Supplementary Table 4: Splicing efficiency of the three P-element introns. We sequenced the transcriptome of hot (generation 22) and cold (generation 11) evolved populations (evol.), either reared in a hot or a cold common garden (c.g.). Reads were mapped to the P-element with an algorithm allowing for spliced introns (gsnap) and the number of reads supporting the presence (pres.) and absence (abs.) of a splicing event were counted for 5' and 3' splice junctions (table shows the sum of the two junctions). The percentage of reads supporting splicing of the intron (%) was calculated. rep.: replicates

			exon 0 - exon 1			exon 1 - exon 2			exon 2 - exon 3		
evol.	c.g.	rep.	pres.	abs.	%	pres.	abs.	%	pres.	abs.	%
cold	cold	8	6	1	0.86	14	1	0.93	0	9	0.00
cold	hot	8	14	0	1.00	12	1	0.92	2	21	0.09
cold	cold	9	10	2	0.83	4	2	0.67	0	4	0.00
cold	hot	9	42	8	0.84	18	12	0.60	4	30	0.12
cold	cold	10	2	0	1.00	6	0	1.00	0	1	0.00
cold	hot	10	6	0	1.00	4	0	1.00	0	4	0.00
hot	cold	8	94	11	0.90	60	28	0.68	0	79	0.00
hot	hot	8	226	42	0.84	118	64	0.65	0	199	0.00
hot	cold	9	22	14	0.61	20	16	0.56	0	40	0.00
hot	hot	9	348	67	0.84	206	80	0.72	0	323	0.00
hot	cold	10	42	23	0.65	34	28	0.55	0	70	0.00
hot	hot	10	140	34	0.80	96	33	0.74	0	142	0.00