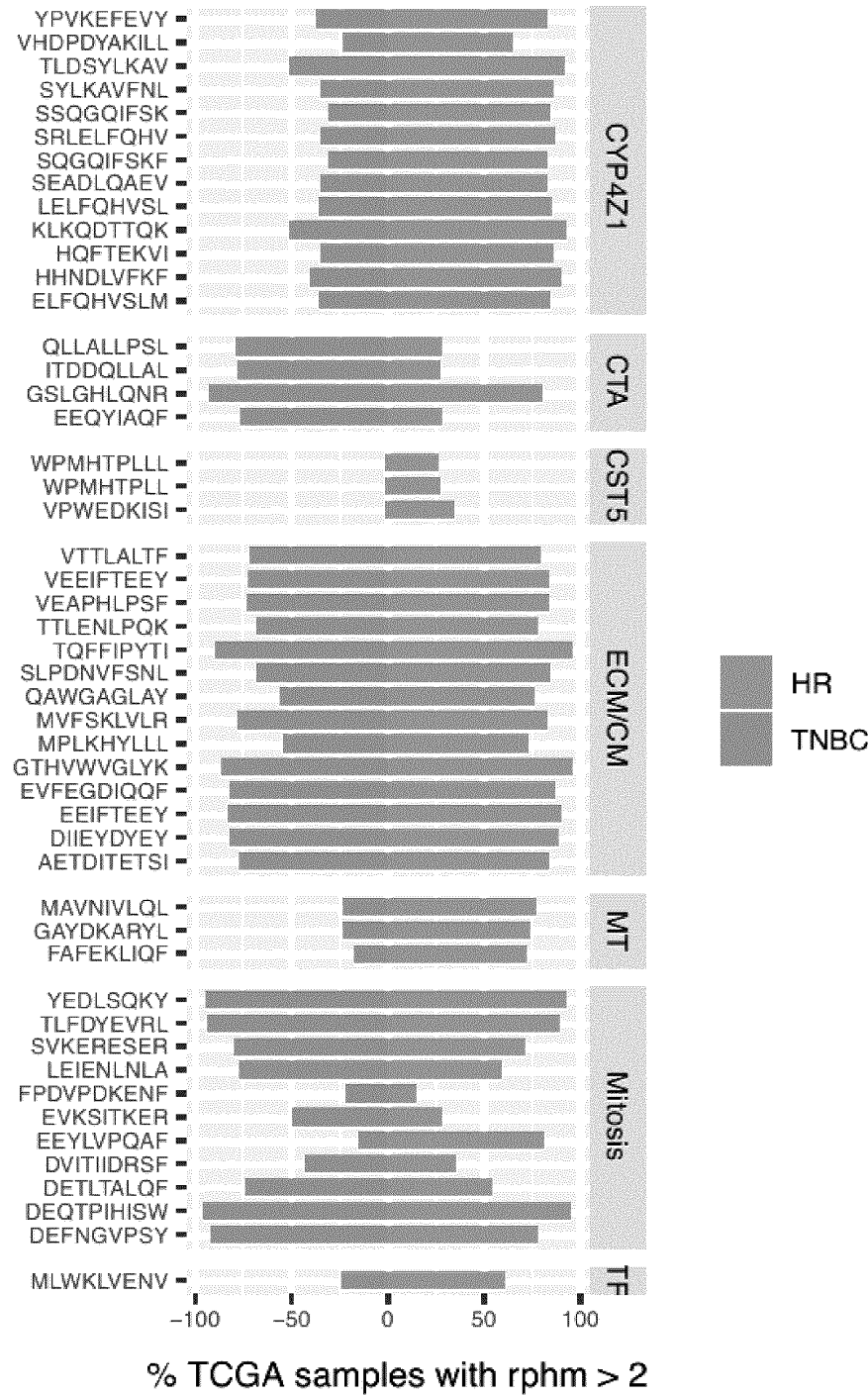


FIG. 5B

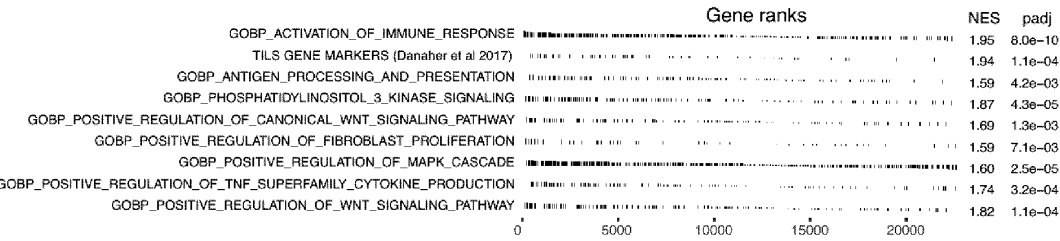


FIG. 5C

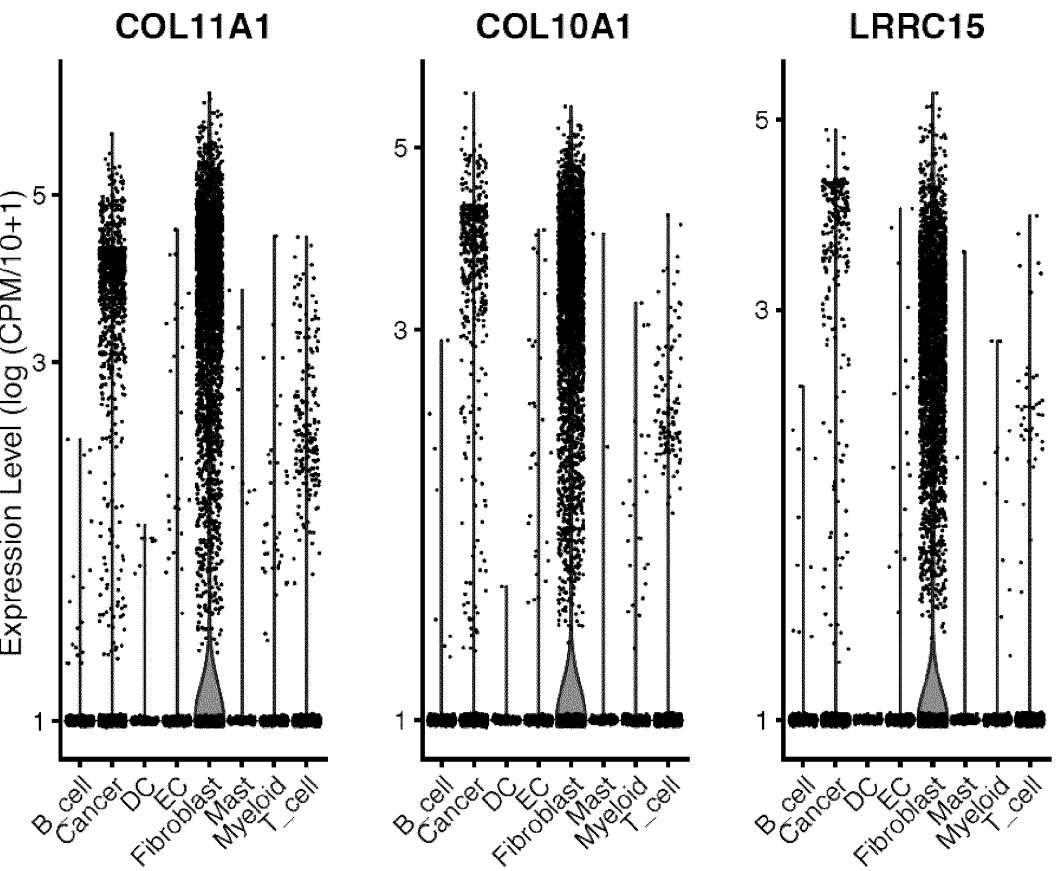


FIG. 6

