Mutation footprints of small-insertion-and-deletions from large cancer genomics data

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**Abstract**

Somatic mutations resulting from various mutational processes are a key driver of tumorigenesis. Mutational signatures, which are distinctive patterns left by these processes, can be identified through experimental exposures or computational deconvolution of mutation catalogs. In this study, we analyzed over 7,000 whole genomes from the PCAWG (Pan-Cancer Analysis of Whole Genomes) and HMF (Hartwig Medical Foundation) cohorts to create a comprehensive collection of ID (small insertions and deletions) mutational signatures using a hierarchical Dirichlet process-based approach. This analysis led to the identification of 15 novel signatures, in addition to the 23 currently cataloged in COSMIC. We identified one novel signature, H\_ID29, associated with TOP1-TAM (Topoisomerase1 transcription associated mutagenesis), using CRISPR/Cas9-induced knockout cells. Moreover, we identified three new dMMR (defective DNA mismatch repair) signatures—H\_ID33, H\_ID37, and H\_ID38—characterizing short deletions or insertions in repeat units within tumors exhibiting high mutation burdens. Notably, five ID signatures demonstrated significant gender bias. Our examination of signature contributions to cancer genes revealed that C\_ID3, associated with tobacco exposure, accounts for nearly 50% of IDs in LRP1B, which is implicated in lung carcinogenesis. This work establishes an expanded collection of ID signatures, validates a novel signature through functional modeling, elucidates distinct mutational processes, and offers insights into biological implications through extended sequence investigation and trait associations. This comprehensive characterization of ID signatures from over 7,000 genomes enhances our understanding of the mutational processes shaping cancer genomes.

**Introduction**

Somatic mutations are caused by various mutational processes and represent a driving force behind tumorigenesis and cancer development (Alexandrov et al. 2014). The mutations can arise from both endogenous and exogenous sources. These mutations can result from both endogenous sources, such as 5-methylcytosine (5mC) deamination or defective DNA repair mechanisms (Davies et al. 2017; Cooper et al. 2010; Grolleman et al. 2019), and exogenous sources, including exposure to chemical carcinogens in tobacco smoke or certain herbal medicines (Alexandrov et al. 2016; Ng et al. 2017). Mutational signature analysis provides insights into cancer etiology, prognosis, prevention, and signatures can serve as biomarkers for mutagenic exposures(Boot et al. 2022; Davies et al. 2017; Dziubańska-Kusibab et al. 2020; Grolleman et al. 2019).

Mutational signatures are distinctive patterns of mutations left on genomes by specific mutagenic processes or exposures. They can be identified through two approaches: (1) exposing cultured cells, organoids, or experimental animals to suspected mutagens or perturbing DNA repair pathways and then sequencing the affected genomes (Boot et al. 2018; M. N. Huang et al. 2017; Kucab et al. 2019; Caipa Garcia et al. 2024; Riva et al. 2020); and/or (2) using machine learning to deconvolute large-scale somatic mutation data(Alexandrov, Kim, et al. 2020; Alexandrov et al. 2014; Nik-Zainal et al. 2012; Degasperi et al. 2022; Chen et al. 2024; Jin et al. 2024). For instance, data mining of liver cancer genomes detected several types of mutational signature due to the aristolochic acid exposure. These consisted of single-base-substitution (SBS), double-base-substitution (DBS), and insertion-and-deletion (ID) signatures. These were further validation in cell-culture experiments (Chen et al. 2024).

While the characterization of mutational signatures has primarily concentrated on single-base substitutions (SBSs), insertion and deletion (ID) signatures also offer valuable insights into mutagenic mechanisms. For instance, the tobacco smoking-associated mutational process not only includes C>A (SBS4) and CC>AA (DBS2) changes but also involves the removal of 1 bp cytosine from polyC sequences of lengths 1-5, as indicated by ID3. However, the investigation of ID signatures has been comparatively neglected. To date, COSMIC v3.4 has collected 99 reference SBS signatures but only 23 ID signatures (<https://cancer.sanger.ac.uk/signatures/>).

