

Table 2. Detailed information for 27 new and previously predicted introns

Gene	ORF	Origin	Size in bases			Sequence				
			Exon 1	Intron	brpt-exon 2	Exon 1	5' splice site	Branch site	3' splice site	Exon 2
BMH2	YDR099W	This study	72	743	98	CGAACC	GTATGT	TACTAAC	CAG	AAGGTT
CGI121	YML036W	This study	446	106	42	AGAAAA	GTATGT	TACTAAC	TAG	ATCTAT
GIM4	YEL003W	This study	38	88	28	ACAACG	GTATGC	TACTAAC	TAG	TCTTTC
HPC2	YBR215W	This study	29	84	19	AAAAAG	GTATGT	GATTAAC	TAG	CAATTG
HRB1	YNL004W	This study	66	342	19	GAAAAAC	GTATGT	TACTAAT	TAG	AATAAT
MCR1	YKL150W	This study	27	88	14	AGAGAG	GTACGT	TACTAAC	CAG	CCAAAC
PTC7	YHR076W	This study	66	93	18	TTTATG	GTATGT	GACTAAC	TAG	GATCCT
URA2	YJL130C	This study	195	320	22	ATTTGA	GTATGT	TACTAAC	TAG	AAATCC
YPR153W	YPR153W	This study	34	134	45	TATGAG	GTATGT	AACTAAC	CAG	ATCATT
ARF2	YDL137W	Ref. 1	61	332	18	CACITT	GTATGT	TACTAAC	TAG	AGATAA
COX4	YGL187C	Ref. 1	122	342	43	TGAAAT	GTATGT	TACTAAC	TAG	ATAACA
IWR1	YDL115C	Ref. 1	23	70	25	CATTAT	GTATGT	GACTAAC	CAG	TAATTG
NHP6B	YBR089C-A	Ref. 1	40	357	14	CGCAA	GTATGT	TACTAAC	TAG	AACATT
RPL24A	YGL031C	Ref. 1	43	456	45	TGAGAG	GTATGT	TACTAAC	TAG	TGATAA
RPL24B	YGR148C	Ref. 1	29	392	66	TGAAAC	GTATGT	TACTAAC	TAG	AAGAAC
RPL29	YFR032C-A	Ref. 2	22	331	50	TAGAAA	GTACGT	TACTAAC	CAG	AAAAATG
RPL32	YBL092W	Ref. 1	40	333	39	ATAAAA	GTATGT	TACTAAC	TAG	ATGGCC
RPS25A	YGR027C	Ref. 1	25	312	34	TTTAGT	GTATGT	TACTAAC	TAG	AACATT
RPS25B	YLR333C	Ref. 2	28	423	32	ATTAAG	GTATGT	CACTAAC	CAG	AACATA
RPS26A	YGL189C	Ref. 2	13	368	56	TAAAGTA	GTATGT	TACTAAC	TAG	ATCATT
RPS26B	YER131W	Ref. 2	21	361	34	GGAAAA	GTATGT	TACTAAC	TAG	ATGCCA
RPS29A	YLR388W	Ref. 2	25	488	22	ATTAGG	GTATGT	TACTAAC	CAG	ATAAAA
RPS29B	YDL061C	Ref. 2	10	409	39	CTAAAT	GTATGT	TACTAAC	TAG	AATATA
RPS8A	YBL072C	Ref. 1	19	308	29	CAAAA	GTATGT	TACTAAC	CAG	TTACAA

RPS8B	YER102W	Ref. 2	19	360	24	TAAAAAC	GTATGT	TACTAAC	TAG	TGTA AAA
SIM1	YIL123W	Ref. 3	275	487	31	TTTTTA	GTAAGT	TACTAAC	CAG	AAATGA
SUN4	YNL066W	Ref. 3	225	346	22	CAAGTC	GTATGT	TACTAAC	TAG	TAATTT

Gene, the common gene name; Origin, the source of evidence for the intron: this study, Spingola *et al.* (1), Planta *et al.* (2), and Lopez *et al.* (3). The sizes in bases are presented for the first exon (exon 1), the intron (intron), and the distance from the branchpoint adenosine to second exon (brpt-exon 2). Sequences are provided for three conserved regions: the 5'-splice site, the branch site, and the 3'-splice site. The exonic sequences that flank the intron are provided for both exons 1 and 2.

1. Spingola M, Grate L, Haussler D, Ares M, Jr (1999) *RNA* 5:221-234.
2. Planta RJ, Mager WH (1998) *Yeast* 14:471-477.
3. Lopez PJ, Seraphin B (2000) *Nucleic Acids Res* 28:85-86.