Supplemental Table S1: Overview of selected *k*-mer counting tools and tool kits

The is not an exhaustive list of *k*-mer counting tools, but an overview of those that are either historically or currently impactful. Most of the tools have their own specialised utilities no other tools does - all of them were developed with a clear intention. For references, see Supplemental Materials.

Tool *Year*	*description*	*url*	*reference*
Jellyfish *2011*	*Very popular and easy to use* k-*mer counter, but substantially slower compared to more recent* k-*mer counters*	*https://github.com/gmarcais/Jellyfish*	*[7]*
Khmer *2015*	*A versatile* k-*mer suite that allow* k-*mer indexing, streaming and building de Brujin graphs*	*https://github.com/dib-lab/khmer*	*[8]*
KAT *2016*	k-*mer counter that is also able to compare two libraries or a library and a genome, powerful diagnostic plots of* k-*mer composition vs coverage*	*https://github.com/TGAC/KAT*	*[9]*
ntCard *2017*	*Very fast,* k-*mer cardinality estimator. The k-mer histogram is a fast approximation and limited to non-repetitive portion of the genome*	*https://github.com/bcgsc/ntCard*	*[10]*
KMC3 *2017*	*Very fast explicit* k-*mer with the capacity to calculate any arbitrary coverages users request by parameters; Interface is a bit more complex*	*https://github.com/refresh-bio/KMC*	*[11]*
Meryl *2020*	*A counter that also implements efficient operations between sets of* k-*mers, like union, intersection, subtraction. Used by Merqury.*	*https://github.com/marbl/meryl*	*[12]*
FASTK *2023*	*The fastest explicit* k-*mer counter, compatible with all the existing downstream tools; using a shortcut to aggregate all repetitive* k-*mers (explicitly counting only to 2^{16}x coverage).*	*https://github.com/thegenemyers/FASTK*	*[13,14]*