

SUPPORTIVE/SUPPLEMENTARY MATERIAL

SUPPLEMENTARY DATA FILE 1

Supplementary Experimentation - Biotinylation Method Determination

Three different biotinylation methods were investigated during the genesis of this methodology. Briefly, the three techniques were as follows: Biotin 1. addition of biotinylated dUTP by terminal transferase (as detailed in the methods section), Biotin 2. Ligation of a pre-biotinylated adapter (5'CGTTAGGCATTGCATTTT-BIOTIN-3', 5'-TGCAATGCC TAACGT-3') after standard end repair and A-tailing procedures, Biotin 3. Addition of biotinylated dNTP following the Illumina Mate Pair Library Preparation protocol. There was little difference between the three techniques in terms of enrichment, GC content, sequencing read depth or evenness of coverage (Supplementary Tables 1 and 2 and Supplementary Figures 1 and 2).

SUPPLEMENTARY DATA FILE 2

Supplementary Table 1. Enrichment Statistics for the *E.coli* Genome Pre- and post- Solution-based Pulldown for the Biotinylation Comparison Experiment

Sample ID	Sample Name	Probe	Read Count	% <i>E.coli</i>	% Human	% Other
S1	<i>E.coli</i> :human 20:80 prepulldown	~	29141301	11.00	39.83	49.17
S2	<i>E.coli</i> :human 20:80 Biotin 1	<i>E.coli</i> 1.5µg	30953918	81.26	5.45	13.30
S3	<i>E.coli</i> :human 20:80 Biotin 1	<i>E.coli</i> 3µg	27274343	81.41	4.80	13.79
S4	<i>E.coli</i> :human 20:80 Biotin 2	<i>E.coli</i> 1.5µg	34698930	82.59	4.05	13.36
S5	<i>E.coli</i> :human 20:80 Biotin 2	<i>E.coli</i> 3µg	30225643	83.08	3.76	13.15
S6	<i>E.coli</i> :human 20:80 Biotin 3	<i>E.coli</i> 1.5µg	33209881	81.04	5.51	13.45
S7	<i>E.coli</i> :human 20:80 Biotin 3	<i>E.coli</i> 3µg	28432180	81.07	5.28	13.64

Details of the enrichment of *E.coli* DNA achieved after hybridisation using probes made with the three different biotinylation methods under investigation.

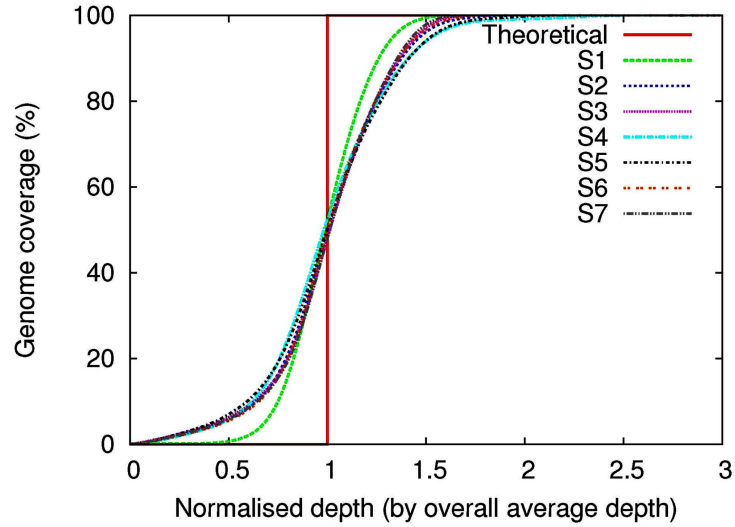
SUPPLEMENTARY DATA FILE 3

Supplementary Table 2. Genome Coverage Statistics for the *E.coli* Genome Pre- and post- solution-based Pulldown

Sample ID	Sample Name	Probe	Average Depth	Peak Depth	Maximum Depth
S1	<i>E.coli</i> :human 20:80 prepulldown	~	112	108	254
S2	<i>E.coli</i> :human 20:80 Biotin 1	<i>E.coli</i> 1.5µg	872	822	2878
S3	<i>E.coli</i> :human 20:80 Biotin 1	<i>E.coli</i> 3µg	771	738	2126
S4	<i>E.coli</i> :human 20:80 Biotin 2	<i>E.coli</i> 1.5µg	993	931	4221
S5	<i>E.coli</i> :human 20:80 Biotin 2	<i>E.coli</i> 3µg	869	822	3063
S6	<i>E.coli</i> :human 20:80 Biotin 3	<i>E.coli</i> 1.5µg	932	905	2996
S7	<i>E.coli</i> :human 20:80 Biotin 3	<i>E.coli</i> 3µg	798	769	2174

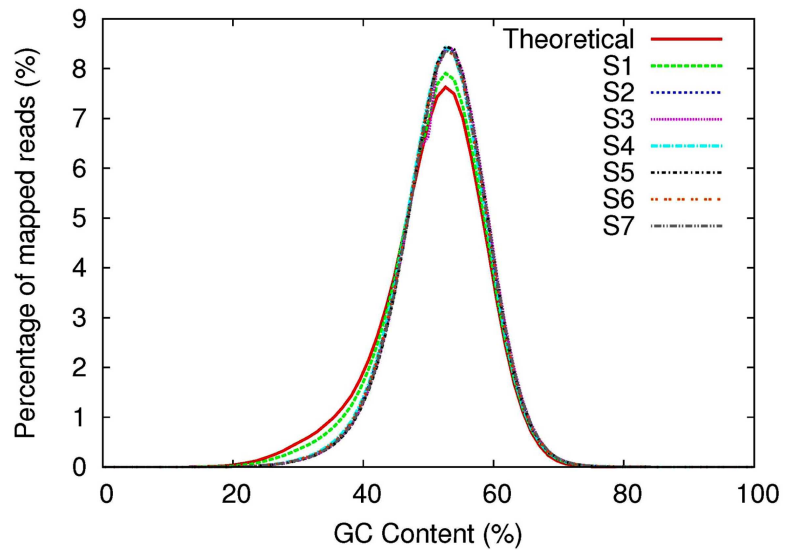
Details of the genome coverage statistics for the *E.coli* genome pre- and post- hybridisation using probes made with the three different biotinylation methods under investigation.

SUPPLEMENTARY DATA FILE 4



Supplementary Fig. (1). GC content of *E.coli* samples pre- and post- solution-based pulldown using different biotinylation techniques during probe synthesis. A figure depicting the GC content of the *E.coli* genome pre- and post- hybridisation using probes made with the three different biotinylation methods under investigation.

SUPPLEMENTARY DATA FILE 5



Supplementary Fig. (2). Genome coverage distribution of *E.coli* samples pre- and post- solution-based pulldown. A figure depicting a genome coverage comparison between the theoretical value for the *E.coli* genome and the DNA obtained pre- and post- hybridisation using probes made with the three different biotinylation methods under investigation.