

Supplementary Note 1

Filtering to improve TSS peak identification

We incorporated two additional analysis steps to ensure that our peak calling results accurately represented lab method performance. First, we evaluated whether specialized filtering programs improved the specificity and precision of each method. All methods, except Oligo capping and GRO-cap, will sometimes add a G base not present in the genome at the 5' end of the sequence read because reverse transcriptase tends to use the 5' 7-methylguanosine (m^7G) cap as a template. We found improved precision with CapFilter¹⁴, which removes peaks containing less than a set percentage of reads with an extra G base at the 5' end of the read (**Supplementary Fig. 2**). We used it with a threshold of 20% extra G reads for all subsequent analysis in this study. We also tested the strand invasion²⁵ and RAMPAGE second read¹⁰ filters, which did not substantially improve performance of the relevant lab methods (**Supplementary Fig. 3a,b**).

Second, in our initial peak calling analysis, we observed low sensitivity for all methods due to a high level of apparent false negatives compared to in the UCSC annotation⁸ (**Supplementary Fig. 4**, dark blue bars). This was expected because transcripts that are expressed in our K-562 sample should reflect only a subset of all annotated TSSs. We therefore considered K-562 specific annotations, previously generated by DNase-Seq^{26,27}, which identifies genomic regions with open chromatin such as promoters, and removed from consideration those TSS peaks without a DNase-Seq peak in K-562 cells, because these are likely to be TSSs that are not active in K-562 cells (true negatives). We used this filtered annotation set in all subsequent analyses.

Supplementary Note 2

TSSs at single base resolution

With 5' RNA-Seq data, it is possible to determine a TSS at single base resolution. Previous studies have shown that the initiator sequence at the -1 and +1 position relative to the TSS is most often a pyrimidine and purine, respectively^{34, 35} and has been shown to be true for TSSs categorized as narrow or broad. In our datasets, we observe this pyrimidine and purine pattern, though the methods do differ to some extent in their biases for the bases in these positions (**Supplementary Fig. 8a,b**). Finding explanations for these differences is beyond the scope of this paper.

Supplementary Note 3

Reproducibility and gene expression quantification

We also assessed reproducibility and gene expression quantification accuracy for each method. For CAGE, ≥94% of the peaks overlapped between any two pairs of libraries across four replicates (**Supplementary Fig. 9a**); for RAMPAGE, ≥90% of peaks in one technical replicate were present in the other; for STRT, 89% and 95% concurred between two replicates. The replicates had similar performance with respect to reads aligning near the 5' end of annotated transcripts (**Supplementary Fig. 9b**) and with ERCC spike-ins (**Supplementary Tables 2-4**). We did not perform replicates of the other protocols: for Oligo Capping, because the Tobacco Acid Pyrophosphatase (TAP) enzyme is no longer commercially available; for NanoCAGE-XL, because it performed relatively poorly. To identify differential TSS usage, it is important for methods to accurately measure relative levels of gene expression. Expression levels measured for replicates of each method correlated well, with CAGE and RAMPAGE performing best (Pearson's $r=0.98-0.99$, **Supplementary Fig. 10a-c**). We also compared the expression levels for each of the lab methods and standard RNA-Seq (**Supplementary Fig. 10d**). Expression levels

measured with CAGE and standard RNA-Seq were relatively well correlated (Pearson's $r=0.86$, **Supplementary Fig. 10d**), whereas RAMPAGE expression levels did not correlate as well ($r=0.78$, **Supplementary Fig. 10d**), which is in agreement with the expression levels measured for spike-in RNAs (**Supplementary Table 4**). While most of the method correlate fairly well with each other, NanoCAGE-XL did not due, at least in part, to it not detecting expression of many genes and being sequenced less deeply (**Supplementary Fig. 10d**).

Supplementary Note 4

Corroborative evidence for other methods

In addition to CAGE, we also investigated how corroborative evidence supported TSSs identified with the other 5' end RNA-Seq methods. Similar to CAGE, methods with good precision, RAMPAGE, STRT, and NanoCAGE-XL (**Fig. 3**), have support for most false positive and intergenic peaks (**Supplementary Fig. 11**). For GRO-cap, we see that most peaks have support from H3K4m3 and DNase-Seq, but not annotation or the consensus of other methods (**Supplementary Fig. 11**). This finding agrees well with previous findings that GRO-cap can identify TSSs in less stable transcripts that might not be annotated or found by other methods¹⁷. Finally, Oligo capping, which has poor precision (**Fig. 3**), had much less support for false positive peaks (**Supplementary Fig. 11**).

Supplementary Note 5

Discussion of excluded methods

The following methods were excluded because of their similarities to other methods or other issues. We did not test 5' SAGE¹ because it is another template switching method similar to

STRT, except that it concatenates 5' tag sequences, TL-Seq², TIF-Seq³, and paired-end analysis of TSSs (PEAT)⁴ because they are variants of oligo capping, DLAF⁵, because it has limitations in recognizing weak alternative TSSs that might be present downstream from a strong TSS, Start-Seq⁶, which uses short, capped nuclear RNA derived from stalled transcripts rather than full-length mRNA, because it is an indirect method that provides inaccurate measurements of the levels of TSS usage and requires the TAP enzyme, and Exo-Seq⁷, which identifies 5' ends based on the m⁷G cap's protection from exonuclease digestion, because it was published too recently to be included in our study. Finally, we note that there are sometimes multiple versions of a method, such as for NanoCAGE^{8, 9} and CAGE^{10, 11}, and we tested only one of each.

1. Zhang, Z. & Dietrich, F.S. Mapping of transcription start sites in *Saccharomyces cerevisiae* using 5' SAGE. *Nucleic Acids Res* **33**, 2838-2851 (2005).
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3. Pelechano, V., Wei, W., Jakob, P. & Steinmetz, L.M. Genome-wide identification of transcript start and end sites by transcript isoform sequencing. *Nat Protoc* **9**, 1740-1759 (2014).
4. Ni, T. et al. A paired-end sequencing strategy to map the complex landscape of transcription initiation. *Nat Methods* **7**, 521-527 (2010).
5. Agarwal, S., Macfarlan, T.S., Sartor, M.A. & Iwase, S. Sequencing of first-strand cDNA library reveals full-length transcriptomes. *Nat Commun* **6**, 6002 (2015).
6. Nechaev, S. et al. Global analysis of short RNAs reveals widespread promoter-proximal stalling and arrest of Pol II in *Drosophila*. *Science* **327**, 335-338 (2010).
7. Afik, S. et al. Defining the 5 and 3 landscape of the *Drosophila* transcriptome with Exo-seq and RNaseH-seq. *Nucleic Acids Res* (2017).
8. Cumbie, J.S., Ivanchenko, M.G. & Megraw, M. NanoCAGE-XL and CapFilter: an approach to genome wide identification of high confidence transcription start sites. *BMC Genomics* **16**, 597 (2015).
9. Salimullah, M., Sakai, M., Plessy, C. & Carninci, P. NanoCAGE: a high-resolution technique to discover and interrogate cell transcriptomes. *Cold Spring Harb Protoc* **2011**, pdb prot5559 (2011).
10. Murata, M. et al. Detecting expressed genes using CAGE. *Methods Mol Biol* **1164**, 67-85 (2014).
11. Takahashi, H., Kato, S., Murata, M. & Carninci, P. CAGE (cap analysis of gene expression): a protocol for the detection of promoter and transcriptional networks. *Methods Mol Biol* **786**, 181-200 (2012).

Supplementary Tables

Supplementary Table 1: Library sequencing metrics

For each library in this study, basic information about its construction, sequencing, analysis, and performance (QC metrics). All samples are from human sources. All K-562 data are from hard clipped STAR alignments; other data are from soft clipped STAR alignments. Metrics are only for read 1, except for Standard RNA-Seq. Reads aligned for CAGE Main and Standard RNA-Seq libraries are limited to PF reads.

Supplementary Table 2: ERCC spike-in RNA 5' end sequence coverage

For each K-562 library, this table reports the % (reads at position 10) / (all reads) for each spike-in transcript. Lowest for each library (red) and highest for each library (green). Used in pool of 8 (CAGE repeat & RAMPAGE repeat, highlighted in yellow). The CAGE Repeat, RAMPAGE Main, & STRT Main data are only from 1 of 2 lanes of sequencing. CAGE Main-6 was to be used to compare method performance for K-562 RNA, but not for spike-in transcripts because they are uncapped.

Supplementary Table 3: Reads aligning to ERCC spike-in RNA

For each K-562 library, this table reports the number of reads aligning to each ERCC spike-in. Used in pool of 8 (CAGE repeat & RAMPAGE repeat, yellow). Used in pool of 32 (green). CAGE repeat data are only from 1 of 2 lanes of sequencing.

Supplementary Table 4: Deviation of percentage of reads aligning to ERCC spike-in RNA between input and output

For each K-562 library and each ERCC spike-in, this table reports the mean quantitation error, the average of the absolute value of the difference between the input and output percentages.

Used in pool of 8 (CAGE repeat & RAMPAGE repeat, yellow). Used in pool of 32 (green).

CAGE repeat data are only from 1 of 2 lanes of sequencing. Calculations were done with reads aligning to the spike-ins added. Percentages shown are Absolute Value (Output - Input).

Supplementary Table 5: Analysis of eRNAs for Paraclu-called peaks in intergenic regions

For each method, corroborative data and analyses are shown to assess how many Paraclu-called peaks in intergenic regions could be eRNAs.

Supplementary Table 6: Analysis of eRNAs for paired peaks in intergenic regions

For each method, corroborative data and analyses are shown to assess how many paired peaks in intergenic regions could be eRNAs.

Supplementary Table 7: List of differentially TSS usage in brain neuron

For each brain-related sample, TSSs differentially used among the samples are listed. PR (peak reads) – only reads aligning to region defined as peak counted. NA values for p.adj are assigned when no comparison was made because PR is not above the threshold of 100 reads in two samples for that peak. Mean expression and Std. Dev are for the gene. Peak name is a concatenation of gene name, position in gene, and number peaks in gene. Scaled values are the percentage of peak reads in a given peak for that sample. One library was prepared from each sample (n=1).

Supplementary Table 8: Comparison of lab methods time, cost, and input

For each method, details about library construction are presented. Cost assumes eight reactions processed in single batch with a BioAnalyzer High Sensitivity DNA chip used for final QC.

Supplementary Table 9: Library sequencing details

For each library type, details about Illumina sequencing are reported.

Supplementary Table 10: External Datasets

Source for each external dataset is listed.

Supplementary Table 11: ERCC spike-in sequences

Complete sequence of each ERCC spike-in is listed.

Supplementary Table 12: Paraclu filtering parameters

For each sample, Paraclu filtering parameters (**Online Methods**) are listed.

Table S1

Method	Replicate	Read 1 trim	Read 2 trim	RNA Sample	RNA source (lot #)	Total Reads	Reads Aligned	% Reads Aligned	rRNA Bases	Coding Bases	UTR Bases	Intronic Bases	Intergenic Bases	Correct Strand Reads
CAGE	Main-1	3 + 6	0	K-562	Ambion (1409009)	8,340,957	7,631,449	91%	9.1%	15%	55%	7%	14%	99.7%
CAGE	Main-4	3 + 6	0	K-562	Ambion (1409009)	8,088,598	7,567,022	94%	13.5%	13%	50%	8%	16%	99.6%
CAGE	Main-6	3 + 6	0	K-562	Ambion (1409009)	7,842,538	7,391,797	94%	9.1%	14%	56%	7%	14%	99.7%
CAGE	Repeat	3 + 6	n/a	K-562	Ambion (1210018)	14,563,335	12,706,814	87%	17.0%	12%	52%	7%	13%	99.6%
Oligo Capping	Main	0	n/a	K-562	Ambion (1409009)	114,389,954	95,512,056	83%	0.6%	17%	63%	6%	15%	99.2%
RAMPAGE	Main	4	15	K-562	Ambion (1409009)	36,370,919	35,866,874	99%	12.7%	22%	53%	3%	9%	99.7%
RAMPAGE	Repeat	4	15	K-562	Ambion (1210018)	5,275,652	5,219,629	99%	11.7%	22%	55%	3%	8%	99.7%
STRT	Main	11	0	K-562	Ambion (1409009)	20,500,952	18,775,073	92%	1.8%	32%	49%	7%	10%	99.5%
STRT	Repeat	11	0	K-562	Ambion (1409009)	7,282,989	6,604,049	91%	1.1%	34%	46%	8%	11%	99.5%
STRT	Repeat-10ng	11	0	K-562	Ambion (1409009)	58,150,901	52,048,326	90%	2.9%	32%	48%	8%	9%	99.5%
STRT	Repeat-100ng	11	0	K-562	Ambion (1409009)	67,949,256	61,071,566	90%	3.7%	31%	48%	7%	9%	99.5%
STRT	RepeatA-1µg	11	0	K-562	Ambion (1409009)	55,966,586	50,909,724	91%	2.9%	32%	48%	7%	9%	99.5%
STRT	RepeatB-1µg	11	0	K-562	Ambion (1409009)	56,280,694	51,143,105	91%	2.7%	32%	48%	7%	9%	99.4%
STRT	RepeatA-5µg	11	0	K-562	Ambion (1409009)	52,227,631	47,471,979	91%	2.4%	33%	47%	8%	9%	99.4%
STRT	RepeatB-5µg	11	0	K-562	Ambion (1409009)	58,957,331	52,929,187	90%	2.5%	32%	47%	8%	10%	99.4%
STRT	RepeatA-10µg	11	0	K-562	Ambion (1409009)	55,749,637	50,211,000	90%	1.2%	36%	44%	8%	11%	99.6%
STRT	RepeatB-10µg	11	0	K-562	Ambion (1409009)	60,248,148	54,231,450	90%	1.1%	36%	43%	8%	11%	99.5%
NanoCAGE-XL	Main	6 + 12	0	K-562	Ambion (1409009)	6,957,156	6,407,741	92%	0.1%	34%	23%	27%	17%	99.6%
Standard RNA-Seq	Main	0	0	K-562	Ambion (not recorded)	59,695,850	54,819,796	92%	0.1%	28%	16%	33%	23%	99.3%
GRO-cap	Main	0	0	K-562	Core et al. <i>Nat Genet</i> (2014)	45,538,197	35,809,451	79%	1.3%	5%	26%	20%	47%	90.3%
CAGE	Main	3 + 6	0	Brain vascular smooth muscle cells	ScienCell	23,538,559	21,104,822	90%	13.1%	15%	60%	6%	8%	99.8%
CAGE	Main	3 + 6	0	Brain microvascular endothelial cells	ScienCell	31,173,330	29,588,075	95%	7.8%	15%	62%	5%	11%	99.8%
CAGE	Main	3 + 6	0	Neuron	ScienCell	15,837,644	14,862,756	94%	7.0%	13%	62%	7%	12%	99.6%
CAGE	Main	3 + 6	0	Astrocyte	ScienCell	17,716,230	16,602,202	94%	10.5%	14%	56%	7%	13%	99.7%
CAGE	Main	3 + 6	0	Fetal frontal lobe	Biochain	22,920,356	21,599,869	94%	5.5%	12%	61%	9%	13%	99.5%
CAGE	Main	3 + 6	0	Adult frontal lobe	Biochain	25,659,539	24,268,652	95%	16.8%	12%	48%	10%	15%	99.4%
CAGE	Main	3 + 6	0	Organoids	this paper	14,728,291	13,366,256	91%	10.6%	10%	39%	24%	18%	98.6%
CAGE	Main	3 + 6	0	<i>In vitro</i> excitatory neurons	this paper	26,257,718	24,499,412	93%	11.1%	12%	56%	11%	11%	99.4%

Table S2

Lab Method	CAGE	CAGE	CAGE	CAGE	Oligo Capping	RAMPAGE	RAMPAGE	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	NanoCAGE XL
Replicate	Main-1	Main-4	Main-6	Repeat	Main	Main	Repeat	Main	Repeat	Repeat-10ng	Repeat-100ng	RepeatA-1µg	RepeatB-1µg	RepeatA-5µg	RepeatB-5µg	RepeatA-10µg	RepeatB-10µg	Main
Capped?	Yes	Yes	No	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	Yes
ERCC-00002	98.6%	99.0%	47.1%		91.7%	98.6%		96.9%	96.8%	96.8%	96.2%	96.2%	96.7%	96.5%	94.3%	93.7%	39.3%	
ERCC-00003	99.1%	98.0%	61.0%		88.6%	99.2%		98.8%	97.8%	98.1%	98.6%	98.4%	98.6%	98.6%	98.5%	98.1%	98.0%	55.5%
ERCC-00012	98.8%	99.2%	61.9%		97.0%	98.7%		96.9%	97.3%	95.0%	95.9%	95.7%	95.7%	96.1%	95.9%	94.6%	95.0%	84.8%
ERCC-00017	96.1%	96.8%	71.8%		81.4%	97.7%		98.2%	98.2%	96.4%	97.0%	96.9%	96.7%	97.3%	97.0%	96.9%	96.8%	60.3%
ERCC-00028	97.6%	98.6%	62.5%		74.0%	98.8%		97.4%	97.9%	97.3%	97.5%	97.7%	97.7%	97.9%	97.8%	97.7%	97.6%	37.8%
ERCC-00031	96.4%	97.4%	32.1%		64.5%	98.8%		97.4%	97.2%	95.7%	95.6%	96.2%	96.1%	96.4%	96.6%	95.9%	96.2%	55.1%
ERCC-00034	98.2%	98.4%	82.6%		77.0%	98.9%		94.4%	91.4%	94.6%	94.3%	93.1%	93.9%	93.4%	93.4%	88.9%	88.0%	34.7%
ERCC-00035	97.7%	98.3%	71.7%		55.2%	99.1%		97.3%	96.7%	93.7%	95.0%	94.8%	94.7%	94.7%	95.2%	93.8%	94.3%	71.3%
ERCC-00041	97.4%	97.9%	64.4%	98.1%	77.5%	99.1%	97.9%	97.2%	96.9%	96.0%	96.7%	96.3%	96.5%	96.8%	96.6%	95.0%	94.7%	81.5%
ERCC-00042	93.5%	83.8%	62.7%	84.7%	36.0%	98.7%	98.2%	93.1%	89.1%	90.3%	90.3%	88.6%	88.3%	90.0%	88.7%	82.1%	79.2%	34.3%
ERCC-00043	96.7%	96.8%	28.1%	97.6%	52.8%	87.0%	79.7%	95.8%	96.4%	95.0%	96.1%	94.8%	95.2%	95.0%	95.0%	93.2%	93.9%	19.1%
ERCC-00044	98.0%	98.6%	66.7%	98.9%	87.4%	98.8%	99.5%	98.7%	98.8%	98.0%	97.7%	98.0%	97.4%	97.9%	97.7%	97.0%	96.7%	65.9%
ERCC-00048	97.7%	98.1%	63.4%	98.8%	59.0%	99.2%	99.7%	98.0%	96.4%	97.2%	96.8%	96.1%	96.5%	95.9%	96.8%	93.7%	93.5%	34.5%
ERCC-00053	97.8%	98.0%	68.0%	98.6%	57.9%	100.0%	99.7%	97.0%	95.4%	96.8%	96.0%	95.8%	95.6%	95.3%	95.5%	94.6%	94.8%	52.7%
ERCC-00057	98.7%	99.1%	80.0%	98.8%	95.2%	98.0%	98.6%	97.0%	96.8%	95.7%	96.6%	96.4%	95.9%	96.5%	96.1%	95.0%	95.1%	38.5%
ERCC-00058	98.6%	99.0%	74.4%	98.9%	92.4%	97.2%	96.3%	95.2%	93.7%	90.1%	91.4%	91.6%	91.1%	91.7%	91.7%	90.7%	90.4%	67.5%
ERCC-00061	95.4%	96.4%	45.2%		88.6%	98.8%		94.3%	96.7%	93.2%	93.6%	93.9%	94.1%	93.8%	93.7%	91.2%	91.5%	55.9%
ERCC-00062	98.4%	98.3%	50.0%		73.3%	99.5%		93.8%	89.5%	93.2%	91.8%	90.6%	91.4%	90.7%	91.8%	85.8%	87.4%	63.0%
ERCC-00069	96.9%	97.3%	45.1%		73.1%	98.0%		95.5%	94.9%	95.2%	94.7%	95.0%	95.0%	95.2%	95.5%	94.2%	94.1%	60.2%
ERCC-00078	96.9%	98.2%	50.0%		78.3%	97.8%		97.2%	97.1%	96.3%	96.1%	96.2%	96.5%	96.6%	96.9%	95.3%	94.7%	51.8%
ERCC-00085	98.9%	99.2%	73.3%		73.6%	98.8%		97.9%	95.7%	96.7%	96.2%	96.3%	96.7%	96.3%	96.1%	93.9%	93.7%	38.9%
ERCC-00096	98.9%	99.1%	50.0%		92.9%	98.4%		96.9%	96.2%	94.7%	95.1%	95.0%	94.4%	94.5%	95.7%	93.7%	93.7%	63.5%
ERCC-00098	97.7%	97.7%	91.5%		87.5%	98.8%		98.0%	97.9%	96.2%	96.7%	96.8%	97.2%	97.1%	97.3%	97.2%	97.3%	66.5%
ERCC-00108	98.4%	98.9%	46.7%		83.0%	97.7%		94.9%	94.7%	94.2%	95.2%	94.1%	94.3%	94.9%	94.8%	92.8%	92.4%	19.3%
ERCC-00111	98.4%	98.1%	35.9%		70.0%	93.4%		92.9%	87.6%	92.5%	93.5%	92.3%	91.7%	91.7%	91.7%	83.1%	81.7%	14.5%
ERCC-00112	96.2%	97.5%	44.4%		91.2%	97.1%		97.1%	94.9%	94.7%	94.9%	95.4%	95.5%	95.4%	95.7%	93.4%	93.7%	67.1%
ERCC-00117	98.3%	98.4%	55.6%		97.7%	98.5%		98.8%	98.4%	97.4%	98.0%	97.9%	98.0%	98.2%	98.1%	97.7%	97.7%	59.6%
ERCC-00126	98.6%	99.0%	73.7%		15.1%	95.6%		96.7%	94.4%	91.3%	91.9%	91.5%	91.2%	92.4%	92.5%	87.2%	87.8%	53.1%
ERCC-00130	98.1%	99.0%	64.6%		91.2%	99.2%		96.9%	96.4%	96.0%	95.9%	96.1%	96.0%	95.7%	96.4%	95.2%	95.4%	65.2%
ERCC-00136	98.6%	98.4%	68.4%		63.3%	98.5%		98.0%	97.6%	98.0%	97.8%	97.8%	98.1%	97.8%	98.1%	97.1%	97.1%	16.7%
ERCC-00145	97.5%	97.0%	43.2%		68.9%	98.4%		95.8%	95.2%	94.4%	94.6%	94.1%	94.5%	95.0%	94.6%	92.1%	92.5%	47.9%
ERCC-00157	97.5%	98.6%	77.3%		90.8%	97.2%		97.3%	94.6%	96.5%	96.0%	96.3%	95.8%	96.2%	96.5%	94.4%	92.9%	55.4%
Average	97.7%	97.8%	59.8%	96.8%	75.8%	97.9%	96.2%	96.6%	95.6%	95.2%	95.5%	95.2%	95.2%	95.4%	95.5%	93.3%	93.2%	51.0%
Median	97.9%	98.3%	62.6%	98.7%	77.9%	98.6%	98.4%	97.0%	96.4%	95.7%	96.0%	95.9%	95.8%	95.8%	96.0%	94.3%	94.0%	55.2%

Table S3

Lab Method	CAGE	CAGE	CAGE	CAGE	Oligo Capping	Rampage	Rampage	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	NanoCAGE-XL	
Replicate	Main-1	Main-4	Main-6	Repeat	Main	Main	Repeat	Main	Repeat	Repeat-10ng	Repeat-10ng	RepeatA-1μg	RepeatB-1μg	RepeatA-5μg	RepeatB-5μg	RepeatA-10μg	RepeatB-10μg	Main			
Capped?	Yes	Yes	No	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No	No	Yes	
% spike reads	0.89%	0.92%	0.02%	0.88%	0.20%	0.47%	0.34%	1.22%	2.10%	1.38%	1.33%	1.77%	1.89%	1.86%	1.81%	2.23%	2.21%	1.36%			
# spike reads	74,151	74,168	1,315	62,919	228,993	170,253	18,072	250,839	153,246	799,677	903,712	993,099	1,062,592	973,024	1,068,625	1,244,371	1,334,158	94,322			
Total # reads	In 32?	8,340,957	8,088,598	7,842,538	7,112,926	114,389,954	36,370,919	5,275,652	20,500,952	7,282,989	58,150,901	67,949,256	55,966,586	56,280,694	52,227,631	58,957,331	55,749,637	60,248,148	6,957,156		
ERCC-00002	Y	2,021	2,123	17	8	8,087	3,538	0	5,527	3,319	21,723	24,143	25,468	25,985	25,181	28,940	26,581	27,526	619		
ERCC-00003	Y	2,448	2,393	82	9	8,592	1,013	0	9,213	5,369	24,836	29,212	30,456	33,672	31,176	33,831	37,007	38,239	4,448		
ERCC-00004	N	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00009	N	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
ERCC-00012	Y	3,272	3,066	21	6	10,589	6,744	0	8,301	5,430	25,985	30,501	33,108	36,935	32,627	36,526	41,835	43,047	3,284		
ERCC-00013	N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00014	N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00016	N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00017	Y	2,590	2,711	39	14	3,420	2,000	0	15,600	10,620	44,014	48,937	57,399	60,891	56,793	62,835	87,996	97,242	3,050		
ERCC-00019	N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00022	N	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
ERCC-00024	N	0	0	0	0	0	0	0	0	0	0	14	21	19	20	5	16	14	12	0	
ERCC-00025	N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00028	Y	3,450	3,330	40	33	8,415	5,747	0	14,111	10,408	43,104	48,654	58,783	61,814	57,954	62,308	85,668	93,039	2,334		
ERCC-00031	Y	2,844	2,697	84	14	14,333	6,324	0	10,407	6,453	30,053	33,150	38,609	40,879	38,995	41,911	56,293	64,526	3,885		
ERCC-00033	N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00034	Y	2,726	2,772	23	3	3,245	7,216	0	3,757	1,813	14,196	16,633	16,297	17,412	15,220	17,142	14,407	15,237	908		
ERCC-00035	Y	3,170	3,327	46	4	2,119	8,657	0	6,263	3,903	17,935	20,998	24,324	25,245	22,655	24,718	30,904	34,828	2,841		
ERCC-00039	N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00040	N	3	1	0	2	0	0	0	0	0	52	28	25	21	17	23	13	17	0	0	
ERCC-00041	Y	2,048	2,064	59	9,122	3,978	6,722	2,861	10,729	6,195	32,665	38,268	42,946	46,453	41,266	45,953	51,933	51,928	5,019		
ERCC-00042	Y	1,179	1,189	51	4,340	929	657	222	2,247	1,032	6,843	8,136	7,239	8,083	7,708	8,745	6,229	6,423	353		
ERCC-00043	Y	906	802	32	6,396	1,961	831	617	4,358	3,859	14,317	17,576	17,276	19,655	18,518	20,708	25,531	26,541	12,340		
ERCC-00044	Y	2,310	2,191	27	8,135	2,214	5,461	2,676	7,321	4,511	24,578	27,042	31,763	33,854	29,753	33,618	38,083	39,992	1,342		
ERCC-00046	N	0	0	0	1	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00048	Y	2,039	2,229	41	11,182	1,976	4,557	3,236	7,684	3,619	24,339	27,836	27,934	30,074	26,793	30,665	27,396	28,902	1,707		
ERCC-00051	N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00053	Y	1,615	1,519	50	9,370	901	5,871	6,066	3,167	2,170	8,809	10,699	10,896	12,384	11,586	11,493	16,198	17,074	2,933		
ERCC-00054	N	1	3	0	1	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00057	Y	1,316	1,224	20	5,416	9,947	1,573	1,549	6,613	4,032	25,865	31,068	32,080	35,112	30,792	33,581	37,887	40,705	467		
ERCC-00058	Y	2,555	2,705	39	8,723	2,205	2,486	845	8,870	5,383	25,798	28,767	33,695	34,522	32,683	35,224	45,625	50,029	3,279		
ERCC-00059	N	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00060	N	0	0	1	0	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
ERCC-00061	Y	1,905	1,963	31	7	3,128	5,663	0	4,860	2,608	16,845	20,437	21,189	22,220	20,551	21,777	22,193	24,189	2,791		
ERCC-00062	Y	2,594	2,364	52	15	2,481	18,773	0	1,773	988	5,379	6,091	5,782	6,649	6,094	6,798	6,995	7,922	7,911		
ERCC-00067	N	0</																			

