

Supplementary Table 2

The primer pairs we found most reliable for sequencing *ASPM* from human genomic DNA

Exon Number	Forward Primer (5'→3')	Reverse Primer (5'→3')	Fragment Size (bp)
1	actcccacgacctctacagc	ccaagagccaccacagtta	579
2	aattaagcagataggtaggagaaa	tcccaaagactcctctgcaa	471
3a	ggaaatgcagaagagcagaaa	cgtacagagagtggcaagca	460
3b	caagcttgtaaaacttggtca	aattctagttcattattagctccatga	426
3c	cccaactgttcttcaact	ctctggtacaggtggccttc	622
3d	tcctaaatcttgcagttcagg	gctctgagggagaaaaatgg	419
3e	gcttcagttgctcggaaaag	cagcaaaagcaagaaaaatca	405
4	agtgcgtggagtacag	ttctccaggctgta	358
5	cccaaatgcttfcagctct	catttaggctaataacagggaat	434
6	gagctaacaggttcgatga	caccacacatacacacaagaagg	633
7	gctgcaaaaatcccacata	tgtcattacgtgcaacacca	526
8	tcctgagctttgtcttttgc	gggtggaggaagggagagta	508
9	tccatagagatattgggagga	ggactcaccagacaggcatt	475
10	cagaatgattggaggatttgtt	ttccagaaaaatgttagtctattcca	316
11	tacttcccactatggagca	cgctatcttccaaagcaacc	479
12	gattccggcaataagtcgtc	tcacagttactggggcaaaa	404
13	gtttgccttggggaaaaa	tcatttgagggaaagtttgc	557
14	tgtgcatgctctcacataa	gcaggtattccaccaaggtc	599
15	cgcaactggttcagtggtta	atccaaaagccttgcaaaa	473
16	gaccttgggtgaatacctgct	acctcccaacccaaaatac	461
17	cgacatgcctggaattatca	agccttctgctgaacaccat	535
18a	ttggatggatttctgaattgg	gcttgaagcaccgaaatct	650
18b	tgcaaagagcttttagagaatgg	aaaatcgaactctgtcttctca	393
18c	gctgcagccattcaattaca	gcagctgctcttaaatgcaaa	500
18d	gatgcaagccaggaaaatg	ttcttctctgattgacctgtg	456
18e	accttgcgaaaagcagatg	gcagcttgatgttcccttct	478
18f	gatgttacagggcgtacaaga	ttttgaatcagaagagcagctt	439
18g	caaaggcaacataaatgtgcta	cacgctgcattttacctga	580
18h	gaagacatattcaacacatgcaca	gcagtttcttgagagagaggaa	538
18i	gcaaagatactgggcaatgaa	taagggttcagaggaatgc	581
18j	ccaagcaaatagagctgcaa	gcccactgaagcttttggtta	633
18k	gacaatggcattctgctgtg	gcctctaaaagcagcctgaa	668
18l	cagggccaaagttgattatga	tgatagcagctcttttctgctg	488
18m	tggtcacaagaaaactggaaa	tggaagataaatggtcacctca	468
19	caccactgttctcagaagactca	gaaaatatcaacaaaaccaacca	486
20	cttcttctgtgtgctgtgt	ttgactgaaatagatgtgtgtgaaa	452
21	acccttggcttacaccttca	tgacagtcagtgctctgtcac	583
22	tgctttctacactctgagttatgagtt	gggtgaaaggctaaatgtgtacg	488
23	aatgcctctgtggaaagctg	tgagttattctaccggctaattgc	453
24	tggtcgataaatgctgtcca	actctgggccatgttctcac	574
25	ccttctgccattcttgagg	tttcatcctaagactcttgcaaca	436
26	aaagtccttgcacttgctg	gcaaaaagcaggttgaaca	447
27	gcgacagagcaagagagacc	accaaacattccattctattca	451
28	tgaagtctcccacctctttg	tgataaaaatgaagaatgtaagaaca	400