The contributions of the Genome Project to the study of schistosomiasis

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In this paper we review the impact that the availability of the Schistosoma mansoni *genome sequence and annotation has had on schistosomiasis research. Easy access to the genomic information is important and several types of data are currently being integrated, such as proteomics, microarray and polymorphic loci. Access to the genome annotation and powerful means of extracting information are major resources to the research community.*

Key words: *Schistosoma mansoni* - genome - database - data integration

Genome sequencing technologies have considerably expanded our range of tools for experimental and theoretical approaches in the quest for understanding the molecular aspects of schistosomiasis and the design of new control tools.

The *Schistosoma mansoni* genome sequence contains over 360 million base pairs divided into seven pairs of autosomes and one pair of sex chromosomes (female = ZW, male = ZZ) (Berriman et al. 2009).

The Wellcome Trust Sanger Institute and an international group of researchers have provided the genome sequencing assembly and annotation (Berriman et al. 2009). The latest draft version of the assembly (Release 4.0) is available online as contigs (50,376) or supercontigs/scaffolds (19,022). Almost half of the genome (45%) was found to be composed of repetitive elements.

Both *ab initio* and evidence based algorithms were used to perform gene prediction and the final automatically annotated sequence includes 11,809 protein-coding gene structures and 13,197 transcripts. It is worth noting that two major Brazilian transcriptome sequencing efforts provided large amounts of expressed sequence tags (EST) (Verjovski-Almeida et al. 2003, Oliveira et al. 2008) that were of critical importance for the identification of the coding regions in the genome. EST data can also be further used for the investigation of transcript variations such as in differential splicing (DeMarco et al. 2006) and alternative polyadenylation (Tian et al. 2007). To infer gene function, several computational analyses were performed using Basic Local Alignment Search Tool (BLAST) (Altschul et al. 1997) for similarity searches, Gene Ontology (Harris et al. 2004) and InterPro (Mulder & Apweiler 2008) for protein domain assignments and limited manual annotation.

SchistoDB: S. mansoni genome database - To establish a central repository for *S. mansoni* genomic data, a database, SchistoDB (Zerlotini et al. 2009) was developed. Similar to other parasite databases with the same architecture (Genomics Unified Schema (Davidson et al. 2001) such as PlasmoDB (Aurrecoechea et al. 2009), ToxoDB (Gajria et al. 2008) and CryptoDB (Heiges et al. 2006), the *S. mansoni* database provides the community wide access to the latest genome sequence, annotation and other types of data integrated with the genome information.

The genome data is structured in a robust relational database coupled with a powerful querying system so that searches can be combined to filter the information based on several criteria. The genome sequences were computationally reanalysed and integrated into a number of public genomic resources.

SchistoDB currently provides over 30 different queries and tools for analysis, retrieving or viewing the data. Users can integrate different search results using the “Query History’’ page, refining the original query iteratively, until a narrow list of genes of interest is obtained. The data can be downloaded in a flat file format for further analysis and each gene possesses its own record page that contains detailed information of all performed analyses (Supplementary data). GBrowse genome browser is used to display gene models, EST alignments, BLAST results, protein features etc and facilitates downloading data in various formats.

Genomic data analysis - Orthology information provided by the OrthoMCL group (Chen et al. 2006) has been integrated into SchistoDB. In this database orthologous genes from 87 species are clustered based on sequence similarity. The immediate result is the ability to infer protein function through evolutionary relationships, since orthologous genes diverged from a common ancestor owing to speciation events. Additionally orthology information allows us to directly compare *S. mansoni* genes to other species to narrow a list of candidate drug targets, for example.

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Using the complete annotated gene set, it is possible to predict the organism's metabolic pathways and gain insight into the physiology of *S. mansoni*. SchistoDB contains metabolic pathway prediction including approximately 607 enzymatic reactions and 112 pathways that were inferred to occur in the organism based on genome annotation and sequence similarity searches. This information can be used to extend the genome annotation and to compare *S. mansoni* with other organisms.

Several tegumental proteins have been identified as potential vaccine candidates (van Balkom et al. 2005, Braschi et al. 2006b) using proteomic approaches. Such research will benefit from the predicted proteome, not only because it enables the identification of mass fingerprints and peptides, but also because these sequences are computationally characterised to have transmembrane motifs or signal peptides and other types of annotation.

Next generation sequencing technologies have become available to *S. mansoni* research groups, allowing the generation of an extremely large sequence data set in each run. Thus, mapping transcript sequences to the genome, for example, will substantially assist intron/exon boundary validation, thereby improving the gene models and genome assembly. Transcript sequences are also invaluable for alternative splicing, single nucleotide polymorphisms and indel studies.

Post-genomic analysis using primarily proteomic and microarray methods is currently being explored by several groups. These experimental approaches, enabled by the genome sequence, have produced essential contributions to a global understanding of how the parasites display sexual differentiation (Waisberg et al. 2008), adapt during development (Jolly et al. 2007) and, for example, how protein expression is compartmentalised (Braschi et al. 2006a). However, these data need to be fully integrated with the genome data to enable the community to make the most use of it.

One remaining challenge is identifying the function of the over 40% of unannotated sequences in the genome. Transgenesis and gene silencing by knockout or knockdown experiments will be essential in that process. These technologies remain largely unavailable. However, recent advances were made with the use of RNA interference (Geldhof et al. 2007, Ndegwa et al. 2007). These methods, in combination with the genomic data, will permit a more profound understanding of the biology of schistosomes and undoubtedly the design of new control measures.