Table S4

Lab Method		CAGE	CAGE	CAGE	CAGE	Oligo Capping	Rampage	Rampage	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	STRT	NanoCAGE-XL
Replicate		Main-1	Main-4	Main-6	Repeat	Main	Main	Repeat	Main	Repeat	Repeat-10ng	Repeat-100ng	RepeatA-1µg	RepeatB-1µg	RepeatA-5µg	RepeatB-5µg	RepeatA-10µg	RepeatB-10µg	Main	
Capped?	In 32?	Yes	Yes	No	Yes	Yes	Yes	Yes	No	No	No	No	No	No	No	No	No	No	No	Yes
ERCC-00002	Y	1.3%	1.2%	1.6%		0.5%	2.0%		0.7%	0.7%	0.1%	0.2%	0.3%	0.4%	0.3%	0.1%	0.7%	0.8%	3.4%	
ERCC-00003	Y	1.4%	1.4%	5.0%		1.9%	1.3%		2.4%	2.2%	1.8%	2.0%	1.8%	1.9%	1.9%	1.9%	1.7%	1.6%	2.9%	
ERCC-00012	Y	2.8%	2.5%	0.0%		3.0%	2.4%		1.7%	1.9%	1.6%	1.7%	1.7%	1.8%	1.7%	1.8%	1.7%	1.6%	1.9%	
ERCC-00017	Y	0.7%	0.9%	0.7%		1.3%	1.6%		3.9%	4.7%	3.2%	3.1%	3.5%	3.5%	3.6%	3.6%	4.8%	5.0%	0.4%	
ERCC-00028	Y	1.4%	1.2%	0.6%		0.4%	0.1%		3.2%	4.3%	2.9%	2.9%	3.5%	3.4%	3.5%	3.4%	4.4%	4.5%	0.8%	
ERCC-00031	Y	1.1%	0.9%	4.5%		3.6%	1.0%		2.2%	2.3%	1.8%	1.8%	2.0%	1.9%	2.1%	2.0%	2.6%	2.9%	1.4%	
ERCC-00034	Y	0.9%	0.9%	0.2%		3.2%	0.4%		0.4%	0.8%	0.2%	0.1%	0.3%	0.3%	0.4%	0.3%	0.8%	0.8%	3.6%	
ERCC-00035	Y	1.5%	1.7%	1.3%		1.9%	2.3%		0.3%	0.4%	0.1%	0.1%	0.3%	0.2%	0.1%	0.1%	0.3%	0.4%	0.2%	
ERCC-00041	Y	1.3%	1.3%	2.1%	1.0%	2.3%	0.1%	2.3%	1.9%	1.7%	1.7%	1.9%	2.0%	2.0%	2.0%	1.9%	2.0%	1.8%	1.5%	1.3%
ERCC-00042	Y	0.7%	0.7%	2.0%	0.9%	1.9%	2.0%	6.6%	1.0%	1.2%	1.0%	1.0%	1.2%	1.1%	1.1%	1.1%	1.4%	1.4%	2.0%	
ERCC-00043	Y	2.0%	2.1%	0.1%	0.5%	2.4%	2.7%	7.3%	0.6%	0.2%	0.5%	0.4%	0.6%	0.5%	0.4%	0.4%	0.3%	0.3%	9.9%	
ERCC-00044	Y	1.2%	1.4%	1.3%	1.5%	3.4%	1.1%	0.3%	0.4%	0.4%	0.3%	0.4%	0.2%	0.2%	0.3%	0.2%	0.3%	0.4%	2.9%	
ERCC-00048	Y	1.8%	1.6%	0.4%	2.6%	3.7%	1.9%	2.7%	0.5%	1.2%	0.5%	0.5%	0.7%	0.7%	0.8%	0.7%	1.3%	1.4%	2.7%	
ERCC-00053	Y	0.6%	0.7%	1.9%	5.8%	2.3%	0.7%	24.4%	0.6%	0.4%	0.8%	0.7%	0.8%	0.7%	0.7%	0.8%	0.6%	0.6%	0.4%	
ERCC-00057	Y	3.0%	3.1%	1.1%	7.3%	0.4%	3.8%	7.4%	0.0%	0.0%	0.6%	0.8%	0.6%	0.6%	0.5%	0.5%	0.4%	0.4%	4.3%	
ERCC-00058	Y	0.5%	0.3%	0.2%	0.8%	2.9%	2.4%	8.4%	0.4%	0.3%	0.1%	0.0%	0.2%	0.1%	0.2%	0.1%	0.5%	0.6%	0.4%	
ERCC-00061	Y	1.1%	1.1%	0.4%		2.3%	0.4%		0.9%	1.1%	0.7%	0.5%	0.7%	0.7%	0.7%	0.8%	1.0%	1.0%	0.7%	
ERCC-00062	Y	1.2%	0.9%	0.9%		1.2%	8.7%		2.3%	2.4%	2.4%	2.4%	2.4%	2.4%	2.4%	2.4%	2.5%	2.4%	6.1%	
ERCC-00069	Y	0.9%	1.0%	1.6%		1.1%	1.5%		0.1%	0.4%	1.4%	0.4%	0.4%	0.4%	0.4%	0.4%	0.5%	0.4%	0.7%	
ERCC-00078	Y	0.0%	0.0%	4.6%		0.2%	0.8%		4.2%	4.1%	4.2%	4.1%	4.1%	4.2%	4.1%	4.1%	4.1%	4.2%	2.7%	
ERCC-00085	Y	0.1%	0.2%	1.1%		0.3%	0.6%		0.1%	0.4%	0.4%	0.3%	0.0%	0.1%	0.0%	0.0%	0.6%	0.6%	2.3%	
ERCC-00096	Y	0.1%	0.2%	1.0%		2.5%	0.2%		0.5%	0.4%	0.6%	0.6%	0.6%	0.5%	0.6%	0.7%	0.4%	0.5%	0.1%	
ERCC-00098	Y	0.2%	0.4%	0.6%		0.9%	3.0%		2.3%	3.5%	1.3%	1.4%	2.1%	2.0%	2.2%	2.0%	4.0%	3.9%	3.0%	
ERCC-00108	Y	1.1%	1.1%	2.3%		1.0%	1.9%		1.6%	2.0%	1.3%	1.2%	1.6%	1.5%	1.5%	1.5%	1.9%	1.9%	2.0%	
ERCC-00111	Y	0.0%	0.0%	1.5%		1.7%	1.4%		2.8%	3.3%	2.4%	2.3%	2.6%	2.6%	2.8%	2.7%	3.4%	3.4%	1.4%	
ERCC-00112	Y	0.6%	0.4%	2.8%		0.6%	1.0%		1.2%	1.6%	2.0%	2.0%	2.1%	2.0%	2.1%	2.0%	2.4%	2.3%	0.5%	
ERCC-00117	Y	1.6%	1.8%	0.6%		24.5%	3.1%		1.6%	1.7%	1.2%	1.4%	1.7%	1.9%	1.7%	1.5%	2.4%	2.2%	0.4%	
ERCC-00126	Y	0.5%	0.8%	3.7%		2.2%	2.3%		2.3%	3.1%	2.5%	2.3%	2.5%	2.6%	2.5%	2.6%	3.6%	3.7%	1.7%	
ERCC-00130	Y	4.4%	4.2%	5.1%		3.1%	7.4%		0.9%	1.2%	0.8%	0.5%	0.9%	0.8%	1.0%	0.9%	1.4%	1.6%	0.4%	
ERCC-00136	Y	1.0%	1.2%	2.7%		1.7%	2.5%		0.5%	0.2%	1.1%	0.8%	0.8%	0.7%	0.8%	0.9%	0.6%	0.7%	1.1%	
ERCC-00145	Y	0.6%	0.8%	0.6%		0.2%	0.2%		1.6%	1.8%	1.7%	1.7%	1.9%	1.8%	1.8%	1.8%	2.0%	2.0%	0.8%	
ERCC-00157	Y	1.1%	1.1%	1.6%		0.7%	2.1%		0.6%	0.9%	0.1%	0.0%	0.2%	0.1%	0.3%	0.3%	0.8%	0.8%	1.9%	
	Average	1.1%	1.1%	1.7%	2.6%	2.5%	2.0%	7.4%	1.4%	1.6%	1.3%	1.2%	1.4%	1.4%	1.4%	1.4%	1.7%	1.7%	2.0%	
	Median	1.1%	1.0%	1.3%	1.3%	1.9%	1.7%	7.0%	1.0%	1.2%	1.1%	0.9%	1.0%	1.0%	1.0%	1.0%	1.4%	1.5%	1.6%	

Table S5

Method	Total Intergenic Peaks	Overlap DNase-Seq	Percent of total	Overlap H3K27ac	Percent of total	Overlap both	Percent of total	Overlap eRNA DENdb	Percent of total	Overlap eRNA ENCODE	Percent of total
GRO-cap	5,890	4,898	83%	5,584	95%	4,676	79%	5,619	95%	5,378	91%
RAMPAGE	654	468	72%	577	88%	439	67%	602	92%	508	78%
CAGE	633	503	79%	586	93%	478	76%	595	94%	527	83%
Oligo capping	503	245	49%	329	65%	236	47%	355	71%	280	56%
STRT	138	113	82%	131	95%	112	81%	133	96%	117	85%
NanoCAGE-XL	23	18	78%	21	91%	16	70%	23	100%	17	74%

Table S6

Method	Total Peaks	Overlap DNase-Seq	Percent of total	Overlap H3K27ac	Percent of total	Overlap both	Percent of total	Overlap eRNA DENdb	Percent of total	Overlap eRNA ENCODE	Percent of total
GRO-cap	10,763	8,486	79%	8,616	80%	6,839	64%	10,411	97%	7,317	68%
CAGE	252	221	88%	237	94%	213	85%	242	96%	213	85%
Oligo capping	170	110	65%	127	75%	104	61%	136	80%	110	65%
RAMPAGE	161	138	86%	152	94%	135	84%	156	97%	138	86%
STRT	50	39	78%	46	92%	38	76%	49	98%	38	76%
NanoCAGE-XL	16	14	88%	16	100%	13	81%	16	100%	12	75%

Table S8

Method	# of Steps	Time (hours)	Cost per library (\$)	Input (μg)
CAGE	14	62	81	5
RAMPAGE	8	29	104	5
STRT	4	9	27	0.01
Oligo Capping	7	41	315	40
NanoCAGE-XL	6	11	177	7.5

Table S9

Lab method	Sequencer	Read length (bases)	Paired end?	Custom sequencing primer (5' to 3')	Index Read	PhiX added (%)
CAGE	HiSeq2500	50	yes, no	no	In-line	1%, 0.5%
RAMPAGE	MiSeq	75	yes	TACACTAGTCGAACTGAAGGTCTCCAGCAGGG	Separate	1%
STRT (10ng)	MiSeq	75	yes	no	Separate	1%
STRT (8 samples, higher input)	NextSeq	75	yes	no	Separate	1%
Oligo Capping	HiSeq2500	50	yes	no	None	1%
NanoCAGE XL	MiSeq	75	yes	GAGATCTACACTAGTCGAACTGAAGGTCTCCAGCA	In-line	30%
Standard RNA-Seq	HiSeq2500	101	yes	no	Separate	not known

Table S10

Method	Sample/Tissue	URL
GRO-cap	K-562	https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR1552480
CAGE (Rep. A)	K-562	https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR390536
CAGE (Rep. B)	K-562	https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR390537
RAMPAGE	K-562	https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR424591
CAGE	MCF-7	https://www.encodeproject.org/experiments/ENCSR000CJO/
Oligo capping	MCF-7	https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR013349 , https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR013351
CAGE	mouse hippocampus	http://fantom.gsc.riken.jp/5/sstar/FF:13-16E8
STRT	mouse hippocampus	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE60361
CAGE	Adult Frontal Lobe	http://fantom.gsc.riken.jp/5/datafiles/latest/basic/human.tissue.hCAGE/frontal%2520lobe%252c%2520adult%252c%25200pool1.CNhs10647.10040-101F4 hg19.nobarcod.bam
CAGE	Fetal Temporal Lobe	http://fantom.gsc.riken.jp/5/datafiles/latest/basic/human.tissue.hCAGE/temporal%2520lobe%252c%2520fetal%252c%252020donor1%252c%2520tech_rep2.CNhs12996.10063-101H9 hg19.nobarcod.bam
CAGE	Adult Temporal Lobe	http://fantom.gsc.riken.jp/5/datafiles/latest/basic/human.tissue.hCAGE/temporal%2520lobe%252c%2520adult%252c%2520520pool1.CNhs10637.10031-101E4 hg19.nobarcod.bam
CAGE	Adult Parietal Lobe	http://fantom.gsc.riken.jp/5/datafiles/latest/basic/human.tissue.hCAGE/parietal%2520lobe%252c%2520adult%252c%252020pool1.CNhs10641.10034-101E7 hg19.nobarcod.bam
CAGE	Fetal Parietal Lobe	http://fantom.gsc.riken.jp/5/datafiles/latest/basic/human.tissue.hCAGE/parietal%2520lobe%252c%2520fetal%252c%25200donor1.CNhs11782.10072-101I9 hg19.nobarcod.bam
CAGE	Adult Occipital Lobe	http://fantom.gsc.riken.jp/5/datafiles/latest/basic/human.tissue.hCAGE/occipital%2520lobe%252c%2520adult%252c%252020donor1.CNhs11787.10076-102A4 hg19.nobarcod.bam
CAGE	Fetal Occipital Lobe	http://fantom.gsc.riken.jp/5/datafiles/latest/basic/human.tissue.hCAGE/occipital%2520lobe%252c%2520fetal%252c%252020donor1.CNhs11784.10073-102A1 hg19.nobarcod.bam
CAGE	iPS	http://fantom.gsc.riken.jp/5/datafiles/latest/basic/human.timecourse.hCAGE/iPS%2520differentiation%2520to%2520neuron%252c%2520control%2520donor%2520C11-CRL2429%252c%2520day18%252c%2520rep2.CNhs13825.13428-144D8 hg19.nobarcod.bam , http://fantom.gsc.riken.jp/5/datafiles/latest/basic/human.timecourse.hCAGE/iPS%2520differentiation%2520to%2520neuron%252c%2520control%2520donor%2520C11-CRL2429%252c%2520day18%252c%2520rep1.CNhs13916.13424-144D4 hg19.nobarcod.bam

Table S11

ERCC Spike-in	Sequence
ERCC-00002	GGGAATTCTCCAGATTACTTCATTCGCCAAGCTGCTCACAGTATACGGCGTCGGCATCCAGACCGTCGGCTGATCGTG GTTTACTAGGCTAGACTAGCGTACGAGCACTATGGTCAGTAATTCTGGAGGAATAGGTACCAAGAAAAAACGAACCTTTG GGTTCAGAGCTGTACGGTCGCAGTCAGACTCGGATAGGTCTCAGAAAAACGAAATATAGGTTACGGTAGGTCCGAATGGCAC AAAGCTTGTCCGTTAGCTGGCATAAGATTCCATGCCTAGATGTGATACACGTTCTGGAAACTGCCTCGTCATGCGACTGTT CCCCGGGGTCAGGGCCGCTGGTATTGCTGTAAAGAGGGCGTTGAGTCCGTCAGTCAGTGCAGCTGCCCCCTTCAGCCTTTGG GTCCTGTATCCCATTCTCAGAGGTCCGCCGTACGCTGAGGACACCCTGAAACGGGCATCGTCGCTCTCGTTGTCGA CTTCTAGTGTGGAGACGAATTGCCAGAATTATTAACGCGAGTTAGGGCAGCGTCTGAGGAAGTTGCTGCGGTTGCCTT GACCGCGGGAAAGGAGACATAACGATAGCGACTCTGTCAGGGATCTGCATATGTTGCAGCATACTTAGGTGGCCTTGG CTTCCTCCCGAGTCAAAACCGCGCAATTATCCCCGTCTGATTACTGGACTCGCAACGTGGTCCATCAGTTGTCGTATA CCAAGACGTCTAAGGGCGGTGTACACCCTTTGAGCAATGATTGACACAACCTGCGATCACCTATACAGAATTATCAATCAAG CTCCCCGAGGAGCGGACTTGTAAAGGACGCCCTTCGCTGGGTATAGCTTCACTGACGGCTAGTACTGGTAGGCCTAGCAC ACATCTGGTTGACTAGGCGCATAGTCGCCATTACAGATTGCTGCCATCAGTACTGGTAGGCCTAGACCCGTGACTCG TGGCTGAACGGCGTACAACCTGACAGCCGGTGCCTGCCTTACCTTAAAAAAAAAAAAAAAAAAAAAA
ERCC-00003	GGGAATTCCAGCAGCGATTAAGGCAGAGGCCTTGTATGCCATTATAAGAAGTTCTCCAGCAACTCCTTCTTAATT CAAACCTAGCTTCAGTTATAAATTCCCTCCATGATTGGGATTTTATAAACCTTTCTTCATATAATTCTATCTTCTTC TAACCGCTCCGAAAAACTCAACTTAAATCCAACCTTAACGCTCATCAGCCATGTCTCCACAGCATAAAAATAGCAGT TGTGGACATGTTAAGACACACTGCCCAATCTCTCTAACATTGATGCTCTAACACTCTGACTTTAGGGTGGCATATCTGTA TTATAAATCCTGGTCTCCATCTGGTTTTGATGGAGGGACATATTCTCAATTCTGCTCTGCTGGACACATTATAACT GAACAACCAAAACCTGTTGCCCTGTAGCTGAATCTAGCCCACCTCTTGAGCTGCTGTTATTAAAACCTTGAACACCA TATTGGGAATGCTCTGAAATGTATCTCAATATAACTCCATTATTCATAGTTCCCTCCATTAGATTCCCTCCATTAGATT ATAGTTATCTTAGGGCTATTAAATATCTTATTCATTTGGTTTAATATCGATAATCCATAAATAAAATATCAACAAAT AATTTAAATAATCTAAGTATAGGTAAATAACAATTAAAAGATTAGAGGGATAGAATTGAACGGCATTAGGAGAATTGTT TTAGATATATTGAAGCCGATGCCAAAATAACAGATATGGCATAAAATTACATCATTATCAAACATTGATGGGTTAA TATTACAGTCTATGAAATAGATAAAGAGACTGAGAATGTTAAAGTTACAATTGAAGGGATAATTAGATTGATGAGATT AGGAAATTATTGAAGTTGGGAGGGACTATTCACAGTATAGATGAGGTTGTCAGGTAAAAGATTATTGAAGAGTTAGAA CACCACAAGATAAAAAAAAAAAAAAA
ERCC-00004	GGGAATTCTCTGCTTCAACAATAACGCTCTTCAAGGCATTGGTATCTTCCCCACTTCCAAGCATTTCAACTAA TCCTATGTATTAACCATTCCCTAAATTCTCTGGGTCTGCTGACAAAGCATGATCAGGACCTCCATATTTTATCTAAGG TAAAGTGCCTCTCAATAACATCCGCTCTAAGGCAACAGAAACTACTGGGCGAGTATTCCAATGTATGGTCAGAATATCCC ACAGGGATATTGAATATACTTTCAAGGTTTAATAGCCTTAAATTGACATCTCATAAGGGTGGTAAGATGAAATACA ATGCAATAAAATAATATCCCTGCATCCATTATTTCTAAACTGCTCCAAATTCCCAATATCAGACATTCTG TAGATAAAATCACCGGCTTGCCTGTTCTAATAAGGATAAAAGTTAAATCACAGAGGAATTGAGGTTGTCAGGTAAAAGATTATTGAAGAGTTAGAA CAGGCACATAAAAAAAAAAAAAAA
ERCC-00009	GGGAATTCCAATGATAGGCTAGTCTCGCGCAGTACATGGTAGTTAGCCAATAGATGCCAGTACGCTGACGGCATTAGAGT ACGCTGATCGGCTTATGACGTATGTGACGCAGCTCTAGCGCAATGTATGTGCTGTTATCGAAGCCTATGGCTGAGTATGTA CGCTATGGCGTCTAGTCGTCTCATACGTCTGATGACCTCGTATCATGTTATAGGCTGCGAAGTCGATGATGGTCACG ACTCTGCGTAGCTGTGTGACTCATTAGAAGGTGTGAGCCTATATGATACGAGTCGATCCTATCTACGTGTCAGTAC TATGTGTGAGTGCTCCGCCCTAGTGCTGATGTGCTGAGTCAGTGGAGTCTCTTAGCATAGTGTCCGCTCATAC ATTAGATGGACGGCTCATTAGTATCATCGTCGGCTGATATAGGCTGGCTCCCTGTATATCGAGGTGAGTCATCTGGATCA ACGTCGACTATGATGTGCAAAGTGTGCTCATGTATAGACAGTGCAGCGTATCATAGGATGCGCGATCTCATACAGCGTT ACGGTCGCTGCGTACTGTATAAGGATGCTGTGAACTGTCATCGGCGATCAATTAGTCTAGTGTGCGTTATTCAAGATCGA GTGAGTACATGATCGTCAGTGTGGATCAATTACAGTTAGGCCGCTGACACATTAGTAACGTCGGAAGCAGTCAGTC GTAAGGCCAGTGTGCTGTCTAGACGACTGTGTGATTCTCGAGCGATTATACATCCGTGACAGCGCTTATAGTGTGCTG ACAGACTGGTGGTTATCCAATGATGACACCTGGAGTCTAATATCTGACCAACGCCCTGTAATCGTATGACACCGCCTGACACG ACTGAATCCAGCTTAAGAGCCCTGCAACGCGATATACAGGCCTGCTACCGATATAAAAAAAAAAAAAAA