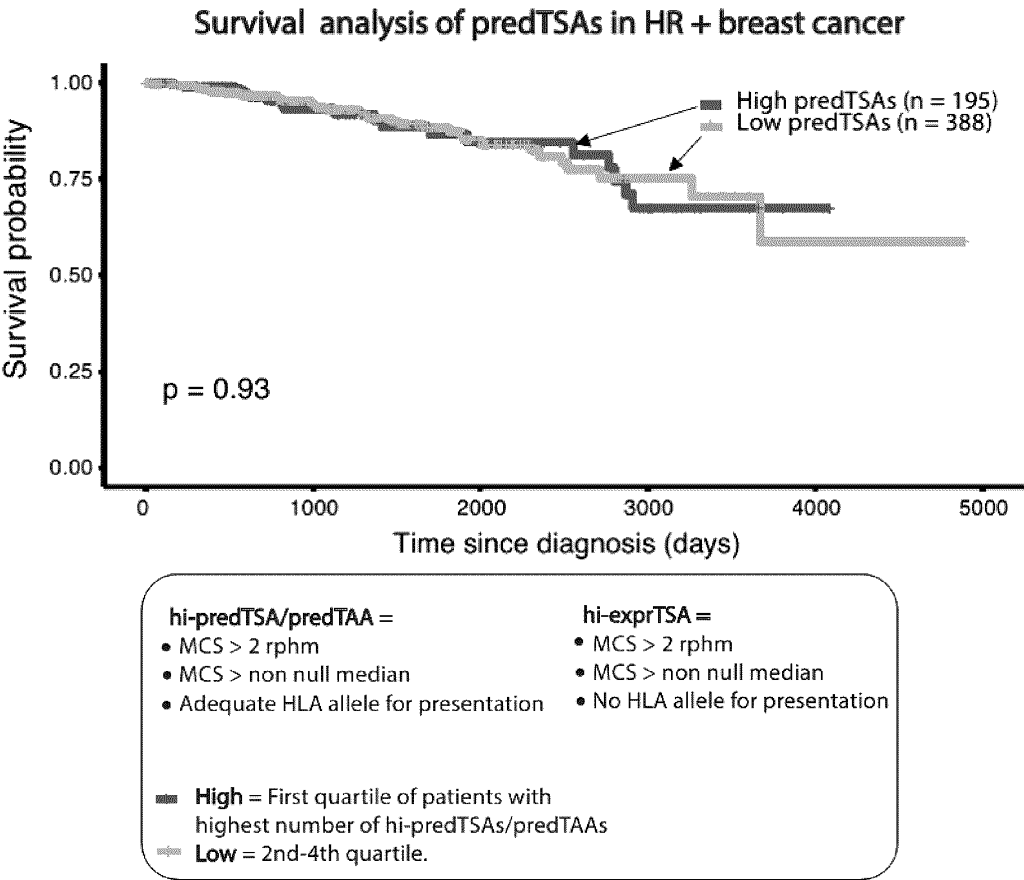


FIG. 7A

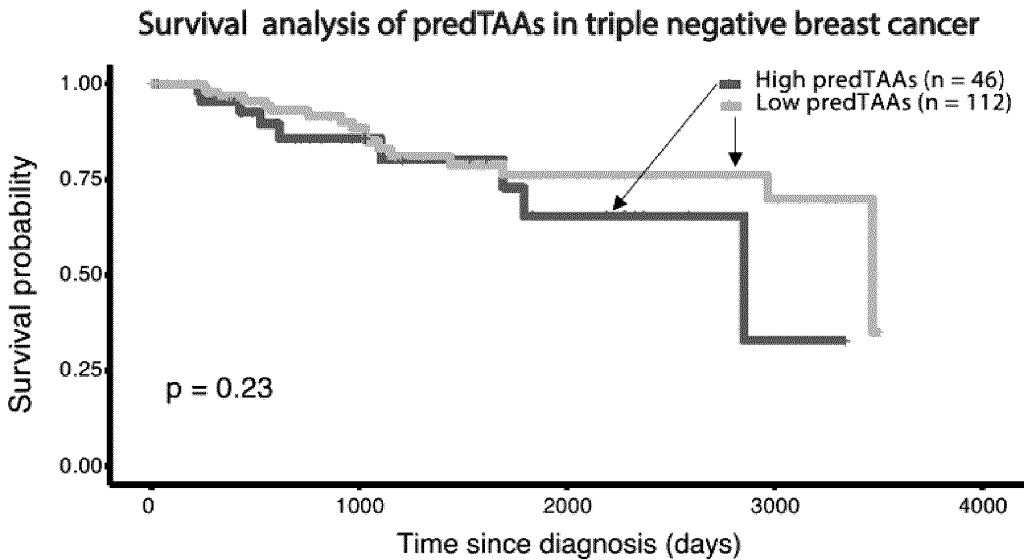


FIG. 7B

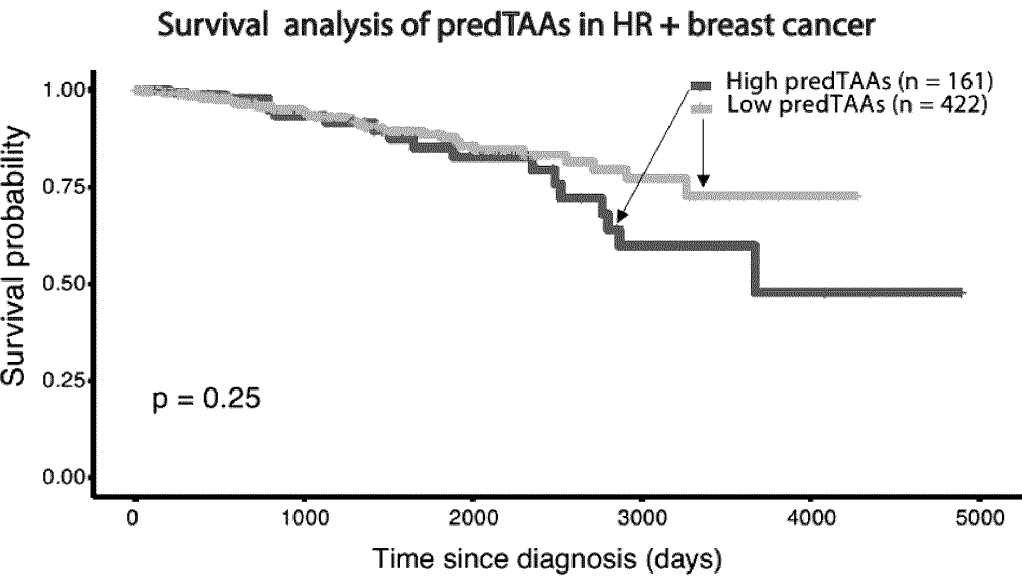


FIG. 7C

