

The repertoire of copy number alteration signatures in human cancer

Xue-Song Liu ¹,

liuxs@shanghaitech.edu.cn

Ziyu Tao ^{1-3*} Shixiang Wang ^{1-3*} Chenxu Wu ^{1-3*}

Huimin Li ¹ Tao Wu ¹ Xiangyu Zhao ¹ Wei Ning ¹

Guangshuai Wang ¹

¹ School of Life Science and Technology, ShanghaiTech University, Shanghai 201203, China

² Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences, Shanghai, China

³ University of Chinese Academy of Sciences, Beijing, China

Abstract

DNA alteration signatures are recurring patterns that are the imprints of mutagenic processes accumulated during the evolution of cancer cell. Despite the importance of copy number alteration (CNA) in cancer progression, comprehensive understanding about the mutational processes and signatures of CNA is still lacking. Here we developed a method to categorize CNA based on various fragment properties, which reflect the consequences of mutagenic processes and can be extracted from different types of data, including whole genome sequencing (WGS), whole exome sequencing (WES) and SNP array. The signature of CNA has been extracted from 2778 pan-cancer analysis of whole genomes (PCAWG) WGS samples, and further validated using 10851 the cancer genome atlas (TCGA) SNP array dataset. Novel copy number signatures associated with haploid chromosome have been identified. The activities of some copy number signatures consistently predict cancer patients' prognosis. This study provides a repertoire for understanding the signatures and mutational processes of CNA.

