

Supplementary Table 1

Summary of libraries sequenced in comparative analysis

Organism	Method	Size Selection	Sequencing Platform	Raw Read Pairs	Mapper	Raw Mapped	PCR Duplicates Removed†	Unique Mapped %	Complexity
E. coli CC118	Sonication, replicate 1	none	Illumina GAlIx (PE36)	14,764,330	BWA	13,096,300	12,719,017	86%	97%
	Sonication, replicate 2	none	Illumina GAlIx (PE36)	15,177,716	BWA	13,283,051	13,018,271	86%	98%
	Endonuclease, replicate 1	none	Illumina GAlIx (PE36)	15,131,182	BWA	13,374,850	12,775,619	84%	96%
	Endonuclease, replicate 2	none	Illumina GAlIx (PE36)	16,171,788	BWA	14,124,278	13,441,857	83%	95%
	Transposase, replicate 1	none	Illumina GAlIx (PE36)	19,812,714	BWA	16,439,998	13,209,901	67%	80%
	Transposase, replicate 2	none	Illumina GAlIx (PE36)	23,239,433	BWA	17,501,733	14,094,636	61%	81%
	Transposase	none	Illumina GAlIx (PE76)	47,445,883	BWA	32,763,991	24,138,660	51%	74%
	Transposase	Ampure >300	Illumina GAlIx (PE76)	49,202,822	BWA	28,370,120	21,618,428	44%	76%
	Transposase	Caliper 350+/-10%	Illumina GAlIx (PE76)	14,781,578	BWA	12,898,508	9,439,353	64%	73%
	Transposase NoPCR (100ng)	none	Illumina GAlIx (PE36)	N/A	BWA	512,202	510,620	N/A	100%
	Transposase NoPCR (200ng)	none	Illumina GAlIx (PE36)	N/A	BWA	1,492,999	1,475,918	N/A	99%
	Transposase NoPCR (50ng), 1	none	Illumina GAlIx (PE101)	spike in	BWA	417,268	414,738	N/A	99%
	Transposase NoPCR (50ng), 2	none	Illumina GAlIx (PE101)	spike in	BWA	416,216	413,342	N/A	99%
	Transposase (500pg)	none	Illumina GAlIx (PE101)	spike in	BWA	882,236	814,763	N/A	92%
	Transposase (100pg)	none	Illumina GAlIx (PE101)	spike in	BWA	1,232,098	1,097,646	N/A	89%
H. sapiens NA18507	Sonication, replicate 1**	none	Illumina GAlIx (PE36)	8,830,236	BWA	8,515,999	8,451,436	96%	99%
	Sonication, replicate 2**	none	Illumina GAlIx (PE36)	8,779,733	BWA	8,471,772	8,403,393	96%	99%
	Endonuclease, replicate 1	none	Illumina GAlIx (PE36)	10,137,423	BWA	8,499,831	8,295,592	82%	98%
	Endonuclease, replicate 2	none	Illumina GAlIx (PE36)	12,477,053	BWA	10,790,123	10,637,932	85%	99%
	Transposase, replicate 1	none	Illumina GAlIx (PE36)	18,378,252	BWA	15,814,133	15,602,480	85%	99%
	Transposase, replicate 2	none	Illumina GAlIx (PE36)	18,559,340	BWA	15,877,850	15,653,955	84%	99%
	Transposase NoPCR (100ng)	none	Illumina GAlIx (PE36)	N/A	BWA	1,044,539	1,037,373	N/A	99%
	Transposase NoPCR (200ng)	none	Illumina GAlIx (PE36)	N/A	BWA	488,026	485,966	N/A	99%
	Transposase (10pg)††	none	Illumina GAlIx (PE36)	N/A	BWA	5,731,004	2,182,087	N/A	38%
CRW10	Nebulization	none	Roche GS FLX Ti*	46,745	gsMapper	43,707	43,707	94%	N/A
	Endonuclease	none	Roche GS FLX Ti*	6,444	gsMapper	5,983	5,983	93%	N/A
	Transposase	none	Roche GS FLX Ti*	47,986	gsMapper	43,917	43,917	92%	N/A
PA1	Nebulization	none	Roche GS FLX Ti*	6,183	gsMapper	6,121	6,121	>99%	N/A
	Endonuclease	none	Roche GS FLX Ti*	9,979	gsMapper	9,412	9,412	94%	N/A
	Transposase	none	Roche GS FLX Ti*	43,639	gsMapper	40,637	40,637	93%	N/A
D. melanogaster w1118	Transposase (2rxn)	Gel 400-450	Illumina GAlIx (PE45)	31,272,321	BWA	30,918,821	28,142,311	90%	91%
H. sapiens YH1	Transposase (5rxn)	Gel 550-575	Illumina HiSeq2000 (PE90)	103,341,810	BWA	82,511,867	81,183,426	79%	98%
		Gel 400-500	Illumina HiSeq2000 (PE90)	68,022,215	BWA	62,183,263	60,709,520	89%	98%
	Transposase (2rxn)	Gel 400-500	Illumina HiSeq2000 (PE90)	67,823,613	BWA	62,293,546	60,817,189	90%	98%
		Gel 500-550	Illumina HiSeq2000 (PE90)	58,597,591	BWA	51,335,787	49,590,370	85%	97%
		Gel 550-650	Illumina HiSeq2000 (PE90)	52,625,788	BWA	47,144,748	45,258,959	86%	96%
		Gel 300-500	Illumina HiSeq2000 (PE90)	68,342,929	BWA	58,105,589	56,850,508	83%	98%
	Transposase (1rxn)	Gel 500-650	Illumina HiSeq2000 (PE90)	54,039,263	BWA	44,013,398	42,200,046	78%	96%
H. sapiens BK229.03	Transposase – Exome Capture	none	Illumina GAlIx (SE36)*	44,472,457	BWA	34,654,705	N/A	78%	N/A

* Single end read only
** Data for sonication method for human libraries taken as single lanes of data from Bentley et al. Nature 2008
† PCR Duplicates removed using the samtools rmdup function.
†† Duplicates removed by using outer mapping coordinates.

Supplementary Table 2

Information content of sequence bias
in vicinity of fragmentation sites

Information Content (-10 to +15bp)

		Average	Maximum
E. coli CC118	Sonication	0.007	0.102
	Endonuclease	0.015	0.108
	Transposase	0.046	0.157
H. sapiens NA18507	Sonication	0.031	0.048
	Endonuclease	0.024	0.144
	Transposase	0.049	0.153
CRW10	Nebulization	0.049	0.063
	Endonuclease	0.050	0.134
	Transposase	0.052	0.109
PA1	Nebulization	0.018	0.035
	Endonuclease	0.032	0.085
	Transposase	0.026	0.053

Supplementary Table 3

		Pearson Correlation of Coverage					
		Son.1	Son.2	End.1	End.2	Tr.1	Tr.2
Spearman Rank Order Correlation of Coverage	Son.1		0.816	0.653	0.678	0.336	0.366
	Son.2	0.854		0.688	0.691	0.320	0.370
	End.1	0.693	0.696		0.795	0.383	0.376
	End.2	0.720	0.720	0.818		0.352	0.401
	Tr.1	0.409	0.421	0.435	0.428		0.835
	Tr.2	0.489	0.497	0.490	0.493	0.877	