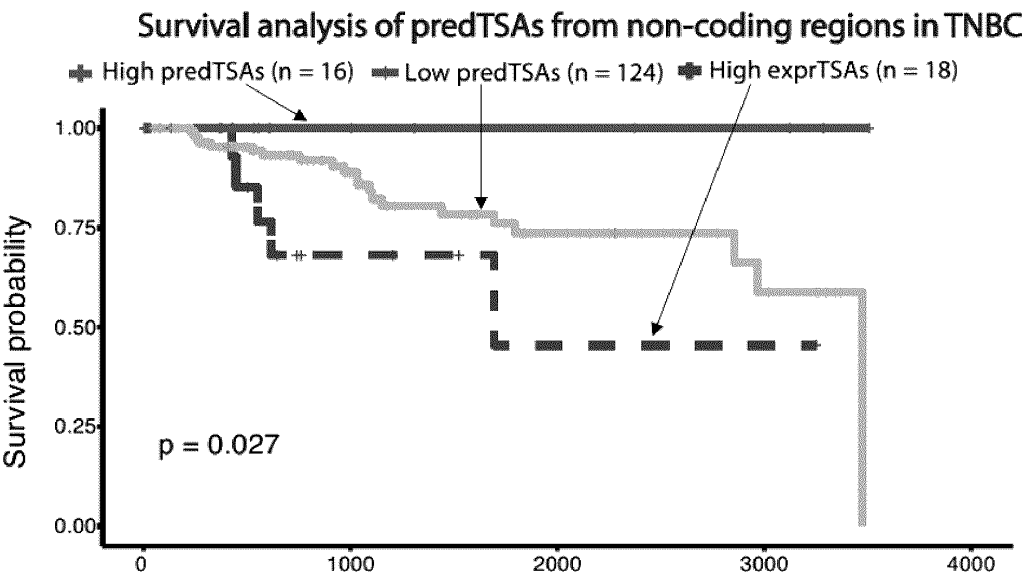


FIG. 7D

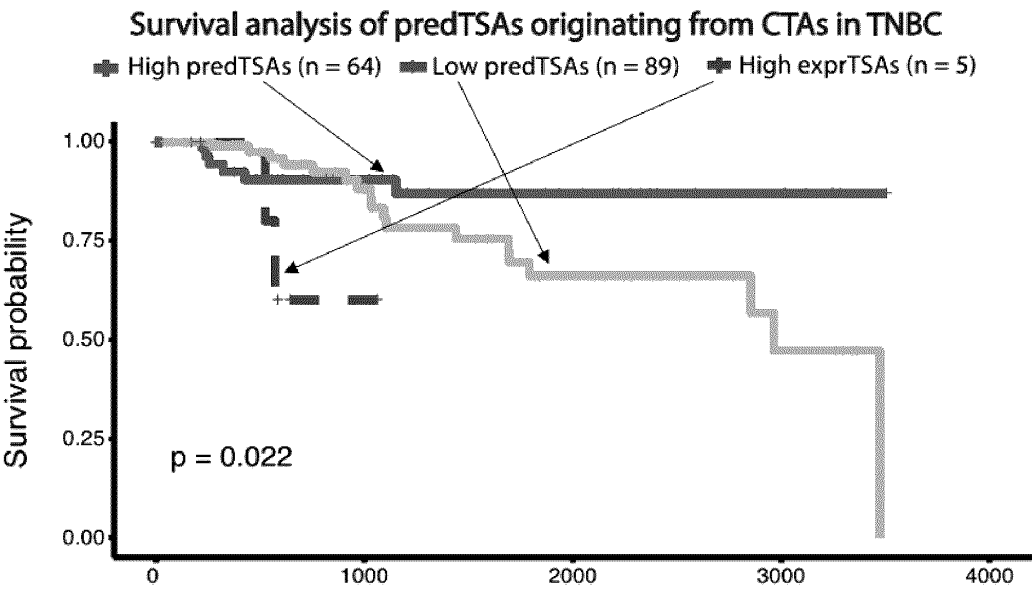


FIG. 7E

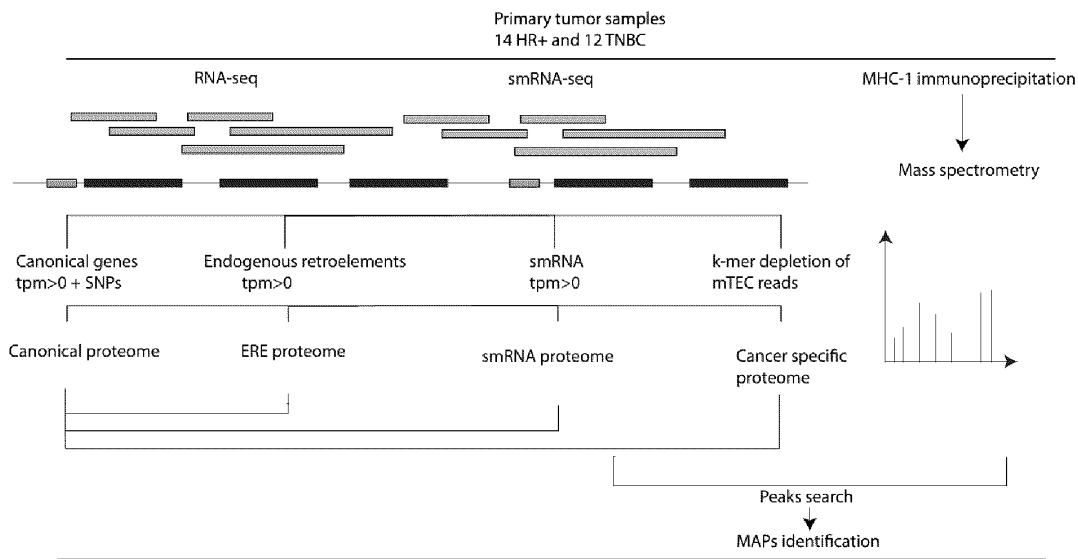


