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Supplemental information

Pan-genomic matching statistics

for targeted nanopore sequencing

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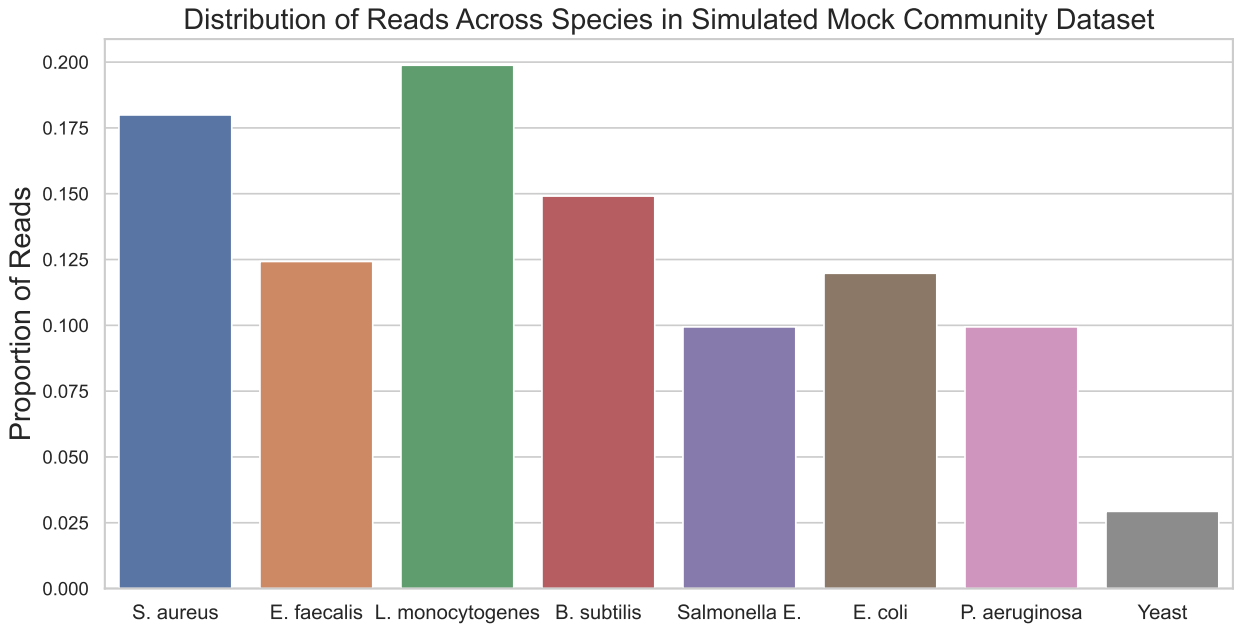
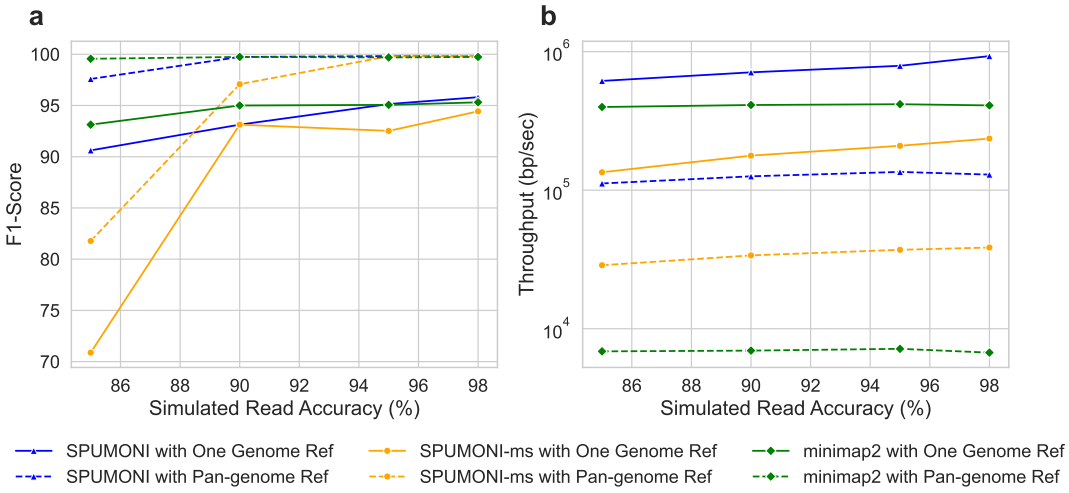


