## Summary Numbers

<table>
<thead>
<tr>
<th>Callset</th>
<th>SNPs</th>
<th>indels</th>
<th>MNPs</th>
<th>others</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>ts/tv</td>
<td>(1st ALT)</td>
<td>n</td>
</tr>
<tr>
<td>medtr</td>
<td>48,997,264</td>
<td>1.30</td>
<td>1.37</td>
<td>4,845,927</td>
</tr>
</tbody>
</table>

* frameshift ratio: out/(out+in)

<table>
<thead>
<tr>
<th>Callset</th>
<th>singletons (AC=1)</th>
<th>multiallelic</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>SNPs</td>
<td>ts/tv</td>
</tr>
<tr>
<td>medtr</td>
<td>12.8%</td>
<td>0.79</td>
</tr>
</tbody>
</table>

Ts/Tv by sample
Hets vs non-ref Homs by sample
Singletons by sample (hets and homs)
Average depth by sample
Number of SNPs by sample
Number of indels by sample
Ts/Tv stratified by QUAL

![Graph](image)

- **Cumulative ts/tv**
- **Per 1% bins**

**Axes:**
- Y-axis: Ts/Tv
- X-axis: Number of sites (sorted by QUAL, descending)

**Values:**
- Y-axis range: 0 to 2.5
- X-axis range: 0 to 1e7
Indel distribution
Fraction of alternate indel allele
Depth distribution
Number of HETs by AF
Substitution types

![Substitution types chart](chart.png)