

## Supplementary Information

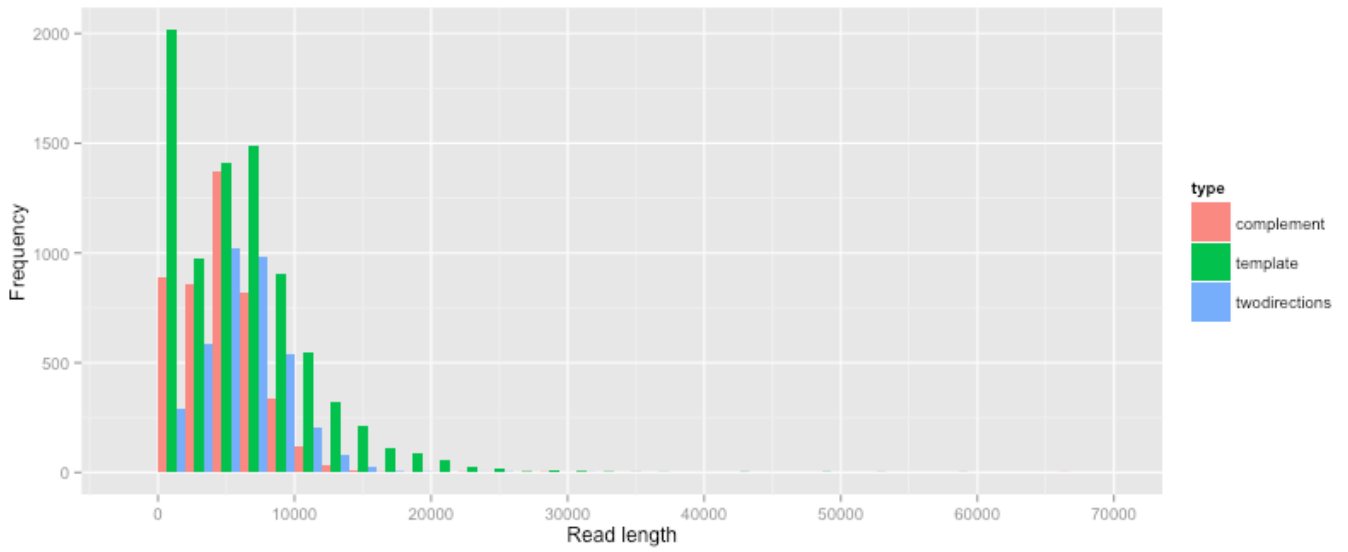
### *Supplementary Figure 1: Schematic of how the MinION reads were used to scaffold the Illumina contigs*