Methodology

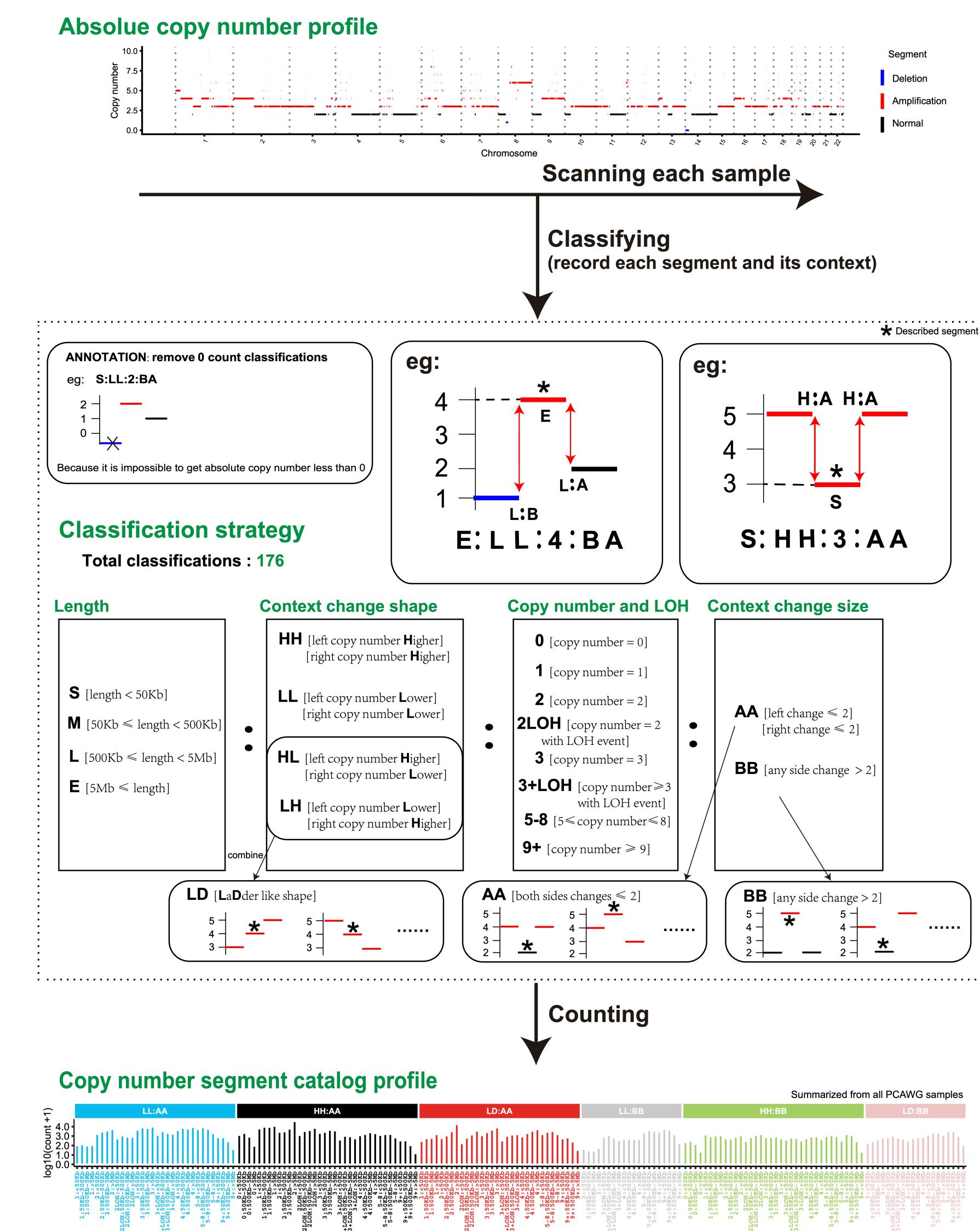


Figure 1: CNA classification strategy for signature analysis.

For each CNA segment, the following features have been considered: 1, segment context, including segment shape and copy number change number; 2, Absolute copy number; 3, LOH status; 4, segment size. In total 176 types of CNA segments have been defined accordingly.

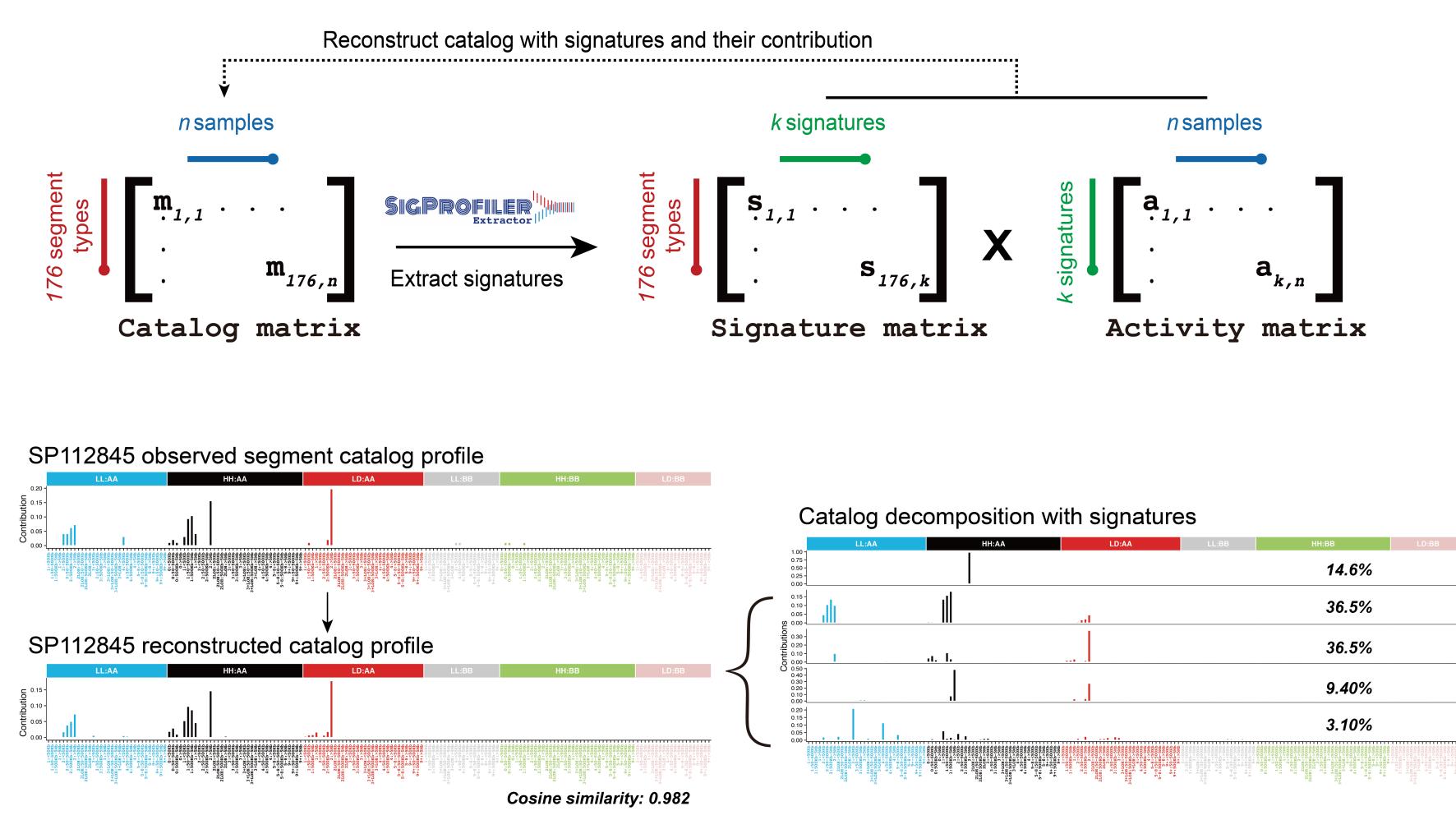


Figure 2: De novo CNA signature extraction with sigprofiler.

