FBrf0104945

From [redacted] **Wed Dec 02 20:56:01 1998**
From: Leyla Bayraktaroglu <[redacted]>
To: rachel@morgan.harvard.edu
Cc: [redacted]
Subject: Annotation for the staufen gene
Date: Wed, 2 Dec 1998 15:55:54 -0500 (EST)

Hi Rachel and Gillian,

Below is a recent personal communication which needs to be archived. Joe has assigned it the following FBrf: FBrf0104945. I have curated the information I need from it, there is (almost) nothing else that you need to do with it. Let me know if you want hard copies of the attached files. As you can see from the body of the message, there are two versions of the sequence alignment, a map of the intron/exon structure, a summary of the exon coordinates he has inferred (which is also included within the text of his message), and a text file of his address.

Thanks very much,
Leyla

----- Begin Included Message -----

>From [redacted] Mon Nov 23 13:06:02 1998
X-Sender: [redacted]
X-Mailer: Windows Eudora Pro Version 3.0 (32)
Date: Mon, 23 Nov 1998 13:05:08 -0500
To: [redacted]
From: "Stephen W. Schaeffer" <[redacted]>
Subject: Annotation for the staufen gene
Cc: [redacted]
Mime-Version: 1.0
Content-Type: multipart/mixed; boundary="====================_911862308==_"
Content-Length: 197193

Annotators of FlyBase,
I am using the data from the FlyBase and Berkeley Drosophila Genome Project to isolate genetic markers for the third chromosome of Drosophila pseudoobscura. I am developing variable genetic markers that span intron regions using conserved sequences from the exons of developmental genes. PCR primers designed for conserved exons allows me to rapidly amplify segments of the pseudoobscura genome without time consuming cloning steps. Ideally, I look for introns of 400 bp or more. I am using the new genomic sequences from the BDGP to help infer the intron-exon structure of genes to aid in this effort. I have just examined the staufen transcript because St Johnston D, et al. Cell. 1991 Jul 12;66(1):51-63 suggested that the gene had three exons and two introns, one of 2 kb and the other 0.4 kb. I used the GenBank sequence of the cDNA in a BLAST search of the BDGP database of genomic sequences and found that GenBank Accession AC004336 or DS03544 included the staufen transcript. The comparison of the cDNA and gDNA revealed that the intron-exon structure of staufen was a bit more complex than St. Johnston et al. had originally proposed. There are six exons and five introns. From my examination of the current literature on staufen, no one has gone back to re-evaluate the structure of the gene.

I have attached five documents that summarize my analysis of the staufen fine structure:
StaufAln.doc, MS Word 97, alignment of the genomic and cDNA sequences
StaufALn.txt, ASCII, alignment of the genomic and cDNA sequences
StaufSum.doc, MS Word 97, summary of positional information
StaufFig.jpg, figure of the intron-exon structure of staufen

Staufen Intron-Exon Structure (text version of StaufSum.doc)

Stephen W. Schaeffer
Department of Biology
The Pennsylvania State University
University Park, PA 16802-5301

These data reflect the intron-exon structure of the staufen locus given the genomic sequence of clone
AC0004336 from the Berkeley Drosophila Genome Project. The following table summarizes the positions of
introns and exons in the cDNA (GenBank Accession M69111) and the genomic DNA (GenBank Accession
AC004336).

	M69111 (cDNA)	AC0004336 (gDNA)

Region	Begin	End	Begin	End	Length
Exon 1 (5' Untranslated)	1	225	9861	10085	225
Intron 1			10086	10712	627
Exon 2 (5' Untranslated)	226	459	10713	10761	49
Start Codon (1st base)	275		10762		
Intron 2			10947	12777	1831
Exon 3	460	2594	12778	14912	2135
Intron 3			14913	14975	63
Exon 4	2595	2792	14976	15173	198
Intron 4			15174	15236	63
Exon 5	2793	3172	15237	15616	380
Intron 5			15617	15676	60
Exon 6	3173	5237	15677	17752	2076
Termination Codon (last base)	3355		15859		

The positions of the introns was inferred based on inspection and consensus splice junction sequences at the
points where the high similarity in the aligned sequences (gDNA versus cDNA) diverged and become similar
again.
Intron 1 GTGAG...AG
Intron 2 GTAAG...AG
Intron 3 GTAAA...AG
Intron 4 GTGAG...AG
Intron 5 GTAAG...AG

Polymorphisms (not a complete list)
The genomic sequence has an insertion of (5 TCGAACTGATA 3) at bases 16178-16188.