\*Chromosomal contig  Insertion sequence  Island contig  MinION read 

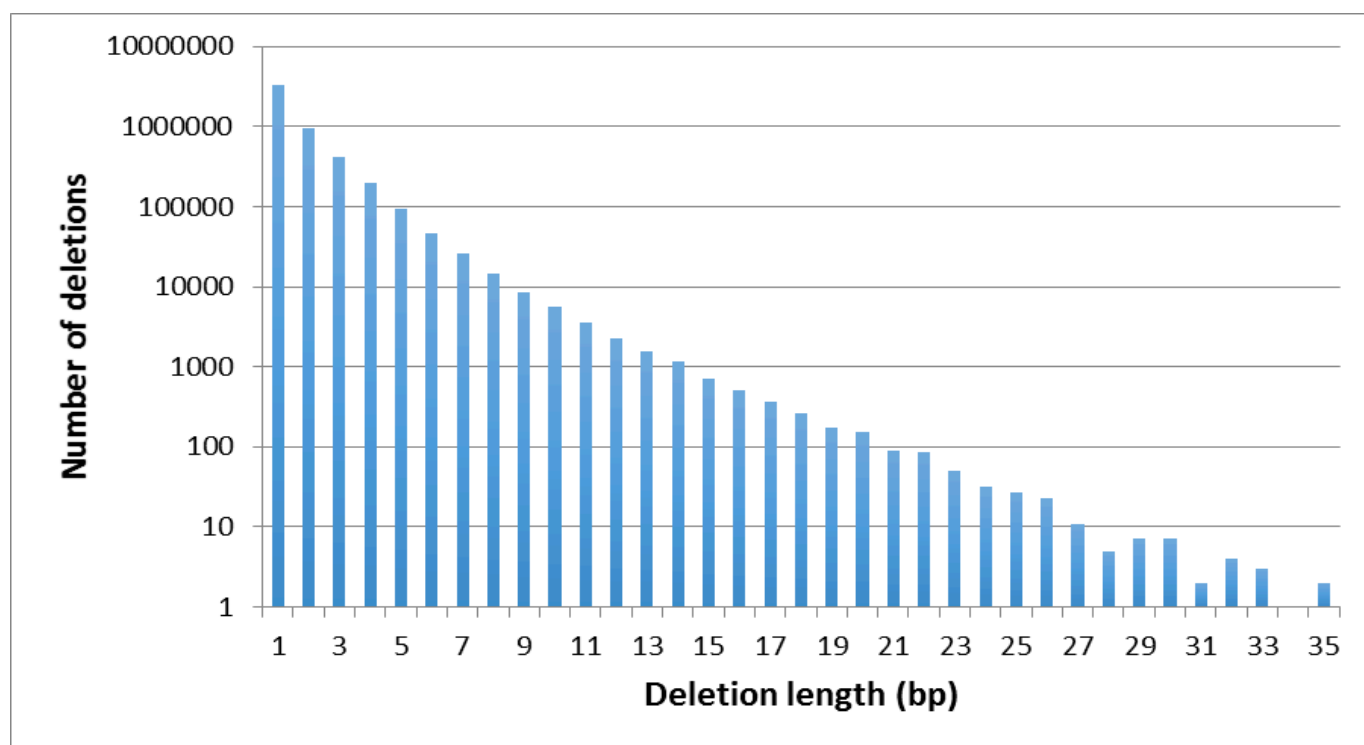
\*Chromosomal contigs flanking the island (15 kb and 65 kb) were identified based on similarity to IncHI1 plasmids on the 5' or 3' terminus

