### SUPPLEMENTARY FIGURE

FIGURE S1: Comparison of the Exon-ORF Plots (EOPs) of representative genes from *H. sapiens, C. elegans, P. falciparum, S. pombe*, and *E. coli* with random DNA ORF plots. The ORF distribution patterns in the three RFs of each gene sequence and its corresponding spliced gene sequence were mapped. The exons and the spliced codingsequence were overlaid on the appropriate ORF and on the RF in which they occurred. For each gene, the gene details are summarized in a table above the plots. A control reference ORF distribution pattern for a computer-generated random DNA of the same length of each example gene was plotted to enable immediate visual comparison (top plot). The plots shown for each gene are: the ORF plot of the split-gene with overlaid exons (middle left), the spliced gene with overlaid complete coding-sequence (middle right), the ARF plot of the unspliced split-gene (bottom left) and the ARF plot of the spliced-gene sequence (bottom right).

### **Introduction to the Plots**

### Representative mammalian (H. sapiens) genes

EOPs of 12 representative human genes are displayed on pp. 3-14. We found that human gene sequences were remarkably similar to random DNA, with nearly all (99.97%) of their ORFs (vs. 99.99% of random ORFs) being shorter than 750 bases and 99.13% (vs. 99.83% of random ORFs) being shorter than 300 bases. The ARFs (amino acid reading-frames; the distances between any three non-stop codons) in human genes also exhibited random characteristics. Our analysis revealed that the vast majority of exons in human genes (98%) are shorter than 750 bases, and >92% are shorter than 300 bases. Very rarely did human exons not conform to the random sequence model. Note that the human genes are also highly intron dense, having an average of 8 introns per gene.























### **Total Spliced Exon Length: 1197**







### Representative invertebrate (C. elegans) genes

EOPs of three representative *C. elegans* genes are displayed on pp. 16-18. *C. elegans* gene sequences are also very similar to random DNA with 99.95% of their ORFs being shorter than 750 bases. The ARFs in *C. elegans* genes also exhibit random characteristics. The vast majority of *C. elegans* exons (98%) are shorter than 750 bases, and >90% are shorter than 400 bases. Very rarely did the *C. elegans* exons not conform to the random sequence model. *C. elegans* genes are fairly intron dense, having an average of 5 introns per gene.







#### Representative parasitic protist (P. falciparum) genes

EOPs of two representative *P. falciparum* genes are displayed on pp. 20-21. *P. falciparum* gene sequences are non-random only with respect to the lengths of a small subset of ORFs that specifically contain the non-conforming exons of genes. The ARFs in *P. falciparum* genes exhibit random characteristics. Nearly all, 99.87%, of the ORFs in *P. falciparum* genomes are shorter than 750 bases, and 69% of exons are shorter than 750 bases. The 31% non-conforming *P. falciparum* exons occur conspicuously within the rarely occurring non-conforming ORFs against a background of random ORFs, indicating that these must have been derived from splicing of short exons. *P. falciparum* genes have a relatively low density of introns (with average of 1 intron per gene) compared to *H. sapiens*, *A. thaliana* and *C. elegans*.





#### Representative yeast (S. pombe) genes

EOPs of two representative *S. pombe* genes are displayed on pp. 23-24. *S. pombe* gene sequences are non-random only with respect to the lengths of the small subset of ORFs that specifically contain the non-conforming exons. The ARFs in *S. pombe* genes do exhibit random characteristics. Nearly all, 99.77%, of the ORFs in *S. pombe* genomes are shorter than 750 bases, and 67% of their exons are shorter than 750 bases. The remaining 33% of non-conforming *S. pombe* exons occur conspicuously within the rarely occurring non-conforming ORFs against a background of random ORFs, indicating that these must have been derived from splicing of short exons. Of the eukaryote genomes we examined, *S. pombe* genes had the lowest density of introns (with an average of 1 intron per gene).

# Exon ORF Plot for Gene cdc5

[Genome: Schizosaccharomyces pombe]									[Gene Name: hypothetical protein]
Gene ID	): <b>254</b> 3	3583		Gene Symbol: cdc5			ymbol: cdc5	Gene Length: 2577	Number of Exons: 6
Exon	1	2	3	4	5	6			
Length	19	20	15	120	449	1651			

## **Total Spliced Exon Length: 2274**

TAA: TGA: TAG: Exon:

# **Random Sequence ORF**



Exon ORF (Before Splicing)

Exon ORF (After Splicing)



GTT : | ACA : | CTG : |

### Exon ARF (Before Splicing)







### **Exon ORF Plot for Gene cki2** [Genome: Schizosaccharomyces pombe] [Gene Name: serine/threonine protein kinase] Gene ID: 2541341 Gene Symbol: cki2 Gene Length: 1492 Number of Exons: 4 2 3 Exon 1 4 Length 126 70 149 963 **Total Spliced Exon Length: 1308** TAA: TGA: TAG: Exon: **Random Sequence ORF** -111 1kb 1 1492 Exon ORF (Before Splicing) Exon ORF (After Splicing) RF1 1111 1kb ++ 1 1kb 1492 GTT: ACA: CTG: Exon ARF (After Splicing) Exon ARF (Before Splicing) 11 11 11 RF3 -1kb , [ 1kb 1

### Representative bacterial (E. coli) genes

EOPs of two representative *E. coli* genes are displayed on pp. 26-27. E.*coli* gene sequences are non-random only with respect to the lengths of the small subset of ORFs that specifically contain the non-conforming coding sequences of their genes. The ARFs in *E. coli* genes exhibit clearly random characteristics. We found that 99.2% of the ORFs in the *E. coli* genome are shorter than 750 bases, and that 43% of their coding sequences are shorter than 750 bases. Distinct from the eukaryotes, a majority of the *E. coli* coding sequences (57%) did not conform to the random sequence model. All of the non-conforming coding sequences in the *E. coli* genes in the *E. coli* genes lack introns altogether. Consistent with these observations, the *E. coli* genome is the smallest of those examined, and contains only contiguously coding genes without introns or intergenic sequences.