Table S11

ERCC-00012	GGGAATTCCGAGAGATGTTGTAGGTGCGGAATGTGTGCGGTCTACCTAGTGTAGTGTGCGATGAACCTACACACAACGTG GTATAGTGGCGATCTTAGAGTGATCCTATCACTCCTACGCACCAGAAGGGATCTGCATACCAGGCGGAGAACCTTGAAGGC GGCTAGATCACTGAATTGCGGAATCGCATTTCGCATTCTTAGGATCTAACCTTAGACCTCCGCGTGCATTGCACCTGCT TGGTACAGAGTTACAAGCCCCCGCAGAAGAATCGATAGAGCCGCGTGGGACCTTGATGGTATCTCTGCCTCAGCTAACCTGCTAGGTCCG TCCCCTGGGATGATCAGGACTCGGGATAGTAAATTGCGGGTTGAAGCCGACTTGCCGCCTAGGCAAAGCACAAAACATC GGACATGTAGAAGTCTCATCGAACTCCTTCCCGTTATGCAGATACTTCAACTGTGACTAGTGGGTTCGGGAGCACCCGCA CTACTTCATTCTTGGCGGTGGCCACTTATGTGACTGTACATGGACTCTACTCATACCAATGTAAAGTATAGTTAACGCC CTGTCCACTCTACTCAGGCGTAATCATCGCGGAAGGCTATCCACAGCCATCAGCGGTCTACATGTCCCAGCAGATTCACCTG TCCTGCGGGTCCCGCTCACAGCCTATTCTGAGGCTCTAAAGACTATGCGAACCAAGGTGTCCAGTCAGACGACGAAGTC GGGAAGGAAGCATGGATACCAAAAAGGTTTATATACTGGGTTACCTAGGGATGTTTACCGGACTGGTCAGCCTCGGTG CGCTCGGCTAGGCCTACTGCATGGGGCTGTGGCAATTGGTATTCTCAGGACTATGGACAAAAA AAAAAA
ERCC-00013	GGGAATTACCGAGCTCAGATGTGAAGGATCTTCTGGAGGATTAAAAAAATGATTATCTGTAAACCCCACGTGAACTTGGT ATCATGCGGAAGCAGGGCGAATCGTGGCTTAACTCATGAAGAGTTAAAAAAGCACATTAAACCAGGAATCTGACAAAAGA ATTGGATCAAATTGCCAACGTTTATTAAAGAACGAGGGTCAATCCATCTTCTAGGGGTATAATGGGTTCGCGGGAGCA TTTGCATCAGTTAATGAAGAACCTGTTACGGCATACTGGCAGCAGGGTCTGAAGGACGGTACATCATCAGTATTGAT ATCGGTGCTAAATTAAATGGTTATCATGGTACTCTGCATGGACATATCCGTTAGGAAACATCAGCGATGATGACAAAAAACT TCTGGAAGTGACAGAGGACTTTATATAAAGGCTTGAGGAAGCAGGAAACCAAGGTGAACGTTGTCGAATATTCCACGCAA TACAAACGTATGCGAAAATGAGCAGTTTCAAGTGTAGGGAGTATGCGACATGGTGTGGCAAGACTGCTATTGAACCTATGGTAA CCGCAAATTCTCATTACGGTCCGCCAACAAAGGACCACGGCTTAAACCTGGCATGGTCTCGTATTGAACCTATGGTAA CGTGGCAGCGCTACGTGAAAACATTGGCTGATAACTGGACGGTTGAACGGTAGATGGAAAAAGTGTGCTCATTGAAC ATACGATTGCGATTACGGAAACGGTTTGAATACTGACGAGAGTAAAAA AAAAAA
ERCC-00014	GGGAATTCGAGCTCGTACCAAAAGAACAGAACAGGAAAGTAGAGGGAGATCAAGATGTCAAACGAAACAATTAAATTAGTCATTGCG GGACCGCGTGGAAAGAACGGGGCAGGAAGCTGTTAAATTGGCAGAACGAAACACCACATTGACCTGTAGGGGCCATAGACCA TACATACGATCAGCAAAATTATCTGATGTGATGCCTGTTGAGTCAGATGCTTCATTACACAGATATCCTGCGCTTTA CAGAAACACAACCGGATGTCTGATTAAACAACGCCAACCGGAAATCGAAAAGTACATACAAATTGCAATTAGACGACGTA GTCCGTCCAGTTGTCGGAACAACCGGTTCTCAGAAGCTGATTAAAAGAGCTCACATCTTAAACAGAAGAAAAGGATCGG AGCCATCATCGGCCAAATTGCGCTCGTGCATACTGATGATGAAATTTCAAAAATGGCTGCCACTATTGAGGATG TTGAGATTATTGAGCTTCATCATGACCAGAAGCTTGACGCACCAAGCGGAACTGCGCTTAAACAGCGGAAATGATTCA GTCCGTAAGAAAAGCAGCAAGGACATCCGGATGAAAAAGAAATTCTCCAGGAGCAAGAGGAGCGGAGCAAAACGGTATTG CTGCACAGCGTCCGTTCCGGACTGATCGGCATCAGGAGTCATGTTGGCATGGATGGCAAACGCTTCAGATACGCC ATGATTCTATAACCGTGCTTCTTCATGTCAGGCGTTAAACTGTCAGTCAGACAAAGTCATGAAGATTGATCAGCTGTG GGTTAGAAAATATCATTGATTAGACGGGGGATAAACAAATGAAAATTGCTTGTGCGCATGACAAGAAAAACAGGATAT GGTCAATTACGACTGCCTATCGGATATTAAAGAATCATGATCTACGCAACCGGAACCACAGGGTTGAAAATTGAT AGGCACAGGTCTCAAATTGAACGTTCAATCCGGCCATTAGGGGAGACCAGCAAATCGGCACTGATCGCTGCCAAT GCACTCGATTTGTCAATTGCGGCCACCGCTGACCGCGCAGCCGATGAACCGGATGTCGGCATTAATCGTTATG TGATGTGATTCCATTCCGCTGCCACAAATATGGTACTGCGGAATTCTGTGCGCACACTTGATGAAGGTGTTTGAAT TCCGTGACCTCTCGGGAGAAGAGCGAATGTATAATGCTGACGTTCTTGCGCCACAGTGATGATGTCAG CGGAATGGCGGCACAATAGCGAAGTTGTCACAGGAAAAAGTAATGATATGCGATTGACAGAAGCGGAACCTCT CTAACGGTACGGTCAGTTGCGTAAAGAACGAGCAGCTGAAGCAGCCGATATTAGGCGCAGATAAAAGAATTGCTAACG CTTCCAGACCGCGGCCATAATGAGTGTACGGCAATTGGTCAATTGTCAGTCATCAGAATCTGCGCCAAAGCGGT TTTATGCCGTATAAAAGATGCCATCCGGATCACGGCAATGCGCTGCAGGGTGAAGAAGCGATCTTCCGCGGAA TCCATAAAATATAAGACGAAAAAGCCTTCCGGCGATAAAGTCAGCAAGGTTACTATTATGATAAAATGGTTTCTCAG CCGGATTGTTATTGATATCTGGATACAATAGAGGCAAAGAACAAAGCCTCAACGCCCTACAAAGCCAGTTACGGTAAAGAACGG GCGTGGAGTATGCCGAAGGTTCTTCCAAACGGATGCTGAAGCTGAAAAA AAAAAA

Table S11

ERCC-00016	GGGAATTGGAGCTCGTTAACGAATGTAATTAGGAGGCAAGAGAGTTGTGGCGCGGACTTGCAGCTCGTAACGCTCTAAA AGGGTTATGCCGCTGAGGCAGGGACCATAGTCAGGAAGGTTGTCCGATCCGCTCAGTTGTCAGAGTAGAGGAGTTCTGTGTT GCCGATACTGCCGAAAACGTCATACCGAAGCAATTCTGTCGCACTCTGTATGTCCGTCCCCCACCTCGAGTATGAGTTTA AAGTCGTGCAGAGACATAGCTCGCAGACTCCCTGTGATGCCGGCGACACATGCTCAATGTGCCTGAACATTGCA TTCGAAAGAATGTCCTTATCTTGATGCCATTGTAATGCAACGCTCTCCTTCAATTGACACGAGGTTGTAGATGGCTGTTA CTCGCGGACGTTAAATAAAACTATCAGCGTCAGCGATTAGGAGGCTTACGGGGAACCTACAATTGTCGCCGATGGTCCG AAGGCGCCATGTCCCTCAGCGGAGCGACAACAATTACTACTGGAGCTATTGTAATACGCAACAAAGCGTCCAGACATTG CCGCTGACCTCCAGTCGATGGACGGGGAGAACAGCTGGAGCAATGCATTCGCTGAGGGACATCCAATCACGGAATCAA GGAAGAATTACCAATTACCTGTAACGAAACCAATTATTACTGACGCAGAGTGAATCACATCTATAGCGTTACGACCCTC CAGAGTGTACCGACGGCGATGTGTTGACCCCCGTGTGACTGGTGTCTGATCCGCAACATGTTACTCATCACTA CGTTAAAAAAAAAAAAAA
ERCC-00017	GGGAATTGGAGAACTGAAAGTGAGTCCAACGAGAGAGGTCATCTGTCAGTGAGAGCTGACTGTCGACAAACACTAGTC GGTCCAGGCATGGATTGCGACCTCACAACTTAAGGAGGCGTAAATCAGATGACAGCGCGACCTGTAATGGGTGACCTGC TAGTGGAGGTGGCGCGGTGTCAGATAAGGATCTCGATGTAGTACCCCTCACATAACTTGCTCCCTGAAATAACATTGCA TCACTCTAATGAATCCCTTAAGCCAGGAGCGTTAGTGTCAAACGCAACGCCCGGTTCATGATCCTGGATGGCTGGTCAAC CAGGGAGATGTCACTCTAATAGGTGCCAAATGTACCGCAGAACCTCGTAGGCCGTTGCCAAATTGGACCCGAGGTATAATGTA GACGGGCACGCTGACTGGCAAAAGATTACAATCCCAGTTACCATACAGTCGCCCGGTAGGATGGGGCATGAAGGCAATAT GTTGGCGCATCCCAGTCTTCCGTAGAAACAGTGGCTAACGACGGAGATACTGCCGGCAAGAACCTTGACCAAGTATGCGC GCCTTGTGAGTCTCATGGACTTGCTGCACCTACAAATCCGAAAGGGCGTTAGTGCTGACTCCCTGGAATATCT TAATCCCAGCTCATGGACGGAGGAATGTGTTAGACCATAAACAGAGGCTGGCCAACAATCAGAGGAAAGTAAGCCCC GCAAAAGGATTCTGCGGGAACCGAATTACACACGTAAGGACGTACCTGCTCTACCCCGAACCAACTGTCAATACGATAATG CGCCCAAAACGAGGGATCGAGACGGTGGAGTGGCAGTCCAGCTAACAGGTGCTGCCGAAACTAGCTGCCAGGGTGAAG CATGGATTCAAAGCCAATGACCGAAGAAAGTCCGACATACAATTACTCGGCTTTGGCAATACCCAGGCAGAGGTAAGCCC AAGCCATACCGGAATGACCTGAGATCCACTTAGTAAGTCTTACGAGATGATCCGACCCAGGACTGGAGCTAGCGGTTGCG CAAGTAACCTCATGTATCGCTGGGAATAATGTTCTGGAAAAA
ERCC-00019	GGGAATTCTTAATGGTTTACATACTTGACGGATTGCACTGAGTGTATTCCGCTCCATCGTATGGTAACCCATAGGGC GTGTCATTCACTCGGATAGTGTGTTGACCGCGTCGCTCCATGTCGCTTTCAGGAGAAATAGTACAGGCTGCTGGCTCA TGTTCCTCTACGCTGCACTGCGGCATAGAGGTGGTGCATCTATATTGAGATAACTATTCAACCGCGCACTCG AATATCCCCTCTTGAGCAAGAGGCCAATAAATGCTAAAAACGAGCGATTGTCACGACATAAAGGGAGACTGTAAGGTC CTAGCGCTGTCTGTTAGTGTGAGAGCCCTAGGTAAACACGGTGTGTTACCCCTAGAGCGTGAAGGGCTGTAGATATCTGA ATCTCGACCTTGGTAGATGGGCTAGGTCAAAAGCGGTAGCGATTGCACTTGATACACTCTCCCCACTAAGTATG TAAGGCCTGACCGGAGATTGTCCTGCTCACCGAGGACGATAGTGGGCCCGGTAATCTGCCCGTAGGGAGTACGAGC AGTGCACCGTTGAAACAAGCACAGGAGGTATGAAGCATCAGACCTGAAAAA
ERCC-00022	GGGAATTCCCCGGCCAATTGCCCTATAACTAGAGCTGAGGCCACCATAAGCGATTTCGCACTAGCCGTAATAAAT ATAATGATCCCGCGGTGAGTAATTCTACGGAATGCAACGGAATGTCAAGCAGAAGGACGTGATGTGCAACCTACTCCCTT TCCCAAGTAAATGTACGGAAATTATCGTTGTTACCGACAACCATGGGCCACGTGGCCAGTTGCCCTATTAGGTGGATA GGCACTGAGTACAGAATATAAAGCGTGACGGATGAAACGCAACCCATTGTCACCGATTGACTAGTTGACCTATCACCC CTACTGTGTCAGACGTCGTTACTAAAGGCCGTGCCCGGAAGCTCATTAAAAAGAACCTGTAAGTAAGCCGGCAGA TATCTAGCAAAACATAGTCCCCCTCTGCTCAGAGGTATCCATAAGTGAATTACAGATGGAGTGCAAGGTACAGACCTCC CTCCCAACTGGTCTGCAAGGACGTTGCTATATCACTTCTGGCGTCTTATGGGTTACCCCTCGCAGTGGCATCGCATCGA CTGACACACCTGCATTCTATTGCTACTGACGGCGACGAGTTTGAGCGTCACTGCGGAGTTAAGGTCAATTGGG GAATAGAACCATAGCGTTGGGTTGTGACTTTCTCCCTAGATAACCGTTGCTGACTGCGCTACATGGATAAAAAAA AAAAAA

Table S11

ERCC-00024	GGGAATTACGGAGGAGCTTGGCATACTAGGCTAGCGAATCTGCAACTAACGCAAGTTACATCCTAGCTAGCGAAGGGCGTC CCAATTTCGCTAACCCGACGCGACGCATAAAAGCGAGAATAACGCCAACGGGATGTACAATGGATGTTGATTATGCCCTCG GGAATGAGGGATGATTGCAAAAACAAGTCAATACCTAACCAATCCGCTAATGGACACCGTAATCGTGCCAACGTTAAC TGGTCGGTAGGTGGCAGGCAAAGCGCTAGTATCCCTAGGCGCACACTATAAGTTACAACACTGCGAGAATTGACACTATGAGC GCGCATACTGGGGCCAGAATAGGCAATACCATGTGCGTCCCTGTGTGAACAGCTCGCGGCCATCAGAAGTTGGGATTGACGCA TGATCTTGATCGAGCATACGGCTCCACCAACCCATAGTACTTGGTAACTATAGCAATCAAGCACCGTGAGCACAACGCTAT CCAAATTACTACATTAACGGAAAAAAAAAAAAAA
ERCC-00025	GGGAATTGGGGTCCATTATAGTCAGGGTGGTAAAGTAGCATTAGAACCTACTACTTAGCCCGCAACTCGTCTATTAA AAAGTCGGAAGGATTAGGGAAGTTAACCTCCGTTAGGGCCTCATTGGCGCGCCTCCACGTATCTGTATTCCCGTGTCCCGACT GGCTAATAAGAGATATGGTGCAGCGTAAACGCCGACCAGAACCTCCGGTGTGCCCGGTTATGTTACTCGAAAGAAATAGACCC CTTGCGCCATGTCATCTTCACTACGGGTAGTCTCTCGGCCAGGCTTGAATCGCTCATCCGCTCTCAATGGTTCTGTCC TGACCTCTGGAGTTAATCTTGTCTCATAGAGTAACCAGGGCACGCACCACGCTAGTTGGTACCACCACTAGAACGCCGTT CGCTGGCTAGTGTAAATATTCTGGAGGTCAAGCCACAGGTCACATGAGCCTACTCGTCTCGTAAACACCCGCTAGCCATG ATTAACAAATAACAGTGAATTAGTGTGTTGACCCCTAGTGTAGGTCGCTGGTACTTAGCAAGGGAGTTGCATATGTGGTCT CTGTTTGGGTTATATCTATTCATTGACACCCTATTGGTTATCACAGTCTTCCACAGGACCATACGGCTGTAAAGAA TACCCCTCTAGCGTTGGAGAGAATAAGTCGATGTTCAATTCAACAAACCGAGCAAAGGCTTGTGACAGCTCTACTAGTATT CACTACCAAAACCGTACCGACTT TAGGGCGGTAGAGAGAATTGCCATTGCCACAGGTTCTCCAGAATACAGGTCCAGGCG GCCCGCAGCATGGAGTGCCTGAACCTGGGGATGCCAAGATTGTAGAGGCCTAACGAGTTGATAACGCCGGACTACG GGCATTGTCTGCCGTCTGTTCAAGTAAACGATCAACCGAGACCAGGTTATTCCCATGTCGTCCTTCAAGGCTTACTAGT CGGAGATAAGGCTGATGTTAGGTGCCTGCTAGCAAAACGCCACAGCTTATGAGCATACGGCTGGCGTAGGTCTAG AGAGGGTATGTAAGATCTCTCTATCGGTGTGCGTCTACTCTGCCCTTCGACACAAATGTACATCGCGGGAAACGGATA CGCCTACGCCCAAGGTTAGCGTATCAAAATGCAACGATTGGATGTCAACCTGGATAGGAGCGACCGATTACGTGT TAATTGGCCCTGTACCTTCTGGTCCGTTGATTACTCATCCCCAGGTTGTTATGGTCTACCGTGGAAACCTCGTCAATGA ATACTTGAGCGCATTGAAGTGTCCCTACATCGGGCTATCATAAAAATTCCCCTTAACAAAGGTTGTCGACGTCAAC GGCCCTGCAGTAGCGTTCTGGACCCGGTTGAGTACCCAGAGCAGACTACGTATATCCAAGTGGTTATGTCCGACGGCA TTTGCCAGGTTAGTATCTCGGAATGAGTTGCGTCTACGGCTAATCGAGAGCACTTGTCACTACGCGCAATTACTACATGG AGTGTATTGTTGAGCGCTGATACAGTTCTCTATCAAGGTCGCAAAGGTTGCTAGAAAAGGGCGTGCAGCAGTCTA CTGCTACCGCGACTTACGACGAAGTTAGGCATCAGACGACCACATGACGGAGAATTACGTACGCCACTTCAGACGTTCTGC CTGCGTGTCTGCAATATAGCGTAGAACGAAGCTCGGTGACTGCTATAGGAATAGCCTGATACGAGCGCACAAACAG AACGAACCAGCGAAACTACCCAGATAACATCGCTCCCCGGCATTACTCTGACGGGGTTGTCACTAGGCTGGTGGTCCTT GCCTCTCATGTCATTCCCTTGTGGCTGTTGGAAAGTACTGATACTAGAGTAGCCTAGTAATACCTAAAAAA AAAAAA
ERCC-00028	GGGAATTCGAGCTAAGAAAGTATTCCATTCCGGCTCATGGTCCCGGCTAGACCTGCAAGATCGAAGGTACTCAATGACACCA GTGACTGAGCGGTCAAGCCCGAAATAGCCAGAAATGTTACCATCCCCCATGTTACACAAACGTCGGCTGACGGAAACCC AGAACCTATGGTGAATAGACAGTAAACGAGCGCAAAGCGTGTGCCAACGGCTCCACCGAATGTAGAACATGGTTAGGG CGTACAGGGAAACCGCAATGCGAGGTTCCGCAAGTCCACCTATAATCTGTGACCGCTCGTAGAACATGGTTAGGG AGTAAATCAAGCCACCTCTGACAGAACGACGAGTCAGTGAATCGACTCACACCTCAGAGTCCACTCACGTGCTGTAAGTC AAAACCCAGTGAACCTCTAACCGTGTAGCGCTCTAGAACACATTAGGCGCCACTGAGGGCATATGGATGAAGCGTGATACG AATTACCTCAACGAATGCCAGCTGGAGGAGGATAGGGACTATGTCCTCGTCAATGCTCCGTCAAATGCCCTTCTAAATAC CTTTGACCTCTGTGTGGATGGGCTAGAACCAAGGACTAAAGCGGTGCACGAGGCCCTTGGATATGTCCTTCTTGG GAGGGCCACAGCCAAAGCCACCCATCACAGCTGAATCTAACCGTGGAGGATCTGAGGCTGAGGACTAACACCC AAGCGCTAGCTCCTCCCCGGTCAAGTAGTAATGCCGGATGACTTGCCTAGCGATCGAGCCCTGAATTACG CGTCAAAGGAAATGATCAGATTAAAGGGCTGTCGGGAGGGATGTGAGGCCACTAACACCC GTCTTCATCGGTACGCTCGAAAGCGCAGGTGGCTCCAAATCGTGGGAGTTAATCGAGCTGCGGATTGG ACGGCAGCGAACATAATCCCGCTGATGTGAAGTCGATCTACAAGGTAACACGGGAATATAATT CAGTTGAACCGGGTGGAGCCTGACTTGGCACTTGGGCTGTTGGAAAGTACTGATACTAGAGTAGCCTAGTAATACCT AGCCTGCACTTGGAACGCTGCATAAGGGACCCACAGCCCCAAAAAA

Table S11

ERCC-00031	GGGAATTGGGAGAAAGCTTCTGCCTAGTTACAGCACGAAGATTGGGACCCATCGATCAGCGCCTCCGTGCAATGGCGCT TGGTACACTCTCTAAAATGCAGTCGGTAGCGGGCATGTAGTTACTCGGGTGTATTAAGCTAGTGAGAACCTTATATCGAA CTGTCTACCAAATTGATGTATCTACATTAGCGTACGATGAGACAATGAACCGTGTCTACGCTCGGGAGCATTACCCCTATCA TGAGCCTACAAGCACCTGACTAGACCAGGAGACAACCTGAGCGAGACACTAGCGAGAGGTGCCATATAAGGTACATTGTC GGATGTCAACATCGATTTCATCCCCTGGGGATGCAACTAACACCAGTAATGTCCTCCACGACCCCTACCGAAAAA CTTACTCGTATGAGTACTTCGCGACCGACTCGGTGTAGTTCCAAGCAGGCCCTGGCTAGACCCATTGTACCACCG AGGATCATCGGAATCCATAATCGGCCACAAACTAGCCGGCTGGAAACCTTGTGATATCATGAACGAGGAGTAAGAGCTGGTTA GTGAATCACCTTGAGGGCGAGGAACACAACAAATTCTGCGGTTAGCAGGAAGGTTAGGAACTCGCTCATAGCATATTAGTAC CGCTATCTCCTTCCCTGGCGACATCTCCAAAGTTAGGCTGATTCTGCCCTGTGATCGCTATCCTTATTGTGGCAGA ATATGTCGATGCAAAAACCTTAATTGCGCTTCATACATCATCCCCGAGAACTCCACGGCTCCACTCCGTTATCACCGT GGGTGCTAAATGATACGAAGTGTGGCAGTCTATGTTAACTGGAGCATCATATTATTCTGTTACGGATGAAGGCCTATAT CAATGATCATTAAAGACATTCCGTACATCGCTACATGCAAAGAGGCTTCCACCCGTGTTCGGTGATTCAAGGTGAGCGA CCATTATCTGCGGCTCATACCGAACCGCCGTGATAGAGTCTCGCATCAGGTACACCATGTCGACTGATAGTAACTGTG GTCGAGTTATGCGTGTGACACACCCTGAGGCGCCCTATTAAAAAAAAAAAAAA
ERCC-00033	GGGAATTGGAGCTCGCACGCCCTATTAACTGGAAACCTTCCAAGATTGGAGAGCATATAAGTTGGGCCGAAAGCTCAGCTG TGAGCTTGCAAACACTGTCTTAGGAGCTAAGACAAATAGAGAACGGGCCATCAGCATTAGCAGCTGCAATTATTGGAAAA ACACCATATTATGGATATCACTTAGATGAAAATAGAAAGACAAACACATATCATTGAGTTAGATGGACAATTATCTAACTT TAAATATGGAGAGAGTTTATGGAGCTTAGGTTACTTAGTTGGGAAGATTGTTAAGAATGGCATTCCATATTGAAAATC TATATAAATTAAATCAAATAACGATAATTAAAATCCTGGGAGCTGCAATGGCTGCAAGTGGTGTATGCCCTATATCAC GCAAAAAACTGACAGCTGAATGCAGAGTTAAGAACAGTTGTTAATGATAAAATTGAAAAGATATCTATTGGAGTTGAGGAGAT AAAGGAAGCTTATGAAAATTAAATACAACAAATGAAGAGCCAGATTAAATTGTTATTGGTGCCTCACTGCAGTTAATGG AAATTAAAAATTGCTGAACCTTAAAAAATTGAAATGCTGATTGTTGGCTGCTCTTCATATTAAAGCA ATAGCAGATAGAATGGGATATACAAAGATTATTGAAAAGCTGGTGGAAAGGTAGTTAAAGACACCTGTATGGTTCTCC AATTGAGGATTAGGTTGTTGAAAAGAGTTGCAACAAACTCTGGAAAAGCTGCTGTTATCTACCAAGCTTGTAAAGAGTGAAG TAATTGGAGATATTGAGGAATTGTTAAAAGGGAGATAATGCTGAATCCAATACTTATTGGCTATTGGCTATTGGCTATT GAATCATTGGGAGTTGCCAGAGTATTCAACGGTTGGATAGGGAAAGTTGATAGCTTTTAGAGAACATATTAAA TCTACAAATTGCAAATAATAGAGATTGGTTGGCTCACTGAAACGTTATTACTCTATTAGTTGAGGTT AGCTTTTTGTTGATAATGCTTACCATCTCCTTAAACTATATTCTATGGTTGGCTATTGGCTATTGGCTATT TTGGCTACAAATCATTATCGAATTCTGCAAAAGCCGATTGAATATATAAAAGGTGATTAGAGGGAGCAAGGAAAGCT GTTCACTGATAGTTAGCAGAGATGCCCAAAGTTGGATAAGAGCATGTATTATCGGCTGCAAGTGGAGCTTATCCGAGAA CATACAGACAGTATAATTGGAGCTTATTCTATGCTATATTGGTTGGCTGGAGCCTTGTATAGGGCGATAAAATA CATTAGATGCAATGATTGGTTATAAAATGAGAAATATCTATGGTATGGGAAGTTAGCAGCAAGGTTGGATGATATTGCCAAT TTTATTCCCTCAAGAATAGCAGGGATTGCTAATAATTACTGCCCTATTATAAAGGAGATGTTAAAAGGCAATATATGG GTTTTAAAAGAAGCTAATAAGGTTCCATACCAAACCTGGTTATACAATGGCTACATTGGCAAATGCATTAATATAACTT TGGAGAAGATAGGATATTATAAAACTTGGTAGTGGAAAATAGATGTTGAAAATCTTAAACGCTTTAAGGCAGTTGATTAT ACAGTCGTGTGTTAATTATTACCTAATTGGTGGATAACATGATAAGTAAAGCTTATTACACTACAGAGATTCCA GAGGATAGATTGAGCTCTGAGTTGTTAAAGATAGTCAAAACCTTAAACTTAGGATTAAAGTTGCTATAGTCGATAGTGATAGGGC TAAAACAAACATTAGCTACTTTGGCAAATGAGCTTTAAACTTAGGATTAAAGTTGCTATAGTCGATAGTGATAGGGC AGAAGAGCATTACCTCCAGCAAAAAAAAAAAAAAA