The cDNA has an insertion of (5 ACGAT 3) between 17405 and 17406 of the genomic sequence. This is an
expansion of a 5 bp repeat that is found in three copies in the genomic sequence and four times in the cDNA.

I hope that this information is helpful to all concerned.
Steve Schaeffer
----- End Included Message -----

<This message contains 5 attachments (not printed)>

Staufen Intron-Exon Structure

Stephen W. Schaeffer
Department of Biology
The Pennsylvania State University
University Park, PA 16802-5301

These data reflect the intron-exon structure of the staufen locus given the genomic sequence of clone AC000433(from the Berkeley Drosophila Genome Project. The following table summarizes the positions of introns and exons in the cDNA (GenBank Accession M69111) and the genomic DNA (GenBank Accession AC004336).

	M69111 (cDNA)		AC0004336 (gDNA)		
Region	**Begin**	**End**	**Begin**	**End**	**Length**
Exon 1 (5' Untranslated)	1	225	9861	10085	225
Intron 1			10086	10712	627
Exon 2 (5' Untranslated)	226	459	10713	10761	49
Start Codon (1st base)	275		10762		
Intron 2			10947	12777	1831
Exon 3	460	2594	12778	14912	2135
Intron 3			14913	14975	63
Exon 4	2595	2792	14976	15173	198
Intron 4			15174	15236	63
Exon 5	2793	3172	15237	15616	380
Intron 5			15617	15676	60
Exon 6	3173	5237	15677	17752	2076
Termination Codon (last base)	3355		15859		

The positions of the introns was inferred based on inspection and consensus splice junction sequences at the points where the high similarity in the aligned sequences (gDNA versus cDNA) diverged and become similar again.
Intron 1 GTGAGÖAG
Intron 2 GTAAGÖAG
Intron 3 GTAAAÖAG
Intron 4 GTGAGÖAG
Intron 5 GTAAGÖAG

Polymorphisms (not a complete list)
The genomic sequence has an insertion of (5' TCGAACTGATA 3') at bases 16178-16188.

The cDNA has an insertion of (5' ACGAT 3') between 17405 and 17406 of the genomic sequence. This is an expansion of a 5 bp repeat that is found in three copies in the genomic sequence and four times in the cDNA.

4

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staufgDNA  ATTATTTTTCGAGTTTCATCCGCAGCCACAGTGCAAAATAGGTTTATCAATTTAATTTAA 60
staufcDNA  ATTATTTTTCGAGTTTCATCCGCAGCCACAGTGCAAAATAGGTTTATCAATTTAATTTAA 60

staufgDNA  GTGTTAAAGTAGTTCTAAAGTGTTTTTTAAGTTGCGCAAACGATCGAGGCCAGCCCGCAT 120
staufcDNA  GTGTTAAAGTAGTTCTAAAGTGTTTTTTAAGTTGCGCAAACGATCGAGGCCAGCCCGCAT 120

staufgDNA  GAATGGATGTGCATGTGTCCATCGATCGAACGGAGTATTTGCATTCAGTTGTTGTGATTT 180
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staufgDNA  TCCCGTGACCATTGCGTACGAAAATCGTTTTGGGAGCGCAAGAAGGTGAGTTGCGTCTGC 240
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staufgDNA  CAGGGCCCTTTGTGCGGACAGGGAAAACATTGTTTGTGTCCGTCTCATCCATGTTCCTTT 840
staufcDNA  ------------------------------------------------------------