FIG. 8

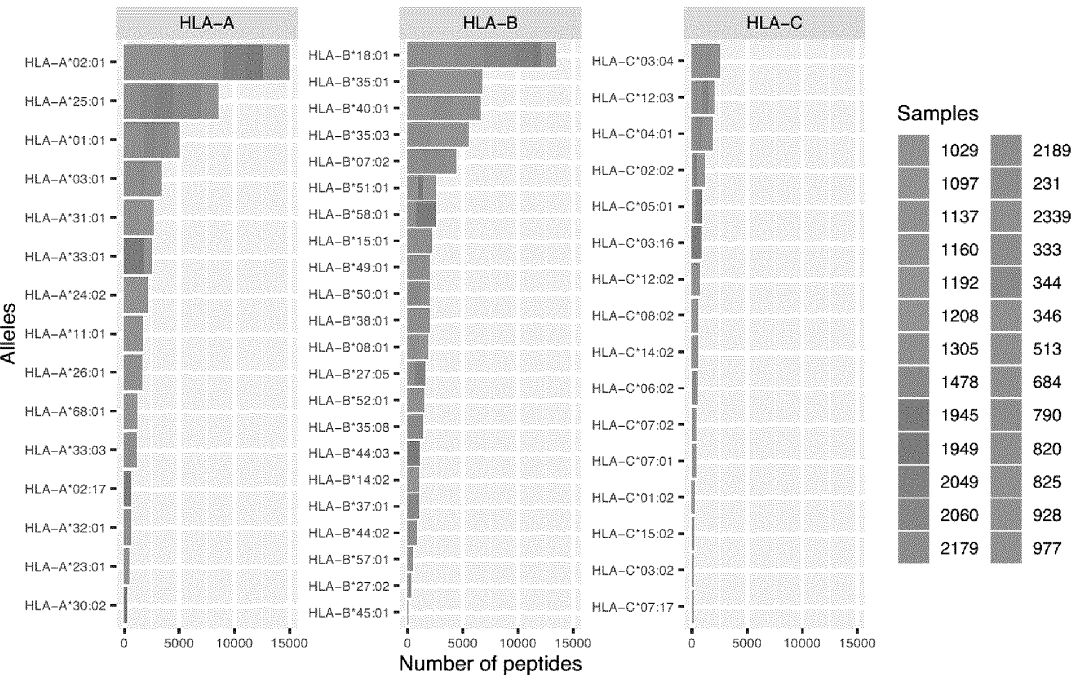


FIG. 9

Percentage of the transcriptome represented at the immunopeptidomic level per cumulative samples