Table S11

ERCC-00034	GGGAATTCCGTATTACCCAGCACTCGTATGGCGCCCCATCGTTGATCAGCAGGAGCATATGTTGCTCTGATTGTATCACCTCGCGAGAAAGACCCCTTGAATACACGAGCTGCCGCCGGATAACGATGTAATAGCCTATGGAGGGGAAGTAGTCATGTCTGCGGACTATTGGTAAGAGCACCCTCGTACGTGGACACGAAGCTGTTGGCCGCACGCAAGTACCTCCCACCTAGAAAGCGATAAACCCAACGACCGTGTCAACCCTGGCGTCTCTCAACCAGGTATGCAATCACGACATTGGCCAGATGTAGGGCGTCTGGTGGATTGAAACTCGGATCGATCACGTATGGCTAGACCTTACAACACCTGTGCGTGCCTGCGTCTGGCGATGGTGGTAGCGGCCGGACGATCGTACTGTAGGCAGCCAAATGCGGATCTTAGGTTGACCGATTGTACATCTGCCATAGCCCCTTTCGTACAACCTTATAAAAGGGTCAGGCCACTGTGTGAATCAGATGGCAAGGCCGTACGGTATAGAAACATACGTTCTCTGGCCACGACCAATAATTATGCACTGTTGGCTCGGAAGGGTGTGTGAAGGATAACTGTGCCCTTAAGTAAAGCTACCGTACCGCCGGTCTCTGATGCTACGACCAAAGTGGTTGACATTACGCCAGTAATGGACTAAGGTTGAATTGAGCGGATGGGCTCAACTGCGTCGTAACCGGTAGATAACAGGGCATACGAGCCTCCATTAAACGGCATCATCCCGCTAGTGCTGGTCAACCGACTGTCTATTGAAGTCAGGTTGGCTACATCAGCTGGAACGTTCCCTAGCTACTATAATCAGGCAATCTGTCCGAAGAGCCCACACCCGTACTTGGCCGTAAGGGAGCCCTAAATCAGTTAAATAACGGGAAAGGAGTCTGCCCTCCGGTGATCCATCTTACCAAAAGACATGTCCACGCCTGTGGCTCTGAAGATGGCGACACATGTCTACCCCTGGCATAACGCCAGCTGATAAGAGTGAACACGACCATCTGACACAGGCCGGCATAGAAGACCAGCGCAATCGGAGGGCCACACATAGGAGTGTGAAAATCTACATCAACATACTCGGCCGTGGCTGAACGAGGGAGTGCTTACAATCCGTTGGCTGGCAGATTCCGGAAATGAGCAAACGCTTCCCATGAACACACTCACAGCATAAGCCTACCTTGTCAACATCGCCCCGAATGCAGAGCCACCTACTGGGTTGTCTGAGAACACTCCATGGTCAAAAAAAAAAAAAAAA
ERCC-00035	GGGAATTGGGAGAGGTATGTAAGGTGAATCCTGTGGCTGTAGGAAGCAGTTCATATGACCAACGGGCCCTAGGGTATACTCCAGAACATGAATGTTACAGAAAATAGGGGAACCTGGTCGCTCCTAGGTAAGGTTGCCTGTCCCCGACTGTACGAAGGTCCGGTCAACGGAAGCAGGCACACGCGCTATCTGAGTCAAATACTTGATCCGGCCGGAAAATTAGAGGTGACGGCTTCCCACTACTGATCTCACTGACGTGCAATCATCCTGTGTCCGGAGCAATGACAGTGTCCAGTCTGTATGGACGAGCTGGACGATTACAGATAAAGGACAGTCCGGGAGGAGTGTGAAGGATAACTGTGCCCTTAAGTAAAGCTACCGTACCGCCGGTCTCTGATGCTACGACCAAAGTGGTTGACATTACGCCAGTAATGGACTAAGGTTGAATTGAGCGGATGGGCTCAACTGCGTCGTAACCGGTAGATAACAGGGCATACGAGCCTCCATTAAACGGCATCATCCCGCTAGTGCTGGTCAACCGACTGTCTATTGAAGTCAGGTTGGCTACATCAGCTGGAACGTTCCCTAGCTACTATAATCAGGCAATCTGTCCGAAGAGCCCACACCCGTACTTGGCCGTAAGGGAGCCCTAAATCAGTTAAATAACGGGAAAGGAGTCTGCCCTCCGGTGATCCATCTTACCAAAAGACATGTCCACGCCTGTGGCTCTGAAGATGGCGACACATGTCTACCCCTGGCATAACGCCAGCTGATAAGAGTGAACACGACCATCTGACACAGGCCGGCATAGAAGACCAGCGCAATCGGAGGGCCACACATAGGAGTGTGAAAATCTACATCAACATACTCGGCCGTGGCTGAACGAGGGAGTGCTTACAATCCGTTGGCTGGCAGATTCCGGAAATGAGCAAACGCTTCCCATGAACACACTCACAGCATAAGCCTACCTTGTCAACATCGCCCCGAATGCAGAGCCACCTACTGGGTTGTCTGAGAACACTCCATGGTCAAAAAAAAAAAAAAAA
ERCC-00039	GGGAATTCGAGCATGGCTAACTGAATGCGCCTGCAGTATCTTCTTAGTATATCAAGATCCGTAAATAACGGTTGCGCGACTACGGTTACCGTCTTATAAGTGAACAAAACGGCTACCAAGCATGCGTATTTCGCCACCCATATAAACCCACTTCGTCTCAAGGAATCCAAAAGTCGGACGGCGTGGCTGTCACTCTCGTCAAAGGTTGCAAACCGAGTAAAAGACGCGATAGATAGGCCATAAGTGGCCTCCCTTGCCAAAATCACGACGAAGTGACTAGTGCAGGCGTCGTATACTACTCCTCATGTTCAGCCCACGCTGCATTGGTAGGCTGTTAGAACGCGTACCGCTGACCGACAGGGGTATGATGACCTCGCCATGGGACCCCTTGTATTCTGGGGCGGGATGTAGAAATCAAAGCTGTTACTAACCATGTAACGCTGCTAAAGAGATTGGCTGTGACCGGCTCCGGACACTGCGTCAACGCGAGTCGCTCACGATCGGCCGTGCGCATTTCGTGAATCATGTATACTGGTTCTCGTTAGATAACATGTAAGCTGAATGGGCCCTACCCAACCGGTTGGGTCTATAAGGCAGATGTGCGACGCACCTATTGGTAGGCCATCTTATGGTTGCCCTTGTACTGAGGGTACCGCAGAGGTCCACTGGTAGCTCACACTATGATCTAGGAGCAGTTGGCGGTAAACGGCAAAAAAAAAAAAAAAA
ERCC-00040	GGGAATTCAACTACGATCCCATGAGAACACCTGTAGATACTCAGGTCTCCGGACCTACGCCCGGACGATGATAAGTCGAGAAACCACCGGATTGCCAACAGACGGCCTAGCCCATCGAACTAGGGAAATGAACTATATCGTAACCAAGCCGGTAGCTCGGTGGTAGACTAGATGTTAGCGTTAGTCAGTCAGTCAGCTGTTACGTGTAACGCCATTGAGACCCCTTACCCCTTACCGGTCGGCGGATACGTCCAGCTCGTCACTGCGTTGAGCCTCTACACGATCCAAGTTACCAAGCTAACGCGCAGTTAAGGTACGTCGCTCGACCAAAACGAGAGTTCGCAGCAAGGGGAGGGAGTGGATTCTTAGGAATGAGGCTGAACCTAACCTCGCTACATTCTATTGTTTCCCGATCGGCTTCATCGGGACGCCGGAGACCGCACCTTGGCCGTTAACGCTGGACGGGATGCCACGGTCTGTTCCACAAACCGGTCGGAGCACCCCTCTATGCTGCGTCTATGCCCTCCGGTGGTTGAGGTGAGCCATGTTAGAATCCGGTTGTATTAGACAGTATTGTGCTTGACGTGCGTGGTATCGGGTGGTTGTGAAGGATAACAGATAATTCTATGGGAGCAGCGATGGGGCTTCCTCAGTCGGTCTACGGCCCACCAACAAACTCGGGATACAAATTGAGCACCCCGGGACCGGAAAAAAAAAAAAAAA

Table S11

ERCC-00041	GGGAATT CGAGCTCGGTACCACCGAGCTCAAGATGCGTTAATTATGTGGGTGACGATAAATGAGTGAGCAAAAGACATGTAC GTATTAGGAATTGAAACAAGCTGTGATGAGACTGCTGCAGCTATTGTGAAAAGCAGGGAAAGAGATCATTCAAACGTAGTAGC CTCTCAAATTGAAAGCCATAAGCGCTTCGGAGGCCTGTTCCGGAAATTGCTTCAAGACATCATGTTGAACAAATCACTTGG TTATAGAAGAGGCCTTCGCAAAGCTGGCATGACGTATAGTGTATTGATGCGATTGCAGTAACAGAAGGTCCGGACTGGT GGAGCGCTCTTATCGGAGTGAATGCCCTAAAGCATTGAGCTTGATATAACATTCCGTTAGTAGGCCTCATATAGC CGGTCAATATACCGAACCGCTTGTAGAAGACATCGTGTCCCCTGACTGGCATTGGCTTCAAGGAGGCCATACAGAAC TGGTTATATGAAGGAACATGGATCATTGAACTGATGCTTGGGGAAACCCCTGATGATGCGGCAGGAGAACGCTACGACAAAGTG GCGCGGACGATGGGATTGCCATATCCGGTGGACCGCAAATTGACAAGCTAGCTGAAAAAGGGAAATGACAATATTCCGCTTCC TCGCGCATGGCTTGAAGAAGGCTTACAACCTCAGCTTAGCGGATTGAAGTCTGCGGTGATCAATACGCTTCATAATGCAT CCCAAAAAGGGCAAGAGATTGCTCCGGAAGATTGTCTGCCAGTTCCAAAATAGTGTGATCGATGTCTGGTAACCAAACG GCGCGCGGGCAAAGGAATATGATGTCAAACAGGTCTTTAGCCGGAGGAGTAGCTGCAAACAGAGGCCCTCAGAGCTGCATT AGAAAAGGAATTGCCAGCATGAAGGGATTACGCTTGTCAATTCTCCATTAGCTTATGCACGGATAATGCTGCGATGATTG CTGCTGCTGGTACAATTGCTTTGAAAAAGGAATTGCCAGCATATGATATGAATGCCAGCCGGCTTGAATTGACTTCT TATCAAAGTCTCACGAGATAATGCGTGAGACTCCGGTACAAAAAAAAAAAAAA
ERCC-00042	GGGAATT CACCAACTCTGGCCTTGTGCTATTCCCCAAGCACACAATCCAGTATAACATCTTCCACAAACTCTACAGCCA AGAGCAACCATTGCGAGCAGTTCCAATATAGACAGCATCTGCTCCTAAAGCTATAGCCTTAAATACATCTGCTGAACATCTGAT TCCTCCACTTGCTATGCTAATTGCTTCTCAAACCTCCTCTCAATCTTGATCTACTGCGGCAATAGCCTTCTA TTGGGATTCCAACATGGTCTCTGAATAACCTTTGGTCTGCCCTGTCCTCCTTATATCCATCTATAACAACACTGCGTCAGCA TCACTTGTGCTATTCCAACAGCAATAGCTGGAGCATTATGGACAGCTGCAATTAAACAAACACTGGCTTTCCATCTTGT TGCTTCTTCAAACCTCTAAACTATTGAGCTAACTCTCAATTGAGTAAATGTCATGGTGAAGGAGCTGGTGAAGATAGCATCAC TTCCCTCAGGAATCATTGCTGCTGAAATTCTGCTGTAACCTCTCTCCAGGTAAAGTGCCCTCCAATTCCAGGCTTAGCT CCCTGCCCTATTAACTCTATTGAGAACCTTCATAAGATACTCTCATTAACTCCAATCTTCAACTTGCAACTGGGT AATTATGTGGTCTGCATAAGGGTAGAGAGCTTTGGCAATCCTCCTCACCAGTCCATGAATGTTCCACATTCTTAACTG CCTTAGCAAATGATAGGTGAGCCTTAAAGACAAAGCTCCATAAGACATATGGCAATCATTATTGGGGTATCTAACTTAAAG TTTGGAGCTATTGTTTAACTTAGCTTTAACTCTTGTGCTCAATTCCATTGGCTCTCAATGGTCATGGATGGTTGTAACCTGCATGCATC AAAAACAATCTAAAAAAAAAAAAAA
ERCC-00043	GGGAATT CAATAACCTTACAATGCTTAACAAGAGGAAATTGTGTTTGCCAATTAAAGACCTAATTAAATAGTTAACCA TTAACCTTAGTTGTTCCAAGGCATAATATAGAGAGTGAGATAACAGGATGAGCTATTGAGGAGTTATTGAGTATGCGATTG CAAGGCAGTTGCTGATTAGATGAAGATTAAAGGTTGTTCTGTTAATGTCCTCAGCAAAGTTAGCTATAAACAGAGCTTAAATGAATATCCTCAAA TAAATAAAAGAAAACCTTCCAATACTCTATGCTCAGCAAAGTTAGCTATAAACAGAGCTTAAATGAATATCCTCAAA GAGAAGGTAAGAAAAGAGAAATATAGAGCTTGATCCATTAGTTGGATTAGGGATGTTAGATGGAGTATCCTCCATATCT ACAAATTGCTTGGATGTCCTCAACTATGGAGAATTGGAATTGTTACAACAAATAGCACCACATCATCTTAG AGGCTGGAACACCACTAATTAAAAGTTGGTTAGAGGTTATTGAAATAATGAGAGAAATTGGATGGCTTATTGTTGCT GATTAAAAACCTAGACACTGGAAGGGTTGAGGTAAGATTGGCATTGAAAGCAACAGCTAATGCACTGGCAATAAGTGGAGT AGCACCAAAATCAACAATAATTAAAGCTATCCACGAATGTCAAAATGTGGTTAATCAGCTATTGAGTATGAAACGTCT CTGAACCTCAAAAATTATGATTCTTAAATTAAAGCCAGATGTTGTTATCTGCATAGAGGGATTGAGGAGACATT GGAATTAAAAAGGAATTGAAATTAAAGGAAACTGCTTATTGCAATTGCTGGAGGAGTTGGTGGAGAATTGAAAGAGCT TTTAAAAGAATATCAAATTAAATCGTTGGTAGAGCAATTACAAATCAAAAGACCCAGGAAGAGTAATTAGGATTATAAA CAAGATGGGTTAAAAAAAAAAAAAA

Table S11

ERCC-00044	GGGAATTGGAGCTCAGATAGTGA CTTAGGGTAAATGCCAAGCCGTCTATAAAAGCGGTAGCGAGAGATCTTAGAACCTCCCGGC GAACGCCCAACTTATGCGATGTCCAGCCCCAAACGGTTGATTAGATCGGTAGCTCCGA ACTAAAGAGACCCTAACGCTATC CGTGGACTGTGAGGTAGGCCGTCTTAAGTGGCTCGTGA ACTAACGCCTGCTGCTATGTCCAATGAAGGGTACATGCC CTCTTCCCGTACTACGCCGATACAAAGTCCCAGCAGCTACGAAATATAGCGCTTAACCATGGGCCACCATAGGTGCCTG GTACAGACGTGTCAGACGAGCCCTGGCTAGCTCATATTGCGGCCATTATAAACCTCAGCGCTGGTCATGTCTGTAC ACAACGCTCCGGTCTCGACGCTCAGTCGGTACCCAAGA TAGCGGACTCTCAAAGAACGATTCACTAGTCAGTAGTCGCCGTACCC TGTAGGCCTTAAGAGGTCTAATTAGCTCTAGGAAACACAACCCGGATTGGGATACGCCACAAACAGAATCCAGCCGCAT CGCACCGCTGAAGTCCTCCGTCTGTGAGTCGACACATAGGATCGGGCACGGAGAGATCGGGGTTGAAGTATGGAGCG TAGGTCTCGATCTCGTACAAAACGACTATGACCATTGGCGTTGACTCATTATCGTTACGATTTACGGTGGCAAACGAAGC TACCAAGTAGATGCCGACGTCGAGTGGATCCACGCAGTCCGAGACAGCGCACACTCGCTGTAGAGGGTTCAATCGACTAAG ACGGCGGGATCTACTACTCTCGCAGTTAGATTAACTGTATCTCCGAATGCCGTTCTAAACCCGTACGTTGATGGTGCATTACAGCAAGAGG GTGAAGCACC GGTTTCGCCGTTAGGTAAAGTAAAAATATGACCTTACCC TACGTTGATTGTGGTCAAGTACCGTACGATAACCGATA GGGTTATAACGCAATCTATGTCGATGCTATGTTATTGACCCCTGCCGTAAGATTATTCACTCGTACGATAACCGATA ATCCC GTATAACCTGTGGTATTATAGGC GACAATTGCAAAAAGGGCGAATTAGCGCTGAATTCTGCAGAAAAAAAAAAAA AAAAAAA
ERCC-00046	GGGAATTCATCTCCTCTAACTTGGAGAGGTAGGAATGGGAGTATTGCACTTGTGGTAACGGTATTGCAATTATTGATGGTT TTTACTATGTTGGGTATGCTGTTGATTCTAAAGGACTGAATATTGCGTGCAGTATGGGATTCTAAAGATAATGTTAAG AATTGCTGGTTTTGCGACGTTGGTGTATTCTATAGCTCATTATGGCGTTATATGGAATCATTGGAGTGCCAGT AATTCTACACGCCTTATATTAAAGACAAAAGAAGTGTCTAACACAACATCCACACTACTACTCCTGTCATATTCTTC CTGAATTGCTGATTCTTATTGGATTCTGATATTCTATTGTTATGGCTATTACATCTAACAGAATTGGTGAAGTAAAT GGTGAAGCTTATGAATTGTTGGAGTGAGAGGATAAAGATAGGGAAGTTGTTGAAGTTATTGGCTGTGAGAGAGTGC TGAAACGTAAAAAAAAAAAAAAAA
ERCC-00048	GGGAATTCTCTGTAAATCCCGTAAACGAGTAGTACGAATCCGGACTTGAATACACGCGTCAATCCCTTTATATCCTAGAAC GACCGTGTGGACGGCAACTCAGAGATAACGCATATCTATGTGCTCGCTTGCCTACAAAGAACGAGACGGCACCAAACGGACG ACATATAGTGACATGGTCAACCGTACGCCTGCTCGTAAGCCGACGGCTTTGAAGAGGGTGGCGAATCATGCGTTGT CTTACTATTACATGCTAGCTTGGTTGGGCATCTGGGACAACGTCTATGTACAATAAACACAAAGCCGCTAGTTATCTCC GCGAGTCCGCCAATACATTGGCGGTGACTTGAGACCGCTAAATGCACATAGAACGCTCAAACATGGTAAGACTATAGATA AGCGCGCGAAAACACGGCATTGGAATGATGTACTGGGAATAAGACGACGTCGCTATGCCCTCTCCGGAAAGGCGGTGTAT GTGCCAACCGATGTTCTTAAATGTAACGGACAGGTGCTGAGGTGGCTTCGTTGGGGCGCCGTTGGGGGAGATTGCG TCAATTGACTGTACGATCGACTAGATTAGGCAGATTAGTGTGCCACCTGAATCAATAGAACAAATACAGTTATGCC GGTGCAGTACTATACAATGGGTTGGCGCATCTGCATGTCATGCTGTATGGCAATCGACCTCTAGTCTGGGGTGTAC GAGGCGCTCTCTTATTAGGAATAGTGCAGGACCCGAAACGCCATAGGGAAAGGGTGAGCGAGGTAGCAGCGTAATAATTG CGCGTGGGCAGGAAATGCTTAGTGTCTCAAGACCTAACGACGACAGCGTACCTGTTACTACCTCTGAAGCTCTCG ACGTTATAGATATTGGCATCCCTAAACACGAGTACCTGCTACGACAGAAAAGTGACCTGAA AAAA
ERCC-00051	GGGAATTCTTACAATAGATGCGTTAGAGTAGCTGGGGATTGGCTCTTAAAGTAGCTTGGGACATGCTCACGCAGAAA TTCCAAAACAAAGCACAAACCGATGAAAGATTAGACCTGAAAGATATTGATAGTATAGTTATGCTCCATTGGCTATT TTAATCTCTGGCCCTGGAGCTATAACAACACCAGATTAGCAAAACCCAGAGTCTTAGAGAAAGGGTTGT TCTCTCTATAAAAAAAAAAAAAAAA

Table S11

ERCC-00053	GGGAATTACATCTGTATAAAAACACTACAGGGTGGAACATGGTCTATATAAAATTAGAAGATCAAAAACGATCCCTGT CCATCAATACCTCAGCGGTATTAGGATATTCTGTTGGATTAAAATTACTGGACATGGAGCTCAGAGCTTAAGCAA TATGGCTGGTCTTATGCTGGAAAGGAATTGGATTACGAAATGAATAATGGTTATGAATTAAAGGATATTAAAGATATTG AAAGATTCTTAACCAGTTAGATTGCAAAGATAGAGATGAATGAGGAAGAGGATGAAATTAGTAAAGATATCAAATGC AATCTCTGCCAAAGAGAATTGTGGCTATGAATTGAAGGAACAGCATGCCCTGGGAGGATTGTTAATTGGATTATAAG TGAAACTTAAAGTATAATTAGGCTACCAAATGAATTAAAGCCAGCTGAAACATGTATTATAAATTAAAGAAGAATAAA ACTTATCTAATATTAAAAACTCCAAAATCTCATAAGGATGCTTAATACAATAACATCCTCCAACCTCCATCAATTTCCTGT ATTTTCAGCATCTATCTTCTAACCTCATCTTAATCTCTTCCCTCAATTATTGCAATTAAAGGGCAAACCTTTTACAAT TTCCACATCCTAACGATTAGATAATAATCTCAACAAAATTATCCCTCTTAACACTATAGCTCCATTGGACAGACGTTATA CATTTAAACAGAGTTGCATTCTTTATCAATTGCAATTAGGAAGTTGTTACAATCCAGCTTATAATCAACTGG AACTATTAAAGATTAAACAAATCCTTCCCTGCCTGAGCTATAGCATTGTTACTAAGCTATCTGCAATTGCCATTAAACAACT TAGCAACGGTATTCCAGTAGCTGGTAGCAAATTAAATCATACTTCTAACGCTCAATTCCAGTGATTGTGATGAGT AAGGATGTTCTAAAAAAAAAAAAAA
ERCC-00054	GGGAATTCGATAAAATTGGTTTGCCTTCAGCAATTCAACTTAATTCTTATTAACTGCCTTAGAAAATGTTGAACCTCCA CTGATTTAAATATAGGGAGCAATGAGCGGAGAAGAGAGGGAGGAGCTTAGAATGCTAAAGATGGCAGAGTTGGA GGAGAGATTGCAATCACAAACAAATCAGTTGAGTGGAGGGCAACAAACAGAGAGTTGCTATAGCGAGGGCTTGGCAAACA ACCCACCAAAAAAAAAAAAAAA
ERCC-00057	GGGAATTCGAGCTCTAGTGCATCCTCGTGGCATCGTCTCAGTAGGTCTGCAGTCAGCTAGTGCATGCAATGCGTCTG AGCCTGAGCTACAGCGATATAGCCTGGATTGTGAGCGTATTGCTGTCAGAACCTCAGCTCATGTATGATGCTGTACCAT CCTGCGATACTGAAGATGCACCGCTATAATGCGAGGCTCTCCGCTAAAGTGGAAAGCTGCTCGTTCTCAATGCGAGCGAGTCGA ATCCAATGCCGTAGCTGCGATAACGATGCCGCTGACTCTACGGTAATGCACTCGATCCTCTACATTGATAGCAGATAGTCTAACG GGATAGCATAAGTGCAGGGCTCTAGCATGTAGTCAGAGGTGCTCAGATATAAGTCATCGCTGCAATCAGCTAGTCATCTTGTG AGGATGCTACTCACTGCGTGCAGAAGATTGCGACCTCAGAGGATGGCACTCGTCACTAGAGTGTGTTCTCGGATCGACA CTGCTGGTCTGCGAATGACTCGCATTCACTAACATGGAGCATCGTTATCTAAAGGGATGCACTGTTATCGTCGAGTGGCGTC ATGTCTATGCAGTGCAGGCCTATGTCTCATTAGCGAGTCGTATGTATCATGTCGGGCTCGAATGTTGCACACGTCTGCGTAATG GTGACCGCTAGTCCCACATGGTCTCGTAGCCACAAATGCTTAGGTAGACCGACGTTATCGCGCTATACCGATGTCAAC GCGAGTTAGACCGTATCGTCCCCAGTGCCCTAAGATGGTCAAGCGTCTCCTACGTTAGTATCAGTTCCATTGGTACGTC TGGCGTACTTCTGAAACGTGATGGCGCTGGTTACCGTATATGGGCTCGGTTGACCTCTATTGGCGTTGACCGAAT TCGGTATCCTCGTCTAAATGGCGAACGTCGTCGCTATAGGCAAACGTCTGCGGTCATGGCAAATGTTACTCGTGTG AAGAAATTACTCGCTGTCAAAAAAAAAAA
ERCC-00058	GGGAATTGGGAGAGTAGGGCCCACTTGTCGATTGTTGACTAAACATGGAGAAAGCATTCCGAGGGTGGCAGATCCGCCTA AGCAAGGTACCATTTAATCCGGTCCCACGAAAGAGTTAACCTATACTGCTCAGATGGGCCATGGTGCCTGGAGGCCACTTT CTGCGAATTGTCACCACTGCCCTCTCGTGTGATCAACATACTATCTCTGCGGAGACCACCACTCACGTGTAGGTGA GCCATGTTGAATCCCATCAGGCACCCGTCGGCGTATGAGCGTCTGGAGGCTACCAACAAACTTACATAAGACCGGAAC GAGAGTCTGGCATCGTGAACAGAGGGCACGAGAGTGAGCTGTGAGTCCTGACTGAGCATGTCCTGAAACTGTGATAGATT AAGCCATGGACCAAGGACCAAGAGATCGACGGGCTGGATATTGCCGCAAGGCTGAAGGTAACACCTTCAGCTTCAAATGCT TGAATACTCAGCGTCCATCACTCGACCGGGTTAAGCTAAGATCTGGTGGCGGTAGCCGTAAACGAATTGGCATTGGAC AAGACAAATCAACCAAAGAATCTACGGTTGCCATGCCATGGCTCGTAACGACACCCGAGGTCTTTATGGCGCAGGCA TCGACGCTGAAAACCTCCGTTGCTGAGCAGGTTATAACGACATCAAGCGACAGCACAAGAAGGCGGGAAACTGTG GACTCCCGCTATGTCAAATACGCTGAGTCACCCAAACAGAAACGTTATCCGCTTGGCAAACGAATACATGGAAAGTGGCG GTCGGATACCAAGATAAGTGGTGTACGAATAGCCCTCGCTGCTTAATCATGGGATGGTACATCGTATTGCTATTGGAT GCAAGACGAATCCTGGCAACAGCCCTCGGACTCAGTAGGTCCATGGATTAACTACAAACAGGAAGCCGGTCAACTGTG ACTACCAGTATTGAGCTGGATAAAGAGGGCTCGGCACCATGGTATAGTGAATAGGAACCATGAAACTCCCATGTCGCAAGC ACTAACAGAGCTGTAACCTCCCTCCATTAGCGGTAATCGGAAAAAA