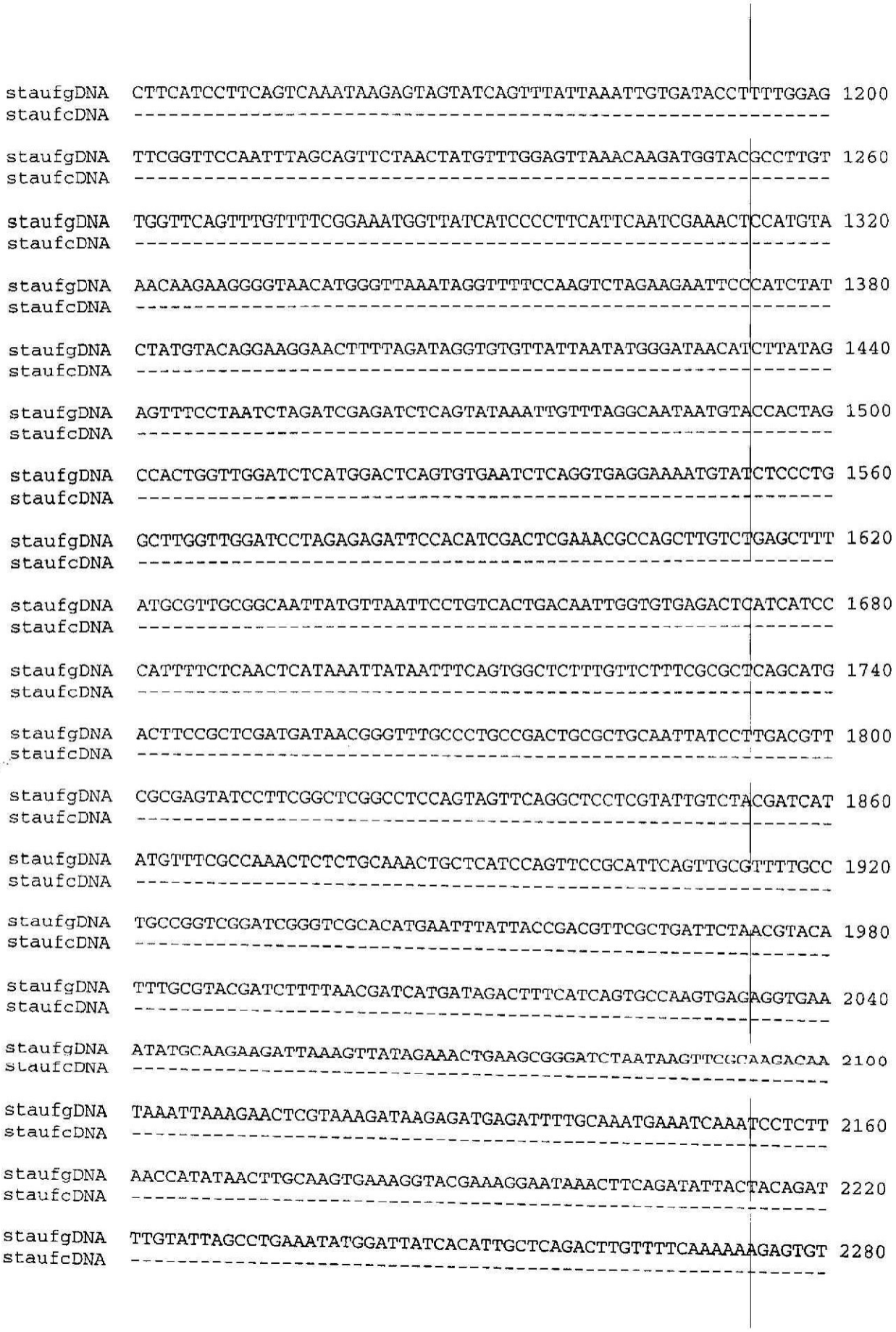
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staufcDNA  ------------CTGCGGTCGCTGGTTCATACGGGAGTCCTAAAGGTTACAGCTCAAGAA 273

staufgDNA  AATGCAGCACAACGTTCATGCCGCCCGGCCAGCGCCCCACATCCGAGCTGCGCACCATCA 960
staufcDNA  AATGCAGCACAACGTTCATGCCGCCCGGCCAGCGCCCCACATCCGAGCTGCGCACCATCA 333

staufgDNA  CAGCCACAGCCATGCCCACATGCATCTGCATCCCGGCATGGAGCAGCACCTGGGCCCCAG 1020
staufcDNA  CAGCCACAGCCATGCCCACATGCATCTGCATCCCGGCATGGAGCAGCACCTGGGCCCCAG 393

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staufcDNA  TCTTCAGCAGCAACAGCAGCCGCCACCGCCGCCCCAGCAGCCTCCACATCGCGACCTCCA 453

staufgDNA  CGCACGGTAAGCCATCTATGTCGTTGACGCTATCAGGAATAACAATTAAACCAGATAATG 1140
staufcDNA  CGCACG---------------------------------------------------- 459
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staufgDNA CTTCATCCTTCAGTCAAATAAGAGTAGTATCAGTTTATTAAATTGTGATACCTTTTGGAG 1200
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staufcDNA ----------
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staufcDNA ----------
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staufcDNA ----------
staufgDNA CCACTGGTTGGATCTCATGGACTCAGTGTGAATCTCAGGTGAGGAAAATGTATCTCCCTG 1560
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staufcDNA ----------