<paragraph needs revisiting> The classification of ID mutational signatures typically involves the examination of several key features, including indel length, sequence context and indel type. Indel length refers to the number of nucleotides inserted or deleted, ranging from a single base pair to larger genomic fragments. Sequence context encompasses the nucleotide composition surrounding the indel site, which may provide insights into the underlying mutagenic mechanisms or sequence preferences. In this context, we do not consider complex indel events involving a combination of insertions and deletions. It considers insertions and deletions of single base pair of C or T, longer fragments from repeats or microhomologies, and result in 83 indel types (ID83).

In this study, we collected somatic mutation data from >7,000 tumor genomes from two large pan-cancer collections: the PCAWG [Pan-Cancer Analysis of Whole Genomes (Alexandrov, Ally, et al. 2020)] and the HMF [Hartwig Medical Foundation(Priestley et al. 2019)]. By systematically analyzing and classifying indels mutational signatures in these cancer genomes using a Hierarchical Dirichlet Process based tool, we established a repertoire of 32 ID mutational signatures including 15 novel signatures and some update of known signatures. By investigating the genetic background and validation in the in-vitro experimental system, we validated a novel ID mutational signature caused by TOP1-TAM (Topoisomerase1-transcription-associated mutagenesis) in the context of RNASEH2B deficiency. In addition, taking the advantage of higher MSI (microsatellite instability) rate in the HMF dataset, we found 3 new ID signatures significantly associated with defective DNA mismatch repair deficiency.

**Results**

***De novo* ID mutational signature discovery from large cohorts with mSigHdp.**

As Non-negative Matrix Factorization (NMF) is widely used for signature discovery analysis, the tool based on a non-parametric Bayesian approach demonstrates significant advantages. This approach allows for the automatic inference of optimal solutions and the sensitive and accurate extraction of mutational signatures from large cohorts. The development of Hierarchical Dirichlet Process (HDP) based extraction model mSigHdp allows a more sensitive and accurate extraction of indel signatures from large scales of genomics data (Liu et al. 2023). We performed *de novo* mutational signature analysis using mSigHdp on a total of 7,013 whole-genome sequencing (WGS) samples. This dataset comprises 2,780 genomes from the PCAWG cohort and 4233 genomes from the HMF cohort. The extraction was performed in three ways: (1) aggregating all samples together, (2) tumors with high tumor mutation burdens (TMBs, details in Method) and (3) analyzing each individual tumor type separately to identify tumor-type-specific rare signatures (Figure 1A).

We then consolidated highly similar signatures from all extractions and removed the ones that can be reconstructed by other signatures. Next, we compared our mSigHdp-extracted signatures to those in COSMIC v3.4, and categorized them into three groups: (1) previously reported signatures (matching COSMIC v3.4 with cosine similarity > 0.85), labeled "C\_IDX" (Figure 1B, Figure S1); (2) merged signatures combining multiple COSMIC v3.4 signatures; and (3) novel signatures not fitting the previous categories, labeled "H\_IDX" (Figure 1C). Our analysis concentrates on groups (1) and (3), omitting merged signatures as they are explicable by known signatures from (1). In total, we identified 32 ID mutational signatures.

**Previously report signatures**

Our analysis successfully reproduced 17 out of 23 COSMIC (v3.4) ID signatures. The remaining 7 signatures were either derived from whole-exome sequencing (WES) data (e.g., ID15 and ID16) or from studies not utilizing PCAWG or HMF data (e.g., ID20, ID21, ID22), potentially exhibiting different disease backgrounds. In summary, mSigHdp's capability to identify nearly all COSMIC signatures underscores its reliability in mutational signature analysis..

