**Table**. Single nucleotide polymorphisms by type and region for resequencing data inferred by SnpEff.

Note SNPs can be counted in two or more categories.

<table>
<thead>
<tr>
<th>Category/Impact</th>
<th>Number of changes</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coding</td>
<td></td>
</tr>
<tr>
<td>Missense</td>
<td>173,485</td>
</tr>
<tr>
<td>Nonsense</td>
<td>2,520</td>
</tr>
<tr>
<td>Silent</td>
<td>247,674</td>
</tr>
<tr>
<td>Noncoding</td>
<td></td>
</tr>
<tr>
<td>Upstream 5'</td>
<td>1,676,362</td>
</tr>
<tr>
<td>Downstream 3'</td>
<td>1,692,488</td>
</tr>
<tr>
<td>Intergenic</td>
<td>1,821,797</td>
</tr>
</tbody>
</table>