Human dataset

- Mapping by minimap2
- Aligned to hg19
- Detecting poly(A) tails with LoRTIA
  - Potential poly(A) sites
  - Calculating A-content
  - Filtering poly(A) sites
  - Human TESs and artefacts

HCMV dataset

- Mapping by minimap2
- Aligned to LT907985

**b**

Genome

- Highest peaks in ±10nt window
  - AND
  - At least 0.1% of overlapping reads
  - AND
  - At least 2 reads

**c**

<table>
<thead>
<tr>
<th>Genome</th>
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<th>Number of As: 4</th>
</tr>
</thead>
<tbody>
<tr>
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<td>1 2 1 0 1</td>
<td>A A A A G T C G G A A</td>
</tr>
</tbody>
</table>

**d**

More reads end in not A-rich regions than in A-rich regions OR Higher minimum percentage of overlapping read in more A-rich regions