<table>
<thead>
<tr>
<th>Derivative chromosome junctions</th>
<th>Patient-derived(^1) (No.)</th>
<th>Current study(^2) (No.)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Percent with insertions(^3)</td>
<td>29.1% (46/158)</td>
<td>17.9% (15/84)</td>
<td>0.05</td>
</tr>
<tr>
<td>Mean insertion length ± SD</td>
<td>5.8 ± 8.9 bp</td>
<td>26.9 ± 50.3 bp</td>
<td>0.04</td>
</tr>
<tr>
<td>Median insertion length</td>
<td>3 bp</td>
<td>5.3 bp</td>
<td></td>
</tr>
<tr>
<td>Percent with microhomology (≥1 bp)(^4)</td>
<td>64.4% (56/87)</td>
<td>79.8% (55/69)</td>
<td>0.03</td>
</tr>
<tr>
<td>Mean microhomology length ± SD</td>
<td>1.36 ± 1.43 bp</td>
<td>1.94 ± 1.35 bp</td>
<td>NS</td>
</tr>
<tr>
<td>Median microhomology length</td>
<td>1 bp</td>
<td>2 bp</td>
<td></td>
</tr>
</tbody>
</table>

\(^1\)Data compiled from tumors from 79 patients comprising the 74 leukemias and 5 sarcomas used in Table 1A, for a total of 158 derivative chromosomes. Data from the 63 lymphomas were excluded as most junctions contained insertions that were ascribed to be P nucleotides.

\(^2\)Data compiled from the 43 neo+ mouse ES cell clones from the current study, excluding 2 complex junctions (p5rE18-t7 der(17) and p5rE18-t37 der(17)).

\(^3\)Insertions include duplications, templated and nontemplated nucleotides and vector sequence.

\(^4\)Only includes junctions without insertions, since microhomology use could not be evaluated in those with insertions. In addition, some junctions could not be evaluated for microhomology use because insufficient sequence information was provided.

References


