

**MinION/PacBio raw read data**



**Demultiplexing raw read data**  
(minibar or qcat)



**Quality and size filtering**  
(Nanofilt)



## **NGSpeciesID**

**1**

**Read clustering**  
(isONclust)

**2**

**Consensus sequence generation**  
(SPOA)

**3**

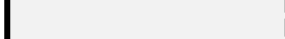
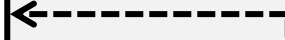
**Reverse complement merging**  
(Parasail)

**4**

**Consensus sequence polishing**  
(ONT: Medaka; ONT & PB: Racon)  
(optional)

**5**

**Primer detection and  
removal**  
(optional)



**Final consensus sequence**