Table S11

ERCC-00059	GGGAATTCACTTGATCGTAACCGGGTACCAATGACCATAACGGGTATTAAAGGTCGACCCCTCGGTCTCAACTTGTGTA TGGGACTTCAAGTACCTAGCTCGTCGGACGCTTAGATGACTTATCCATAGTCCTAAGTCGGGCCGGTTAACGCCCTAT TAGCGTGTGACTCTCTAGGAGCGGCTCGCACAAATTACTGCTCAATCTAGATACGTTGCCTCGTGTAGAATATCAGCTAATAGGGTCGGCTCA TCAGATCTAGCACTCGTCAGTACGATGGCAAGTCGTGCCTCGTGTAGAATATCAGCTAATAGGGTCGGCTCA ACAGTGTATCCGGTGGACAAGCACTGACACCGCATGACGTTGTCAAGAGTCGCATAATCTCAGAATCCGTACAGCCGATCG GGTCACGGCTATAAAACAGCGTCATCAGCTAGGGTATCGCTCGGTGTACTGACTTGGGCCACGTCTTCCTCGCACAT TAGGCTAGATTAaaaaaaaaaaaaaaa
ERCC-00060	GGGAATTCATCGACAATAACAAAGAAATAGAACTTTAACACCAGAAGGAAAATTTGAAGAAAATTGGTTATGTTGA TTACTATGAGGCAGGGTAGTTAAAATTAGCTGAAGAACAGCAAAAGAGATGAGGACGTTATTATATTAAAAATCATGGAG TAGTTGTTAGGTAAGATTGATAGATGCATATATAAAAGTGGAGGTTTAGAAGAACAGCTAAACTACACTTTAAC CTTCTGTAAAGAAATAGTGGGATTTTAAATTATTAACTCTTCTAATTCAACTAACAAACTCCAAATTGTGTTCTG TGTGAAGTGGCATGTTGGTCGTCAATCTCATCTAAGATGTGGATTGCTGTGCACTCTAACGATTGGCTCCTCCCC TCCTTAAACAGCTCTTAGCCTTCAGCAGCAGCTCTAATGTTCTTGAACGGTTATCGTTAATTATCTCATCAA ATCAAAGCAaaaaaaaaaaaaaaaaaaaaaaa
ERCC-00061	GGGAATTGGAGAAGCTGGCAAACACTACCGGGCATAGATAAGACGCGGGCCAAGCATGCCACATTGGGACTTCCAT GTTACGGGCATGGAGGCGCAGCTATCCCACCCCTCGTCGCAAGATGGACAACCGAGCGCGTAGTAATCGCGAATGCCAGG CACTTATTGTAGAGGTGAATCGCTAACTACTCGGTGTAAGTTCCGTCGATGAACAGGCATCGGAGAGGGCTACGGCCA CCCAGTAGTCAGCTCAGGAGTCATAAGGAAGCAGATTGACCGTGGCGCAGACTCGCGATATGAATAAGACTCTAGGGGTGT ACAATTGATCGTTCGCTACGGATCGTCGACCTCAAAAGTTAACGCGAGGGTCACCTGCTCCGCGAGCAGCCTTGTC CAGGCCTAGTCCTGCATTGACCTATCGCACCGAGCGTCTACCCAGCTAGTACGAAATTAACTGATAGAGATGGTTAAC CCTCAGAGCGACTGGTTAAGTCTAGGACGGACAAACGGTACGATTACGTTAGCATCAAGTGGTGCCTGATCTCGTATA GACAACGTGAGAGTATTGGATGTATGGCTAGTTACGACAGCATGTGGCATTATTCTCATGTTTGCAGGGAGCGACTCAA TTTATCCGAACCATGGGAGATCGTCATTGTTGGTCAAAAAAAATCACGGCCCTGATACTGGTCGAAGTTGCGCCCTATGC TTACACGGCGCACGCCGCGTGGAGCGATCGAGACCTCTCGGATCTGAAATAACCCGCAACGTGAGGTAGTGTACGCATAC ATTGCCACGCTAACTGATGCGTTGATTCTCGGAGTCTTACCATGAGAATTGGCATATGAAATCCTGTCATACCACGG GTCGATACTTGTCTCGTCTGAAGCAACGAAGCATGTTGACCGTCAAGATGATTTCGGACAGAGTGAACGATATA ACACCTCTGGTCTTACAATGATTGAAGACACGTGAGACGCACTAGAGGCTAACCTGGCAGATTGTGATCTCGATGGTAAT GAAGTCGCCGTACTATCTTACTGATGACGCGACTACCAaaaaaaaaaaaaaaa
ERCC-00062	GGGAATTCACTATTGGAGAGAAAGATATGCCAGACCTATTAGTAGCTCCACAGGCCTAATAAAAGAGGCAGTATCATTAA ATTGGAAAGAGTGCTGTTGAGGGATGATTAGAAGAAGTTCAAATAAAATTATTCAAATAATCAAATAAAAGTAATACTTATAC TGAATATTGAAATTATTATTGGAAATTTCACAATATAGGTGATATTGTCGATTTAGGATTTAGGATTTGGAAAGATATTAG TCAAAAAAGAGATACATTAGGAAGAAATTGACGTAACTGTTTAGGATTAATAAGATTATGGATTTGGAAAGATATTAG GAAGAGGGCTCATGGAGTTATTACGAATGTGGAAAGAGAGCTGGACTGGCATTAAATCCAAAAGTATTGAAGATGTAGTT AAGTTTGAGGAATATAAAATTGGAAAGGTGGAGATAGTTAATAAGAGCCATTGTAATTAGGGTTATGAATGTATCTC TTGTTCTGGACTTCCTGAGGTGGAGAGACATTATGTTGGTTGAAGGAGGCTTATTGCTGGATGCTTAGAAAAAATTAA ACAAGAGAGTTAGAGTGAAGAAACTCACTGTGCAGGTTGGGCATGATTCTGTCAGTTGAGGTAAGTCCTTAATGA TATTTTTCATCTCATTTATTATCTAAAGCTTCAAAACCTCTTCTATGTCTGCAAAACGGCTATTGAAGCAAT CCTCTCCCCAATACCTAAACAGTGTGTTGGTAAAGATATCAAAACATCAAACATTATTTTGCTCCTCAATAA CTAACTTCAACTTTCTAAGATGTCTCATCTATCTCATTCTTGTGATGGAACATTTCATCCATTTAAATCATACTCC CTAACAAATCCATTGAAAGTTACAATACATCCAAATTCCCTTGATTTCAATACATCCATCTTGTGAAACTCT TCATACTCGTTaaaaaaaaaaaaaaaaaaaaaaa
ERCC-00067	GGGAATTGCCGTACTTACACCCCTACGGTGTGATCTGGCGCTCGTACATTACACTTGTAGTTGAAGGTCGGCGATGAGG CGTTCGTTGGCAACCTCGTTACATTGCACAAATGCCGATTGGCTACTATATATACTCCCTGATCAAGGGTCGAGTTGTC TGTGCATTAGCTCGGAGCTAATGAGCACGTCGGTCACGGACACTGCGAAGCACGACGAAATGGCTCTCATGCGATTGTC CTTGTGCGACAAATTGTCAGGCGGGACGGGCCAGGAATGACAATAGAACATTAATCTAATTGACGCCATGACGT ATTAACATTGGCATGCAAATCACCGATTAAAGATCCCCTGTACGGCTGCGTCCACACTAGCATGATGTAATCGATTG GCGGTGACCGCTGATCCTAACAAAAGGGGTGGTCAAATGAAACAGTAGGTGCGAGCAAACGTCTGGTGTCTAATGG CAAACATCTGCAATCAGCGAACCTCGGGTATGGCAACTCACTAATTGTCGTCGACGACAAATTACGAGGGAGGCACCTA TGAGTTATCTCGCTGTGATATCTCCTCGACTAGCGCGGTAGTCaaaaaaaaaaaaaaa

Table S11

ERCC-00069	GGGAATTGGGAGAAGTACCAATATCAGACTCCCGAGACATAAGGGGTGTGCACGGCATGGATGTGCTAACCTCCTGGCT CTATAAAGCAACACTCATGGCACCGTGTGCTGAAGGCTCCAAACGGGTGATACCAGAAGGGTCGATTCTTCTTCCAATACA TTGTCGGGTCAATGCTGGAGGCCAGGAGACGAAATCCTCGGTAGGTTACTTGAAGGGTCAACACAGAGCTCAAATTT GTCCAGGGTGGTCACCAGGGTCTCGAACAGAGGTGAAACGGATAAATACCGAAACATTATAACCCCTGCCAGTCATTA TAAGCAAGCGCTGACTTGGACACCACAACGTGTGGAACCTCAGGTAAGCTGGTCCGGGAATCTGGTGCAGCAGCCCCA TTGAGTAGGCAATCCAAACCTGCAAACAATAGGTGCCATCCGGTCAAATAATGTGGGAGATGCGCACATCATGAGAGCGAC GTATTGAACTCAAGGGACGGTGGTCCCAGGAGAGGGATTACACATGTTGAAGCTCTTCAAATCGATTATCCAATCTGCGC ACTGTAAGTAACCAACCGCAATAATCCCCAGAACACTGCCCTGGTATCTATCGATTGGAAGTCCAGACTCTAGTGATGCCG GCTGGTCGGACAAGAAAACATAATTGCAAAGGGCCCTGTCTCATTGGCGTCTTGTACCCAAACACCATACTGGGAGGG TGGTGCGGCGCATATCAACGACTAGAGGCCGTAGAATGAGTCTTCAACACATATCGCTGAAGAAATGTCACTCCATGGT GCTGATATAGAAACATATCCTCGGGACTTCATGCCGGCACAAGGCTACAAGATGGACTGGAACGCCGTCAACCTCGTA ACAACTCCCCATGCAATTCACTCACCAGTAGCCTATAATGGGAATGTAGACGGGCCCTATCTCAAATGTGTCACCTCTA TCCCCACCAAGTATAGTCGACTTAAGGGCGATCAAATGGCGCGTGCATACAAATCCGGTCCAAGCATGACTCATGGCA GTACGCCGGTTAGTGGAAATACGGCTGTCAAACGCTGGTCAAAAAAAAAAAAAAA
ERCC-00071	GGGAATTCCATGCGAGAGGCCCTTGAGGCCGATCGCATACAGAGACTATTGCATCAAGGTAACACTTATTAATCCCCA TCGTCTATAATCGCTAGATTCTAGGTATTTCGGATCTCTAGTTACAGAACATGTTAATTGGGCTCGGGCTCTGCGCCAG GCCTTCGTAGTCCATACCACGATCTGTATTTGCACCTTCGCTATGCTGAGGTTGTTGACATAAGGATTAACGTGTTGGTG TGTCTACTCGGCTACCTCCTGGTTGGCGTCAAACAACTCCAAGATTATCTCATACTATAAAAAGACGACATGCACCGCCG TCCTTAAGTGCCTACGACAGAGGGCGTTATCTCTCGGTCTCGGTCTCGGTGCGCCTTCACGGAGCAGCATGACCTGCTAACCTG CATCAGCCAATGTCCCGTCTCGAGCTGGCTACGGATGCGTAGCAGAACAGGTGCTAACTCTTCTATAACCCGGAGATGAACTA CCACGCTTCTCGGTGGTCCCGCGAAAAGAACGAAAGCAAGGAGATTCTCGGACCTGGCCATTCACTACATAACAGAGTTAAG ACTTAGATCAGCGAGCAGGTGTACGCCCGGACCTGGCTACTTAAAAAA
ERCC-00073	GGGAATTCTGTGATAATTCGACGAGGGGTTACATATTCTGAGAGGGGTGATTAAGTCTGCTTCGGCCTGGATGGTCTGTCT ACGTGTGCGTAGTTCTGTCTAGCGTCGAGGATTCTGAACCTGTCCATAGTATCCTGTAAGCGTCCAATGTACCTATATCGTG GACCCAAAGTCGATACGTCCGATTAAGCGACGTTGGTCTAGGTAAGAATTATACCCCTGGGTTACGAATTATGGCTGTGCCT AACGAATCTGGGACGTGCTAAGTAATCTGGTCCCGACTAAGATGTACGGTATCGTGGACGCTGACCGGACTTATGCGTC GCCTTCCGAGTTATTGGATGGCGTCCGTCTATTGGATACTATTCCGTGCGTGTGCGACACGTTCCGAGCATATGCTAACAG TTCCGTCACTATGTAACGCTTGACGTAGATTGCTATCAGGTTACGATGACTGCTAAGCCATTACGCGACATTGCAAAGTTA CGTCGCATTCTCACGTTACGGCTGATTCTCTAGGCTTACGCGCATGAGCTTAGGTTCCGGGACTATCGAACGTGTCATT GGTACTAAAAAAAAAAAAAA
ERCC-00074	GGGAATTCTGGACATTAATTAGGGCTGAAAGCCCTAACTTAATGGACGGGAGGTATCCCAATAGGAGGTTCCCTATGGTT TTCAAAACAATCACCACATGCTATTAATGATATTAAATCCCAACTATACCAAAAGAATATCCCAATTATCCATAAAACTGTA ACTAAGTGGCTCTCTCATGGTTTATACTCAATATAAGCCTTGGTAGGGATAGATAGCCACCTATATAGTATAGCTTCCC ATCTTCTTGAGAGTTGGTTATGCTCATCCACTCATACCCAGCACTTAGATATTAAAGAGGCATCTACAT AAGGCATCATTATAACTAAAAATGGATATATTCCCTATAAAACTACTGCTAAGACAGCTAAGAAAGCTCCAATTGGTAGAGTT CCAACATCTCCTGGAAAACCTTGTGGATATTGTTAAATATCAATAGCCCTAAATAGGATGCGAGAGAATATCAAAGCGGA AAAAATCCAAAAAA

Table S11

ERCC-00075	GGGAATTCTCCTACACGTTCCCTCATCTGAAACCATAACTACCAACTGGATTTAATGGAGTGCAAACCGTTCCAACAATGGCAGTCAGTTGGCAGTTCTCTCTCAAAATCTTATCACATATAACACCTTAGGAATTTCTCTTAATCTCTGGAAATCTCATGCTCATAGATGTCAAATTCTTATACCTCTCCCTCAATCCAAAACCACATTAAACAACCTGGAAACCTCTCCAAGAACATCTATGCTTCAAAAACCTTCAACTGCTCTAATATATTCTTTCAACCTTGCGCTCTCCACTGATGACTGCTTAAACATTATAGCCATTAACACATCTATGGCTCAAAGCCA GCAACAACCATTGGAGCTTGATTTCACACAACCCATAATAAGGCTTAATCCGGTATTGAAACATGTCCTGGGCA TATAAATGCATCTAAATAAACTCCCTATTTAACAAAGAACCTCCATAACTGGAGGAGTCTGCCTGGCAATTAGGATAAAGAAGTTATTAACATCTTATTTAACCTTATAGTTCAAGCCCAGTAGTGGAGCAGTGGTTCAAGACCTATTGCCACAAAAACAAACTCTTATCTCTCCCTTAGCCATCTTACTGCTTCACTTAACTATAGACAATTCTAACATCACAACCCCTCAGATTGCTTTCCATCAAAGATTTCACTCCCAGCTCTACATATCTCAAGAGTGGTTATTACATATCCATTGTCAGCTAAATATGGCTGTATCTTGTGAGTTACACAAACTGGACAACCCGGCCCTGGAACAACGGTTATTCCTCTGGAGAACATCCCTAACTTACAGATCGTGTGCTCATGACTCCACAGACGTGCATAATCTTAATTATCTTCTCA GCAAGTTGTTAAAAAAAAAAAAAA
ERCC-00076	GGGAATTCTCCTCATGTGAGCGGACTACTATCTACAGCTGGTAATACTCTCAGAATTCTAACTACCAGTCGAAAGTAGGCGAGCTGGTGGCTCTTGAAGCGAGAGAACCAAGGTGCTGGCTATTGTCGCCCCGTCTACGGCTAACCGGGGGTTCTGCCATCCGGTTAGCGCAGAAATAGTATTAGTCGGTCAGTGGACCCCTCCTGAATATCTATACTTAGCGGCGGATTACCCGGCCCTCTTCATTGCGAAAGATTGGGAACCGCCTCTGGCTGTACGCCCGCAGGGCTAGGTGAGGTACTATGTGAGGTATTTTCTCAATGTTAGATCATCTATGTTAGTGGATCTGAGAGATCACGTGGACCAAAGCTGATTGATTACGGGACTGGCGTAAGTGTGCCCCGAGTAGCTCTAGATCCGGCTAGATCCGGCTAAATTCCCTGCGGTGCCTTAGCCACCACTCCTACGACGGGCCGATCTGGTTATTCTCGCTAGACACGGGTTCGGGAAAGTGGAGCATCGTTAGCTGCCAAGATGTGTATGTTGCGCCACTCTCGCACCGTTTATAGTCGTTCTATTAGAGATGGTTGCACATGGCGTTCTCATCGTAAAAAAAAAAAAAA
ERCC-00077	GGGAATTCAAGTTTTCACTTATGACTTCTCACTCCATACGAAAGACAGATGGTTGCTCCAATGAACCCAGAGGGAGTTAGGTGATGATTCCCAAGTCCAACATGGAGTTATGCTTACACGTATGTTGGACAGACCCCTGTATTGAGCAGACTTAACTTAACTGATATACAGCTAAATTGAAACAACAAATCTCTTAAATTGTTGAGAATAAAAGGATACTATCTTATCCAATATTGTATTCCAAAAAA
ERCC-00078	GGGAATTGGGGATTGGATTGCAAGGCATATTAGCAAGTTAACGCCGATCACTCTCCGGCAGTGCTCCATTAAATACGGGCCCTCGCAATCGCGTGTGTTACACATAATGCCGTATCCATCTACTATGCCGCCAGGGTCAAGAAATGCATATCCCGCCTACCCCTTAGCAATCGACATTGTCTTGCTGGACGCGCATGATTGAGTTACGGAACCTCGCAAAGTATTCCCTTGTGGTCCGTGCCCATGCTCTCTGGCGTAGCTTACAAGGACTAGGCCGTAGCCTGTAATTAGGAACCGAGCACCAGAGAACATCAGGGTACAGTGTGGTAGACGAAATGATCGTGGCTGAGGGAATTAGGAGGCCGGTCCAATAGTCATAACACCTGACGGAAGTACGGCTGCAGGATCTAATCATATAAGTTCAGAAATTGCAACGCGCTCTAAGAACGGACCAGTGTAGACACAATACAACCTAAAGCGCAGATCTGAGAGAGGGTGCACAATCCAGGCAAAGTCCGTTAGAAGGTCAACCTGTGGTGCAGCGCTTGCTCCTAAAGATTGCGCTCTCGGGAGCGACGCGACTGCTAGGGACTGGTAAACGTTGGCGCTGTCCAAGGTACCCCTCAGTCTGTATTCTAGCCCTCAAATATGCAATCCGACCCGGCTTAGATTATAGCAGAGGGTCTCGAGGACTGTAATGTCTTGCAGACAGGAAAGGTTGGCGGTACGTACCTCTACGGTCGAGGCTGGGTGTATCATGGAGTAATCTATATTCCCTACACGCTTGCTTGCCTTACCATACAACACCGCAGTCATTACGCGTACATATACCAGCAATTCTTACGGACCGTTAGGAAGAAAATGAAAGGAGTGGCTGGCCATAATTGCAACCGAAGCTACTGGTCGGACCCATAGCGCGTGTGCAAAAAAAAAAAAAAA
ERCC-00079	GGGAATTCGATGTTGGAGTTACGGAGACCCGCCATGTTACGAAACAGGTGCGAGATAATGTGGAGCAGATTACGTTGAGCGGGCTCTGGGGACCCAAAGGATGAACGGGGTGTGTTCAAGAGCGATACCAACCGCAGCTCTCTTTAAAGATTGAGCGCTAGGTGTTCTACAGTAACTCAATTAGCGTGAGCCAAGGGCGAGCCACGGGCCAGTAAGCTATTAGGTTTACATGGCTCGATACCGAAACACGTGACCGTACTGACTTGGACTGGTACGAGAGGCCGAGAGTTAGTGTGCGCACCACAGTCCAGAAGTCCGGCCAGATCAAAGACGCTACTGACTTGGACTGGTACGAGAGGCCGAGAGTTAGTGTGCGCACCACAGTATTGGCGTGTGCTCATGTTAGATTAAACAACCCGGGGCGAAGTTGATAAGCGTGTCTAGATTGGAACCTACCACTGTTAAATACACGACGCCATCTCAAATCGCACGCAACAGGGGGCTCCACCAGATACTCCCCAGGACAGGTGGAGATACCAACACGAAGGAGGTCTCGTGTGAGCCTCGTCGATATACCAAAAAAAAAAAAAAA

Table S11

ERCC-00081	GGGAATTCTTATCGGGGTGTTGATAAGACTCCTAGGCACGCCAACGACGTTAAAGGGAGGTCGCTCGATCAA GAGATCCATACAGCAGGCTCTATCAGTCTATCTGACGCCAGTGCCATTGGACGGATGTCGAGGGTTGCGGTGGGAACG ACCATACTACTGTCTTACGACGTGCGGGAAATTGAGGTTAAGTGTGTTGCCACCTACAATAACGAAGAATTAGCCACC AGTTGGCGTTAGAGTTGTCAAGACGTTGGCGTATGGGATGAACGTCGCTAAACGTTGGTCAGGGCTCCATATACATCT GCCGTGCCCTTAATCTCCATACAGACCCCCAGGCGGAATGATAAGTCGATACCAGGACAATGACGGCTCAACGTTTC ACTTTCCGAGGTGGCGACCCCTAGTGTGACGCTGGTACATCAGACACGTACACCGCAGTGGGTGTAATCAAGCAGGA CCATAACTGATAGTCACCAAAAAAAAAAAAAAA
ERCC-00083	GGGAATTCGAGCTCGAGTTATAGTCTTTTGATTGCCTCAACTAATGCCTCCTTGTAGGAGCTCCAATAACTCAACAT CCCCATTATTACAATTGTTGAACTGCCATTATCCCATTGCCTTTGAGGATTCTCCATAACGTTATGTATTCT ACTTCACACAGCATCCGGCATTTCATTGCTACCTCTCAACAACACTCTTAGCTGCAGGACAGTGAGGACACATTGGTGTGATGT AAAAAGCTCTATCTTACCTTGACATACTAACACCTTAAACCTTAAGTTATAATAAAAATTATCCAAATTTTAT AAATAGTTCCAAAATAGAATATTAAATTAGGCTAAAATTAATGACCACATGTCCAAACTGTCTGAAGTGTCAATT GCTCAACAAATACCTTCATTCTGGTGGAAAGCTACAAACAACTCTGGCTTAATTCCAGCGTATTTCTTGAACC GTTACAACCTAAAGTCATGTTAGGAGCTTCTGTATAAAACTGCCCTACAGCATTGCACACAATGACTGAATTCTGAGA AACTGCCTGGAATCTCACCTTATGGTAGAGTATTGCTGAACTAACCTCAACGCAATTGGCTCTCAATAAAATACA ATTGAGTCTGGAATGAAGTCGGTTCATCTAATGGAGCATAGACTGTTGCATAAAATTCTCTTCAACTTTGGTATTGCATC AACTGTTTTTAGCTGCCTCTCATCTTAAAGTTCTTAATTGACATATAATTCTCTGCTAATGTTCTGGATTTCTTAATCTT TTCTAAAGACCCCCATTGCATAAGCTCCTCCCTACAGAGGTGTTATCAACTGTTGCATAATAATTCTCTTCTAATCTT GCCATTAAATCATTACAGTGTCTTTCTCGTCTAATGTTCATAGCCTCTGGATTCTCCTGGATTTCGATTTGCCATT TTACAGCGACAAATGGAAAAAA
ERCC-00084	GGGAATTCGCGAATTGTCGGGCCTCGTTGACTATCCTATTACGGGATCTCAGGTGTGGTATCCCTGGTGAGACATTG GACTAGTGTAAATTGACAGTCATCGTATCGGGATACCTCAAGTTGTTATCGGAGGGCTTATCGGTGATACTGTGTAATCCCTC GGCGAAAGATGTATCGTGAGCATTAAATTACGTGTTCTATATCGGACGCCATTCTTACCCGAGAAAGATATCTCTGT AAGTTTCAGCAACCGCGTCTAATGTATATAACTTGGATCATCAGATAGGCCATTACACTCTCGGTGCTGCCGATATCC GACGAGCGGGCTTGCACTTGATCAGCGCTGGTAGAGCTGGATAAGCGAGGTCAAGCGATTGTTGCCCTCCGG TCCCACGTAGATCGTTGCCTGCATTATAGGTAGTGGCTCGCAGTCCGAGGCACTGGAACGATCCTACCAACAT AACGGTCGAACTCGGTGTCGGATGACCCGGACGGGACGCCGCGCTCACACAGGTATCTGGGTGACACCGAACGG GCTGGCGACACAAATGCTCTAACCGCTGTGAATCTACTGCAGAACTATGGTTGCTAGCGCGCCGGTATCTACCAGCA AAACATAGGAGCGTGGCGAAACTGGTCACTGAGTGGAAATATCCGAGTGCAGCTGCCATTAGTGGGGCGGTATCGGGGT GATTGAAGGTAGGCTAACATTAGTCATCTGGTAGGGCATATTAAACGGCTAGGCTGGGTTCAAGATAGGACTGATAT ACTTGATGTGCCCCGTTCTCAGCGTGCAGCTATGCAGCGACAGACGTTGGAGCCTTAATCAAGTACGCATCGGAGCATA GGTCACTGGGCATTGCAGTGAATTAAACCATCCCGTCCCGTCTCAGTTGCAGGGTGGGAAAAAA AAAAAA
ERCC-00085	GGGAATTCGATTGCCTGACGTACATAGACGAGATAGGTAAGCCTATTGCAAACCTCCGCTTGCTACTACAAGGACCTCG GAAGTGTGGAGAATCGAACCTACAATTTCGCCAGGATCACGCCGGTATCTCTGCAATTCTAAAGATGGAGGATAGTTTGG AACCCAAATATCCCCAGCCTACGGTTAGGTGCAAGAATAGAGCGTACCGAGCGTCCGGCGCCATTGTAGTCTGTATTGT TGAATTAGCCTCTTCAGAGGGCTAACGCCAGCACAACATGCTTACCTGGCTAATTGACTAAGTGTACGGTACACAACGAC TACGTACGTAGCACACAGTTGAGGTTATCTCTGAGCGCCCCGTTAGAAACTGAGGGCTCAATTATAGTACCTTAACCGTTGC GCTGTCTGGGAAGGTATTTAATACGGATTACCGCTCCACCGGAGCGTTCCGTTACCTAACAGGTGGACAAAC TGCTCATTCAAGGGCGCTCCATCGCAGGGTTGCAATTATTTCTAGCTAGAGGTGTAACCAGGCCGGCAGCGAACGTCCGC ACTAGCAGGTACACAATCAGGCATCGAACATGTACTCATTAGTCCGAATTAAAGTCGGATACTGCCTTAAGTCGATCTG AATCATAGCCGCTCATTGCCAGTAGACGGGATCTGCTGAGTGGTAATCAGTCTACCCGTGGGTCGTTCTGCCGAG TGCTGCATTCCGCTACGCGCGTATTCAACAAGGGTAATCCCTCCGACAACCTCAGTGTATCATCCGCTCAAGGGGAA AAAAAA

