

A

	Signal Peptides	Exon/Intron Boundary	
<i>D.mel</i>	MKT-LALFLVLVC--VLGLV-QA--WEWPWN---RKPTKFP I P S P N P R	↓	--DKWCRLNLGPAWGGR-C 55
<i>D.sim</i>	MKT-LSLFLVLVC--LLGLV-QS--WEWPWN---RKPTKYPI P S P N P R		--DKWCRLNLGPAWGGR-C 55
<i>D.sec</i>	MKT-LSVFLVLVC--LLGLV-QS--WEWPWN---RQPTRYPI P S P N P R		--DKWCRLNLGPAWGGR-C 55
<i>D.yak</i>	MNT-VALLLVLVC--IVSLV-QS--WTWPWQK--KKP-KFP I P S P N P R		--DKWCRLNLGPGWGGR-C 55
<i>D.ere</i>	MKA-VSLLLVLVC--IVGLV-QS--WTWPWQK--KPEVKFP I P S P N P R		--DKWCRLNLGPGWGGR-C 56
<i>D.ana</i>	MKN-FNILLLVAYAIMVAMV-SS--ERMTWLKTLSPWRPMPMSAR		--HKWCRLNLGPLWGGR-C 60
<i>D.pse</i>	MKVATSAMLLML--VEAAVGVPA-WGRMTS---RRPT--PKQSQAQF		--QKWCRLNFGPAWGGRG-C 57
<i>D.per</i>	MKVATSAMLLML--VEAAVGVPA-WGRMTS---RRPT--PKQSQAQF		--QKWCRLNFGPAWGGRG-C 57
<i>D.wil</i>	MQAPISILLLL----VLAIVSQSMA-----NPNPERGGDKG		KWCRLNLGPAWGGR-C 47
<i>D.vir</i>	MQATFSIIFIL----LSILCCSRG-----EYKTTKWPRYPNKWCRLNYPYLGGR-C		47

B

<i>D.mel</i>	CCAAGCCCAATCCTC P**S**P**N**P**R	gtaagtgtt - 45 bp - tctttcgtag	-----GTGATAAGTGGTGCCGT -----**D**K**W**C**R**
<i>D.sim</i>	CCAAGCCCAATCCTC P**S**P**N**P**R	gtaagtctta - 54 bp - tctttcgcag	-----GTGACAAGTGGTGCCGT -----**D**K**W**C**R**
<i>D.sec</i>	CCAAGCCCAATCCTC P**S**P**N**P**R	gtaagtttta - 45 bp - tctttcgcag	-----GTGACAAGTGGTGCCGT -----**D**K**W**C**R**
<i>D.yak</i>	CCAAGCCCAATCCTC P**S**P**N**P**R	gtaagtgtga - 32 bp - tcttttgcag	-----GTGATAAGTGGTGTCGT -----**D**K**W**C**R**
<i>D.ere</i>	CCAAGCCGAATCCTC P**S**P**N**P**R	gtaagttttt - 31 bp - tctttcgcag	-----GTGATAAGTGGTGCCGT -----**D**K**W**C**R**
<i>D.ana</i>	CCTATGACTTCGGCTC P**M**T**S**A**R	gtaactgtct - 42 bp - ttttttcaag	-----GTCACAAGTGGTGCCGA -----**H**K**W**C**R**
<i>D.pse</i>	CAAAGCCAAGCACAAT S**Q**Q**A**Q**F	gtaagtaaat - 54 bp - tcgcctacag	-----TTCAGAAATGGTGTAGA -----**Q**K**W**C**R**
<i>D.per</i>	CAAAGCCAAGCACAAT S**Q**Q**A**Q**F	gtaagtaaat - 54 bp - tcgccaacag	-----TTCAGAAATGGTGTAGA -----**Q**K**W**C**R**
<i>D.wil</i>	AATCCTGAAAGAGGAG N**P**E**R**G**G	gtatgtaaac - 41 bp - ccgattcaag	GTGATAAAGCAAATGGTGTCGT **D**K**G**K**W**C**R**
<i>D.vir</i>	ACGACCAAATGGCCAC T**T**K**W**P**R	gtaagtaaac - 52 bp - attgccttag	GTTATCCCAATAAATGGTGTCGT **Y**P**N**K**W**C**R**

Conserved Domain

Figure S2 Comparison of amino acid sequences and gene structures of SP orthologs. (A) Comparison of amino acid sequences of SP orthologs. Black and gray boxes indicate highly conserved amino acid residues. A black bar and an arrow indicate signal peptides and exon/intron boundaries, respectively. Aligned sequences were inspected and manually adjusted to maximize homology. (B) Schematic presentation of exon/intron boundaries of SP orthologs. Boxed and unboxed regions indicate exons and introns, respectively. Putative amino acid residues were shown below DNA sequences. Gray boxes indicated splicing consensus sequences.