We selected the signature extraction solution as the maximum signature number which meets the following criteria: 1. No over fit. 2. Stability should be at least local maximal. 3. Mean cosine distance should be as small as possible. Based on the rules, we selected 14 signatures for PCAWG copy number data.

Results

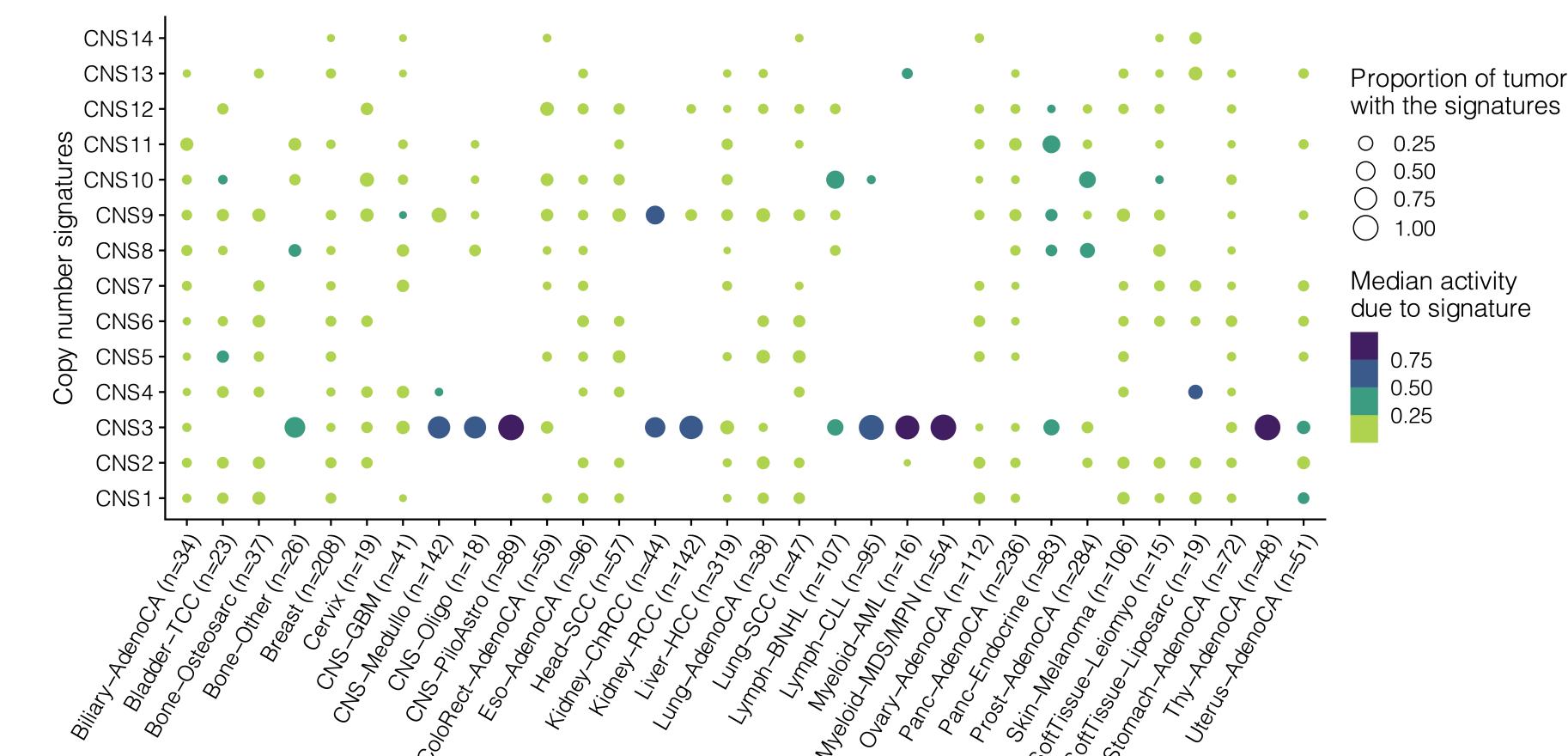


Figure 3: Proportion of tumors with the signature and the median activity of the signature are shown for 32 PCAWG cancer types. For each individual tumor, only signatures that contribute to >=5% of the total are counted.