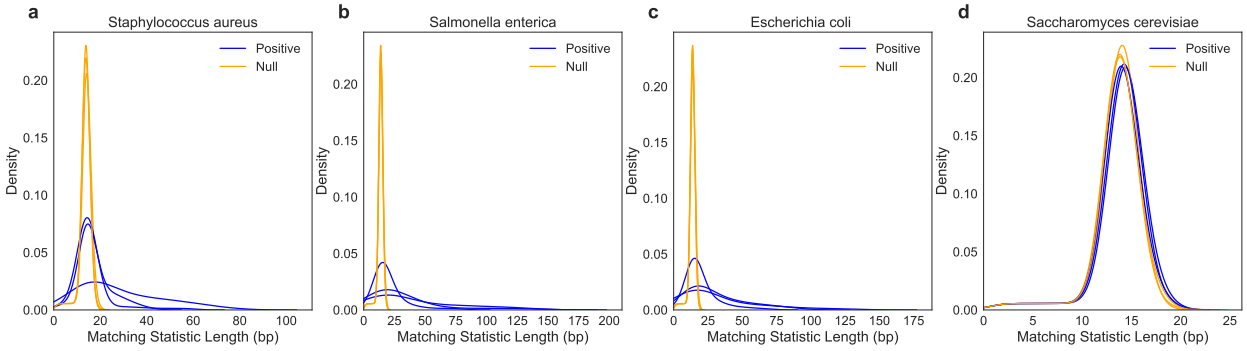
Supplementary Figure 1: Proportion of reads from each species in mock community in the simulated mock community dataset which is related to Section 2.3.2.

Number of Genomes Included in Each Mock Community Index		
Species\Reference:	One Genome Ref.	Pan-genome Ref.
Staphylococcus aureus	1	574
Enterococcus faecalis	1	49
Listeria monocytogenes	1	225
Bacillus subtitlis	1	165
Salmonella enterica	1	880
Escherichia coli	1	1370
Pseudomonas aeruginosa	1	274
Saccharomyces cerevisiae	1	1

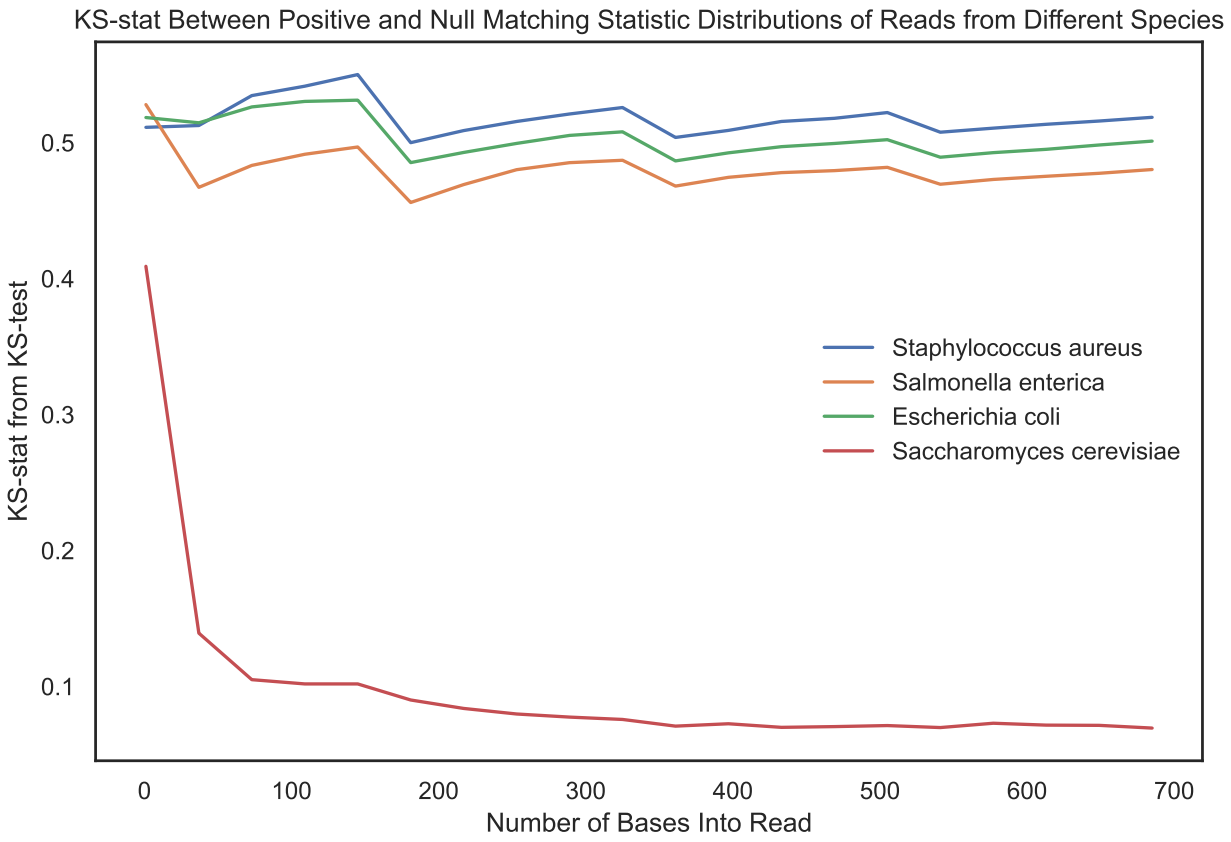
Table S1: Number of genomes for each species in the different references used for the mock community experiment which is related to Section 2.3.2.