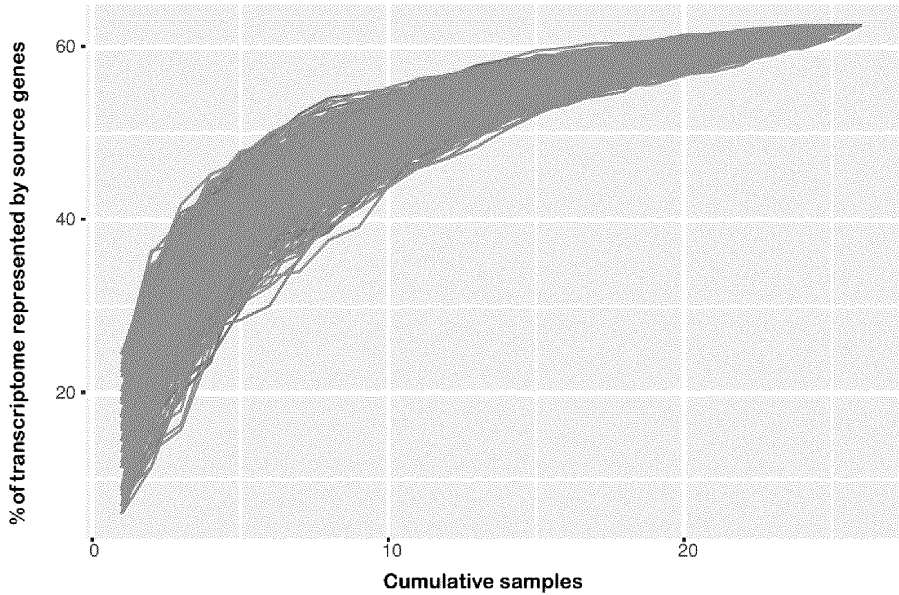


FIG. 10A

Histogram of the total number of MAPs generated per source gene

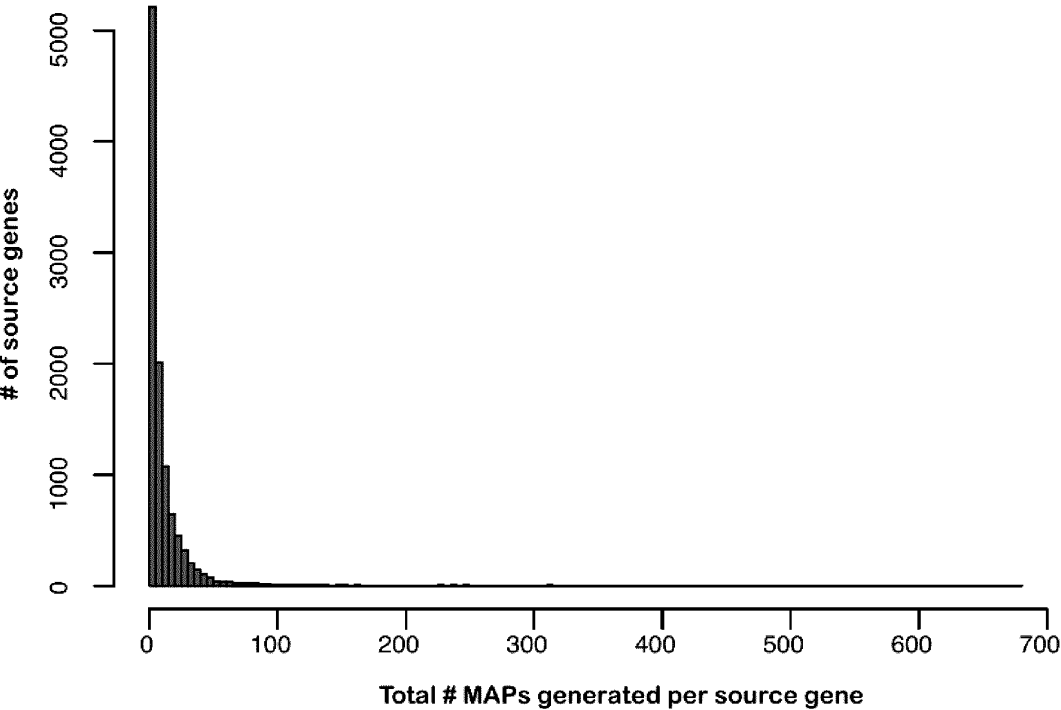


FIG. 10B

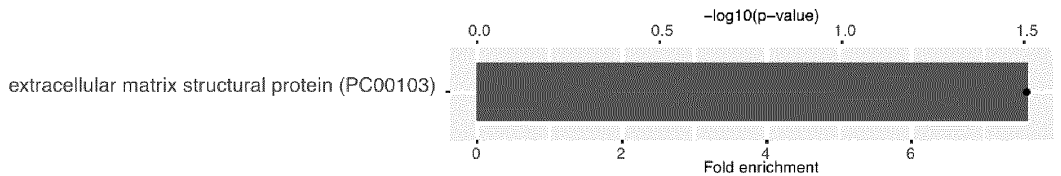