Signatures	Representative sample profile	Prominent features	Potential mechanism
CNS1	SP11669	(A) CN amplification (34 copies) with different size flanked by higher copy (8-20 copies); (B) Adjacent CN change is irregular; (C) Localized amplification with various fold.	Likely Chromothirosis due to MMBIR
CNS2	SP120844	(A) Localized CN amplification(3 copies >5Mb); (B) Adjacent CN change is within 2;	Unknown
CNS3	SP105708	(A) Long DNA segment (>5Mb) without copy number alteration (CN=2).	Genome without CNA
CNS4	SP116225	(A) Many, massive high CN amplification (copies>5); (B) Adjacent CN change is within 2 copies; (C) Poor overall survival	EcDNA or neochromosome
CNS5	SP117200	(A) Mostly large-sized (>500kb) DNA segment with amplification in different levels(3-8 copies); (B) Adjacent CN change is mostly irregular; (C) Oscillating CN with 3-4-3-2 (minor) pattern are observed.	Likely BFB
CNS6	SP17443	(A) Many DNA segments of various size (>50kb or 50kb-5Mb) (CN=2 or 3 with LOH); (B) Adjacent CN change is irregular.	LOH and amplification
CNS7	SP11603	(A) Shallow CN deletion (size>5Mb) flanked by neutral segment with adjacent CN change; (B) Adjacent CN change is within 2 copies; (C) Localized oscillating CN with 2-1-2 pattern.	Chromothripsy
CNS8	SP116048	(A) Large size (>5Mb) DNA segment with CN change less than 2; (B) Adjacent CN change is mostly 4 copies; (C) The signature is associated with WGD.	WGD
CNS9	SP116887	(A) DNA segment of small to medium size(0-3Mb) (CN=0 or 1) interspersed with large sized (>5Mb) neutral segment(CN=2); (B) Adjacent CN change is within 2.	Homozygous deletion
CNS10	SP135354	(A) Large size (>5Mb) shallow deletion along with large sized (>5Mb) neutral segment; (B) Adjacent CN change is within 2;	Haploid chromosome
CNS11	SP17676	(A) Large size (>5Mb) DNA segment (CN=3) along with large size (>5Mb) neutral segment flanking LOH; (B) Adjacent CN change is within 2;	Triplid chromosome
CNS12	SP13654	(A) Localized high number of amplification (CN=4-8) and shallow deletions; (B) Adjacent CN change is mostly 2 copies.	Unknown
CNS13	SP9163	(A) Evenly distributed small size(<50kb) segment (CN=1-4) flanked by large size (>5Mb) neutral segment CN=2; (B) Adjacent CN change is within 2 copies; (C) The signature is strongly associated with HRD.	HRD
CNS14	SP9163	(A) Evenly distributed small size(<50kb) segment (CN=1-4) flanked by large size (>5Mb) neutral segment CN=2;	

Figure 4: Representative CNA profile, prominent features and potential mechanisms for each identified CNA signatures extracted in PCAWG dataset.

An important purpose of CNA signature analysis is to identify the underlying mutational processes for CNA, and classify CNA based on mutational processes. Potential mutational processes for CNA include intrinsic inducers and extrinsic inducers. Intrinsic CNA inducers include: double-strand break repair defect (HRD etc.); cell cycle defect; DNA replication defects; telomere loss, etc.