6

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staufgDNA  ATTAACCAATTTGCTTGCTCTATCCTCCGTTTTGCAGTCTGAATCATCACCATCTCCACG 2940
staufcDNA  ----------------------------------TCTGAATCATCACCATCTCCACG 482

staufgDNA  CTCAGCAGCAGCAGCAGCAACAGACGTCGTCGAACCAAGCCGGCGCCGTCGCTGCGGCTG 3000
staufcDNA  CTCAGCAGCAGCAGCAGCAACAGACGTCGTCGAACCAAGCCGCCGCCGTCGCTGCGGCTG 542

staufgDNA  GGGCTGCCTATCACCACGGCAACATCAACAGCAACAGCGGCAGCAACATCTCCAGCAACA 3060
staufcDNA  GGGCTGCCTATCACCACGGCAACATCAACAGCAACAGCGGCAGCAACATCTCCAGCAACA 602

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staufcDNA  CGCCCACCAAGCAGACCCCATTCAAGCCGATTAAGGTTAAGACACCAGGCAAAAGTGGTG 2282

staufgDNA  CAGCTGCCCGAGAAGGTTCGGTTGTGTCGGGCACTGATGGTCCTACGCAAACGGGCAAGC 4800
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staufgDNA  CGGAGAGACGTAAACGCCTCAATCCGCCGAAGGACAAGCTGATAGACATGGACGATGCGG 4860
staufcDNA  CGGAGAGACGTAAACGCCTCAATCCGCCGAAGGACAAGCTGATAGACATGGACGATGCGG 2402

staufgDNA  ATAATCCCATTACAAAGCTAATTCAACTGCAGCAGACGCGTAAGGAAAAGGAACCCATTT 4920
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staufgDNA  ATGCCGAGAGTAAAAACAACACGGAGAGTAGCAGCAACAGTACGAGTAACACACAAAGCG 5700
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staufgDNA  GCTTACCAACGGAACAGTCAACCCCAACTAGAAACTAACCAATTTCCTCAATTCAGGTCA 5820
staufcDNA  ----------------------------------------------------GTCA 3176

staufgDNA  ACTTCTCGGACTATCCGAAAGGCAATCATAACGAGTTCCTGACCATCGTGACATTGTCCA 5880
staufcDNA  ACTTCTCGGACTATCCGAAAGGCAATCACAACGAGTTCCTGACCATCGTGACATTGTCCA 3236

staufgDNA  CACATCCGCCGCAGATCTGCCATGGCGTTGGCAAGAGCTCCGAGGAGTCGCAGAATGATG 5940
staufcDNA  CACATCCGCCGCAGATTTGCCATGGCGTTGGCAAGAGCTCCGAGGAGTCGCAGAATGATG 3296

staufgDNA  CTGCAAGCAATGCCTTGAAAATCCTCAGCAAGCTGGGGCTCAACAATGCCATGAAATAAG 6000
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staufgDNA  AGCATGATAAGAGCAAAGCAAAGAAAAAACAATTGAAATACCCGTCCACAAAGCAAACCT 6120
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staufcDNA  GAGAATTGAATAACGAA----------GTAACCGAAACTGAACAGAGGCGAACACTTAA 3705

staufgDNA  CCAGAACCGCAACGTTGTTAATCCAAATCGAGAATCGAACAATAACTAGACTTAATGAAA 6420
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staufgDNA  ACCCAACAAAATCATGAATGAACAGATGCATATATACATATGTGCAGTACCTAAACTTAA 6480
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staufgDNA  GATTAAAGCTCATTAACCACTTGAATTGAATTGATGAACAAAGGACTATTGATACCTCTT 6540
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staufgDNA  CATAAGCATCGGCGAATGTCGGAAAGCCGTATACCGTACCCCATGACCGGTCGATTTGCC 6840
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staufgDNA  ACAAGCTAAAAGCTGAACATCCTTATGAATAATGAATCGTGTTGTTTAATCTGTCATGGT 7077
staufcDNA  ACAAGCTAAAAGCTGAACATCCTTATGAATAATGAATCGTGTTGTTTAATCTGTCATGGT 4425