FIG. 11A

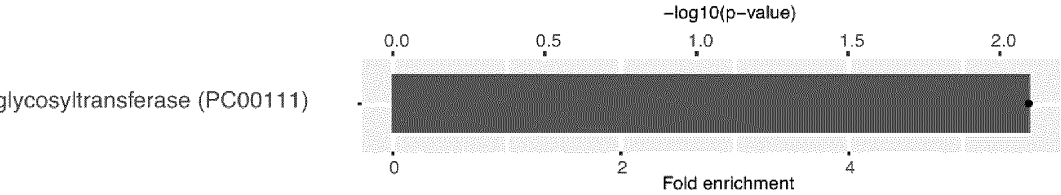


FIG. 11B

Small-RNA database construction

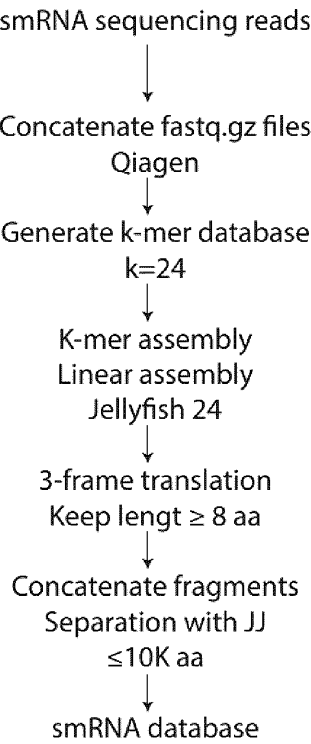


FIG. 12A

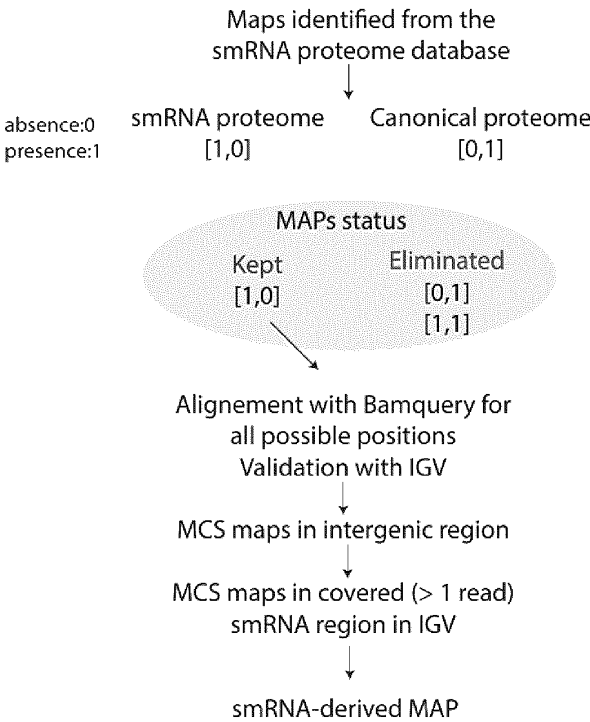