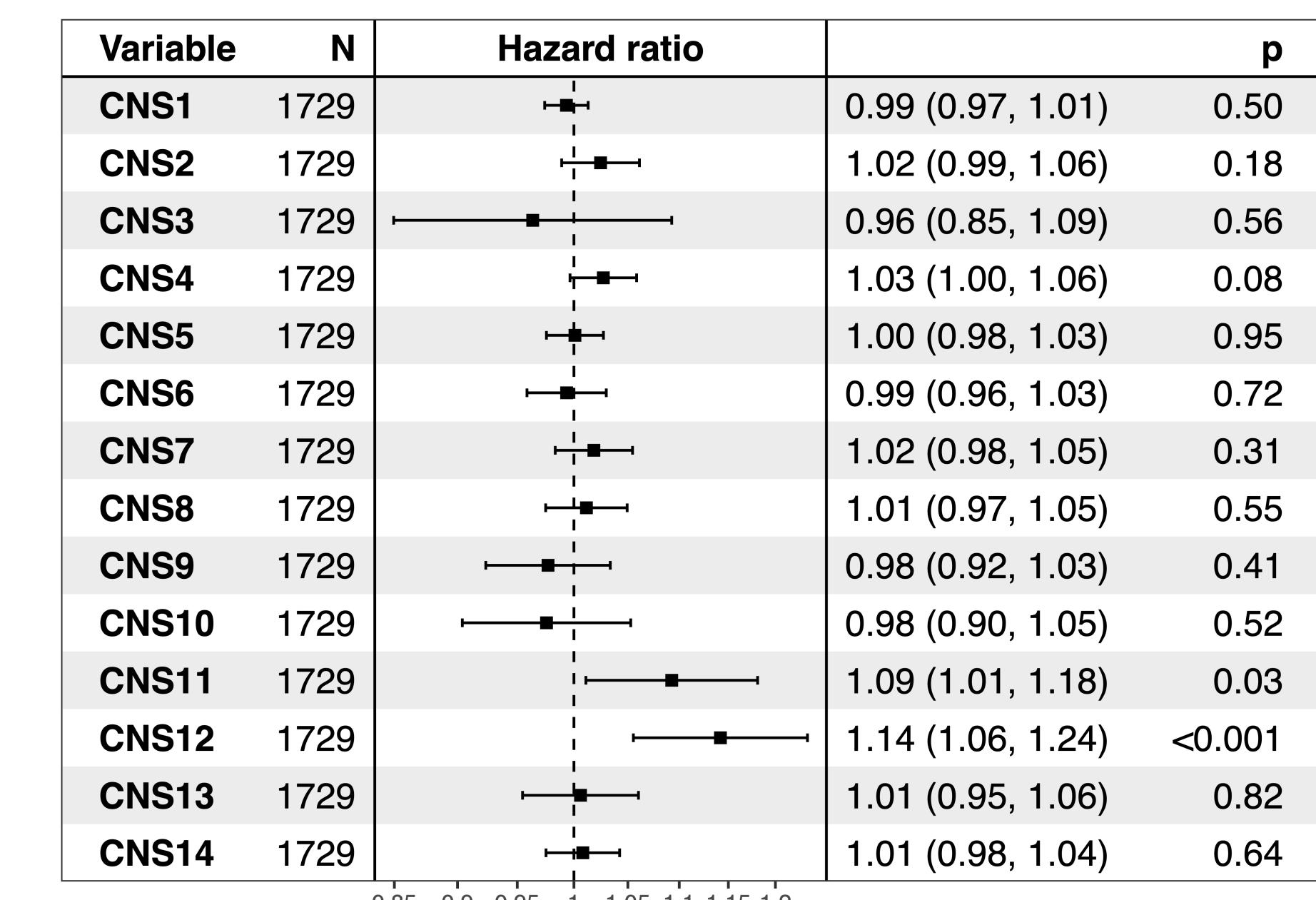


Figure 5: CNA signature activity and cancer patients' prognosis.

The CNA signatures extracted from cancer patients could be cancer prognosis biomarkers. In pan-cancer level, activities of CNS11, CNS12 are significantly associated with poor OS.

Conclusion

- We developed a unified and comprehensive method for copy number signature analysis.
- Our method can be applied in cancer patients with copy number profiles generated with WGS, WES or SNP array data. - Our copy number signature analysis method is based on a novel and comprehensive method to catalog copy number segments.
- copy number signatures could be biomarkers to guide cancer precision medicine.

More

You can scan QR code at bottom center to see online analysis report. All code and related data are published at https://github.com/XSLiuLab/Pan-cancer_CNA_signature.

Acknowledgments

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Recent works of our lab

- Wang, Shixiang, et al. "Copy number signature analysis tool and its application in prostate cancer reveals distinct mutational processes and clinical outcomes." PLoS genetics 17.5 (2021): e1009557.
- Wang, Shixiang, et al. "UCSCXenaShiny: an R/CRAN package for interactive analysis of UCSC xena data." Bioinformatics (2021).
- Wang, Shixiang, et al. "Sigflow: an automated and comprehensive pipeline for cancer genome mutational signature analysis." Bioinformatics 37.11 (2021): 1590-1592.

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