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staufcDNA  ATCGTGTTATGTCATTAAAACTGAAGAAATCCCCGCCCCAAATAAAAATATGTAAAATGT 5205

staufgDNA  AATTATACGAATAAAAAGTGAAATAAAGTTGGAAGTGAGTGTTTTTGATTGATTTGGGAA 7912
staufcDNA  AATTATACGAATAAAAAGTGAAATAAAGTTGG                            5237
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2222

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2936

staufgDNA
GCGATTCGCAAGCCACAGAGGCGGCTAGTGAGAGTGCACTGAATACCTCAACCGGCAGCA
5580
staufcDNA
GCGATTCGCAAGCCACAGAGGCGGCTAGTGAGAGTGCACTGAATACCTCAACCGGCAGCA
2996

staufgDNA
ATACGAGTGGTGTGAGTAGCAACAGCAGCAATGTTGGAGCCAACACGGATGGTAACAACC
5640
staufcDNA
ATACGAGTGGTGTGAGTAGCAACAGCAGCAATGTTGGAGCCAACACGGATGGTAACAACC
3056

staufgDNA
ATGCCGAGAGTAAAAACAACACGGAGAGTAGCAGCAACAGTACGAGTAACACACAAAGCG
5700
staufcDNA
ATGCCGAGAGTAAAAACAACACGGAGAGTAGCAGCAACAGTACGAGTAACACACAAAGCG
3116

staufgDNA
CTGGTGTGCACATGAAGGAGCAGCTCTTGTACCTTAGTAAACTGCTGGACTTTGAGGTAA
5760
staufcDNA
CTGGAGTGCACATGAAGGAGCAGCTCTTGTACCTTAGTAAACTGCTGGACTTTGAG----
3172

staufgDNA
GCTTACCAACGGAACAGTCAACCCCAACTAGAAACTAACCAATTTCCTCAATTCAGGTCA
5820
staufcDNA ----------GTCA
3176

staufgDNA
ACTTCTCGGACTATCCGAAAGGCAATCATAACGAGTTCCTGACCATCGTGACATTGTCCA
5880
staufcDNA

ACTTCTCGGACTATCCGAAAGGCAATCACAACGAGTTCCTGACCATCGTGACATTGTCCA
3236

staufgDNA
CACATCCGCCGCAGATCTGCCATGGCGTTGGCAAGAGCTCCGAGGAGTCGCAGAATGATG
5940
staufcDNA
CACATCCGCCGCAGATTTGCCATGGCGTTGGCAAGAGCTCCGAGGAGTCGCAGAATGATG
3296

staufgDNA
CTGCAAGCAATGCCTTGAAAATCCTCAGCAAGCTGGGGCTCAACAATGCCATGAAATAAG
6000
staufcDNA
CTGCAAGCAATGCCTTGAAAATCCTCAGCAAGCTGGGGCTCAACAATGCCATGAAATAAG
3356

staufgDNA
CATAAAGCGCTGAAAATTTCACAAAACCCTTATTAACTGCAATTTTTGTTGTTGCACATA
6060
staufcDNA
CATAAAGCGCTGAAAATTTCACAAAACCCTTATTAACTGCAATTTTTGTTGTTGCACATA
3416

staufgDNA
AGCATGATAAGAGCAAAGCAAAGAAAAAACAATTGAAATACCCGTCCACAAAGCAAACCT
6120
staufcDNA
AGCATGATAAGAGCAAAGCAAAGAAAAAACAATTGAAATACCCGTCCACAAAGCAAACCT
3476

staufgDNA
TAAACAAAATCCAAAAACCAAGCTGTGTGCAAATTCAAAAAAAAAAAAGAAGAAAAATGA
6180
staufcDNA
TAAACAAAATCCAAAAACCAAGCTGTGTGCAAATTCAAAAAAAAAAAAGAAGAAAAATGA
3536

staufgDNA
GAAATGTAAGAGAAGCAATGCAAGAAACAGTTTTGAAATAGCAAATTATTAGTTAATACC
6240
staufcDNA
GAAATGTAAGAGAAGCAATGCAAGAAACAGTTTTGAAATAGCAAATTATTAGTTAATACC
3596