Furthermore, several noteworthy differences were observed, and we believe that mSigHdp provides a more biologically reasonable analysis: (1) In contrast to the C\_ID9 identified in our extraction, the COSMIC ID9 signature exhibits a near-depletion of the INS:1:T:5+ motif. This discrepancy may arise from the prevalence of the INS:1:T:5+ peak in almost all tumors. Biologically, a mutagenic process removing a single thymine base from polyT sequences of lengths 1-4 would likely occur in longer polyT sequences as well. (2) mSigHdp C\_ID5 signature incorporates elements of both COSMIC ID5 and ID8, despite having a 0.94 cosine similarity to COSMIC ID5. This can be attributed to the co-occurrence of these signatures in tumors and their shared correlation with aging. We found no tumor samples supporting COSMIC ID5 alone, justifying the merger of these signatures. In our analysis, while neither C\_ID5 nor C\_ID8 showed correlations with patient age, their sum strongly correlated with patient age (Figure S2A, Spearman coefficient = 0.12, p-value = 0.0038 in HMF, Spearman coefficient = 0.18, p-value = 0.0036 in PCAWG). (3) Compared to COSMIC ID17, mSigHdp C\_ID17 signature enhanced the pattern of deletions at repeats and microhomologies, showing similarities to ID8 deletions. Boot et al. identified and validated an association between the TOP2A (Topoisomerase 2A) p.K743N mutation and ID17 (also known as ID\_TOP2A) using a yeast model. Our analysis revealed that our C\_ID17 signature demonstrates a closer resemblance to the ID\_TOP2A signature identified by Boot et al. than to COSMIC ID17 (Figure S2B, C, cosine similarity = 0.982).

**Signature activity**

We evaluated the activity of our 32 mSigHdp signatures using mSigAct, a tool incorporating statistical analysis for the presence of a given signature (Jiang, Wu, and Rozen 2024). Because tumors with large amounts of indels carry1bp T deletions and/or insertions on polyTs (DEL:T:1:5+ and/or INS:T:1:5+). The predominant peaks affect the accuracy of signature assignment analysis because other signals are hidden. We therefore proposed a new way to perform signature assignment analysis for MSI tumors: we firstly removed the DEL:T:1:5+ and INS:T:1:5+ to make other peaks more obvious, as well as the DEL:T:1:5+ and INS:T:1:5+ deletions from the mutational signatures, resulting in ID81 catalogs/signatures. Then these ID81 catalogs were reconstructed by the ID81 signatures. After this, we put the DEL:T:1:5+ and INS:T:1:5+ back and reconstructed the tumors, then perform the signature assignment analysis of the difference between catalogs and reconstructed catalogs with C\_ID1 and C\_ID2. In this way, we can reveal more detailed information in MSI tumors that cannot be observed when DEL:T:1:5+ and INS:T:1:5+ are present.

Consistent with previous studies, C\_ID1, C\_ID2, C\_ID5, and C\_ID8 were observed across most cancer types, with C\_ID3 showing a strong presence in lung cancers and C\_ID13 showing a strong presence in skin cancers. The novel signatures identified by mSigHdp were generally active in fewer cancer types compared to COSMIC signatures, except H\_ID24 and H\_ID25 which were widespread across cancer types (Figure 2). We analyzed correlations between our ID signature assignments and the SBS signature assignments by Degasperi et al. in PCAWG and HMF samples (Figure S3). Our analysis confirmed strong correlations between C\_ID3, SBS4, and SBS92 exposures, all linked to tobacco-induced lung cancer (Spearman correlation coefficients: 0.75 between C\_ID3 and SBS4, 0.63 between C\_ID3 and SBS92, Figure 3A & B). In addition, a strong correlation was also observed between C\_ID13 and SBS7a, both associated with UV exposure (Spearman correlation coefficient: 0.81, Figure 3A). The analysis also revealed a module of four signatures associated with cell replication: SBS18 (associated with reactive oxygen species), SBS1 (5mC deamination during cell replication), C\_ID1 and C\_ID2 (replication slippage) (Figure 3C). We identified a correlation module including C\_ID14, SBS93, SBS17, SBS88, and SBS35 (Figure 3D). SBS17, SBS88, and SBS93 are frequently observed in gastrointestinal (GI) tracts, while SBS35 is associated with platinum treatment. This correlation suggests a possible etiology for C\_ID14: platinum treatment in GI tract cancers. Interestingly, we identified a dMMR (defective DNA mismatch repair) module consists of five signatures: SBS44, C\_ID17, H\_ID33, H\_ID37 and H\_ID38 (Figure 3E). Interestingly, only 1 out of 7 dMMR SBS signatures was observed strongly associated with indels. This suggests a distinct mutational process hidden behind SBS44 from other SBS signatures.

