	length	Donor site		Acceptor site	
21506829..21507115	286	tgaacttacg	GTaatatcc	tgtttttcAG	atttcagatt
21503350..21504064	714	ttttcaagcg	GTaagtgttt	caccttttAG	atattagctt
21504108..21504985	877	tacaattgtg	GTacgtgatt	tttttttcAG	agcattggac
21503350..21504985	1635	ttttcaagcg	GTaagtgtta	tttttttcAG	agcattggac
21505027..21506774	1747	ccggtttgct	Gcaagtattt	tttattttAG	ctcctttttt
21505134..21507115	1981	accagccaag	GTatttaata	tgtttttcAG	atttcagatt
21505134..21508851	3715	accagccaag	GTatttaata	tatctgatAG	tcggggaact
21503350..21507132	3782	ttttcaagcg	GTaagtgttt	attaccattt	ggctatgagg
21505134..21540689	35555	accagccaag	GTatttaata	tgatttaaat	tatcatgctc
21505089..21540689	35600	cgtgttttt	ttttgcgct	gatttaaatt	atcatgctc
21505134..21594560	89423	accagccaag	GTatttaata	tttccatcAG	tgtcccgtct
21503500..21661658	158158	tcctcctact	GTtttggaat	cgccggcgct	gcttccggtg

Table S3: Sequence upstream and downstream of the donor and acceptor sites of *flam* introns.

Grey represents intron. Consensus sites are written in capital letters and underlined.