**Checklist of software used in STORK**

R version 3.5.1 or R studio with R version 3.4.0 and above1

cutadapt 2.4 with Python 3.7.82

BEDtools v2.28.03

samtools 1.2 (using htslib 1.2.1)4

Blat suite5 (https://genome.ucsc.edu/goldenPath/help/blatSpec.html)

pblat v2.06 (https://github.com/icebert/pblat/releases/tag/2.0)

Bowtie2 2.3.57

H. sapiens GRCh37 reference Bowtie2 Index (<https://genome-idx.s3.amazonaws.com/bt/GRCh37.zip>)

STORK analysis script (https://github.com/VivianWei1328/STORK\_test)

**References**

1. Team RDC. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL <http://www.R-project.org>. R Foundation for Statistical Computing, Vienna, Austria 2012.

2. Martin M. Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnetjournal 2011;17:10-.

3. Quinlan AR, Hall IM. BEDTools: a flexible suite of utilities for comparing genomic features. Bioinformatics 2010;26:841-2.

4. Li H, Handsaker B, Wysoker A, et al. The Sequence Alignment/Map format and SAMtools. Bioinformatics 2009;25:2078-9.

5. Kent WJ. BLAT--the BLAST-like alignment tool. Genome research 2002;12:656-64.

6. Wang M, Kong L. pblat: a multithread blat algorithm speeding up aligning sequences to genomes. BMC bioinformatics 2019;20:28.

7. Langmead B, Salzberg SL. Fast gapped-read alignment with Bowtie 2. Nature methods 2012;9:357-9.