**Novel Signatures**

**MSI signatures**

Leveraging the higher proportion of microsatellite instability (MSI) tumors in the Hartwig Medical Foundation (HMF) dataset, we identified additional MSI-associated ID signatures beyond COSMIC ID7: H\_ID33, H\_ID37 and H\_ID38 (Figure 5A). COSMIC v3.4 lists seven SBS signatures associated with mismatch repair (MMR) deficiency: SBS6, SBS14, SBS15, SBS20, SBS21, SBS26, and SBS44. These signatures often co-occur and show overlapping peaks. For instance, SBS44 and SBS20 have nearly identical C>A mutation patterns, while SBS6 and SBS15 share a predominant CCG>CTG peak. We observed similar patterns in ID signatures, with H\_ID33, H\_ID37, and C\_ID7 all showing >1bp deletions at repeat sequences, but they preferentially characterize different ID types.

C\_ID7 is characterized primarily by 1 bp deletions of C or T from long C or T sequences, while H\_ID33 mainly represents TT deletions from 4-5 TT repeats. H\_ID37 is primarily associated with TTT deletions from 3 TTT repeats (Figure 5D). In contrast to these deletion patterns, H\_ID38 predominantly describes insertions, including 1 bp and 2 bp insertions at long repeats. It consists of two main scenarios: when a sample predominantly features insertions, these primarily involve TT repeats (e.g., CPCT02030532T, DRUP0105003T in Figure 5D); when a sample has a more balanced mix of deletions and insertions, a wider variety of dinucleotide insertions is observed (e.g., SP94933, SP102133, CPCT02450014T, WIDE01010606T in Figure 5D). These microsatellite instability (MSI) signatures account for over 50% of indels in MSI tumors, but are less prevalent in microsatellite stable (MSS) tumors (Figure 5C). Notably, some MSS tumors exhibit a high ratio of MSI signature activity, likely due to their strong MSI characteristics, such as high indel and single-base substitution (SBS) mutation loads, despite being classified as MSS. Furthermore, we investigated the potential of the MSI signature activity ratio as a biomarker for detecting MSI status. An area under the receiver operating characteristic curve (AUROC) analysis was conducted to compare the MSI ratio with pre-labeled MSI status, resulting in an AUROC of 0.81, indicating strong predictive capability

**RNaseH2B deficiency preferentially removes 2bp nucleotides on genome**

We identified a novel mutational signature characterized by 1-3 bp deletions from two repeats or microhomology (Figure 4A). The primary peak mainly represents the deletion of CT from 5’-CTCT-3’ (or AG from 5’-AGAG-3’), as indicated by the extended sequence analysis of five samples exhibiting the highest H\_ID29 activity, two of which are from the PCAWG cohort (Figure 4B). These PCAWG samples show significant H\_ID29 activity, with a skin melanoma genome (SP103894) containing 3,772 H\_ID29 mutations and a breast cancer genome (SP5559) containing 949 H\_ID29 mutations (Figure 4D). Analyzing additional samples allows for the identification of rare signatures within the PCAWG datasets.

