Supplementary Table 1. PCR primers for mutation analysis

<table>
<thead>
<tr>
<th>Gene</th>
<th>exon</th>
<th>Forward primer sequence</th>
<th>Reverse primer sequence</th>
<th>Length (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>SF3B1</td>
<td>exon 14</td>
<td>5'‐AAGGCGGAGAGATCATTTCTAA‐3'</td>
<td>5'‐CTTCTAAGATGTGGCAAGATGG‐3'</td>
<td>402</td>
</tr>
<tr>
<td></td>
<td>exon 15</td>
<td>5'‐AGGTAATGTGAGCATTAA‐3'</td>
<td>5'‐AGCAGCCAAACCCTATTTTT‐3'</td>
<td>298</td>
</tr>
<tr>
<td>U2AF1</td>
<td>exon 2</td>
<td>5'‐TGCTGCTGACATATCCATGT‐3'</td>
<td>5'‐AGTCGATGACCTGCTCCT‐3'</td>
<td>324</td>
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<tr>
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<td>exon 7</td>
<td>5'‐ATTAAAGCGTGGATGGCAAG‐3'</td>
<td>5'‐ATGCAATGATTGCGAGAAGC‐3'</td>
<td>314</td>
</tr>
<tr>
<td>SRSF2</td>
<td>exon 1</td>
<td>5'‐CGGAAGGCAACTGCTGAGA‐3'</td>
<td>5'‐GTCCCTGACGTCCTTTAC‐3'</td>
<td>476</td>
</tr>
</tbody>
</table>

Supplementary Figure 1. Cumulative incidences of AML progression were compared in patients with or without mutations of SF3B1 (A), U2AF1 (B), or SRSF2 (C). The results of the statistical analysis ($P$ value) are shown on each panel.
Supplemental Figure 1

A. SF3B1

- Wild type
- Mutation

Number at risk
Wild type: 91
Mutation: 15

B. U2AF1

- Wild type
- Mutation

Number at risk
Wild type: 96
Mutation: 8

C. SRSF2

- Wild type
- Mutation

Number at risk
Wild type: 94
Mutation: 10

CI of AML progression

Days

P = 0.229

P = 0.611

P = 0.534