

Software tool	Version	Underlying algorithm	Data structure	Types of reads accepted	Organism	Journal	Published year	Programming language	In the publication compared to	Tools webpage	Software dependencies	Default k-mer size	Read trimming
BLESS	1.02	k-mer spectrum	Bloom filter and hash table	SE/PE	Human, E. Coli, S. aureus	Bioinformatics	2014	C++	SGA, QuorUM, Lighter, BFC, DecGPU, ECHO, HITEC, Musket, Quake, Reptile	https://sourceforge.net/p/bless-ec/wiki/Home/	MPICH 3.1.3, OpenMPI 1.8.4, Boost library, google sparseshash, klib, KMC, murmurhash3, zlib, pigz	N/A	YES
Fiona	0.2.8	k-mer spectrum	partial suffix array	SE	human, drosophila, E. Coli, C. elegans	Bioinformatics	2014	C++	Allpaths-LG, Coral, H-Shrec, ECHO, HITEC, Quake	https://github.com/seqan/seqan/tree/master/apps/fiona	N/A	N/A	YES
Pollux	1.0.2	k-mer spectrum	Hash table	SE/PE	Human, E. Coli, S. aureus, mixed genome data	BMC Bioinformatics	2015	C	Quake, SGA, BLESS, Musket, RACER	https://github.com/emarinier/pollux	64 bit Unix-based OS	31	YES
BFC	1	k-mer spectrum	Bloom filter and hash table	SE/PE	Human, C. Elegans	Bioinformatics	2015	C	BLESS, Bloocoo, fermi2, Lighter, Musket, and SGA	https://github.com/lh3/bfc	N/A	N/A	NO
Lighter	1.1.1	k-mer spectrum	Bloom filter	SE/PE	Human, E. Coli, C. elegans	Genome Biology	2014	C++	Quake, Musket, Bless, Soapc	https://github.com/mouris/Lighter	N/A	N/A	NO
Musket	1.1	k-mer spectrum	Bloom filter and hash table	SE/PE	Human, E. Coli, C. elegans	Bioinformatics	2012	C++	SGA, Quake	http://musket.sourceforge.net/homepage.htm	N/A	N/A	NO
Racer	1.0.1	k-mer spectrum	Hash table	SE/PE	Human, E. Coli, C. elegans, Drosophila, other bacteria	Bioinformatics	2013	C++	Coral, HITEC, Quake, Reptile, SHREC	http://www.csd.uwo.ca/~ile/RACER/	OpenMP	N/A	NO
Reptile	1.1	k-mer spectrum	Hamming graph	SE	Human, Acinetobacter sp., E. Coli	Bioinformatics	2010	C++	SHREC	http://aluru-sun.ece.iastate.edu/doku.php?id=reptile	Perl, GNU make, C++ compiler	24	NO
Quake	0.3	k-mer spectrum	Bit array index	SE/PE	Human, E. Coli	Genome Biology	2010	C++, R	SOAPdenovo, EULER, SHREC	http://www.cccb.umd.edu/software/quake	N/A	15	YES
SOAPdenovo2 Corrector	2.03	k-mer spectrum	Hash table	SE/PE	Human, PhiX174, Drosophila, Saccharomyces cerevisiae	Giga Science	2012	C/C++	SOAPdenovo1, ALLPATHS-LG	http://soap.genomics.org.cn/about.html	GCC 4.4.5 or later	N/A	
ECHO	1.12	MSA*	Hash table	SE/PE	Human	Genome Research	2012	Python	SA, SHREC	http://uc-echo.sourceforge.net/	GCC 4.1 or later, Python 2.6, numpy, scipy	1/6 read length	YES
Coral	1.4.1	MSA*	Hash table	SE/PE	Human, E. coli, S. aureus	Bioinformatics	2011	C	COMPASS 3.0, HHalign 1.5.1.1 and PSI-BLAST	https://www.cs.helsinki.fi/u/imsalmel/coral/	N/A	N/A	YES
RECKONER	0.2.1	k-mer spectrum	Hash table	SE	Human, S. cerevisiae, C. elegans, M. acuminata	Bioinformatics	2017	C++	Ace, BFC, BLESS, Blue, Karect, Lighter, Musket, Pollux, RACER, Trowel	https://github.com/refresh-bio/RECKONER	KMC2, KMC tools	N/A	NO
SGA	0.10.15	FM-index search	FM-index	SE/PE	Human, C. elegans, E. coli,	Genome Research	2012	C++	Velvet, ABySS, SOAPdenovo, Quake, HITEC	https://github.com/jts/sga	Google sparse hash library, bamtools, zlib, jemalloc (optional), pysam, ruffus	31	NO
ShoRAH	1.1.0	clustering	not specified	SE	RNA viral population	BMC Bioinformatics	2011	C++, Python, Perl	no comparison	https://github.com/cbg-ethz/shorah	Biopython, NumPy, Perl, zlib, pkg-config, GNU scientific library	N/A	YES
KEC	1	k-mer spectrum	Hash table	SE	RNA viral population	BMC Bioinformatics	2012	Java	ShoRAH	http://alan.cs.gsu.edu/NGS/?q=content/pyrosequencing-error-correction-algorithm	FAMS; ClustalW2 or Muscle (optional)	25	NO

*MSA - multiple sequence alignment