staufgDNA
TATTTATTTATTTATGTGTGCACGTTGTGCAAACTGGTGTTATTATTTTATTTATTTGTT
6300
staufcDNA
TATTTATTTATTTATGTGTGCACGTTGTGCAAACTGGTGTTATTATTTTATTTATTTGTT
3656

staufgDNA
GAGAATTGAATAACGAATCGAACTGATAGTAACCGAAACTGAACAGAGGCGAACACTTAA
6360
staufcDNA
GAGAATTGAATAACGAA----------GTAACCGAAACTGAACAGAGGCGAACACTTAA
3705

staufgDNA
CCAGAACCGCAACGTTGTTAATCCAAATCGAGAATCGAACAATAACTAGACTTAATGAAA
6420
staufcDNA
CCAGAGCCGCAACGTTGTTAATCCAAATCGAGAATCGAACAATAACTAGACTTAATGAAA
3765

staufgDNA
ACCCAACAAAATCATGAATGAACAGATGCATATATACATATGTGCAGTACCTAAACTTAA
6480
staufcDNA
ACCCAACAAAATCATGAATGAACAGATGCATATATACATATGTGCAGTACCTAAACTTAA
3825

staufgDNA
GATTAAAGCTCATTAACCACTTGAATTGAATTGATGAACAAAGGACTATTGATACCTCTT
6540
staufcDNA
GATTAAAGCTCATTAACCACTTGAATTGAATTGATGAACAAAGGACTATTGATACCTCTT
3885

staufgDNA
AGCTGCATGCGGCAATCGCTTTCAAAAATAAATACAAAATTTCTGAGCACCTCGGTGCAG
6600
staufcDNA
AGCTGCATGCGGCAATCGCTTTCAAAAATAAATACAAAATTTCTGAGCACCTCGGTGCAG
3945

staufgDNA
GACAAAATTGAAGGATATCCGCATTTGCGAATAAACCAGGCAGGCTGTCAATGGAGAAAC
6660

staufcDNA
GACAAAATTGAAGGATATCCGCATTTGCGAATAAACCAGGCAGGCTGTCAATGGAGAAAC
4005

staufgDNA
TGGACAAATTTTTGATTTATTTTTCAAAGCACGACAACCATGAACCGTTTGTGGTCATAT
6720
staufcDNA
TGGACAAATTTTTGATTTATTTTTCAAAGCACGACAACCATGAACCGTTTGTGGTCATAT
4065

staufgDNA
GCTTGATGAAACTCGTCGAATAATGAATCTATTATACGTATACTATATTTAAGTGTTAAG
6780
staufcDNA
GCTTGATGAAACTCGTCGAATAATGAATCTATTATACGTATACTATATTTAAGTGTTAAG
4125

staufgDNA
CATAAGCATCGGCGAATGTCGGAAAGCCGTATACCGTACCCCATGACCGGTCGATTTGCC
6840
staufcDNA
CATAAGCATCGGCGAATGTCGGAAAGCCGTATACCGTACCCCATGACCGGTCGATTTGCC
4185

staufgDNA
AAAACTTTCAGCAAATATTTGCAATGTTTTGCTGGATTTTGGTTGATTGATAGGAAGTGG
6900
staufcDNA
AAAACTTTCAGCAAATATTTGCAATGTTTTGCTGGATTTTGGTTGATTGATAGGAAGTGG
4245

staufgDNA
AAGAAA---GGGCGTTCACGTCGAACATACAACATAAAATACAATTTACATAATCGTTAT
6957
staufcDNA
AAGAAAAGAAGGCGTTCACGTCGAACATACAACATAAAATACAATTTACATAATCGTTAT
4305

staufgDNA
AATTATATTTATGAATGTTTAATAAGCCATTTTTGTAAATGTTCAGCTTTTGGCGAGTGT
7017
staufcDNA
AATTATATTTATGAATGTTTAATAAGCCATTTTTGTAAATGTTCAGCTTTTGGCGAGTGT

