**TextS1.** FALCON config file parameters

[General]

# list of files of the initial bas.h5 files

input\_fofn = input.fofn

input\_type = raw

#Here, we used FALCON’s ability to determine the required length cutoff (set length\_cutoff = -1) given a desired seed coverage and estimated genome size.

#80-fold seed coverage is the recommended level (according to PacBio) for Falcon-Unzip.

#We used a slightly high-end estimate of genome size, as suggested by PacBio.

length\_cutoff = -1

seed\_coverage = 80

genome\_size = 120000000

#The length cutoff used for seed reads usef for pre-assembly.

#PacBio recommends using a value of 1 to use all preassembled reads for assembly.

length\_cutoff\_pr = 1

#job\_type, sge\_options, and concurrent\_job numbers will be specific to the cluster environment used so are not given here.

pa\_HPCdaligner\_option = -v -B128 -t16 -M32 -e.70 -l4800 -s100 -k18 -h480 -w8

ovlp\_HPCdaligner\_option = -v -B128 -t16 -M32 -h1024 -e.96 -l2400 -s100 -k24

pa\_DBsplit\_option = -a -x500 -s200

ovlp\_DBsplit\_option = -a -x500 -s200

falcon\_sense\_option = --output\_multi --min\_idt 0.70 --min\_cov 4 --max\_n\_read 200 --n\_core 6

overlap\_filtering\_setting = --max\_diff 100 --max\_cov 200 --min\_cov 3 --bestn 10 --n\_core 24