Table S11

ERCC-00086	GGGAATTGAGCTTTCTTGTACTTTCCATAACTCCCTAATTGTTCTATAATTCTCTTCAAAGAGTCCTTATCATAACCAAATACATAAACTCTAACACTCTATTCCCTTTGATTCTATTGTGCAATCAATGTCCATCCTGATAATCTCTCACAAAGCTC CAAAAGCTCTCATCACAACTCACTTTGATGAAATAATCTTCTCATAGTATGCCAAAATAATAAAAGTAATTACAAATTACCATAGCTTATATAATAAAAGTTGCATGAACAAAAATGTTGTGGTATATCATGGACGAATTGAAATGATAAGAGAAACACATCTGAAATTACAGCGAGGAAGAGTTAAGAGAGGTTAAAAAAAGATGAAAATCTGTTACATAGGTTGAACCAAGTGGTAAAATACATTAGGGCATTACTCCAATAAAAAAGATGATTGATTACAAAATGCTGGATTGATATAATTATATTGTTGGCTGATTTACACGCCTATTAAACCAGAAAGGAGAGTTGGATGAGATTAGAAAAATAGGAGATTATAACAAAAAGTTTTGAAGCAATGGGTTAAAGGCAAATATGTTATGGAAGTGAATTCCAGCTTGATAAGGATTATAACTGAATGTCTATAGATTGCTTAAACTACCTTAAAGGTTGGATGGAGAAGGAAAGATGAGTTCTTCAAAGGAATTTTAGCTGTTGACTCTCCAGAAGAGATTAGGGCTAAGATAAAAGAACATACGCCAGCTGGAGTTGAAAAAAAAAAAAAAAA
ERCC-00092	GGGAATTCAAGATGTATATGATGTCCTTGGACGGGTGGCGCAGTATTACTGCAAGAGAGCGGACAGATTAGTGTGTTGGAGCCGACACATCAAAGGTTCGTCGGGACCGATCTGCAGCCTACGGACATTATCCGTAAGCATGGCGTGTTCGTACTTATCGGAGGCCAGGTATCGTCGCGCGAGTCTCCCCGACGGAGATGGCGTTACTATCTGGCCGTCTCGTACTCTGTTACTTGGCACAGATGCGAGCCCTCGTAATGTGCATCAGCTAAGGGCGATATTATAATGCGACGTTGTACGGATTGTTACTAACGTGTTGGACTAGTGAATATGTCGTTGGCTACCCATGGCTTCGCGCGACACATGCTTAGACTCTTCAAAACTTCGGTGAAGTTCACTCAAGCCCGGGAGCGCCGTCGTAATTCACTAGGGATGGCGGTACCCGTGCCGTCCGATTCGTAGCAACCTGCATCACGATTGTCTTCGGCGACTTATCAGATA CGGTAATGTAATACCTGGCATTGGGACTTCTGCGTTAAGCAGGTTAATGCTAGCTCGAGTCTCCCACGGACACGTAGTGGGTTGTAACGATCGATACCGAGTCTTTGTCTAGTAGACAACCCATTAAGGAGTTCACTAGCAGATCTTGCACCCGATC GTCCGTGTGCGTAATACTTTGTTATGACGAGACATA CGCTCAAGCCCTGGGTAGCTAGTCGGAGGACGTTACCGCGCACAAACCCCTATTGTTACATGTACATCGCATCTGAGGTAGTACACTCCGGCGTACGTGAGTATTGCGCGTAATAAGCGCCTGTTAGCTGATCCCCTCTCGTATCAGGTTAAGCGAGGAGATAGGCTAACAGCTGGTTGGAAAGCTTAAAGCCGTTGGAAAGGTTGGTTGAAATAAAAAAAAAAAAAAA
ERCC-00095	GGGAATTGAGCTTTGATGATGATACTAACCAAAACCTACCAACTAATGTTAGTCATCTGTCTCCTCTTGTGGATTAGGAAATATCTGCTCTGTCTCTCAAACACTCAATTAAATTCCCCATTAAGAAAAAGGAGTGTAAATCAGAAACCTACTTGCGCTGCTGCATGTTGTGGTAACAACAACAATCGTATAATCTTAGCTA ACTCAACCATTAACTCCTCTATCTTAATGTTGGAGATAAGGTC TAAGGCAGATGTTGGTTACCGCTAACAAACCTCTGGCTAACCGCTATCGCTCTCGCTACACATAACCTCTGCTGTTGTCCTCCAGAGAGAGATAGAGCTTTTATGCAAGTTCTACCTCATCCCACAAAGCCGTTCTTAAAGCCCACCTCAACACATCTTATCCAATTCTTTATCCTTAATTCCATGAATTCTGGCCAATGCAACATTATCATAGATGCTCATAGCAAAAGGATTGGTTTGAAATAAAAAAAAAAAAAAA
ERCC-00096	GGGAATTCAAGATAAAACGAATAGCTCGAACCAACATGCACAGCGGTCAAACAGTATGTCCTCCTCTTGTGGATTAGGAGCTGGCGGTGCCTCCCTATCCCTACGAGGCTACCCGGATCGATGACCGAATTGGGACATTCAAATGAGCATCCTAGTCACCGCGTTAAATGAACCTGCCGCTGATCGTGGCTGAGTATAACAAACCGTCAATCTCAGCTAAACCGACGCAGTTTGCTCTTGGATTCTGAGCCCGGGCATGCCCTCGTTATGAACTAGCCTATCGCAGACGGTATCAACAGGAACATCCTCGTGTAGATATTGAGGCTGCTCGTGTGGCACGAAGTGTCTCCGATGCAGTGTCCAGTCATGACCTCGATCCATCGCTATAGGGACGCCCTGCTCGCGTTACTGCCAAGCGAGCGTGGTAGACGACCAGCGCTGACGAGCTGGCGCAATGACGACCTAATTGGCGCACAGTACTAGGCATCGTCATCCAATGCGACGAGTCCTACACTATCTTGGATATGATGGCCACTACACATGCTAGCCGCTGGGAGATTAGCTCGAGTTGCCCTTGCCGATCCCGAAGATAACGCTCTAGTCGGCAATCGCTCTTGGCGAGATGCTAGGAAAGGTTGACTTCTCAGCGGAGCAGAAAGATCATGTTATTGGAAGC ATCAACCTGCGCCGTCTGTTAACTTGTCAATCGCGCACGTAGCCTAGAGCGCCAGGGCGAAATTGCGCTGAAAGTTGCGGCCACAAGCACGATGGCTCTAATAGGAGGTGAATTAGATAGGAAAAGATGGGATGCTACTAGTTACTGCGTCACGCTGAGGGACTCATCCTGGCTACAATCCTATTGCCGAGATAGTATTCTTAGCTCCTGAGGGAGGTCAATTGAATGTGGTATATGCGAAAAAAAAAAAAAA

Table S11

ERCC-00097	GGGAATTCCCTTCATAATACCACCAAAATACCAATTGAAAGTTAGCATATTCAAACAATATAAAATCTCAGATTGGACA TTAATTGGGACTGAAAGTCCCACCTTAATGGACGTGTGGTATCCACACCATAAAGGGGCTACGCCCTTGGGATACTCCCC TAATATTGCTAATTACACCTCGAGCATAAGCGAGGAGGTGTTAGGTTGATGAACCTTTACTAAAAGGTTCATACCAAT AGGAGGTTCCCCCTATGGTAGTTAACATGTACATTGGATATTCTTACTCTTGACATCATCTTAAATGTTGCTCTGCC AGTTCTTAAGTTGTTCAATAGCTTCAGCCTCTTGATGAGATTCAATATTACATTAGATTGACATTTAACCT AACCTCTAATAGATTAGCCCCCTCTGGGCTGGTCAATTCCAACAGTTCAGCCAACAAACCAATAGCATCAAACCCAT GTCATGGCAAAAAAAAAAAAAAA
ERCC-00098	GGGAATTGGAGGTGCAATTACATCGGTTCTGTCCGTAGAGGCTGGAAGGGCATAAGAAGCAGTGATACCAACGCTCTC CCCCCGCGCTCTCGTGAGAGCAGACCATGAACATCGCAGAGGAGAACCTGCATGACTGAATGCGCAGAGCAACTGTCACCAC GTGGTTAATGAGAAGGCAGAACTCAACAGACAGCTCTGGATCTGCTGCATCCCAGGGCAAGAACATCAGGAAAGCAGATGCAGTA ACCATAGGCACGTGAAATGCTCCGCCACACTTGGAGCTATTACCATGGTCGGGCCAACATAAGTGGACAGCTAGAAC GATTCTCAAGCCTGGCAACGTGGTTAGAACTCCAACCCCTCGCACGTAGTATGGCCTGGAGTAAAGAGCGCTCTGTTAGC AAGCACCAGTCTCCGAAAGTACAGGATGTGCATGTTCTAACCAAAGGGTGCAGGGACGATGATTGCTAGTAGCTTGACAA GGCTATCCTAGTCATCCTGAATCCGGCTATCAAAGGAATGCGTGGCAGGTCAAGTGACGAGAGTGGAAAGAGCTTCCCGTTGA CAAGCGGCAAGTAGACTGTGCCTACCCGGCTTCCAGACCTAACGATATCTGCATTGCAGAGTGGTGTGTCGGGCAGCA GTGTGCCTCATTGTCACACTGGAGCCTAACGGCCCAAACTCGATCATTGATGACTACTCGACACAAAGGGTGGTATACAGA AAGAGGCTGTGTCGCCGGAAACGCTTATCCGCACAGTAAACCTCCCAGATGACCTCTCCCTCATAATCACTTAATCTGA GCGCAGGAGGCAGGTGTTAACATTCCGGCCTCCAACCGGACCGTGGAACGACGCGACCAAGTGGTCACGGACATGCCAG TATTGGCCGTTCTGCCGATTCTCAGCTAGAACACCAAGATCGTACTACGTACGCGCTGGATAGATCGACGGCTGTTAATA AGAGTCACTCCAGGCTGTGCTAGGATCAGGGCACCAGGCCAAATATCAACTCAAGGACAAGTTGACGCCCTGCCTCTGGGG TATGGATCAAAAGCCCACGTACCATGTAAGACCGTGTGGATTTCGAAAAAAAAAAAAAA
ERCC-00099	GGGAATTGGAGCTCGGTACCGGGGATGCAAATGAAAGAGGAGACATTATCTTGTCCGTGAAGATGTATTGCCGATGCAAT GAGAAAAACATTAGAAGTCAAAAGCTGTTGATCGAAAAAAAGCAGATTGAGCTAGCAGATGCCGTTCAAAAGGTCATTAA GTAGAAGTGCCTTATAAATACAGGGATGCTGTTTCCATTCTACACCATGGTAAAGAACAAATTATCACACTTTCTT CATTTGGAGGATAGGTGAGGTGTTATCTCAGCTTCTCAGGCGGTAGCTGATTCTGGAAAGCAACGTTCTTCCATTACCA GACCATTCCGCTCAAGGCAGAGCAAATGTGACACTGTCTATCAGTACGTGCGATGGAAGAAGACATTACATTAATGAA TAAGCTCAGGAAGTTGATTGTTGAGAAAAGGTTGAAATATTAGGTTCAGGTGCATAAGGGAGAGAAAATCGTCATGAAAGTC GGTTATTAGGTCCAGCAGCTACATTACACATCTAGCAGTCAGTTCTGTTCAAAACGGCGCGAACATGTTGCTTACCG CACCATTCCGGAGTGTAGATGCAGCCGTTGCAGGCAGTTGATTCGCTTTGTTGAAAATGCTTAAAGGAT CTGTTAATCTAACAAATAGACTATTAAATACATGAACAGCCTTGCAATCGTGGGTGAAATGACGTTGCCGATTACCAGCAC TTGCTCGTCCATCCCTCAAGAGAGATGCATGGAAAGAGCTCGACAAAATTACTCACATTACACGCGATTGCGCAATGCCA TAAATTCTTCATCGACACTTCCCTCGTTCCATATGAATACGCCAATTCTACCGGGCGGCAGCAAAGTTGTCAGTGACC ATCCCGAGCTGAATATGGGGTCAATTGCCAATGATATGGCAGCTTCTACATACGAATTAAAATCGTAAACGGGATATACAG GATTATAGGGACAATCATACAAGATTGTTATCCTGTCTCCGATGAAAACATATCTTGAAGTGAATTCAAATTGAGCTC TAGGCCAAACGACCTTAATGGTCATGCTGCCAGGATGATCAGTCCGGCGCTGCATAGAGTGTGCTGCATTCTT GGAGAAAATTAAACCTGTCAAAATTGAGTCACGTCCGACTAAAACGGATTAGGCCATTATTCTTTATTGATATTGAG AAAGCGTTGATGATGTATTGATTCCAGGGGCCATGCAGGAGCTCGAAGCACTCGGCTGCAAAGTGAGGCTCTGGGTGCATA CAGTCTTACCAATTATAA

Table S11

ERCC-00104	GGGAATTGGAGCTGCAATCTCTAACAGCCTCTGCTAAGTATTCTGCAGCTGCTGCTAACACTCTCAGCACCAGCCTT TTTCATAATTCTCTCAAATGGTGCAACTGGAAAGCTCAGGCCATAATACCACCTACAATAGATTCCAATAAAACTGTTATAAA AATCCTTATTTAAACTTTCGGTCACTTCAATTTGTGAAAGTCTTGAAAATTTCACACATAAGGTTAA AAAGTGTGACACTAAAATTATAAAAACACTATTATAATGTATGTCACAAATTAAAATATAATTGAAAGATAGATAA ACATAAATGGTAGAGTTAATTGTGATATTGATAATTACTATAGCTTCGGTAAAGGAGGGTTGGAAAAACTACAACA TCAGCATCTTAGCAGTAGCAGTCTAAATTGGGAAAAAAGGTTAGCTATTGATGGAGACATATCAATGGCTAATTAGG GATTCTATTCAATATGGAAAAGAAAAACCTCTTACATGAAGTTGAGTGAAGAGGCAGATGTTAGGGATGCAATTACA AACATAAAACTGGAGTTATGCAACGAGTTGCTTAGAAGGTTATAAGAAATCAGATATTGATTACTCCAGAT GTGGTTAATGAGGTAGCTGATGATTGATTATGTAATTAGATGCTCCAGCTGGTTAAATAGAGAAATGGTAGAGATGAGATTGAA ATGTTAATAAAAGGAAAGTTAGTTGAAGTCCCTGAAGATGAAAATGTTAGGTCAGCAGCTTAAAAAGATGAGTGT TGAATATAGAAAGAATTCTCCAGCTCTCAAGCTTATATGAAGTTAGCTCAATAATAGCAGGAGTCCTATTACATTGAAG ATGAAATTAAAATAAAAGGAAAGCTTATAGATAAAATTAAAGAGATTATTAGGATGTATTAATTATCTGATTAAA AATTTAATTATCATCCTTCCAATAAACCGTATATGGGAACGCCCTCTCAATGAACCTTCAGTAAAGCTCACCA AAAATGGATGCATCATCGCTTGTGATGATGCCCTTAGTTCTCCAAATAAACAGTATATGTTGGGAATGCCA TCTCTATCCCTTCTTTCAAATTCTCTTTATCTCAAATTATTCATCAACGGCATTAAATAGTAATCAAATCCATG TTCTAACAAAGTATTCTACCCCTCAAATTAAACTCCAATCTCCATATTCCCTAAATGCACTCTATGGAGGGAGAGTAGC TGGATGATTCAACAATCTCTTATTATCTCCTAGCCCTCTTAATTCTCTACCGGTGTTATAAGTTAAACCGATAG TCATTAAAACCTCTTCTATCTCAACTGTTAGTTCAATGGCTGAATCCAACAATTCTGAGTTGGGATAGTTAA GTGTAATCAAAGTCTAATTGCGTGTCTTATTCCAATCTCTACAATCCCTCAGCCCCTTAACCTAACCAATG GCCTAAACTAAAGGGTTGTCATCAATATTAAACCCAGCAATGAGTTTTATGGGTCTTGCATAGCCAAAGCTAAAG CTAAACCCCTACTCTAAACCCAGCAATAAGCAGTGATATCATAACCAACAGAGCTTAAAGCCGTTAATATACCAAGAAGT ATTGTTAATATCTTACAATTGCTTATTATGTCGTCGACTCTGTTCTGCTTCAATGGGAT TAGGTAGTGTCAAATATCCAAAAAAG AAAAAAAAAAG
ERCC-00108	GGGAATT CCT CT GTGTCATGATCGTGAGTTGTCGCAGTGTCTGTACCAAA ACT CTGGTGGAGCTATAAGCCGTGTTGCGT AAATCAACGGCATGCCCTATGACCGCGTCATGCTAACTGATAACAGCCTGCTGAACAGTGATACGCACACTGATAACTATG CGCAGACGCTGAAACGATGTGACATCGCTCTAGAGTATGAGCCGAATGCACGACTGATACTCGATATGAGCAGCAGTCGG CTATGATTGCAATGCTTGTGAGTATGCTGATCGTGCAGTGTGATAATACGCTCGCATGATATGTATTGCGCTC AGATGCTGGAGATATGCCATGCGTGTCTGACCTTATCGACGCGCATGTGAGCCTATAGACAGCGATGTGAGCACTCTCATGCGGAT TGTGATGACGTTGCGAGTCTGTGACCTTATCGACGCGCATGTGAGCCTATAGACAGCGATGTGAGCACTCTCATGCGGAT CAGTCTATCCTCGCTGATGCTCAGTGTGATACACGCTGATGCACGCTAGTGAGCATCCTGTGCTCGCATATACCGCTGCTGCACTG ATATGAGCCAGTGCTGCTCTACGGAGTGTGCTCGGCTATAACAGCGAGTGCTACGCCCTAAACTGGCTGTCTAGCACTG TAGCTGGTCATGTACTCGACTGCCGTGCATCTACTATAAGACTCTGACATTAGCGTATAGGCTGATACATTAGCTCGGATG CTATCAGCTTGCCTATTATATGCCTGACGCGGGATCTATCAGAACGACTCGGTAGCTCATATACTGGATCACGGTGCAC ACATGCTACACGAGGTCTCAGACTCTATCCCCTGGACTCAACGTGCATCTGCTATGCTGAGCGCGTATCTGTACCTGTCCG ATGCTCTGATCTACACTGCCGTGATCGTTATATGACGAGACTGTGCGCTCATAGCCGACACTGTGCTCGATAAGACCACGCTG TGC GG ATATAA AAAAAAAAAAG
ERCC-00109	GGGAATTCTAGCGGAGTGTCAAATT CGGAAGGGGGCATAATGTTCTTACAATCGCACCAGTTAGCGTGGCGTATACCAT GTTGTTAACAGCGCCATAAGTGCCTGATCCCGGGCAAAACTACGCAACACTGTGACTGGGTGCTAGGTGCGACGAACA CGCAACTAGATCATGGGAGTGCCCAAGTAAAATTGTTGTCAGGGCAACAGTGACGATAGCGCGTAAATGGTATCATG ATTGTCGACCTCGGTATCTTGTACAGTTACGTCAGCGAAGTCTGATCACGTTAACTAGCTCAGGGTATTAATAACC GAAAGGTTCATGTGGATGTGAACTGCGACAGAGACGACCCATAGTCCTTACCCAGGTAGCTGAGGGCGACGCACTGAC CATCGAACAAACTGAGAGATCGAAATAGCCTCACCCCTGAAACCTACAAAGCTCACTTAGCCGTTAACGGTCAAGTTGTC CTAGATCAGAACGTCGGACTCAAAAAAAG AAAAAAAAAAG

Table S11

ERCC-00111	GGGAATTGCCCTAAGTCCGGTCCGCAATTCTGGGACGCTTGAAGCGCAAGTAGAAAACGAGATAGGGTGTCCC ATCTAAACCGCCGTCCAATAGCTTAAAGGCCAGGAAACATTTAATATCCCTAACAGCACGGTCCACCAACGGCATTACGA CTTACGAGTTCGCAGAACAAAGACTTGCAACTGCAGGGGAGCCCTCGATGCATCCGAATGAGGGCGAGCGTCGAGATTA ACCTCGAGCAGTTAACCAGGAAGGATATTCCGGCATCAAGCGTTCTCCCTACTAATATCCTCCTATGTCCCCTAA ACAGCACTCAGCATCTCAAACAATCACAAAACAACCCACCTCATCGTGACCAGATGATAACGTGGGACATTATCTTGGCA ATACCACCAAAATCGTTCTTATGGGTATCGCTCTAACGCAGCGACTTCTGCATAACTATGCCATACAGTTAGGTGCTACC ATGAACATCCCGAGCTGCGTTGCATGTATCGGTATGCCAAGACCATACTCCAATGCTGCAGGGTTAAATTCTCCGTTCT CGTCTAATCTAAGAGAATTGTATAGCTGCAGGCTAACATCCTGGTCAACCCCCACATTGTAACCTCGCTGATTCCCAC TAATTTCTAGGGTTAGTGAAGGTTGATACTCGCAGGGGGATGGTGCTCAATTGGGCCTCGTCAACACACAAGAGAGATCGCACGCGAAA CCGTTAACGCAAGAATATACAGCATATGGCATGTAAGCGAAATAACATCCTCCACTGGGTGACAGCGAATTAGTATCATAG TAGAATTAAGCGAGATCCATGACGTACCGCTACTCAATCATCACGTCTCGGTACACCAAAAAAAAAAAAAAAA AAAAAA
ERCC-00112	GGGAATTCAAGATGCCTGGATAGGTTCAAGTTACCGTACCCACCCACTAACACGACCTTCTGCCCTTGT ACCAACGCCGGCTAACAGGTGGGCCAACTAATATTGTTAAGGCAGGCCTGTACTACTCGATCGTTCATAGCCCCACG ACATAGTTTACTACGTTAGCCGTTAGAAACTCACCTGTTGAGGTTACAACCAGATCGTCTTACTTATGGCAT GCTGGCGTAGACAGGTGCCATTGCGGCCAGTACTCGGATGTTGACTGATCTGGCCTCTGTTCCCTGGTAAAACG TCGCTTCACTCCGGTAAGGGCAATGTAATGACCGTATTCTAAGGTACGGATCTACACTATGTGCGGGCGAATAGACTCGGGC CCGTAGCGGGAGCAAATACTTGTACGCAATCTGTACGTCACACTGATGTCGCGAGACTGCTGCGCACCCAAAGTACCGTAC TAACGTCCGTGATTAAACGGTAGGAATAAACACCGTCTTACAGCTACGTTTCGATTACTACCGAGCGTTGCG AGAACATATGGATTGGAAATAGGCTCGAGTCCACATACAGCCTACGGTAAGTGCTAGGCTCGCAATTCTATCCGGTTGT GAGTCTAGTTGTGCTCCGGCTTGAATGAGCATACTCATGAAAGCGCTGCTACTATGATAAGAGTACACGTACAGGTCTCG CCCGATTGGATTATGGCGAGCTGCCGATTGACGGACATACCTTGAACGTAATCGCGACGAGTGCAGGATTAAGATTCTCCG CTTCATGCAATGTGGTACAGCTGACTATCATTGACACCAAGCCGCTGAGGTATCGCCTGCGATAAGTTAAGAGTG AGACGAAGAGTATTGAGCGCCAGGTAAGATAGTGCCTAAGCATCGGTATCTAGCTTAGTAACCTCTCGATGG GAATACACCTCTGCTTAACGGCTTAATAATTGACGCGTCTGGACGTAGTACTCTGCAGTGCCTAAACTCATAGTAAACGAT CTGGTAGGTCTTTACACACGGTTTATCGCTAGTGCTAAAAAAA AAAAAAA
ERCC-00113	GGGAATTCACACCGCGCACGCCACAGCGCTCATCTCCAAAGAACGCCATAGCCCAGATGCGAGGTGAAAAGTCACAC TAGAGCGACACCAACATCGTTACGCTTACACACCGGACGCTGGATCAGTGGGAAGTGCTCACGCCGGAGCCACTGGCGA ACAGCAACGTTATAACGCCACTCAGTGGTCTGCACGCCAGCCCCGGGTTCTGCCCCATAAGGGCCTAGTACCTTCGAG CCCCCGCGTACTAGGCAGATAAGAACCTCCAGCTCGGGCCTAAACCGATATTCCATGTGGGCAACTGCCATGTTGTT CCAGTCGCTATGGAGTAGCCGCGCTGGTGCACACGACTACAACCCCTGTAATAGGCTGCGTGCCTAAATACACTCGC TGGTGGAGATACTAAAATTATCTGTGGATTGCCGGCATTGAGCCACGGTAACCCCCAAATACATAAGTGTATAATGTCGGA CCCGTCGCAACGGTTGTTAATATGACAGGCCGCTAAAGACGTTACTCCGCCATATGAGATAATATCCTTATCTGAGACGC ATAGCAAATGTAGGAGAGAGAGGTTATAAGGCCCTAGCCTAAAGGTTCTGCGAGAGCAACATCATACCCCTGAGAACCGA CTTTGGGTTAGGGCCTGCCGTAGCTACAATTGATGCTGAAGGTTCACTAGATGTTATGGACGATGACTATAGTG TAACAGGTGAGAGCTTAACCTGGACACATGACACTCAGTTCTGTACCAACTAGGAAGAGCGCCGGGTAGAAGAATAAAA AAAAAAA

