

**Supplemental Table 1. Redesigned dA-tailed adapters results in increased DS data yield.**

	<b>Adapter Overhang Base ID</b>	<b># Starting Reads</b>	<b># SSCS Reads</b>	<b># DCS Reads</b>	<b>Peak Family Size</b>	<b>% Increase in DCS Reads</b>
Sample 1	dA (old)	8.9x10 <sup>6</sup>	3.8x10 <sup>5</sup>	2.7x10 <sup>4</sup>	23	78%
	dT (new)	7.4x10 <sup>6</sup>	4.3x10 <sup>5</sup>	4.8x10 <sup>4</sup>	17	
Sample 2	dA (old)	5.6x10 <sup>6</sup>	9.4x10 <sup>5</sup>	6.4x10 <sup>4</sup>	6	500%
	dT (new)	7.8x10 <sup>6</sup>	1.7x10 <sup>6</sup>	3.2x10 <sup>5</sup>	5	

Data are from the same original DNA sample, but prepared and sequenced on two different days. The DNA was processed as described in the PROCEDURE section. A 20X molar excess of adapters was used for the ligation and 40 amoles of DNA was used for the PCR amplification step (PROCEDURE Step 38).