FIG. 12B

ERE genomic mapping

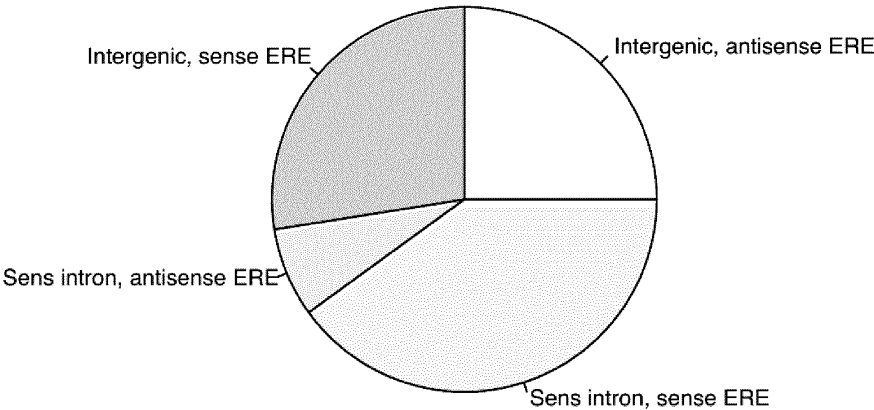


FIG. 13

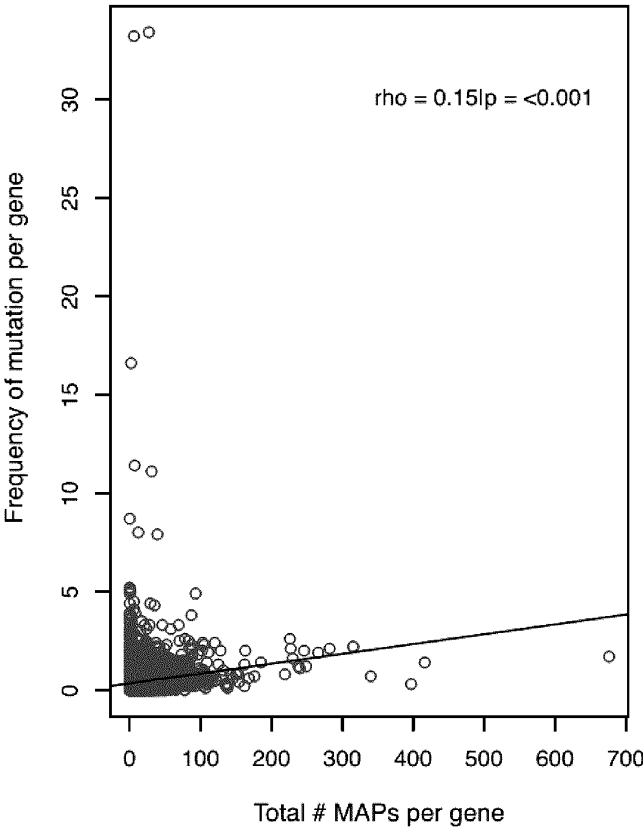


FIG. 14

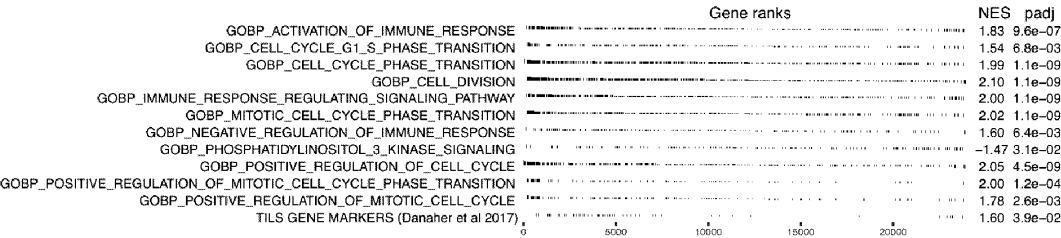


FIG. 15