Table S11

ERCC-00116	GGGAATTCAAGCGTTCACAGCTCGGCAATACCTGTGACGAGCTGCTCGCAAGATTACGCAGTGTGGCTATACTGACAGTGA TGGCGCTTACTTCAGATGTATGGGTGATACTTCGCTATATGGGTGGTCACTTCTCTATGGCGCGTGACAATGTACTATGGAGC GGTCAATGTCAGTACGGATCGCGTCACTAGGTGACTACGCACGCCTCTGGAGTAATCGAGTGCCTCGTGCAAATACGCG GTCATCGTGCAGATAACCAGAGTCATCGTGAGTAGTATGAACGTGTCGTATGCAGCGGTATGCGTGTATAATGGCGTCT GTCGTGCTCATAAAGGTTCTGATGTGCTAGACGTGTCATCGAGCTGCATAGCTATACTCGAGTCACTTGGGATACTTCG ATAGCGTTGTGAATAGTGTGCTAGGCTCCGGGACGTTAAACTGTTGCCAATTCAAGATTAGTCCAGCTCGTACTA TCGAATACACCATCGTCGTATCGAATAATCGCACCTCGTAGGAGTCGGTTGCCACTCGTGTAGTCACCAGGCTCGTTAGA TAGTAGCCCAGATCCTACGAGATGAGCTACGTAACTAGTGTAGCATATAGGGTACGCTAGAATGCCAGGTCGTAGTCGA TTAGTCAGGTTGGATGTCTACTAGTTGACTTGGAGTATGCCATGAAGACTCGTCCCTCGATATCAATACTCGTCCGCAGGTGA ACACTGTAGTCGGTCTAGTGCCACTCTCGGTATGTGTCCTCAATTATCGAGTAGGATTCTAATCAATCGTCGCCGCTCAC TAATTGTCTCGGGTGGCTACTAATGGTTACGGTGCCTGACTAACCGTGTAGGTGTCTAATACATCGTGTACGGGCGATATAA TGCTCGATAACGGCAAATATACTCCCGTCCGGATCCAGATCGCAGGGTATCGCATCGACAGACCTGGTATCGTCGTGACGA ACGTGCTACTCGCTTATCGGCCTGCTACATCAGTGGCATGTTGTAACCCTAGCCGATCTTCTACTACGAGGCTACTA TTCGATCAAACACTCGCCTATCTGGTAATAACTGCGGTGATCTGGTAGCCACTACGTGCGCCTGGTAGCAAATACGGCGAGCTGG TATCACTATCGGCTCAGTGGTCCGACATAGTGCCAGTGGTTCGATAACTGCCGCTGGTCCAATATAACACGCACTCGTCA ATCATACTCGAGCCGATGGTCCGGAATAGGCCCTGTTGACACTATGCCACCTCTGGTCTAATATACTCGCCCTGTTGTCGTATA ATCGAGCGCGTAATCGTATATCCGACTGTAGGTGCGTAACTCGCGACTAGGTGGCTCTAATCTGCGTTGGTTGTCGTACAG TGTCTGGTGTTCGATACCGGATCGGGTCCGTAATCTTGGCATCGAGGTTTCGTACATGTCACGCCGCTCGTTCTCGATTCTCG GTGGTGTCTAGTACATCCAGTGGTAGTCGCTACATCACACGGTACCGGCTAAACCTCTGGCATCCGTATTAAGCGACAT TCCTACGACTTATCAGCACGTCCTACGGTATAACAAGGCGTCTACGGTCAACGACGCTGGTAGCAGTCTATCAGATCGCTA GTACGAGTTAGAGATGCTTAGTACGCCCTCGAATCTATGATGTCGTGCTACGCGATGCACTCGGATTATGGCACATGCACT CGCGTAATGACGCTGCATCGCTCAGTATGATCCATGAGCGCGTAGATGACGCGATGAGCCTCGTATCGAGTCATGAGCTGTC TTTCACATGATACTCGCTCTAAATCATGCGACAGTCTCGACAGCAGCTCAGCATCTATGCATCATGTGCCTCACTAGGA CATCATGCTCGACTCTGAGACACTGATCGAGCATTAAAGACTCTAGAGCGGCCGACTAGTGAGCTAAAAAAAAAAAAAAA AAAAAAA
ERCC-00117	GGGAATTCAAGATACTATCAGGCCCTATGGGCAAATCTGGCCTCCAAACTCCGAGTGTACCGAACCGTAGGAAATTCTTCC CCAAGCGTGTGCAATACTCGTAGCACACCGGGATAAATAGGAAGGAAACATCCGCGGGTCTTACGGTAGAGCTGTGGGACCGC TTCTGTACACGGCGTCCAATCAAGGGCTTGGCATTGGGCCAGATCGAAAGTGTGAACCACAAACGACTCTACGGTGACG CCTCCAAGCGCGAAACTCCAGGCAATGGGAACCGCAGAAAGATGTCCGCTAGACCGCATTAAATACCACATCTGGCCTAGA AGCCCCTCGGTGCTCCAGGGAGGACGGATCGAATTAAACGTGATATGGAACCTTAACTGATCAGGCCTGCCCTACTAATG GCGCGTTGTAACGGCCTTGAGGGATGTCACTATTGAGGCACCCGTTGACCCCTCAGAGATATAACCATTCCGCTATTGTAG CTCTCCTCGTACCACAGTCTGCAAATACTGTCATAGCTATGGAACCGCCCCACGCCGGGATTATGGCCTCTCATGGACTCA GTGTGATCAGAACCTGCTCGAGTGGGACTGGATGCGAGAGCTGATCTGTAGTGTGTTGTCGCCGGAGCACCCGGATG ACAACGCCATATTCCAGTGCCAAATACTCACTGGTAACGGCTGAACTCATGCTAATTCCATTATAGTTCTTAAACATAA GCTTGCCTCGGGCCCATTCCCTGAAACCATGCGGTGAGTCACGTACGCGACCTGAAATTAAGATCCGGACAGGCCGA CCTTAGCCAAGGGTAAGAACCGCTTCACTTAGTGAACATCCTATCCAGTCCGTCAGCATCGTCTACGGTCCGGCTCTGCC GAAAGGTCATTAACAGACAGAAGGATAAATGGCTCCAGCGGATACGCGCATATCGGTTATCGCAGTTACCGTGCAAAACT GCATCCCCGCTGGGATAAGCACATGAGATGGACAAGGCTTCTATGAGTGATTCCAAAGAACATTGCCGACGACCGACCTT CAGGTAATCCACGAGACATATGCTAACCAAGTGGGCCATGGAAAAAAA
ERCC-00120	GGGAATTGGCGTCTCACCTGGCTTGATTCACTGAGTTAAATGGAGCACTTGTGGAGTGCCCGACACAAACATCCGCTAGCCTCAGT CGAATGACAAGTTAGAACAGGAGTGGGCCGATCTCTGCAAACCTCTATTGTCAAGGGTGGTGGACGGTATAGGTTTGCGC CTACCTGAATGCAAGGGCTTACCTCCAACGGCTTAGATGTGCTAGAAGGTACGCCCTCAGTCAGACGCCGGCGTTAG TTAAAGCAGGCTTGTACACATCACGTAGTTCTGCTGCGTTTAAGTCATTAGCTCCAGTAACCCATCAACCATTACCGTA TAGACTTATCCGAGTGTGATCAAATAACGCTGAGCCTTATGATCCTCGTCGACCCAAACAACGCCGGATATACTGTTGGGATAT AAACGAAACACGTACCGCGAGTGACACGCGTTGACGTTACGTTAAACTCGTAGCCAACCTTAACATTCCCTGCACATATG TTAGTGCCTACAACATTAAGGGAAAAAAA

Table S11

ERCC-00123	GGGAATTCTTAAGAGAGGAATAATTACTTTCATCTTACCCACCAAGTTTAGTTCTTATTCTTCACCTAATTTTCGA CCTCCTCCTTGTTAATCTTAGCTTTAACCTCCTCCAATTCTTTGTAACATTAACTTAAATCCCCAGTATTATG TTGAGGAGTATGCTAATAGCCACAATTATACAAAATCATCCTTATCTCCTCCGAACAATCCTTAATAAACCTAGATATG AATGATTCTTCTTCTCAAGTTGTGCTCATTTAGCTCAATTAACTTAGCTGCTATCTCATGACTGCTGAGCGGC TGGAGAATCTGGATACATAATAACGAGAGGTGTTCCAATGCAGCTGCCTCCTAACATGAGGGCCTCTGGAACAACACCTA TAACAGGAACTCTAAAATTGCTCTATAGCTTAACCCCCACTCTGACTCTCATTTGAAACCCTATTAACAATAGCCCCA ATGATGTCAGTCCCAATCTTTGTTAGCGATAATTAAATGCATCTGATATTGGGGATATCTCTGGATTACAACGAC AATTAAACCATCTGCTGATATTGCTATTAAAGTCTCTTCCAATACCTGCTGGACAGTCAATAATTAAATCTCAACTA AATCATGTATTGCCTTAAAACCTCCTCAAGTTCTGGTTAGCTCTGAACTTTCTAATGAAACACCTGCTGGAATA ACTAAAACCTCCTTCAGGACCTCATAAATTGCGCCTTATATCTGCTTACCAACATCGTTAAGGTTACTGGCTT TCCTCTAACCCCAGTATAGGCTCTAAGTTGCCATTGCTATATCAGCGTCAAAACAGCCACTTTTCAAATTGCAA GAGCCACAGCAAGATTGCAGATATCGTGTCTTCCAGTACCTCCTTCCAGATGCTATCGCGATAGCTATTCCATTAATG TCACCATTCTAAAAAAAAAAAAAA
ERCC-00126	GGGAATTCGAGCTGGAGACCGACCGCATTAGTCATATAGTCATAATGAGACGTCACGGATTGAGTATCATT GCTAGAACTGCTTACCTATCTAACGCTCAGGTATGCCTGCGCTGAGACTCAGCATCTCAATGTGACCGAGCTGTGACTCCG CATCCTCCTGCAATATAACCCATCGGCCCTCACGGGTAACGTAGCTCTGCGTACACCTGGCTAGAGGGCCTTACCGGCT GTAAGCTCACTACAATCCAGGTACAGAGTGCCTAACCGGCCATTAGAGGGCCGCTACACCGTCAGAATTAAACGTATGGG CGCGAAGCGCATAATGGTTAGACCTCTTGCAAGGGCAAATAACGATTGCGACTGCCCTTAAGATGGAGAATGGACA AACGCTCATTCTAGTGGAGACATCGACATCGTTACGATGCAACGTCAGTGGCGCATAACACTTGGCTCGGTCTACCGC GACAGTGCACACAAAAACAGTTGCTCTACATTGCTATGCAATTAAACGGATATGCCTTGGCTGGTAATCGTCCGGTGGCCCT AGTTGGCTATGCGCGAACATTATGCCGGATTCCGAAAGCATGTGCCAAATTCCCATGACCCTGGTCCAGGTGAGCTGACAC TGGCGTTAGCACATGCGCGAACAGGGCGGATTCCGAAAGCATGTGCCAAATTCCCATGACCCTGGTCCAGGTGAGCTGACAC TATCAGTCGAAGTTGTTCTTAACCAGGAAAAACGCTGTTCTCCGTTGCTTACCATGGGGCAGGGAAATTCTCGAGC GCGCGAATGTATACACTATTATCTCATGTGCATGCTCAGAGCGGGCTAACCTAATATACTGGTGCATGTCGAGATCAGT TGGGAATAGCGGAGCGGATACGCCTGGAACGCTGGCGTGCAGTAAACTACTGTTCTCCAGTTCCTCCATCATGTTCCGT CTAATCCGGAGATGTGTAGCTGCATTGTGCTCCGTTGCGGACTCCTCGACTGGGTGCCATATGGCTACTGGCGAGAGGAAA TTGCTTTGTATTAGGCCGTGGCACCTAAAAAAAAAAAAAAAG
ERCC-00130	GGGAATTCGAGCTGCATTTGAAAATTCTATGGAAGAGCTAGCATCTGACGAAAACAGCAGACGGAAAGTACTGACCAG CGTCACACAAAAACGGAACAGGGCTGACGCCGCTACATATAGAAAAGGGAGGTAGAAGAGCTGAAGGCACACTGTTGGAAG AGCTTGAAGCTGATCTCTCATCTTAATGAACTGTCGCCAAGTCAGCTGAAGTCATTGGCAACAGCAATTGAAGTGAAG ATGATTGACCGCACGCAATTGATATTAGATATTGCAAAGCAGGGGAGAACGAGAGAACGGCAAACCTCAAATTGAGCTGGC TCAGCTGCAATATGCACTGCCCGTCTGACGGACAAGGGATCAACCTTCCCGCAAGGGAGGAATTGGGCAAGAGGTC CCGGGAAACGAAACTGGAAACCGACGCCGCCATTAGAAATCGCATTGAAATCAACACAGCTTCCACTGTCATT GCCATAGAACCGGATACCGTGAAGAACGAGAACGGGTGTGCTCAAATTGCGTTGCGTACAAACAGCAGGGAA ATCAACATGGTTCAACCGCCTGACGAGTGCTGACAGCTATGAAAGAACCTCTGTTGCCACGCTGGACCGATGACCAGAA AAATGGCTGCCAACGGCTACAGTGTCTTCTTCAGATACAGTAGGATTATTGAGGATCTTCGACGACATTGATTGCT GCATTCCGCTCAACGCTTGAGGAAGTAAAGAAGCGGATTAAATTCTGCATTAAATTGATTCTCAAATGAGGATTATGCGGG ACATGAAAAAACAGTGTGCTCGGCTGCTGAGGAGCTGAAAGCAGATGATATCCGATGCTGACGGCTAACATAACGTGATC AAAAACTGCCGTATTATACCGACCGCCGGAAAGGGATCACATTGGTCAGTGCAGGAAATTGAGGACGACGCTGCAGCCTT AAAGAAGCGATTAGCGCTATTGCGCCAAGAACGTAACTGTTGAATTCTGGAAAAAA

Table S11

ERCC-00131	GGGAATTCCGCCGGATAAAGGCTTCTCGGTACTATACAAGTTGTCTACGCACATTGCCTGGGTATTAAACTCTAGTAGGA GCGAAACTGACATATCAAACCTCTGGAGAGGCATCTCCAGACATTACGGATGATCAGGTCTCAGCGAACCTCTAGCTGTG CGGATAATTGTGGCCCGCACAAACCGCAAGACACCAGCGTGTCTATTCCACAAACTTCGACATATCAATAACGCAGTAACAAAC GTTAAGTAGGGGGACAGGCAGTGCCTAAGGGCTTGAGGTGCCGATTCGCATCTAATCTAACAGACGAGGTGGCGT AAGATGTACCTCGTTCAATCTAAGTATGAATTGTCCGCTGGTAATGGTCCAATTAAAAGAACATCGTAAACAGACGAGGTGGCGT GTAATTGGGTGGCCCGTCTGGCAAATTGCCCTGCAAGCTGAGCTGAAGCTCGGATTGGATGTCTCGTAAGGAATACTTATTGCGG GTGGTACGCAAATTGCAACCAGTGAAGTAATGTGAGCGTACTTCACCTGCTCCGGTACAAGGCCCATGTGCTCATGTTGG GAAACCTCTCGTAACAACCGACGCTGCAAAGTCATTCCCCTATCGGTACACTATTGAAAACATGACAAACGTATAATG CGTGATGACCGAACAGGTGTAAGTGCACCAACTAGTATTGGCTCTGTCCACATGGTCGGGTTTCCGCCCCCAAACATGCA AACATCCGAAAAAAAAAAAAAA
ERCC-00134	GGGAATTCAAGGCTTGTATTGGTATTGACTTACAAACAGTTAACGCCATTGAATATGATAATGTAGTTGCAATAAAAGGAGA TTTCACCTAGAAGAAAATTGAACAAAATTAGAGAGCTAATTCCAATGATGAAAAAAAGGTGGATGTGGTTATAAGTGACG CCTCCCCTAATATAAGCGGTTATTGGATATAGACCAACGCTCGTTCAATAGATTAGTAACACTGCCTTACAAATAGCTACT GAGATGCTAAAAAAAAAAAAAA
ERCC-00136	GGGAATTCGAGCTTTGACGTTGAAGGAGGGTTTAAGTAATGATCGAGATTGAAAAACAAAAATCGAACCGGTTGAA ATCAGCGACGATGCCGAATTGTAAGTTGCTAGAGCCACTTGAGCGTGGATATGGTACAACCTCTGGTAACCTCCTTACG TCGTATCCTCTTATCCTCACTCCCTGGTGCCGCTGTAACATCAATCCAGATAGATGGTACTGCACGAATTCTCGACAATTG AAGGCCTGTGGAAGATGTTACAACGATTATCTTACACATTTAAAGCTTGCAATTGAAAATCTACTCTGTGAGAGAACG CTAGAAATGATGTACAGGGTAAGGAACGTAAACGGCAGCTGATATTACACAGATAGTGTAGAGATCTAAATCCTGA TCTTCATATCGCAGCTTGGTGAGAATGCGAGTTCCGAGTTGCCTTACTGCTCAAAGAGGACGTGGTATACGCTGCTG ACGAAACAAAGAGAGGCAGTACGCAATCGCGTGATTCCGATCGATTCTATACGCCAGTTCCGTATCTTACAG GTAGAGAACACTCGTAGGCCAAGTTGCAAACACTATGATAAAACTTACACTTGATGTTGGACTGATGGAAGACACTGGACCGAA AGAAGCAATTGCGCTTGGTCAAAGATTAACTGAACACCTTAATATATTGCTGGTTAACTGACGAAGCTAACATGCTG AAATCATGTTGAAGAAGAAGATCAAAAGAGAAAGTTCTGAAATGACAATTGAAGAATTGGATCTTCTGTTCT TACAAC TGCTTAAAGCGTGC GGTTAAACACGTTCAAGAGCTTGCAGAACAGACGGAAGAAGATGATGAAAGTTGAA TCTAGGACGCAAATCACTGAAGAAGTGAAGCGAGACTAGAAGAACATTGGACTCGGACTTCGCAAAGACGATTGACTAGTT CCCTGTGAACTAGGATTTCGGGTACAAAAAA
ERCC-00137	GGGAATTCCAAGCAAACCTAATGAAGCCAGACAGAGATCACAGAAAATCGCTGACTATCCGAGTGCGCGGCGAGCTACAA TCCAAGATGATTATTTTACGACCGGGCGCTGGTCAGGTATATCGCTGGTACAGATGGCGCAAGCATCGTGTCAACACT TCCTTCACGATTCCGTTAGAGCGAGTGGTACAGCACGTACGTTATATATGGGAGTACGGACATGCTCCACCTCGTCAGC CAAGATGATAGATACCGTAGCGTGTGGTCTTATAGCTGCTCTGATGGACTTCGAAAGATCACCGTGCAGCTATTCAAA GCAGCCGGGGAAAAGGTGGTCTGCCGAAAGCCATGACCTCCGATCACTCCTGGCGGTAGTCGTTTATTGCAATTGTC AGTTGCGCGCGCAGGTACATCCCCTGGTTAAATAGAGGCACGAGCGCTCGTTGGTGTCAATATGGCTTACCC CGAGAGAGTTGTGAGCTTGCACGAAAAAAAAAAAAAA
ERCC-00138	GGGAATTCCCTGCTAAAGAGGTTGGTGTATAAGATTGGAGAATTCTAGCCTCTGGTAAAAAAAGTAACACTACAT AGACATAAAAAAGCCACCACAAACCCAGAAATTAAAGTTAGTGGAGAAATTGCTGAGCAAATAAGGATGAAGATG TAAAAGTTGCTGGAGTAGAGCTTGGTTCTGCTCTAGCTACAGCTGTCAATTATTGCTCAAAACCACTATTAAATTGTT AGAAAGAAACCTAAGGATTACGGAACCTAAAGATAGAAGGAGAGCTAAAGAGATAAGGTTGTTATTGTGGAGGA TGTTACTACAACGGAGGAAGTGTGCTAAAGGCAGTTAAAGAGATTAGGGAAAATGGTGAATTGTTGATAAGTTTGTG TTGTTGATAGGTTAGAAGGAGCTAAAGAAACCTACAAAAGAGAATGTTGAATTACCCATTAGTTACTGTTAAGGAGCTA CAATCCACTCAATAATCTAAACCTCTTAGTCCATAGGGAAACCCCTATTGGGATACTCCCCGTCCATTAGTTGCTCCT TTCAGGAGCAATTATGCTTAAAGCTTAAATCCACTCAATAATCTAAACCTCTTAGTTCTCTTTAACCTT ACCAAATTCTCTAATTGCTAACATCTACATTCTTATCCTTAAATCTTATTGGTCTATGAGTGCACATTGTTAA GTAAGTCTCAATATCCTCTTTGAGTTAAATCTTCCACAGCATCCCAGTCGTGAATTAGTATAAGCAACTCCACCA ATGTTCTTAAAGGAATCTGATATTGGCAACTCCTCTCCAATTAAATTTAAATCTAAACATCCACACAAATTCCC ATCAACACTCATCCAAGATAAAATCCTCTGTGGAGTAATCATAATAGATGGGAACAAATTACTCCTGCCCTCATCTGG TGTGGATAAAAAAAAAAAAAAA

