Different CNA tools for tumor fraction

1. Absolute
Carter, S. L. *et al*. Absolute quantification of somatic DNA alterations in human cancer. *Nat Biotechnol* **30**, 413–421 (2012).

2. Sequenza
Favero, F. *et al*. Sequenza: allele-specific copy number and mutation profiles from tumor sequencing data. *Ann Oncol* **26**, 64–70 (2015).

3. Sclust
Cun, Y., Yang, T.-P., Achter, V., Lang, U. & Peifer, M. Copy-number analysis and inference of subclonal populations in cancer genomes using Sclust. *Nat Protoc* **13**, 1488–1501 (2018).

4. ichorCNA
Adalsteinsson, V. A. *et al*. Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. *Nat Commun* **8**, 1324 (2017).

5. CloneCNA
Yu, Z., Li, A. & Wang, M. CloneCNA: detecting subclonal somatic copy number alterations in heterogeneous tumor samples from whole-exome sequencing data. *BMC Bioinformatics* **17**, 310 (2016).

6. CLImAT
Yu, Z., Liu, Y., Shen, Y., Wang, M. & Li, A. CLImAT: accurate detection of copy number alteration and loss of heterozygosity in impure and aneuploid tumor samples using whole-genome sequencing data. *Bioinformatics* **30**, 2576–2583 (2014).

7. THetA
Oesper, L., Mahmoody, A. & Raphael, B. J. THetA: inferring intra-tumor heterogeneity from high-throughput DNA sequencing data. *Genome Biology* **14**, R80 (2013).

8. GISTIC2.0
Mermel, C. H. *et al*. GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human cancers. *Genome Biol* **12**, R41 (2011).

9. ASCAT
Van Loo, P. *et al*. Allele-specific copy number analysis of tumors. *Proc Natl Acad Sci U S A* **107**, 16910–16915 (2010).

10.shallowHRD
Eeckhoutte, A. *et al*. ShallowHRD: detection of homologous recombination deficiency from shallow whole genome sequencing. *Bioinformatics* **36**, 3888–3889 (2020).

11. CNsignatures
Macintyre, G. *et al*. Copy number signatures and mutational processes in ovarian carcinoma. *Nature Genetics* **50**, 1262–1270 (2018).

12. BoostDM
Muiños, F., Martínez-Jiménez, F., Pich, O., Gonzalez-Perez, A. & Lopez-Bigas, N. In silico

saturation mutagenesis of cancer genes. *Nature* **596**, 428–432 (2021).

Different CNV tools for CN calling

Smolander, J. *et al*. Evaluation of tools for identifying large copy number variations from ultra-low-coverage whole-genome sequencing data. *BMC Genomics* **22**, 357 (2021).

1.

1. BIC-seq2
2. Canvas
3. CNVnator
4. FREEC
5. HMMcopy
6. QDNAseq
7. CNAnorm (similar to QDNAseq)
8. CNV-seq (required control sample)
9. VarScan2 (required control sample)
10. TitanCNA (required control sample)
11. WisercondorX (required control sample)