Summary

<table>
<thead>
<tr>
<th>Genome</th>
<th>ppersica139</th>
</tr>
</thead>
<tbody>
<tr>
<td>Date</td>
<td>2012-08-01 21:59</td>
</tr>
<tr>
<td>SnpEff version</td>
<td>SnpEff 3.0c (build 2012-07-30), by Pablo Cingolani</td>
</tr>
<tr>
<td>Command line arguments</td>
<td>SnpEff  ppersica139 -i txt /snpEff_3_0/SNPs.txt -o txt -v</td>
</tr>
<tr>
<td>Warnings</td>
<td>0</td>
</tr>
<tr>
<td>Number of lines (input file)</td>
<td>1,109</td>
</tr>
<tr>
<td>Number of variants (before filter)</td>
<td>1,109</td>
</tr>
<tr>
<td>Number of variants filtered out</td>
<td>0</td>
</tr>
<tr>
<td>Number of not variants (i.e. reference equals alternative)</td>
<td>0</td>
</tr>
<tr>
<td>Number of variants processed (i.e. after filter and non-variants)</td>
<td>1,109</td>
</tr>
</tbody>
</table>
| Number of known variants (i.e. non-empty ID) | 0 (0%)
| Number of effects | 2,163 |
| Genome total length | 227,252,106 |
| Genome effective length | 219,490,920 |

Change rate

<table>
<thead>
<tr>
<th>Change rate details</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chromosome</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
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<tr>
<td>4</td>
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<td>5</td>
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<td>6</td>
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<td>7</td>
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<td>15</td>
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<td>53</td>
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<tr>
<td>62</td>
</tr>
<tr>
<td>127</td>
</tr>
<tr>
<td>Total</td>
</tr>
</tbody>
</table>

Number changes by type

<table>
<thead>
<tr>
<th>Type</th>
<th>Total</th>
<th>Homo</th>
<th>Hetero</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNP</td>
<td>1,109</td>
<td>1,109</td>
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</tr>
<tr>
<td>MNP</td>
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<td>0</td>
<td>0</td>
</tr>
<tr>
<td>INS</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>DEL</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>MIXED</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Interval</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Total</td>
<td>1,109</td>
<td>1,109</td>
<td>0</td>
</tr>
</tbody>
</table>

Number of effects by impact

<table>
<thead>
<tr>
<th>Impact</th>
<th>Type (alphabetical order)</th>
<th>Count</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>HIGH</td>
<td></td>
<td>1</td>
<td>0.046%</td>
</tr>
<tr>
<td>LOW</td>
<td></td>
<td>161</td>
<td>7.443%</td>
</tr>
<tr>
<td>MODERATE</td>
<td></td>
<td>122</td>
<td>5.64%</td>
</tr>
<tr>
<td>MODIFIER</td>
<td></td>
<td>1,879</td>
<td>86.87%</td>
</tr>
</tbody>
</table>

Number of effects by functional class

<table>
<thead>
<tr>
<th>Functional class</th>
<th>Type (alphabetical order)</th>
<th>Count</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>MISSENSE</td>
<td></td>
<td>122</td>
<td>43.262%</td>
</tr>
<tr>
<td>NONSENSE</td>
<td></td>
<td>1</td>
<td>0.355%</td>
</tr>
<tr>
<td>SILENT</td>
<td></td>
<td>159</td>
<td>56.383%</td>
</tr>
</tbody>
</table>

Missense / Silent ratio: 0.7673

Number of effects by type and region

<table>
<thead>
<tr>
<th>Type</th>
<th>Region</th>
</tr>
</thead>
<tbody>
<tr>
<td>HIGH</td>
<td></td>
</tr>
<tr>
<td>LOW</td>
<td></td>
</tr>
<tr>
<td>MODERATE</td>
<td></td>
</tr>
<tr>
<td>MODIFIER</td>
<td></td>
</tr>
<tr>
<td>Interval</td>
<td></td>
</tr>
<tr>
<td>DOWNSTREAM</td>
<td>787</td>
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<tr>
<td>INTERGENIC</td>
<td>79</td>
</tr>
<tr>
<td>INTRON</td>
<td>294</td>
</tr>
<tr>
<td>NON_SYNONYMOUS_CODING</td>
<td>122</td>
</tr>
<tr>
<td>START_GAINED</td>
<td>2</td>
</tr>
<tr>
<td>STOP_GAINED</td>
<td>1</td>
</tr>
<tr>
<td>SYNONYMOUS_CODING</td>
<td>159</td>
</tr>
<tr>
<td>UPSTREAM</td>
<td>683</td>
</tr>
<tr>
<td>UTR_3_PRIME</td>
<td>30</td>
</tr>
<tr>
<td>UTR_5_PRIME</td>
<td>8</td>
</tr>
</tbody>
</table>
### Base changes (SNPs)