Table S11

ERCC-00142	GGGAATTCCACCTGTCACATTCCAATCGGCTCAGGAAGAGAGAAGTGACGGCTTAGCTGTAGTAATCCGGGATCGACTTAA AAGGGGTGCAGCGACCACGGCGATCGGCATGGCGTCAATAGTCCTCTGTTAGGAGGGTCTTAATGTTAACGCCGAATAT TAGTCATATTTGCTAGCGCTATCAGCGTAAGATATGATTTAAGTACACCAAGGAGAGTAGCGAGATAGAACCACTCGTGG ATCGGTCTTCTTAATTGACTACTATCAGATCCGGCGATGGCGTGGAGTCAAACACTACATTACAGGCCCTGGTTCCATGGG TCAGCGCAAGTACAGGCAGAGATAACACCTCCGGAGACTTCGCTCCACACACCGGAGACCCTAACCGTACCCAAATGTA ACTAGCGCCTCTGGTGTGAGCTACTAGAAAGTAGGCCGGCGTCAGAGGTTGCGCCAAAAAAAAAAAAAAA AAA
ERCC-00143	GGGAATTCATGCAGCGTAGGTATCGACTCTCACTGTGGAGTCGTCTATGATGTCGTGGAGTCCTCTCAGAGTGCTGTAGGTCC TCATAGGTCGTGCTGTCTCTACACCGGTGAGTCTACATTTCTGCGAGTTGGTGTCTCACTGCGGTGTCAGTGATCT CTCCCGGTGACATGAGTCTAGCTTCCGGTATGGTCTATCCCAGCGATGGATGAGACTACTCTGTAAGTGCTGTAATGCTGA CTCGCAATGAGTCGTAGTCCCCACAATGTCTCGATAGTGCGCCGAATGTGTCTGTAATGCTCGAATGTGTAATCGTCAACT CGTATGTGAAGTGCTAGGCTAGTATTGACATCTACGGCGGCTATTGACGAACCTCCGGTATATGCTCTACATCTGAGGGA ATTGCCGACCATATATGGGTCTTGCTGATAACGCTAGGGTGTGCTACTTAGATAGGCGTCTGGCGCTATTGCGGGTGT CTCAGAATATGCGCACGTGCTGGTATATGGCACTGTGTCGCTACGACATACTGGTCCACATATAGACATACTCCAC GACATGACAAAGCGTGCCTACATAGCACAGCGTCTCTAAATAGATCCGGTCTATCGCTGAATGTCTAGGATTCTCGTC AATGATCTACGATCCTCGCTAAGTATTAGCCACCTCGTATAGTATTGCGCACCTGAGGATTATTACACCTGACTCGGTAT AATATGCCGTACCTAGTCTAAAAAAAAAAAAAAA
ERCC-00144	GGGAATTCACTAGGATAAATTGACCCGTATGAACGTGTTGCCGGCTCGGAAATGTTAAGGCTCTGCGCACGCACCTTATCATT CGCAGCCTGTTCTGTCAGCGGGTCAGCCTAGGTTACGGTGGAAACCACCTCGGTATCGTCAGACAGGGATCGAAGGCGATCCA GCCGGTATACTTACGTCACATATACTATCGTAATATTGGCGGTGCTGACAAGTAAATACGGCTAAACCGGTGTTGACCAAC CACTCTCGGGGGTCATAAAATATCACTGAGCCCGGAAGTACCCCGTGACAGACATACGAAAAGCGTGATAACGTATTGTA GGTATTATTCCGTTAGCTGGAGGTAAAGGGTCTGGTCTAGCCGTGTTATGTCTATTATGAGATGGTAAGCTCGTCACC AACTCGTACGCGATCGAAATAGCTTGGACTAATGTCGGCACATAATCAAGTCTACATCAATGAATGGTTCTGATTG CTACCATCAGATATCATGTGAGCAAAAAAAAAAAAAAAA
ERCC-00145	GGGAATTCACTGCTTTCATCCATAAGCGGAGAAAGAGGGAATGACATTGTTCTACACGGCACAAGCAGACAAATCAACA TGGTCATTAGAAATCGGAGGTGATGCTCTATTAGCGGAGAAATATGGTACACCTCTTACGTATATGATGTGGCTT TAATACGTGAGCGTCTAAAGCTTAAGCAGCGTTATTCTGCAAGGCTGAAAGCACAGGTGGCATATGCGAGCAAAGCA TTCTCATCAGTCGAATGATTGCTCGCTGAGGAAGAGGGACTTCTTACGTTAGATGTCGTATCGGAGGAGAGCTATATACGGC TGGTCAGCAGGCTTCCGGCAGAACGCATCCACTTCATGGAAACAATAAGACAGGCAAGGAAACTGCGGATGGCGCTTGAGC ACCGCATTGGCTGCATTGGATAATTCTATGAAATCGCCTCTGAAAGACCTATGTAAGAAACCGGTACTCCATC GATGTTCTCTCGGATCACGCCGGAGTAGACGCATACGCATGACTACATTACAACGGGCCAGGAAGATTCAAAGTTGG TTTCGATCTTCATAACGGACAAACTGAACGGCCATTGAAACAAGTATTACAATCGGAACACATTGAGTCTGGTGTCCATT GCCATATCGGCTCGAAATCTTGATAACGCCGTTTGTTGTTAGCAGGGAAAAACTCTCAAAACTAGACGAATGGAGA GATTCAATTGATTGATCCAAGGTGCTGAATCTGGAGGAGGTTCGGATTGTTACGGAAGATGATGAACCGCTTCA TGGCACTGAATACGGTAAAAATTATCGAAGCTGTGAAAGAAAATGCTCCGTTACGGTTTGACATTCCGGAAATTGGA TCGAACCGGGCGTTCTCGTGGAGACGCAGGCACAACCTCTTACGGTGGCTCTCAAAAGAAGTGGATAAGCTGTAC AATGTTCATCATTGGCGTGCATTAAAAAAA
ERCC-00147	GGGAATTCCCTGCTTAACCTTAATCTGCTTATTACAATATTTAGAAAAATAAAAGTAAAATAAGCAAATCCTTA ATCTTGGTATATTGATGGAGAGGTATGAAATCCCTAAAGAGATTGGAGAAATAATGTTGGCTGTTGTCAGATTACA TAAGACAGATGTCAGTTGCTAAGATAGTTACACCAAGACACTTATGATGAAGATGGTTATCCAATAGATGGAGGTTAATGGAC ACAAGATTGGAGTTAGACCCAGGTTAGTTGCAAAACATGTGGAGGAAGGATTGGAGAGTGTCAGGGCATTGGCA TATAGAGTGGCTAACCAACAGTAATTGATAGGATTGCAAAACATAACAGATATTGAGGCACTGTTGCCCACACTGTG GAAGAGTAGCAATAAGTGAACATAAGAGGAAAGAAATTGGAAAAGATGGAAAATTAGAGAGAGATGGAGGAAACAAGTGG GAGGTTTGAGAGGTTATAAGAAGCTTACAATCTGCCCACACTGTGGAGAGATAAGTATGATATAAGTT TGAGAAACCAACAACTACACAGAATTGATGGAAATGAGGAAAAACATTAACGATGTTAGAGAGATTGAGA AGATTCCAGATGAAGATTGTATCTACTCGGCTTAAACCCAGAGGTTGCAAGGCCAGAGTGGATGGTCTCACGTTGCA GTCCACCGATACTGTAAGGCCATCAATTACCTGGAAACTGGAGAGAGATGAGACGATTAAACCCACAAGTTAGTGA TATCATCAGAATCAACAAATAGATTAGAGGAGAATAGAAGGAGGAGCACCAACTTAATTGAGGATTATGGAATCTGT TGCAGTATCACGTAATACCTACTTCGATAACGAAGCTCCAGGTATTCCACCAAGCTAAGCACAGAAGTGGAAAGACATTAAAA CCTTAGCTCAGAAAAAAAAAAAAAAA

Table S11

ERCC-00148	GGGAATTCCATCTCATTGGTCACGTTACAACCAGTAGACGCCATAGCAGGAGGGTGTGCGACAGGCAGGAAGCTCTCGGGGTCCAAGCATTGCTGCAATGGCGCTTGCTCGATGTTGACCGAAGCTCTAACACTGCATTCAAGTCCGAATCTCTAGATATCTCGAGAGCCAATGGTTAAGGAAGGGCGTAAGTTCAGCGGACACGCTGCAGGATGTAATGATTAAAGCCGTAGTTGAATTATGGAGCGGTGCCCGGAAAGGTATAAATCGGAGGCAGGGTTACGGCGTCAGGATAGTTCATAGCGTACGCAGAACGAGAACCTTATTGGCAAATGGAAGTAGCTTCCACAGTTGTAACAAGCCGTGCCTGCGCATGTTACCAATGGAGAATCGAAAAAAAAAAAAAAA AAAA
ERCC-00150	GGGAATTCACTGATGTGACATCACGCCAATCAATTGGTTACTCCCCTCGATTATGCGGAGTTATCAGTAAGAGCGG GTACCGTTCTGCTGAATGCACTATGAGGGCGACCCCTGATCTTCATTGCTCATAGATGCAAATACCCGGTACTAGTTGGCGAAGTTGGCTAAAGATTGCCACTTACTAGGTGACTGTTAAGTAGAAAGTTGCATGAGGCTGGTAAGTGAGGGCTCAGTGAACAGGATAACCGTACCGTACGATTCCCGTGTGGGCTTGACATTGAGCCAGCCTCCGCTTGACAGAGGCAGACTGTCCGATGCCTAGTATGTTCACTATACGATTCTGGCTAGCTAGGTGTCTGACCCATATTCAAAGATCCGAACCTGCTTGTACTTACAGTACGAGTTGATGCTCTGGGTACCTATTTTGTATCCGATAGTATTGGTTCTGGCGTGTCTCGTAACCCGGGACTAGATTATGGTAATGGGTGTACACACTACTTGACGGGCGTTACCATTTCAGGTGGGCACAAATAGCTAAAGCCTCGTCCGCATTACGCCATGGCTACGAGGCTACCCATAAGGGATTACGGAGTTACCCATAGTAACAGACGAAATTGTTGATAACAGATAGTTAACGCCTTGGCTGAGGAGACCAACGGACTTCAGGGTTAAAGGAAAAAAA AAAA
ERCC-00154	GGGAATTCTCACTAGATCAGAAGTCTCCACTCGAGACTAATCTGGACTATCTATGAGCACCTATTGCGCTGTGGAAGATTGCCCCTAGGTCTGGCGGCTCGATTGCGGGATGAACTGGTGGTCCGAGGAGGCATATAGGAAACGATGGCAGCGCTATT CAGACGTTATTGGTATGGAGTAAGAGGCCGAAACTGGGCTCGATTGATGGACTATGATCAGTCAACTCAAGCGAGGATATC CATACCCACCGACGGTATGGTCAATTAAACCCAGTATTGACTAGTGGAGGTCTAATTGGAACGTATTCCCGCGCACACAGAGATTCACTTACATGGACGTGAAGATTGATGCCGGCGACTATTATTGCACGACCTTGCCTGCCCTCAGTGCGCCCTTTTGTCCACGACGCAGGCTGGACCAAGCAGCCGAGGCTGCGCTCCGGCATCAAAGTCCACGAGTTACAGCCAGCGGGTTAAGGGTATTAGCATCTCGAGTGA AAAA
ERCC-00156	GGGAATTCCACAAGAATCCCTGCTAGCTGAAGGAGGGTCAAACATAACACCTTACGGCAGGCTAAGTGAAT ACTAACCCACCGGCAGCCGTTGATGAACTGTTGACCCCTGGCTCGAGACATTGGTGTGCTAGTACTAGGTGACTGGTACCGATTCAAGGTTGCCATTCTCTTATCGAGAGCCCGAGGTAGACTATCTTCAGATGATGCCATACGTTCACTCAATCGCGCGCATGACGGTGGGCTACGAACATTGCTATCCGCTAGATGTGGTAGAAATATGTCAGGGTTCTGTCGAATTGCTCGCAACCGTGGCTGTGAGCATAGACCCAAACCGACTAGTCGAATCTTAGGTTGTATGCTAGAACGGCATGGTATAAGCCGTCTCAA AAAA
ERCC-00157	GGGAATTGGCTTGTACCTCCGTCAATTGTTAGAACCCGTGAAGGCCAAGTAACAGGCCAGGGTTAACATGTACGGACATACCTCCACGGAAGATTGGGATGAAAGTTGATACCCAAACTTCATTAACACAAAGGCATGTTGGCGAGTACTGTGCTTACACCAACAGGGCGGCTCAACTGGTTGGTAGCCAGCAGTACTAGCTTACACCAATTAGGCCGTATGCATTCTACTGCTTATCCGGGGTGTATGCACTGCCAGGGCGGAAGTGAACACCGCTTGACGATGTGTTGCATAAGCGGTTACACAGGCCTACTCTCGTCAGCCGACTACTAATATTGCCGGCGCCGGTAGATAGCGAGGCTTGGGGTAGCTTAAGTGCAGGCTAGGCTCAGTTGACGATACTTACCGGTTACACCCCTTATGATGGGTATGAGGCACGTGGCCATTCCGGACCCGATGCTGTCGTCTCGTGGCAATAGCGCAGGATTACAGGTGACTAGTTCAGCTGTTGGATTCCAAGTAAGCTCGCATAGAGCTGGACTCTCGGAACGGCTGACCGCATTCCTGCATCAATACGCCAGCGGGTCCGATAGCATCTGCCATTAGATCCGGGGGATACTGGTCAAAGCTCACTACGGGACTAGAGTGGCTAGTGCAGATGCGCAGCGCAGATATGCTATACGAGATGAGCTCAAATTGAGTTATGACGATAACGCTAGGATCTGACGCACTGACCCGGTGTGACAACCGGTTAAAGTGAAGGCGAGCAGGAGGCGGTACAGGAGTATACTTTAATGGTGGCGCTCCCAAATCCCCGATCTGCCACGATTGCCATAAGCCGTATGTTAGAGGCGGTCACAGCAAACCTCAGTTACCGGTTGATGATTACGATGCCGGAGCGAACGACTACGCTCGAAGTTGGTTATCTAGAGCAGT AAAA

Table S11

ERCC-00158	GGGAATTGGAGCTTTCAACAGATCATGGAACACTACGGGAGAAATAAACATTGGATAGAAAATGTAACATTAAAAATGATG CAAATCATATTCTTAAATTAAACGAATCTTAATATGGGCAGTAAATAAATCTGTTATGAGTTGTATTGGAATCCATT AACAAATCTATCTGGATAGATGGGAGTAATTACACTATAACTCCAAATATTGACATACCTCCAGGAGAAGTATGGAACCTAA AACCTACAACCTCACATTAGTAGGGAGTCCAATCGTTGGCAAACGTCTCATTACACTGTCAAAAAAAGATTATATCCTT TAAATGAAGTAAGTCAAATAGGAAGTCCTATGTTGTTGAGGAGATTATGTTGTGGTAGTTATTGATTAAGGTGACT AAGCATATTGTCGGATGCGGATGGGACTTATGATATTATAGTTGTGGAGAATTGGTAGTGTGAAGACTCCTGAGTA TGTGTATGTTATGATTGATTCTAAGAACCTCACCCTCAGATGAGTGGGTTAATCAATCAAGTATGTTGATTGCTGAAG GAAATCACACCATTACAACAAATCCAAGGTATAATTAAAGCATGTGGTGGCGTTACATGCAATATATCCAGGAGCAGATGGG GACGGTAACTGGAACGACACTGCTGAAATACTTGCAAATAAAACAGTAGTCATACACTACAAACTAAACGGAACCTGGCGAATT CTACCCAAGCGACGCATTATCGTTGGATCGACCCCTACAAACTCACTACCAACACCTCACCAAAATAACAACAGTAG CCGGAACAGTAGAAAACAACTTGAGATATTAAACTGATAAACGTTATCTTGGATTAGGTATTAACAAAGAGGAAT ATAAGGAATAATAAAATAAGTGGGGATGATGATGAAGAGATTGCAATTACTCTTATTTCCTGCATTATAACACCACT TTGCAAGATGTTGAGGAAAAAAAAAAAAAA
ERCC-00160	GGGAATTCTCCTGGTTGAAATCAAATTACTATAGATTGCATGCAGAAGTAGGGCTTACAAGTTGTTCTAATTCCGTTG AACAAATAGCGAATGTATGATGGTCGGTCATTGCCGCAACCCCTGAAGCAGTGAGCGTGGTAGTAACCACGTACTAGAAGTCC AAGGATGGTGCACTAGCTCAATTGCCATTGCTGGAATAGTGTGGTAAACCACGCACCGGGGAGCCCGTTCTGTTGC GATAACCTCATATAGTCCCAGTCTCGGACGCGACCTGCAGCGTAATTAAAGGTCAAGGCTATGATTCAACCACCGTGTAG GAGTTATGCGCCTTATCGCAAGGTAGTTACTCTTGCCAGTGGGATGAAATTGCGAGCTGCCCTAGTAGCGTTAGTACCGT CATAAAGCCACTCTAAGAGATCGAAATTATACAGTAGTACTAACAGCAGACCTGCAATATCAAAGTTATAAGCGCGTCGACA CGCCTCGCTAAGAAAAACTACTCCATTAAAGTCGAGGACAAATGCGGTCTGATTCACTAGCGAGGCCATTGCACT GTGGTCTGCCGTGGCTCGATAATACCATGATAACTACTGACTGCGCAGTTGAGCGACCGCAATGGGAGTGTGTTC TTTATTCAACTGCGTGGCTATCCTACTTAGGAGTTGTGGATACCAGATTCTCGCGTGGAAAAAA
ERCC-00162	GGGAATTCTCCACAGATTCCATGTGTCATTCTGAATATCTTCCAGCTAAGTGCTCTGCCACCAGAACAACTATGT TGTATTGTTGCTTAATATACTCTAAATTGCTATCTCAATGCCCTCTGGATATTGCTGATGTAATTGTTACTGACCTT GCCCTCTCTGGCAAACAAACTCTATTCCATTGCCCTCCAAACCAGCCCTTGTGCTTGTAACTCTCATGTCTTTAAC CCTATTCTCGATTCTCCTCTAAACTAAATCTAATGCAACATTAAAGGCATAGGTTAAATTAACTGATGGTGTATGGGG TTGTTTTCTCTTCAAGTATTAAAGCCAATAAACTAAGTAGAAACCAACTTGTCACTATTCTCTTAATAACT TCCCATGCCCTTCACTGACTGTTATTGCAAGCCAATCCTGGAGCTGCCAACATTGAGAACAGTAACACAGATATC ATGTGGAATAAAAAAAAAAAAAAA
ERCC-00163	GGGAATTCATAGACTAGCCTGCCGGTCAATAACTGATGACGCCGGAGTCACCTGATAACCCATAGCGGAACAGTCTAACCTAC GCGAGATACTCTACCGCACATAGGTAACCTATTGCTGACTAGCAGGCCTTATTCCGGTCTATGAGTATCTTACCTGGTCT AGGTATCTAATTGCGGGTCTGGTACTACATTGCGATGGGCTCTCGCTCGTCTATGAGGTCTCGTCTCGTGAAGTCAA TGTATCCGAAGTCGTAGTGATAATATGGAACCTAGGCGCAGTTGACGAACGTATGCCGATATTGGAACGTGCGCTGGAAAT TCGCCACCTAGATCGAAATTATGGAACCTCGTCGCTTATTGACACCTTGGAGCCCTCTAAAGCTGAGTCTGGTTCTT ATTAGCGAGGAGCATTGCAACTGAGCCGAATATCGTAAGAACACCCCGCAGCGACTGTAACACTAACATGGGAAACTTATT ATAGGGCCGGTCCAGGTCTGCAAGCAGTAAAAAAAAAAAAAA
ERCC-00164	GGGAATTAGGAGCTCCAGTAGTTCCCTCAAAATTCTGATAAGATTCAACTTATCCTCTTTCTGGTGTGA GAAGATGCTCTGCCCTGGTCTCTCTGTCAGCTTTGGATATCCTCTTCAAGATAAAGGCAGATTAGTTGGACATCCAT CAACAACTGCTCCAACAGCCTTCCATGACTTTCTCCAAAATGTAACTCTAAACATATCCCCATAGGTGTTCTTAATGTC ACCAAAAATTCTTAATTGCTTAGTTACATTAAAATAAAATAGTCAAAAAATAAAAGGTTATCTGTAGAGA ACATCCAAGTGTGCTGGTCTTAACTTAACTTCTTCTCCATAATCTCTCAACTGCCCTCTAAAGTCATCCATTGT TACATAGTCCCTTAACTCCCTAATTGCAATTGCTCATCCCTGCCCTGTGCAAGATTGCCCTTAACTCAGCCCTACACATCCTCAG TCATCTTAGCTATTCTCTAAATTGACATCTCCGCTAAATTCTTCTGTATGAACTTCAATATCTCAATCTACCC TTCTCATCAGGAGCTGGACTCTATGATTCTATCAAATCTCCAGGTCTTAATTGCAAGGGTCTAAAGTGTCAAGGCTGTT TGCAGGGCCCAATTCTTAACATCTCCCTTGCACTGAAATCCCATCTCTGCCAACAACTGCATTAATGTTCTCTGAACTT CCCTATCTCCACCAGTTAAAGCGTCTGTTCTTGCTGCAATAGCATCTATGAATATGATTGAGGAGCTTT TCTTAGCCAATTGAAATATCTTAACTAACGGAGCCCCCTCTCAATAAAACTTCTTAACCAATTGAGAACAAACTCT TATAAAGGTAGCATTGTTCTGTAGCAACAGCTTAGCTAATAATGTCCTCCAGTTCCCTGGTGGGCCGTAAGAGAATACC TTTGGTGGTAAAAAA

Table S11

ERCC-00165	GGGAATTCGATATGCGTTACGTGAGTCTGATAGCAGTTCACTACCTGGATATCTGATCCACTAGCTCGATCATGCTCACCCATAGTTATCTGCATCACTCGTACTGAAATGCTCACATCGCAGGTAGAGCAGCAGTCAGAGCTGCAACCTGAGATAACGACGGCATACTGCGTCAACGTCAAGGCAATGTGTCGGAACGGCAGCTACGTCGCCTCACGGAGTAATCGCGTCCCTCTAGGTATAGTGCCTCGGTTCAAGGTATATGCGCAGGACATATCACGGACGTATCGCTATCAGACGGACGCTCTCGGACCTAAACCGTAGCTCTCGGCAAGATCGCCTCGTCTGAATATAGGCCCTAGTGCTGCAAATGTCACCGCTATCTGTAAGGGTCCGCTGTTGAGTTAGGCCTCTCGTTGGATGTGAGCTCGGTTGCTGGATGGTGCAGCTTACTTCGCTACCTGCTGTTGCATCAGTCCTCTGCATCTATAATCGGTATCTCTAGTAGACCATATAGCCATCTAACGCGTCGATATTCCACCTAAGTGGCGCTATTGAACTAAGTGGCAGCGAATGGACTATCGCTCCTCGATATGTACGGATAGGCCACGGCATGTACGAGCATAAGCCGAACGTGACGAGCATACCCGACACTGATCTGAGAGTCGCTTAAATCATCTCGTGTCTAGAGCTTATCGCCATGTCTGTCAACTGTACTGTCATCCTGTAACTGTAGCGTATGTGAAAAAAAAAAAAAAA
ERCC-00168	GGGAATTCCAATGAACACTAGCTATTCTCTTAACAAATAACTTCTCCAGAAAATTCAAATGTATCATCTCAGGATTCCACCTAAAAACATCATGTAATATAATATCATCAATTGGTGTATTCAAACAATCTCAGTTACTCTCAGTTCTTAACAAAATCTCCTTATAAAATCAATCTAACCTGCATACATATGGCATTAGTTGTTCAAGCATAATCTTGAATGTTCATTGGTTCAGCATTCAACCTCCTTATAACTGCCTCTGGGGATTTGCGTGTATCGTTGATAACGCCAAATGTCCTGTAGTTATTGCTTGAAATAATCTCGCCTCCTCACCTCTAACCTCTAACAAATTAAATAATCTGGTCTTGCCTTAAAGCCGCTTTAATAAAATCCATCATAGTTATTTCATATTCTCTCCACCGAATCCACTTCTGTAGTTCCAGCAATCCAGTTTCATGATAACACCTAATTCTGGATCCACAGTACCTCAATAGATACTGATTTGATTGAGGAAGGATGAAAGAGAGAATGCATTAAAGGGTGGTTTCCAGTAGCTACCTCTCCAGCAACCATAATAGAAATTAAATATTCAATGAGTAACCAAAGATATGCAAGCATCTCTGGAGAAATACTCCCATACTCTTAAATCTGGCAATATAGGAGTGTGTGAATTTCATTGTAATGTTGAACCATACTTGAGATATCCCTTCAAGGGTTACATTAGCCTGCTACCATCTGGAGAGAACCATCCACTATTGGATTAGCCAATGTTAAAGATTTCACACCTTGGGCTAAGGATATAACAAACGAGTCTAATTCTCATCAGTTCAAATTAAATTGTTCTTAAATGTTGTCTTAAATGTCGTTTCTATGAAACACATACGGCTTCCAAACACCTGTGCAACTGATACCTCCAAATTCTCATCTTCATAAGAGCATCTATTCCCATACTCCAATGAGGTAAAAAAAAAAAAAAA
ERCC-00170	GGGAATTCTATTGGTGGAGGGCACAAGTTGCTGAAGTTGCGAGAGGGCGATAAGTGAGGCAGACAGGCATAATATAAGAGGGAGAGAATTAGCGTAGATACTCTCCAATAGTGGTGAAGAAAATTATATGAGGCTGTTAAAGCTGTAGCAACTCTCCACGAGTAGGAATTAGTTAGCTGGCTTTAATGGGAGGGAAGATAACTGAAGCAGTTAAAGAAATTAAAGAAAAGACTGGCATTCCCGTGATAAGCTTAAAGATGTTGGCTCTGTTCTAACAGTTGCTGATTGGCTGATTTGGTTGGAGACCCATTGCAGGCAGGGTTTAGCTGTTATGGCTATTGAGTAAAGGTTAAAGGTAGGGTGCTATAAGATAATTAAATAATTGGTATGAAACCGTAGCTTGGTTATGAAAGCTTAAAGGAGGAGCTCTATGATTGTCTTAAACAAAGATTATTGATGTATATACTGGAGAGGTTGTTAAAGGAATGTTGAGTTGAGAGGGATAAAATACCTTGTGGATTAAATGATGAAATTGATAAGATAATTGAAAAAAATAAGGAGGATGTTAAAGTTATTGACTTAAAGGAAATTTATCTCAAACATTATAGATGGCATATACATACTGAAATCTCCCACATCTCATCCCATCAGAGTTGAGAAATTGTATTAAAAGCGGAGTTAGCAAAGTAGTTAGACCCGCATGAAATAGCAAATATTGCTGGAAAAGAAGGAATTGTTATGTTGAATGATGCCAAATTAGATGTCTATGTTATGCTTCTTCCTGTGTTCCAGCTACAAACTAGAAACAAGTGGAGCTGAGATTACAGCAGAGAATATTGAAGAACTCATTCTTAGATAATTGCTTAGGTTAAAAAAAAAAAAAG
ERCC-00171	GGGAATTCTGGAGATTGTCTCGTACGGTTAAGAGCCTCCGCCGCTCTGGGACTATGGACGGGCACGCTCATATCAGGCTATTTGGTCCGGTTATTATCGTCGCGTTACCGTAATACTCAGATCAGTTAAGTAGGGCCATATGCCTCGGAATAAGCTGACGGTGACAAGGTTCCCCCTAACGAGACGCTGCAATAACACAGGGCATACTAGTAACCAGGCAAGAGCTCAATCGCTTAGTTCTGGCGGGATTGAGGAAAATGCGACTGTTCTTAACCAAACATCCGTGCGATTGTCGCACTCGTAGACGGCATCTCACAGTCAGTGAAGGCTATTAAAGAGTTAGCACCCACCATTGGATGAAGGCCAGGATAAGTGACCCCCCGGACCTTGGAGTTCTGCTAATCAAAGAAGAGCTAATCCGACGTTAAAGTTGCGCGTTGATTACGCAAGGATTGCGACCAAAGAACGAGAAAAAA

Table S12

Sample	Method	Number Reads (millions)	min density	min sum	min value	max width	min width	min pos with data
Comparison (K-562)	CAGE	20	5.4	81	1	300	3	0
Comparison (K-562)	RAMPAGE	20	4	60	1	300	3	0
Comparison (K-562)	STRT	20	8.8	132	1	300	3	0
Comparison (K-562)	Oligo capping	20	4	60	1	300	3	0
Comparison (K-562)	NanoCAGE-XL	6.9	9.2	138	1	300	3	0
Comparison (K-562)	GRO-cap	20	7.2	108	1	300	3	0
Comparison (MCF-7)	CAGE	13	9.2	138	1	300	3	0
Comparison (MCF-7)	Oligo capping	13	3.4	51	1	300	3	0
Comparison (mouse hippocampus)	CAGE	13	2.4	36	1	300	3	0
Comparison (mouse hippocampus)	STRT	13	6.6	99	1	300	3	0
Reproducibility (K-562)	CAGE	7	2	30	1	300	3	0
Reproducibility (K-562)	RAMPAGE	5	1	15	1	300	3	0
Reproducibility (K-562)	STRT	5	3	45	1	300	3	0
Brain-related human samples	CAGE	13	3.2	48	1	300	3	0
FANTOM5 (Temporal, Occipital)	CAGE	10	2	30	1	300	3	0
FANTOM5 (Parietal)	CAGE	6	2	30	1	300	3	0
FANTOM5 (iPS, Frontal Adult)	CAGE	20	5.4	81	1	300	3	0