**Supplementary Figure 2: Read length histogram of MinION data divided by read type**

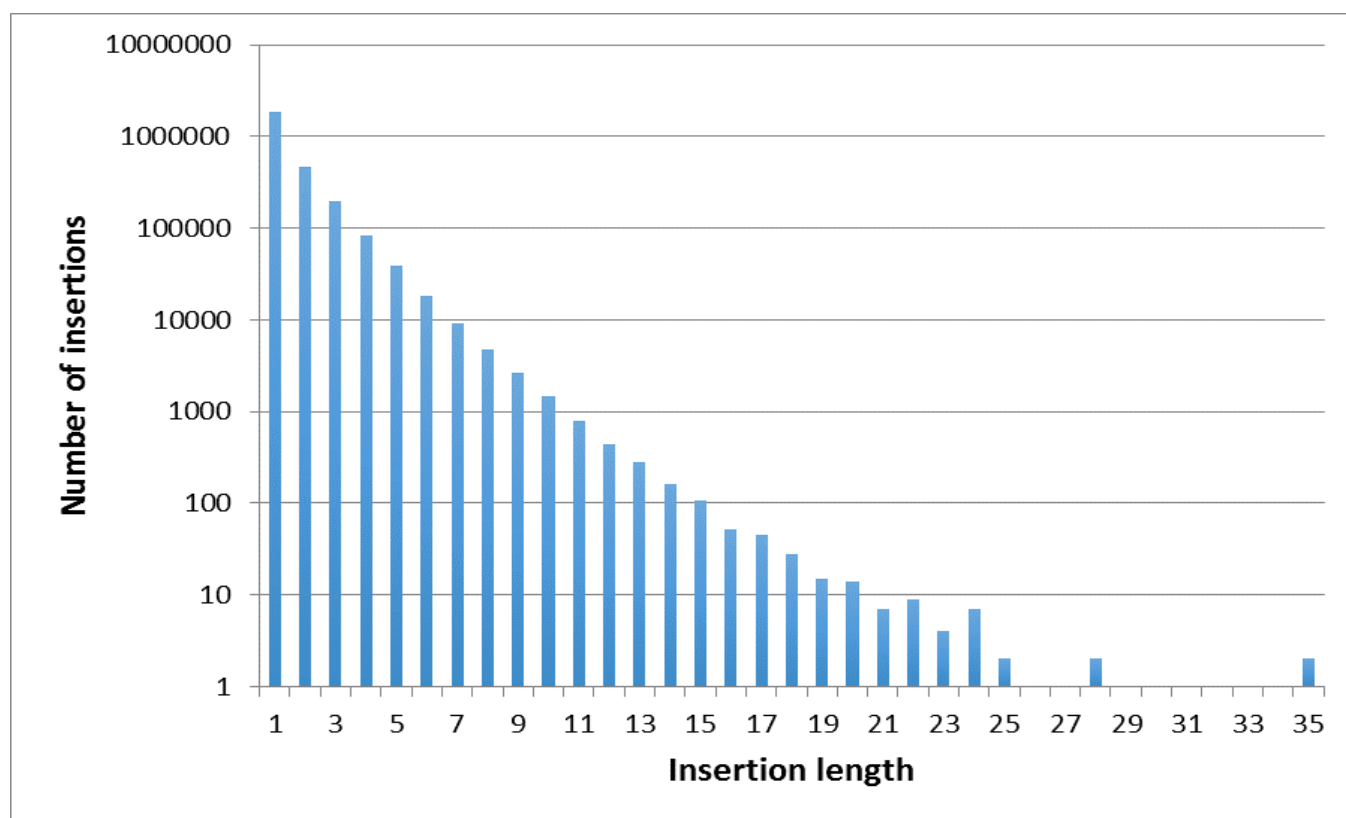


Bin width = 2000 bp.

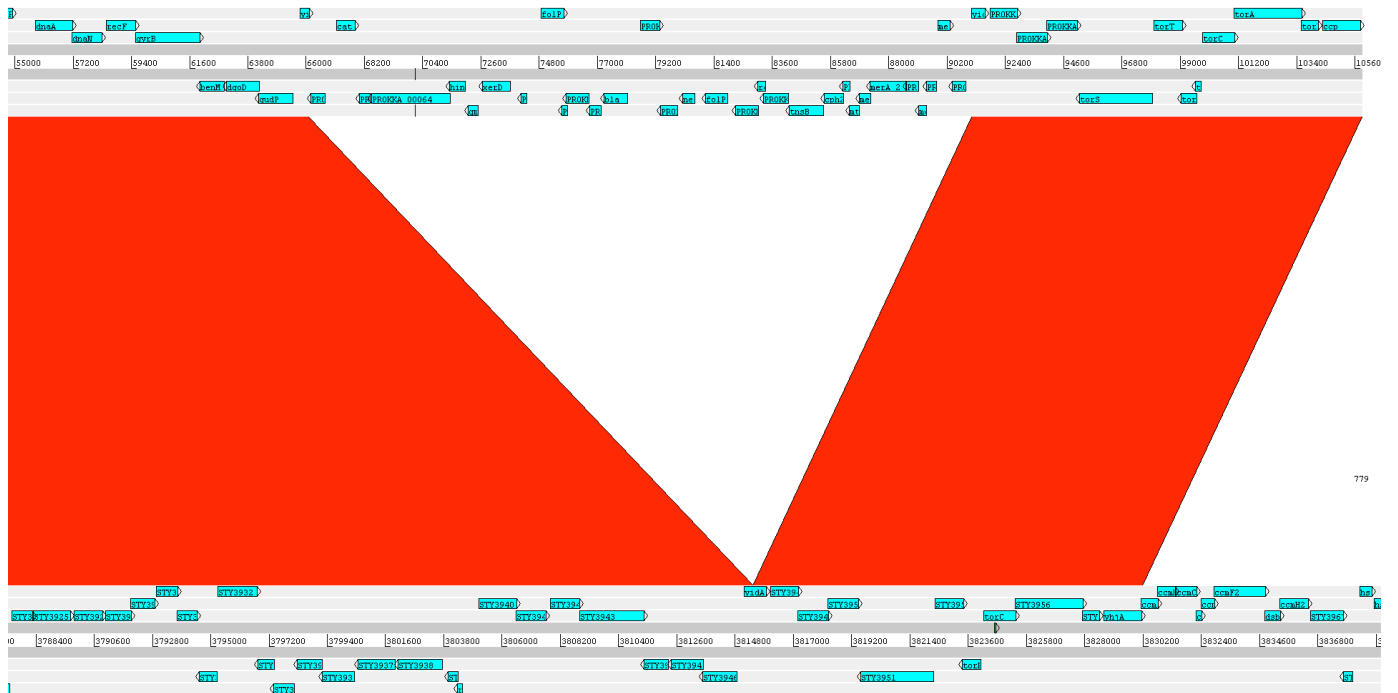
**Supplementary Figure 3: Distribution of deletion lengths in MinION data when mapped to reference using LAST**



**Supplementary Figure 4: Distribution of insertion lengths in MinION data when mapped to reference using LAST**



**Supplementary Figure 5: Artemis Comparison Tool graphical representation of the context of the insertion point (*yidA* gene) of the *S. Typhi* chromosomal resistance island**



Top: *S. Typhi* haplotype H58 - H125160566; bottom: *S. Typhi* CT18. Red indicates 99% similarity and the cut-off minimum was set at 800.