We re-examined the rnh201Δ *Saccharomyces cerevisiae* genomes and observed patterns of 2 bp deletions similar to those of H\_ID29 (Williams et al. 2019; Lujan et al. 2014). We established an RNASEH2B deficiency model using the CRISPR/Cas9 system in the HEK293T cell line, and whole genome sequencing revealed patterns consistent with H\_ID29. Previously, Reijns et al. developed RNASEH2A-deficient mammalian cell lines and Rnaseh2b-KO mouse intestinal cancer models, and identified (Reijns et al. 2022). Our findings indicate that H\_ID29, rather than ID4, closely resembles the mutational spectra from these knockout models, providing a more accurate representation of the genomic footprints associated with TOP1-TAM (transcription-associated mutagenesis) during the cleavage of embedded ribonucleotides in the absence of RNASEH2A and/or RNASEH2B (S. N. Huang, Ghosh, and Pommier 2015; Sparks and Burgers 2015; Chon et al. 2009).

While TNT is predominantly found at deletion sites for both H\_ID29 and C\_ID4, our extended sequence analysis indicates differences in sequence context: H\_ID29 tends to delete CT/TC within tandem repeats, whereas a common TCTNT motif is present in microhomologies. Collectively, this study presents H\_ID29 as a novel mutational signature identified through de novo extraction from cancer genomic data, proposing that H\_ID29 is associated with TOP1-dependent deletions in RNASEH2A and/or RNASEH2B deficient cells.

**Extended sequence context characterization of novel signatures**

We observed that some signatures share dominant peaks, prompting an investigation into whether they represent distinct mutational processes. To address this, we examined the extended sequence contexts of samples with high activity for these signatures to understand the preferential sequence context of the indels.

DEL:C:1:0

Both H\_ID24 and C\_ID9 exhibit a similar pattern of 1 bp C deletions (DEL:C:1:0). However, analysis of their extended sequence contexts revealed that H\_ID24 preferentially deletes C from 5'TTTCX3', while C\_ID9 favors C deletion from 5'XCTTT3' (Figure 6A). These findings suggest that H\_ID24 and C\_ID9 arise from distinct mutational processes: H\_ID24 preferentially removes cytosine 3' of poly-T sequences, whereas C\_ID9 removes cytosine 5' of poly-T sequences. Additionally, DEL:C:1:0 is also prominent in H\_ID32, where the extended sequence surrounding DEL:C:1:0 shows a balanced ratio between A and T.

H\_ID27 and part of H\_ID28 both display 1 bp C insertions (INS:C:1:0), but they characterize two distinct processes: H\_ID27 preferentially inserts a cytosine 3' of poly-A sequences, while H\_ID28 inserts a cytosine or guanine 3' of poly-G sequences. Based on these observations, we conclude that H\_ID27 and H\_ID28 result from two distinct mutational processes rather than an over-splitting of a single process. Furthermore, we noted that both H\_ID27 and C\_ID14 exhibit high levels of INS:C:1:0. Extended sequence analysis indicated that the INS:C:1:0 of these two signatures preferentially occur within poly-G sequences (Figure ). Several HMF samples strongly support the presence of H\_ID27, leading us to propose that H\_ID27 is a variant form of C\_ID14 which is composed of more DEL:T:1:0. We also found that the primary mutation types in H\_ID28 share a similar pattern in extended sequence context analysis; specifically, the insertion of repeats, along with 1 bp C and 1 bp T, tends to occur 3' of poly-G sequences.

**Gender comparison**

We investigated whether mutational processes, as represented by mutational signatures, exhibit gender-specific patterns. We firstly exclude the samples with gender characteristic including prostate cancer (only in males), uterus cancer, breast cancer and ovary cancer (only in females). To assess gender-specific prevalence of mutational signatures, we employed Fisher's Exact Test. From a total of 5,000 patients with available gender data, we identified 7 signatures demonstrating significant gender-specific associations: 6 signatures (C\_ID3, C\_ID5, C\_ID8, H\_ID25, C\_ID13, H\_ID30) showed a significant prevalence in male patients. Conversely, only 1 signature (C\_ID12) was more commonly observed in female patients (Figure 5D). Some of the observations can be explained biologically, for example, C\_ID3 is associated with tobacco smoking which has a higher proportion of male patients.