#### Ts/Tv (transitions / transversions)

**Note:** Only SNPs are used for this statistic.

**Note:** This Ts/Tv ratio is a 'raw' ratio. Some people prefer to use a ratio of rates, not observed events. In that case, you need to multiply by 2.0 (since there are twice as many possible transitions than transversions, E[Ts/Tv] ratio is twice the ratio of events).

### Frequency of alleles

**Note:** Number of times an allele appears once (singleton), twice (doubletons), etc.

### Codon changes

How to read this table:
- Rows are reference codons and columns are changed codons. E.g. Row 'AAA' column 'TAA' indicates how many 'AAA' codons have been replaced by 'TAA' codons.
- Red background colors indicate that more changes happened (heat-map).
- Diagonals are indicated using grey background color
- **WARNING:** This table may include different translation codon tables (e.g. mammalian DNA and mitochondrial DNA).

### Amino acid changes

How to read this table:
- Rows are reference amino acids and columns are changed amino acids. E.g. Row 'A' column 'E' indicates how many 'A' amino acids have been replaced by 'E' amino acids.
- Red background colors indicate that more changes happened (heat-map).
- Diagonals are indicated using grey background color
- WARNING: This table may include different translation codon tables (e.g. mammalian DNA and mitochondrial DNA).

|    | A | C | D | E | F | G | H | I | K | L | M | N | P | Q | R | S | T | V | W | Y |
| A  | 17| 1 | 1 | 1 | 3 | 5 | 2 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| C  | 1 | 1 | 1 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| D  | 7 | 4 | 1 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| E  | 1 | 4 | 1 | 2 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| F  | 5 | 1 | 1 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| G  | 1 | 15| 1 | 1 | 1 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| H  | 3 | 3 | 1 | 1 | 1 | 1 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| I  | 6 | 1 | 2 | 1 | 1 | 3 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| K  | 3 | 8 | 1 | 4 | 2 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| L  | 2 | 22| 2 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| M  | 1 | 1 | 2 | 2 | 2 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| N  | 1 | 2 | 2 | 6 | 2 | 2 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| P  | 1 | 1 | 10| 1 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Q  | 1 | 2 | 2 | 7 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| R  | 1 | 2 | 4 | 2 | 7 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| S  | 2 | 1 | 2 | 2 | 1 | 17|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| T  | 3 | 1 |   | 13|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| V  | 5 | 1 | 2 | 4 | 3 | 13|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| W  | 1 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| Y  | 1 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

**Changes by chromosome**

**Changes histogram: 1**

<table>
<thead>
<tr>
<th>Changes/100Kb</th>
<th>0</th>
<th>2</th>
<th>4</th>
<th>6</th>
<th>8</th>
<th>10</th>
<th>12</th>
<th>14</th>
</tr>
</thead>
<tbody>
<tr>
<td>Position</td>
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<td>2000000</td>
<td>3000000</td>
<td>4000000</td>
<td>4500000</td>
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</tr>
</tbody>
</table>

**Chromosome: 1**

**Changes histogram: 2**

<table>
<thead>
<tr>
<th>Changes/100Kb</th>
<th>0.5</th>
<th>1</th>
<th>1.5</th>
<th>2</th>
<th>2.5</th>
<th>3</th>
<th>3.5</th>
<th>4</th>
<th>4.5</th>
<th>5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Position</td>
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<td>3500000</td>
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<td>13000000</td>
<td>17000000</td>
<td>20350000</td>
<td>23700000</td>
<td>28700000</td>
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</tr>
</tbody>
</table>

**Chromosome: 2**
Details by gene

Here you can find a tab-separated table.