## Table S5. Genomic integrity index predicts downstream molecular analyses in single CTCs and WBCs.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Molecular assay</th>
<th>n</th>
<th>GII 0*</th>
<th>GII 1*</th>
<th>GII 2*</th>
<th>GII 3*</th>
<th>GII 4*</th>
<th>P Value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>CTCs</td>
<td>PIK3CA Exon 9</td>
<td>261</td>
<td>5/20 (25.0%)</td>
<td>12/20 (60.0%)</td>
<td>36/48 (75.0%)</td>
<td>67/77 (87.0%)</td>
<td>93/96 (96.9%)</td>
<td>&lt;0.00001</td>
</tr>
<tr>
<td></td>
<td>PIK3CA Exon 20</td>
<td>261</td>
<td>7/20 (35.0%)</td>
<td>16/20 (80.0%)</td>
<td>41/48 (85.4%)</td>
<td>73/77 (94.8%)</td>
<td>93/96 (96.9%)</td>
<td>&lt;0.00001</td>
</tr>
<tr>
<td></td>
<td>PIK3CA complete</td>
<td>261</td>
<td>3/20 (15.0%)</td>
<td>11/20 (55.0%)</td>
<td>33/48 (68.8%)</td>
<td>64/77 (83.1%)</td>
<td>91/96 (94.8%)</td>
<td>&lt;0.00001</td>
</tr>
<tr>
<td></td>
<td>ERBB2 qPCR</td>
<td>246</td>
<td>3/11 (27.3%)</td>
<td>8/16 (50.0%)</td>
<td>28/47 (59.6%)</td>
<td>65/77 (84.4%)</td>
<td>88/95 (92.6%)</td>
<td>&lt;0.00001</td>
</tr>
<tr>
<td></td>
<td>aCGH</td>
<td>40</td>
<td>not assessed</td>
<td>not assessed</td>
<td>3/4 (75.0%)</td>
<td>6/8 (75.0%)</td>
<td>28/28 (100%)</td>
<td>0.023</td>
</tr>
<tr>
<td>WBCs</td>
<td>PIK3CA Exon 9</td>
<td>122</td>
<td>2/3 (66.7%)</td>
<td>2/5 (40.0%)</td>
<td>12/14 (85.7%)</td>
<td>35/40 (87.5%)</td>
<td>53/60 (88.3%)</td>
<td>0.048</td>
</tr>
<tr>
<td></td>
<td>PIK3CA Exon 20</td>
<td>122</td>
<td>1/3 (33.3%)</td>
<td>2/5 (40.0%)</td>
<td>14/14 (100%)</td>
<td>36/40 (90.0%)</td>
<td>56/60 (93.3%)</td>
<td>0.0003</td>
</tr>
<tr>
<td></td>
<td>PIK3CA complete</td>
<td>122</td>
<td>1/3 (33.3%)</td>
<td>1/5 (20.0%)</td>
<td>12/14 (85.7%)</td>
<td>33/40 (82.5%)</td>
<td>50/60 (83.3%)</td>
<td>0.0004</td>
</tr>
<tr>
<td></td>
<td>ERBB2 qPCR</td>
<td>105</td>
<td>0/1</td>
<td>0/2</td>
<td>13/14 (92.9%)</td>
<td>30/35 (85.7%)</td>
<td>48/53 (90.6%)</td>
<td>0.00036</td>
</tr>
<tr>
<td></td>
<td>aCGH</td>
<td>10</td>
<td>not assessed</td>
<td>not assessed</td>
<td>1/1 (100.0%)</td>
<td>1/1 (100.0%)</td>
<td>8/8 (100%)</td>
<td>not assessed</td>
</tr>
</tbody>
</table>

* GII = Genome integrity index; GII 0: no fragment detected by QC2-assay; GII 1: QC2-assay negative for the three long markers, but KRAS fragment detected; GII 2: 1/3 long MseI fragments of QC2-assay detected; GII 3: 2/3 long MseI fragments of QC2-assay detected; GII 4: 3/3 long MseI fragments of QC2-assay detected

§ Tested by Chi-square