**Signature attributions to cancer genes**

We examined the contribution of mutational signatures to indels in cancer genes, focusing on 581 Tier 1 genes from the Cancer Gene Census (Sondka et al. 2018). We excluded DEL:1:T:5+ and INS:1:T:5+ from our analysis, as these indels are primarily contributed by C\_ID1 and C\_ID2, and single-base thymine insertions/deletions in poly-T regions rarely have significant biological impacts. The genes most frequently affected by insertions were CAMTA1, ERBB4, FHIT, FOXP1, LPP, LRP1B, NRG1, PRDM16, PTPRT, and RUNX1. Several signatures with known causes contribute to these insertions, including DNA replication slippage, defective MMR, defective HR DNA damage repair, and UV exposure (Figure 6C). Deletions most frequently affected CAMTA1, CUX1, ERBB4, FHIT, FOXP1, GPHN, LPP, LRP1B, NRG1, and PRDM16 (Figure 6C). These deletions are primarily caused by DNA replication slippage and defective MMR. Notably, the tobacco smoking signature (C\_ID3) contributes to nearly 50% of cytosine-deletions and thymine-insertions in LRP1B. Previous research has linked LRP1B mutations to lung cancer pathogenesis (Ding et al. 2008). Our analysis potentially uncovers the mutational processes responsible for LRP1B mutations.

**Discussion**

Using a novel nonparametric Bayesian approach, we analyzed over 7,000 whole-genome sequencing (WGS) tumor samples encompassing 25 cancer types from the Pan-Cancer Analysis of Whole Genomes (PCAWG) and Hartwig Medical Foundation (HMF) cohorts. As the first study using >7000 genomes for ID signature analysis, our study established a comprehensive collection of 32 ID mutational signatures. We identified one indel signature associated with RNaseH2B deficiency, validating this finding via CRISPR/Cas9 system. Additionally, we found three ID signatures strongly linked to microsatellite instability (MSI) status, which implement the understanding of indel footprints left my defective MMR mechanism. We also performed an extended sequence context analysis to understand more information behind the formation of mutational signatures.

We attempted signature extraction using SigProfilerExtractor, an NMF-based model recognized for its strong performance in signature analysis (Islam et al. 2022). However, this method proved ineffective for our large cohort, yielding an optimal solution of K=12 but failing to identify either novel signatures or previously established COSMIC signatures. Similarly, we employed the minimum-volume NMF model, MuSiCal, across all genomes, which resulted in an optimal K=13 (Jin et al. 2024). This limitation is likely due to the challenges Non-negative Matrix Factorization faces in managing the high data sparsity associated with indels (see Supplementary figure). In contrast, using mSigHdp, we identified 30 mutational signatures in the extraction of all genomes, with 24 included in the finalized collection. Our study highlights the effectiveness of mSigHdp for mining large datasets and demonstrates its ability to reveal novel signatures in highly sparse, low-count data.

As sequencing technology advances, numerous national cancer research initiatives are underway. Mutational signatures have proven valuable in predicting cancer treatment efficacy and tracing disease etiology. By integrating more data into mutational signature analysis, we anticipate discovering additional signatures that characterize genomic mutational processes. Furthermore, we expect the development of mutational signatures as clinical biomarkers to enhance cancer diagnosis and treatment strategies.

