

Table S4

<i>Site</i>	<i>Number of sequences reads</i>	<i>Total number of bases (million)</i>	<i>Average read length</i>	<i>GenBank nonredundant proteins</i>
<i>Indian WWTP Downstream 1</i>	75,765	27.68	365	45.1%
<i>Indian WWTP Downstream 2</i>	44,281	16.16	365	40.2%
<i>Indian WWTP Downstream 3</i>	39,764	14.27	359	43.1%
<i>Indian WWTP Discharge site</i>	88,374	32.81	371	42.3%
<i>Indian WWTP Upstream 1</i>	53,045	19.10	360	44.9%
<i>Indian WWTP Upstream 2</i>	39,034	13.78	353	47.5%
<i>Swedish WWTP Downstream</i>	37,895	13.98	369	35.7%
<i>Swedish WWTP Upstream</i>	63,365	22.91	362	42.3%
<i>Total</i>	441,523	160.69	364	42.9%