SOLiD™ Overview

SOLiD™ Sequencing involves the serial ligation of probes in which a dye reports the subset of four possible dibase pairs (5' to 3') is ideal as it enables fragment library paired end sequencing. To this end, novel ligation chemistries were developed to support 5' to 3' read lengths of up to 35 bases. This paired end sequencing technology will be incorporated into the SOLiD™ V4 platform, increasing effective read length, maximizing throughput per run, and meeting relevant research needs, such as whole genome studies.

Paired End Sequencing on the SOLiD™ Platform

A.) 5'-phosphorylated primer is hybridized to the adapter region of the templates to be sequenced; B.) Fluorophore at the 1st and 2nd positions from the ligation junction. SOLiD™ Sequencing in the forward direction involves: F.) 3'-hydroxylated primer is hybridized to the adapter region of the templates to be sequenced; G.) Ligation of dye-labeled probe to primer extending from bead; H.) Cleavage, etc.; I.) The 3' phosphate is removed for the next round of ligation; J.) Additional cycles of ligation, cap, image, repeat ligate.

Schematic of Paired End SOLiD™ Sequencing

Paired End Sequencing Throughput

Paired End Sequencing Human Genome

DNA Fragment - 200 Bases

Figure 1: Paired end sequencing on the SOLiD™ platform. Plotted is the % of reads per template for forward reads (F3 Adapter) and reverse reads (F5 Adapter). Paired end sequencing is shown to increase effective read length, maximizing throughput per run, and meeting relevant research needs, such as whole genome studies.

Figure 2: Pairing statistics for paired end sequencing on the SOLiD™ platform. The % of reads per template for forward reads (F3 Adapter) and reverse reads (F5 Adapter) is plotted for different adapter sizes. Paired end sequencing is shown to increase effective read length, maximizing throughput per run, and meeting relevant research needs, such as whole genome studies.

Distribution of Small Insertions

Figure 3: Distribution of small insertions (1-3 bp) in dbSNP. The % of reads per template for forward reads (F3 Adapter) and reverse reads (F5 Adapter) is plotted for different adapter sizes. Paired end sequencing is shown to increase effective read length, maximizing throughput per run, and meeting relevant research needs, such as whole genome studies.

Distribution of Small Deletions

Figure 4: Distribution of small deletions (1-3 bp) in dbSNP. The % of reads per template for forward reads (F3 Adapter) and reverse reads (F5 Adapter) is plotted for different adapter sizes. Paired end sequencing is shown to increase effective read length, maximizing throughput per run, and meeting relevant research needs, such as whole genome studies.

Table 1: Summary of SNPs/Indels

<table>
<thead>
<tr>
<th>Length</th>
<th>Read Pairing</th>
<th>Pairing Rate</th>
<th>% in dbSNP</th>
<th># Insertions</th>
<th># Deletions</th>
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<tbody>
<tr>
<td>25mer (F5)</td>
<td>35 x 50</td>
<td>99.05%</td>
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<td>20000</td>
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<td>35mer (F5)</td>
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<td>50mer (F3)</td>
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CRISPR/Cas9 genome editing in human cells

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Summary of Identified SNPs/Indels

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