**Materials and methods**

Data source

We considered two large pan-cancer whole genome cohorts: the PCAWG cohort which comprises 2780 whole-genome–sequenced samples; and the HMF cohort, comprising 3417 whole-genome–sequenced tumor samples. The mutational spectra used for mutational signature extraction were provided in Table S1. Variant calls for 2,780 WGS samples from the ICGC/TCGA (International Cancer Genome Consortium/The Cancer Genome Atlas) Pan-Cancer Analysis of Whole Genomes Consortium and clinical traits were obtained from the ICGC data portal (<https://dcc.icgc.org/releases/current/Projects/>, now the repository is retired, the data was downloaded on 9 May, 2024). Variant calls for 3417 WGS samples from the HMF cohort were obtained from xxxx. Clinical traits such as cancer type, age and gender of the HMF genomes were found from supplementary files of Priestley et al., 2019. These data was also provided in Table S2. The COSMIC Cancer Gene Census was used to identify known cancer driver genes (Sondka et al., 2018).

**Mutational signature extraction**

We used mSigHdp (v 2.1.2) for de novo mutational signature extraction analysis. when applying to all samples de novo mutational signatures were extracted using the cancer type to construct the hierarchy; when applying to samples of each cancer type, the de novo mutational signatures were extracted with 2-layer HDP mixture models. In both scenario, we used the following parameters: seedNumber=1234, burnin=1000, bunin.multiplier=20, post.n = 200, post.space = 100, num.child.process=20, gamma.alpha=1, gamma.beta=100.

For SigProfilerExtractor, de novo mutational signatures were extracted from each mutational matrix using SigProfilerExtractor and default parameters (v1.1.24). NMF was performed with finding solutions between k = 10 and k = 30 signatures; each factorization was repeated 100 times.

Match mSigHdp signatures into COSMIC reference signatures

The mSigHdp signatures were matched to previously identified COSMIC signatures (v3.4). We compared all de novo signatures to COSMIC signatures and categorized them into three groups: (1) known signature: if a mSigHdp signature has a cosine similarity of ≥ 0.85 with a COSMIC signature; (2) merged signatures: if a mSigHdp signatures can be reconstructed by at most 4 COSMIC signatures with a reconstructed similarity of ≥ 0.85; (3) novel signatures: the signatures do not fit into the known signatures or the merged signatures.

Signature attribution analysis

The 32 ID signature activities were attributed to each sample using a two-step approach: first, we used find\_best\_reconstruction\_QP function of SigTools R package (v1.0.7) to which provides a fast signature attribution analysis with quadratic programming optimization; second, we used the PresenceAttributeSigActivity function and default parameters in mSigAct R package (v3.0.1) to further refined the result from the previous step.

Cell line culture and RNaseH2B CRIPSR

Need help here

MSI/MSS status and high/low TMB status

For PCAWG genomes, the MSI status was evaluated by the PCAWG working group and obtained from the synapse repository (<https://www.synapse.org/#!Synapse:syn8016399>, the data was downloaded on May 2022). For HMF genomes, the MSI status was downloaded from the supplementary data of Priestley et al., 2019. Based on the MSI status from the literatures, samples with >14000 IDs and >15000 SBSs were labelled as high TMB tumors. The thresholds were selected based on the minimum number of mutations of the pre-defined MSI tumors.

Gender enrichment by Fisher’s exact test

To evaluate the presence of mutational signatures in male and female, we used Fisher's Exact Test to determine the statistical significance of signature enrichment by gender. We quantified the frequency of the presence of each signature (exposure > 0) in both groups and applied the test to assess associations. A p-value threshold of 0.05 was established to indicate significant enrichment.

Extended sequence context

To analyze a specific signature and indel type of interest, we first identified the 5 genomes with the highest exposure to the corresponding signature. From these genomes, we extracted all indels of the relevant type. We then examined the nucleotide sequence within a 21-base pair window centered on each indel site (±10 nucleotides from the indel position). For each position within this window, we calculated the frequency of each nucleotide (A, T, C, and G). The logo was plotted based on the frequency matrix by seqLogo function of seqLogo R package (version 1.71.0)

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