

Chinook salmon genome assembly pipeline

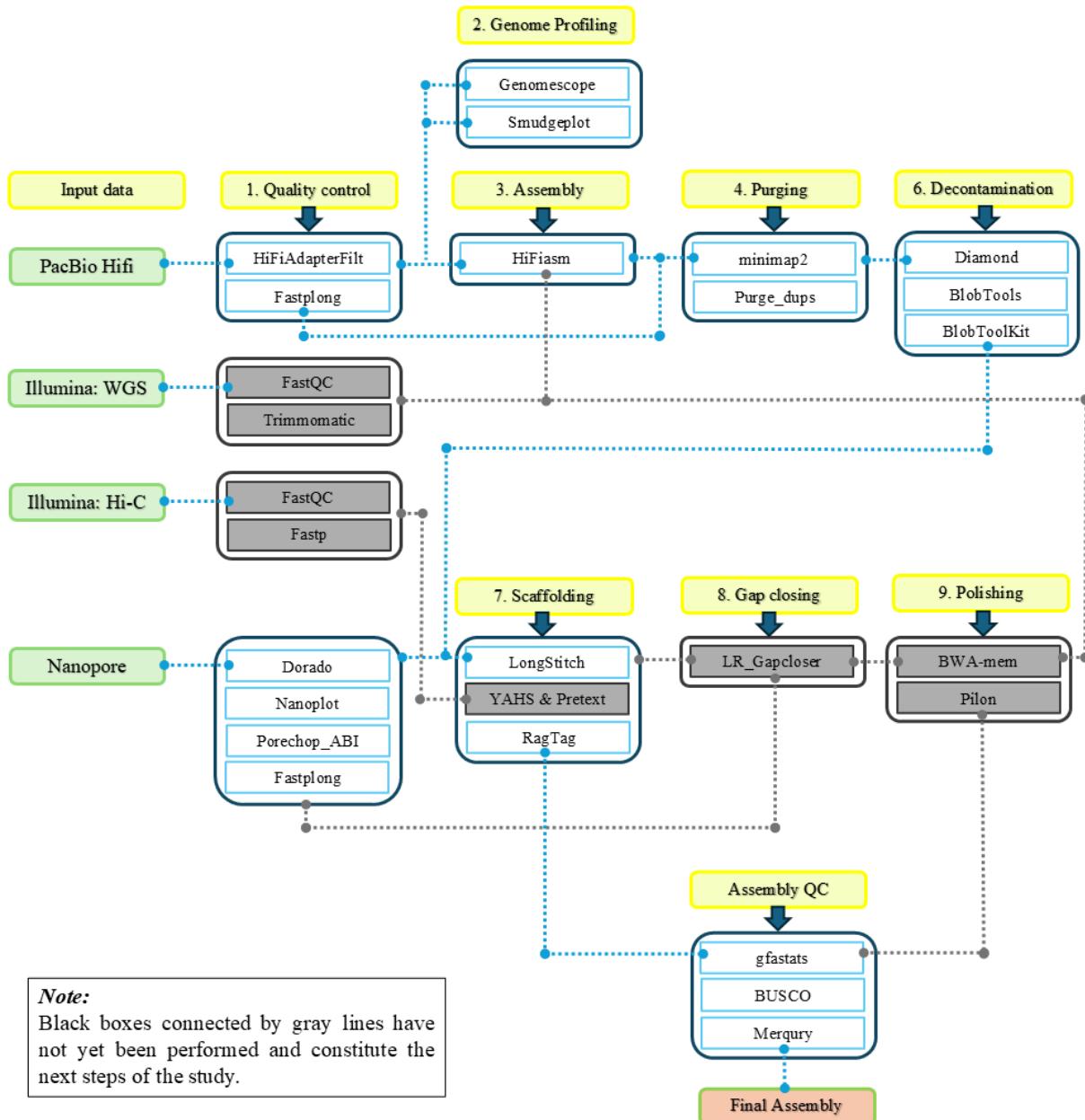


Table 1. List of softwares used to assemble the genome of Chinook salmon.

Step	Software	Version	Parameters	References
Quality control	HiFiAdapterFilt	v3.0.0	default	Sim et al., 2022
	Fastplong	v0.5.0	PacBio HiFi reads: -q 20, -l 5000 Nanopore reads: -q 10 -l, 10000	Chen, 2023
	Dorado	0.9.6+0949eb8d	basecaller --no-trim, --device cuda:all, --emit-fastq, --recursive dna_r10.4.1_e8.2_400bps_sup@v5.0.0	Oxford Nanopore Technologies, 2025
	Nanoplot		default	De Coster et al., 2018
	Porechop_ABI	0.5.0	-abi, --guess_adapter_only	Bonenfant et al., 2022
Genome profiling	Genomescope	v2.0	-k 51, -p 2	Ranallo-Benavidez et al., 2020
	Smudgeplot	v0.4.0	default	Ranallo-Benavidez et al., 2020
Assembly	HiFiasm	0.21.0-r686	--primary, -k 51	Cheng et al., 2021
Purging	Minimap2	2.30-r1287	read depth analysis: -I 4g, -x map-hifi self-alignment: -x asm5	Li, 2018
	Purge_dups	v1.2.6	cutoffs: -m 30, -u 200	Guan et al., 2020
Decontamination	Diamond	v2.0.13	blastx, --db diamondnr.dmnd, --eval 1e-5, --max-hsp 1, --max-target-seqs 1, -outfmt 6 qseqid sseqid bitscore, --more-sensitive	Buchfink et al., 2015
	BlobTools	v1.1.1	Taxify: -m prot.accession2taxid	Laetsch and Blaxter, 2017
	BlobToolKit	v4.4.4	default	Challis et al., 2020
Scaffolding	LongStitch	v1.0.5	k=32, w=500 (with seven rounds of scaffolding)	Coombi et al., 2021
	RagTag	v.2.1.0	default	Alonge et al., 2022
Assembly QC	Gfastats	v1.3.11	default	Formenti et al., 2022
	BUSCO	v6.0.0	-l actinopterygii_odb10, -m geno, --augustus	Tegenfeldt et al., 2025
	Mercury	v1.3	default	Rhie et al., 2020

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