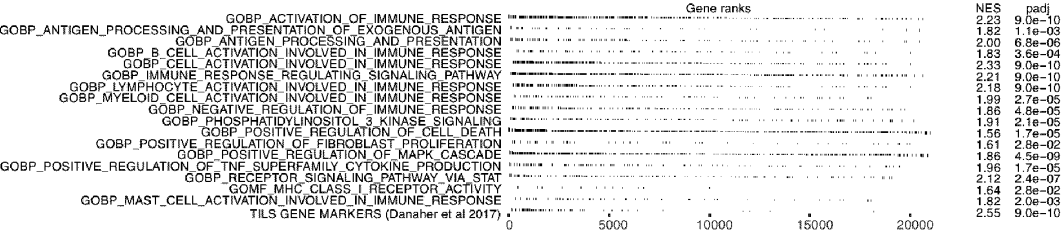


FIG. 16

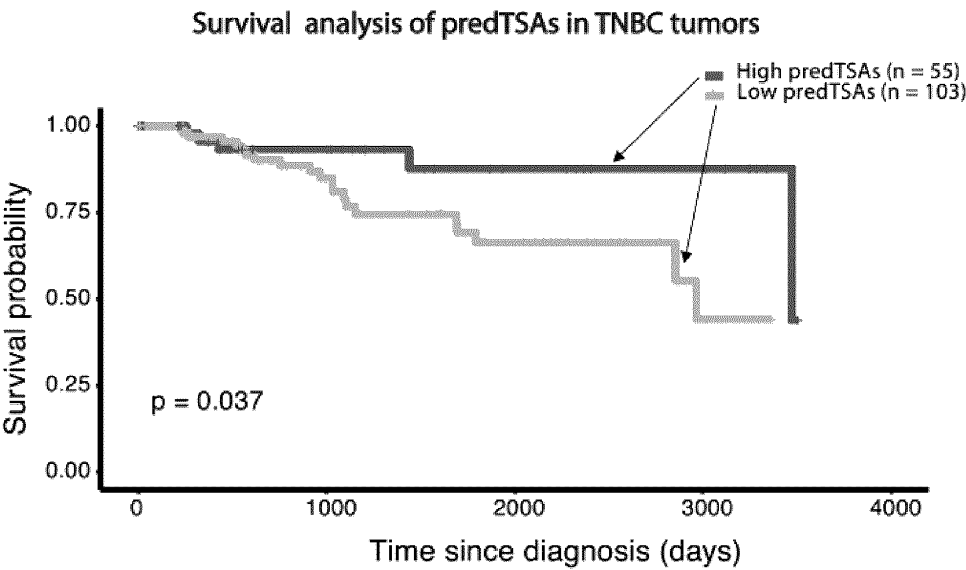


FIG. 17

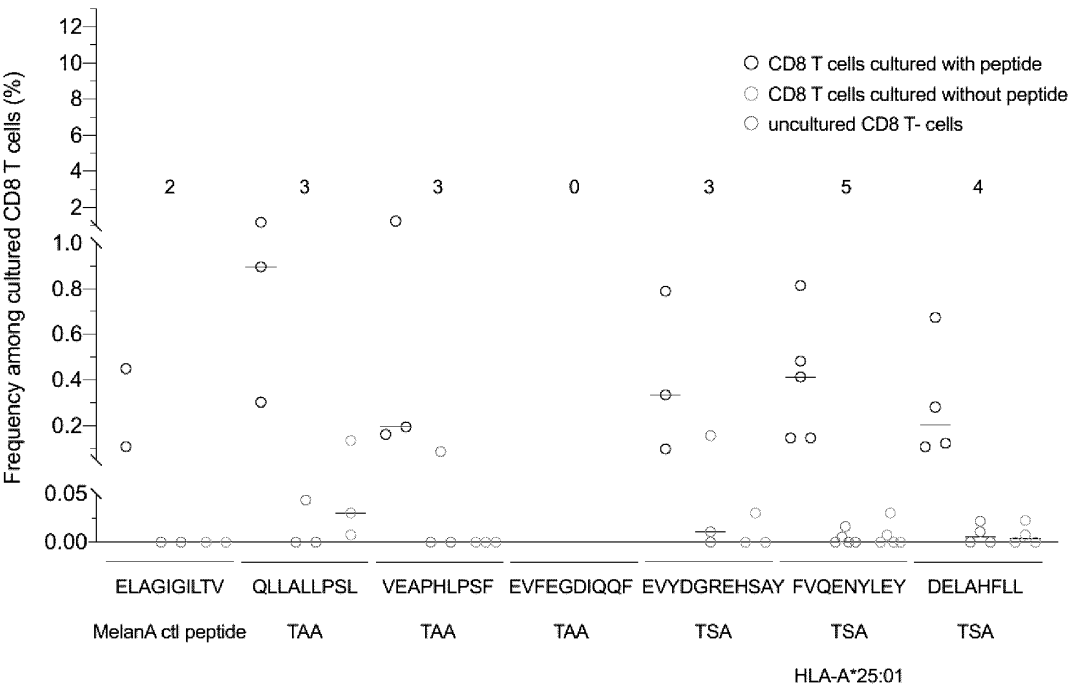


FIG. 18A

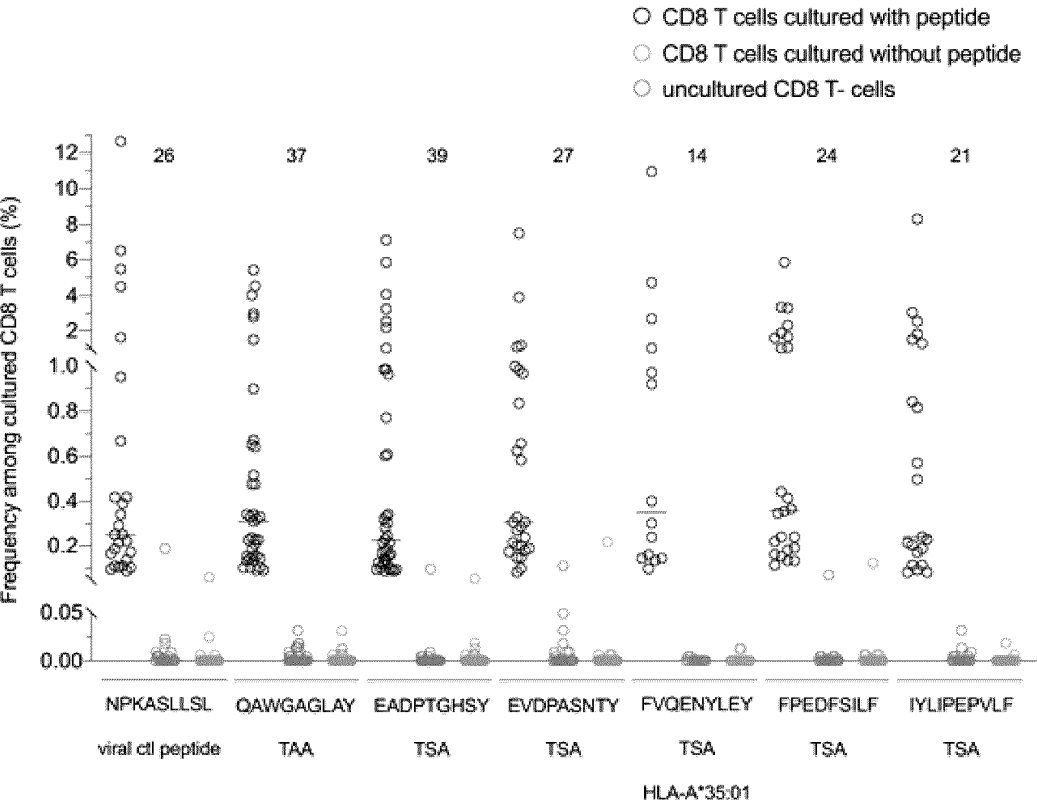


FIG. 18B