Supplementary Figure 2: Visualization of (a) F_1-score, (b) throughput with varying simulated base-call accuracies which is related to Table 2.



Supplementary Figure 3: Distribution of matching statistics against positive and null indexes for three randomly chosen reads of (a) *Staphylococcus aureus*, (b) *Salmonella enterica*, (c) *Escherichia coli*, and (d) *Saccharomyces cerevisiae*. Each density curve is based on the first 720 bases ($\sim$ 1.6 seconds) of ReadUntil data for each read, which is related to Section 2.3.3.



Supplementary Figure 4: Each line represents the average of the Kolmogorov-Smirnov statistic (KS-stat) across all reads from that respective species in the mock community. The figure (related to Section 2.3.3) shows that for bacterial species (*Staphylococcus aureus*, *Salmonella enterica*, and *Escherichia coli*) the KS-stat is relatively larger at ~ 0.5 since the reads are matching to sequence in the positive index. While for the yeast reads, the KS-stat is small at ~ 0.1 since the distribution of positive and null matching statistics are quite similar to each other.

Algorithm 1 Matching Statistics

given text T and a pattern p
//first pass: get pointers
$j \leftarrow 1, pos \leftarrow SA[j]$
for $i \leftarrow p.len$ to 1 **do**
  if $p[i] \neq \mathrm{BWT}[j]$ **then**
    if $j < \mathrm{Thr}(j, p[i])$ **then**
      $j \leftarrow \mathrm{BWT.pred}(j, p[i])$
    else
      $j \leftarrow \mathrm{BWT.succ}(j, p[i])$
    $pos \leftarrow \mathrm{SA}[j] - 1$
  else
    $pos \leftarrow pos - 1$
  $pointers[i] \leftarrow pos$
  $j \leftarrow \mathrm{LF}(j)$
//second pass: get lengths
$\ell \leftarrow 0$
for $i \leftarrow 1$ to $pointers.len$ **do**
  $pos \leftarrow pointers[i] + \ell, j \leftarrow i + \ell$
  while $j < p.len$ **and** $p[j] = T[pos]$ **do**
    $\ell \leftarrow \ell + 1$
    $pos \leftarrow pos + 1, j \leftarrow j + 1$
  $\mathrm{ms}[i] \leftarrow \ell$
  $\ell \leftarrow \max(\ell - 1, 0)$
Return ms

Algorithm 2 Pseudo Matching Lengths

given text T and a pattern p
//first pass: get pointers and pmls
$j \leftarrow 1, \ell \leftarrow 0$
for $i \leftarrow p.len$ to 1 **do**
  if $p[i] \neq \mathrm{BWT}[j]$ **then**
    if $j < \mathrm{Thr}(j, p[i])$ **then**
      $j \leftarrow \mathrm{BWT.pred}(j, p[i])$
    else
      $j \leftarrow \mathrm{BWT.succ}(j, p[i])$
    $\ell \leftarrow 0$
  else
    $\ell \leftarrow \ell + 1$
  $\mathrm{pml}[i] \leftarrow \ell$
  $j \leftarrow \mathrm{LF}(j)$
Return pml

Supplementary Figure 5: Matching statistics (Algorithm 1) and Pseudo Matching Lengths (Algorithm 2) computation using the thresholds (which is related to Section 11.2.2). Given an array a, $a.len$ refers to the length of the array. Given a position j in the BWT, $\mathrm{LF}(j)$ is the LF-mapping, SA is the suffix array sampled at run boundaries, $\mathrm{BWT.pred}(j, c)$ is the position in the BWT of the first character c preceding position j, $\mathrm{BWT.succ}(j, c)$ is the position in the BWT of the first character c following position j, $\mathrm{Thr}(j, c)$ is the position of the threshold for the character c between the run of c preceding and following position j in the BWT. To avoid overloading the notation, we consider the variable pos to be $(pos \mod T.len) + 1$. Furthermore, note that if $\mathrm{BWT.pred}(j, c)$, the threshold value is guaranteed to be smaller than or equals to j, i.e., $\mathrm{Thr}(j, c) = 0$. Similarly, if $\mathrm{BWT.succ}(j, c)$, the threshold value is guaranteed to be greater than j, i.e., $\mathrm{Thr}(j, c) = T.len + 1$.