**Supplementary Table 1: (A1) Read statistics for a single 30 hour run of S.Typhi strain H125160566 (with overnight incubation of the library to improve 2D yield and accuracy as recommended by Oxford Nanopore), broken down by read type; (B1) Statistics on mapping of reads from for strain H125160566 Illumina assembly; (A2) Read statistics for a single 48 hour run of strain 08-04776 broken down by read type (B2) Statistics on mapping of reads from for strain 08-04776 to the 08-04776 Illumina assembly**

**(A1) Read stats**

	<b>Number of reads</b>	<b>Median length</b>	<b>Max length</b>	<b>Total length (Mbp)</b>	<b>Median phred</b>	<b>Median accuracy</b>
Total	8968	4589.5	58917	44.005356	5	68.38%
Template	5364	4025.5	58917	25.584794	4	60.19%
Complement	1987	4365	19439	8.741678	4	60.19%
2D	1617	5899	25941	9.678884	8	84.15%

**(B1) Mapping stats**

	<b>Number of reads mapped</b>	<b>Number alignments</b>	<b>Total length alignments (Mbp)</b>	<b>Median accuracy</b>	<b>Median gaps</b>
Total	4898	7150	29.6	65.53%	18.59%
Template	2185	2964	13.8	64.44%	17.27%
Complement	1300	2293	6.5	61.75%	23.56%
2D	1413	1893	9.3	71.79%	14.66%

**(A2) Read stats**

	<b>Number of reads</b>	<b>Median length</b>	<b>Max length</b>	<b>Total length (Mbp)</b>	<b>Median Phred</b>	<b>Median accuracy</b>
Total	10227	3353	83819	42.265801	4	60.19%
Template	7227	2723	83819	28.075045	3	49.88%
Complement	1840	3752	17257	7.419795	3	49.88%
2D	1160	5937.5	19044	6.770961	8	84.15%

**(B2) Mapping stats**

	<b>Number of reads</b>	<b>Number alignments</b>	<b>Total length</b>	<b>Median accuracy</b>	<b>Median gaps</b>
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	<b>mapped</b>		<b>alignments (Mbp)</b>		
Total	4773	7262	25.456267	65.96%	17.28%
Template	2816	4014	14.78298	65.61%	16.49%
Complement	973	1639	4.924954	62.70%	22.21%
2D	984	1609	5.748333	70.18%	14.24%

**Supplementary Table 2: Number of substitutions detected in the mapping of the MinION reads to the Illumina de novo assembly.**

		Reference			
		A	T	C	G
Substitution	A		616349	1142384	1145988
	T	620140		1155658	1135436
	C	1010539	1122063		1157663
	G	1132170	1003170	1165458	



**Supplementary Table 3: PCR primers used in this study**

<b>Primer name</b>	<b>Primer sequence</b>	<b>Target (contig) feature</b>
1_fw	ACGAAAGGGGAATGTTTCCT	48 (chromosome) – 61
1_rev	ACTGAGTGTTTCGGGTCCATC	(island)
2_fw	GCCGATCAACGTCTCATTTT	
2_rev	CAGCGCTCAGCTATGATGAC	25 (chromosome) – 50
3_fw	TCCTTGCCACTTGTGCATCT	(island)
3_rev	AGCGAGACGATTCCTAAGCG	
4_fw	TAGTTGGCCTTGCTCACACC	
4_rev	TCCTGGTCGATTTTCTGCCG	64 (island) – 56 (island)
5_fw	GGTCATGCTCGACAGGTAGG	
5_rev	AGGCTTTGGCCAGCGATATT	65 (island) – 56 (island)
6_fw	GCAATTTCCGTTGCACCAGT	
6_rev	TGGGCTCGTCAGGATCAAAC	65 (island) – 50 (island)