<table>
<thead>
<tr>
<th>Cancer Type</th>
<th>Sample Count</th>
<th>Total Somatic SNVs</th>
<th>DNA Only Method</th>
<th>Triple BAM Method</th>
<th>RNA Rescue Calls</th>
<th>RNA Rescue Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>Uterine Corpus Endometrioid Carcinoma</td>
<td>177</td>
<td>27900</td>
<td>27390</td>
<td>6325</td>
<td>510</td>
<td>2%</td>
</tr>
<tr>
<td>Lung Adenocarcinoma</td>
<td>263</td>
<td>85044</td>
<td>79347</td>
<td>21484</td>
<td>5697</td>
<td>7%</td>
</tr>
<tr>
<td>Kidney Chromophobe</td>
<td>66</td>
<td>4163</td>
<td>3957</td>
<td>1042</td>
<td>206</td>
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</tr>
<tr>
<td>Thyroid Carcinoma</td>
<td>430</td>
<td>20849</td>
<td>19836</td>
<td>2882</td>
<td>1013</td>
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<tr>
<td>Skin Cutaneous Melanoma</td>
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<td>584431</td>
<td>573925</td>
<td>70091</td>
<td>10498</td>
<td>2%</td>
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<tr>
<td>Low-Grade Glioma</td>
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<td>13852</td>
<td>12837</td>
<td>3926</td>
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<tr>
<td>Prostate Adenocarcinoma</td>
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<td>14630</td>
<td>12653</td>
<td>4631</td>
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<tr>
<td>Kidney Renal Papillary Cell Carcinoma</td>
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<td>28662</td>
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<td>1316</td>
<td>5%</td>
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<tr>
<td>Adrenocortical Carcinoma</td>
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<td>9891</td>
<td>9748</td>
<td>1863</td>
<td>143</td>
<td>2%</td>
</tr>
<tr>
<td>Cancer Type</td>
<td>Sample Count</td>
<td>Total Somatic SNVs</td>
<td>DNA Only Method</td>
<td>Triple BAM Method</td>
<td>RNA Rescue Calls</td>
<td>RNA Rescue Percent</td>
</tr>
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<tr>
<td>Uterine Carcinosarcoma</td>
<td>57</td>
<td>8987</td>
<td>8776</td>
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<tr>
<td>Stomach Adenocarcinoma</td>
<td>327</td>
<td>134,895</td>
<td>127,405</td>
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</tr>
<tr>
<td>Liver Hepatocellular Carcinoma</td>
<td>236</td>
<td>32,854</td>
<td>32,113</td>
<td>7,056</td>
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</tr>
<tr>
<td>Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma</td>
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<td>62,252</td>
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</tr>
<tr>
<td>Pheochromocytoma and Paraganglioma</td>
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<td>2,993</td>
<td>2,820</td>
<td>761</td>
<td>173</td>
<td>6%</td>
</tr>
<tr>
<td>Pancreatic Adenocarcinoma</td>
<td>137</td>
<td>23,692</td>
<td>22,850</td>
<td>9,653</td>
<td>842</td>
<td>4%</td>
</tr>
</tbody>
</table>

**Table S1: Summary of TCGA samples analyzed by RADIA.** RADIA has been run on over 3,300 TCGA samples across 15 different types of cancer. The RNA Rescue mutations make up two to seven percent of the total somatic mutations across the 15 types of cancer. Variant Call Format (VCF) and Mutation Annotation Format (MAF) files can be downloaded from the TCGA Data Portal (https://tcga-data.nci.nih.gov/tcga/). Open-access somatic MAFs can be visualized and downloaded via the UCSC Cancer Browser (https://genome-cancer.ucsc.edu/).