4365

staufgDNA
ACAAGCTAAAAGCTGAACATCCTTATGAATAATGAATCGTGTTGTTTAATCTGTCATGGT
7077
staufcDNA
ACAAGCTAAAAGCTGAACATCCTTATGAATAATGAATCGTGTTGTTTAATCTGTCATGGT
4425

staufgDNA
TTGTCCCCACATGTCTTGCTCGTTTTTGAATCCGACCTATTTATTAGTTATGTTATCGCC
7137
staufcDNA
TTGTCCCCACATGTCTTGCTCGTTTTTGAATCCGACCTATTTATTAGTTATGTTATCGCC
4485

staufgDNA
GTAACCCCATTACTCCCCCCTCCCCCCCCTCCCCAATACACACACATTGCACACACCAACT
7197
staufcDNA
GTAACCCCATTACTCCCCCCTCCCCCCCCTCCCCAATACACACACATTGCACACACCAACT
4545

staufgDNA
GAAATTTCGAGAACAATAGTTTTAATTACTTTTATCCCGAACAGCACCAGTTGATTAAGC
7257
staufcDNA
GAAATTTCGAGAACAATAGTTTTAATTACTTTTATCCCGAACAGCACCAGTTGATTAAGC
4605

staufgDNA
GTTAAGTTGCGTTATGTAAAATGTATTTTGTCTAAGCCATCACGTTGGCCACAATGTGCA
7317
staufcDNA
GTTAAGTTGCGTTATGTAAAATGTATTTTGTCTAAGCCATCACGTTGGCCACAATGTGCA
4665

staufgDNA
TGATTGCTTCGCGATTTGCGATCCTAACCTAAGCTTAAGCCCCAGCGAACTGTAACCGTT
7377
staufcDNA
TGATTGCTTCGCGATTTGCGATCCTAACCTAAGCTTAAGCCCCAGCGAACTGTAACCGTT
4725

staufgDNA

GAAATGAAGTCAATCCCAGTATTAAATGTATAGATAGGGGGCAGTTGTGCGTAACTCCCA
7437
staufcDNA
GAAATGAAGTCAATCCCAGTATTAAATGTATAGATAGGGGGCAGTTGTGCGTAACTCCCA
4785

staufgDNA
TTAAATTACTAGACTCACAGATATATATCGTGCACATTGTTTGCGCCACACAAATTGTTC
7497
staufcDNA
TTAAATTACTAGACTCACAGATATATATCGTGCACATTGTTTGCGCCACACAAATTGTTC
4845

staufgDNA
ATTTTGTTAGAAGATTTTGCAGACCCAGCGGATACGATACGATACGAT-----CATAATC
7552
staufcDNA
ATTTTGTTAGAAGATTTTGCAGACCCAGCGGATACGATACAATACGATACGATCATAATC
4905

staufgDNA
GTAGTCAATAAATTTTCATGTGCGAGTGTAGCGGTGTCTGCTTTGCAAAATCTTCACAAA
7612
staufcDNA
GTAGTCAATAAGTTTTCATGTGCGAGTGTAGCGGTGTCTGCTTTGCAAAATCTTCACAAA
4965

staufgDNA
ATTGATTGAAATTATTAATCTTAATGTGAGATGTATTCGCAGGTAGCAACAATGCGTGAA
7672
staufcDNA
ATTGATTGAAATTATTAATCTTAATGTGAGATGTATTCGCAGGTAGCAACAATGCGTGAA
5025

staufgDNA
GATCTGTTCATTAACACCAAATAAAGGCATACGAGTCAAGATGAGAGAACACATTTATTA
7732
staufcDNA
GATCTGTTCATTAACACCAAATAAAGGCATACGAGTCAAGATGAGAGAACACATTTATTA
5085

staufgDNA
GTCTTAAGCCTACGCCCACACACATTCACTAAGTTTTGTCTATCTGTAATGTGACACATA
7792
staufcDNA

GTCTTAAGCCTACGCCCACACACATTCACTAAGTTTTGTCTATCTGTAATGTGACACATA
5145

staufgDNA
ATCGTGTTATGTCATTAAAACTGAAGAAATCCCCGCCCCAAATAAAAATATGTAAAATGT
7852
staufcDNA
ATCGTGTTATGTCATTAAAACTGAAGAAATCCCCGCCCCAAATAAAAATATGTAAAATGT
5205

staufgDNA
AATTATACGAATAAAAAGTGAAATAAAGTTGGAAGTGAGTGTTTTTGATTGATTTGGGAA
7912
staufcDNA AATTATACGAATAAAAAGTGAAATAAAGTTGG 5237

Coding Regions

Transcribed and Untranslated Regions



Intron-Exon Structure of the *D. melanogaster staufen* gene
Cytological Location: 54F6-55C1
Genetic Location: 2-85.5