Table legends

Table S1. Count of somatic mutations in GEL, ICGC and Hartwig cohorts. Overall count of single nucleotide variants (SNV), double nucleotide variants (DNV) small insertion and deletions (Indels), and rearrangements (Rearr), across the GEL, ICGC and Hartwig cohorts, along with the number of samples used. For the GEL cohort, we indicate the proportion of samples that had PCR cycles in the library preparation.

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Table S17. SBS distinct patterns info table. Annotation of SBS distinct patterns into recurrent, mixed and singleton, with corresponding reference signature name.

Table S18. DBS distinct patterns info table. Annotation of DBS distinct patterns into recurrent, mixed and singleton, with corresponding reference signature name.

Table S19. SBS reference signatures info table. Summary table of all SBS reference signatures identified in this study. We report QC status, proposed etiology, transcription and replication strand bias, number of samples with the signatures and other annotations.

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Table S24. DBS reference signatures exposures. Number of mutations associated with each reference signature in all samples analyzed in this study.

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Table S26. DBS conversion matrix. Conversion matrix mapping organ-specific DBS signatures into reference signatures.

Table S27. Examples of trinucleotide mutational catalogs from GEL, ICGC and Hartwig cohorts.

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