Genome sequencing and annotation has impacted how molecular research is conducted in schistosomes. Issues related to data sharing and data standards still need to be fully resolved. However, the organisation of the information and the availability of robust querying tools, enabled by a relational genome database such as SchistoDB (http://www.schistodb.net), have provided a framework that provides faster access to the information and empowers groups that are not equipped to conduct the required computational analysis to make use of the information.

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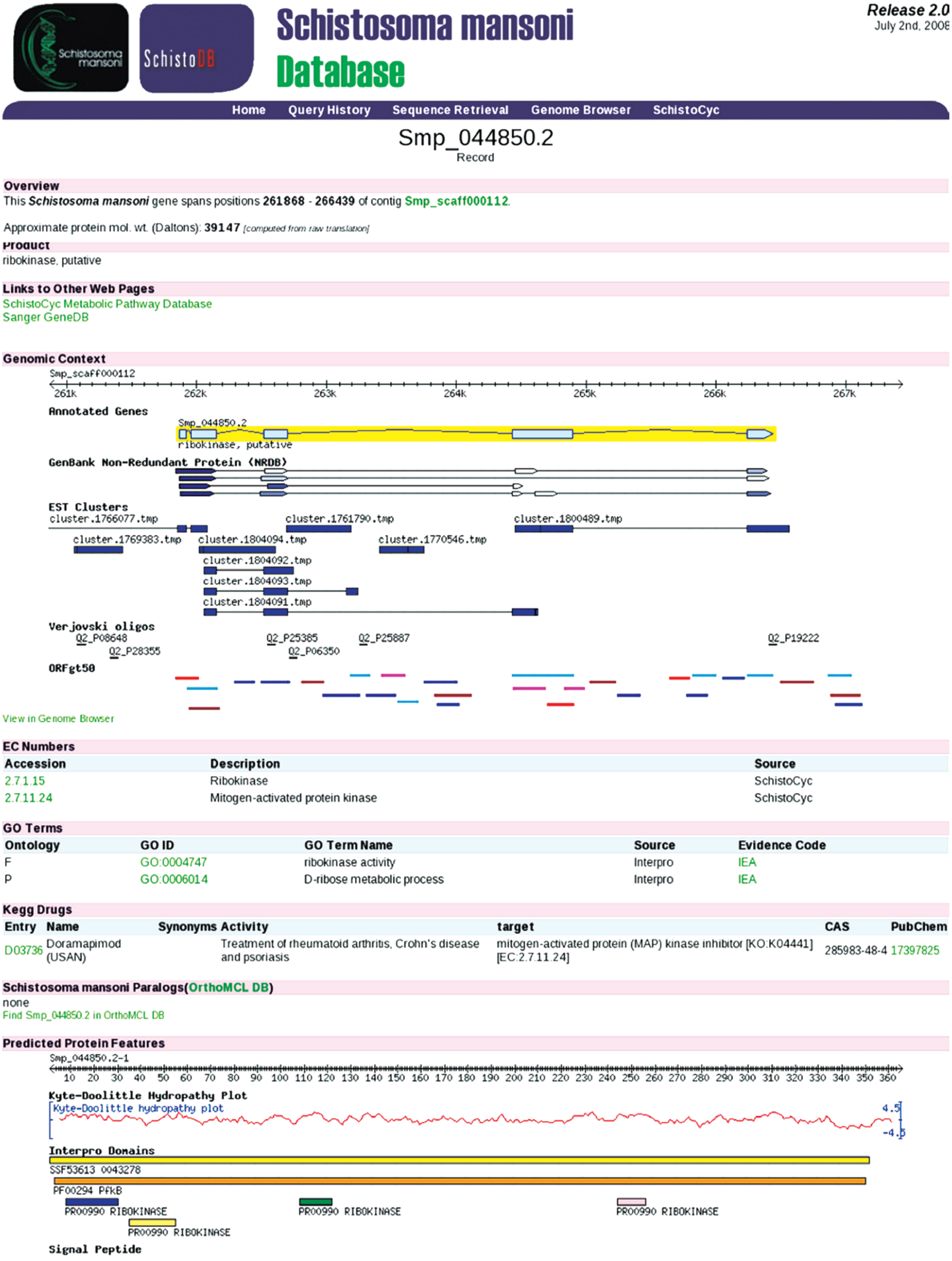


Smp_044850.2

Record

Overview

This ***Schistosoma mansoni*** gene spans positions **261868 - 266439** of contig **Smp_scaff000112**.

Approximate protein mol. wt. (Daltons): **39147** *[computed from raw translation]*

Product

ribokinase, putative

Links to Other Web Pages

SchistoCyc Metabolic Pathway Database
Sanger GeneDB

Genomic Context

View in Genome Browser

EC Numbers

Accession	Description	Source
2.7.1.15	Ribokinase	SchistoCyc
2.7.11.24	Mitogen-activated protein kinase	SchistoCyc

GO Terms

Ontology	GO ID	GO Term Name	Source	Evidence Code
F	GO:0004747	ribokinase activity	Interpro	IEA
P	GO:0006014	D-ribose metabolic process	Interpro	IEA

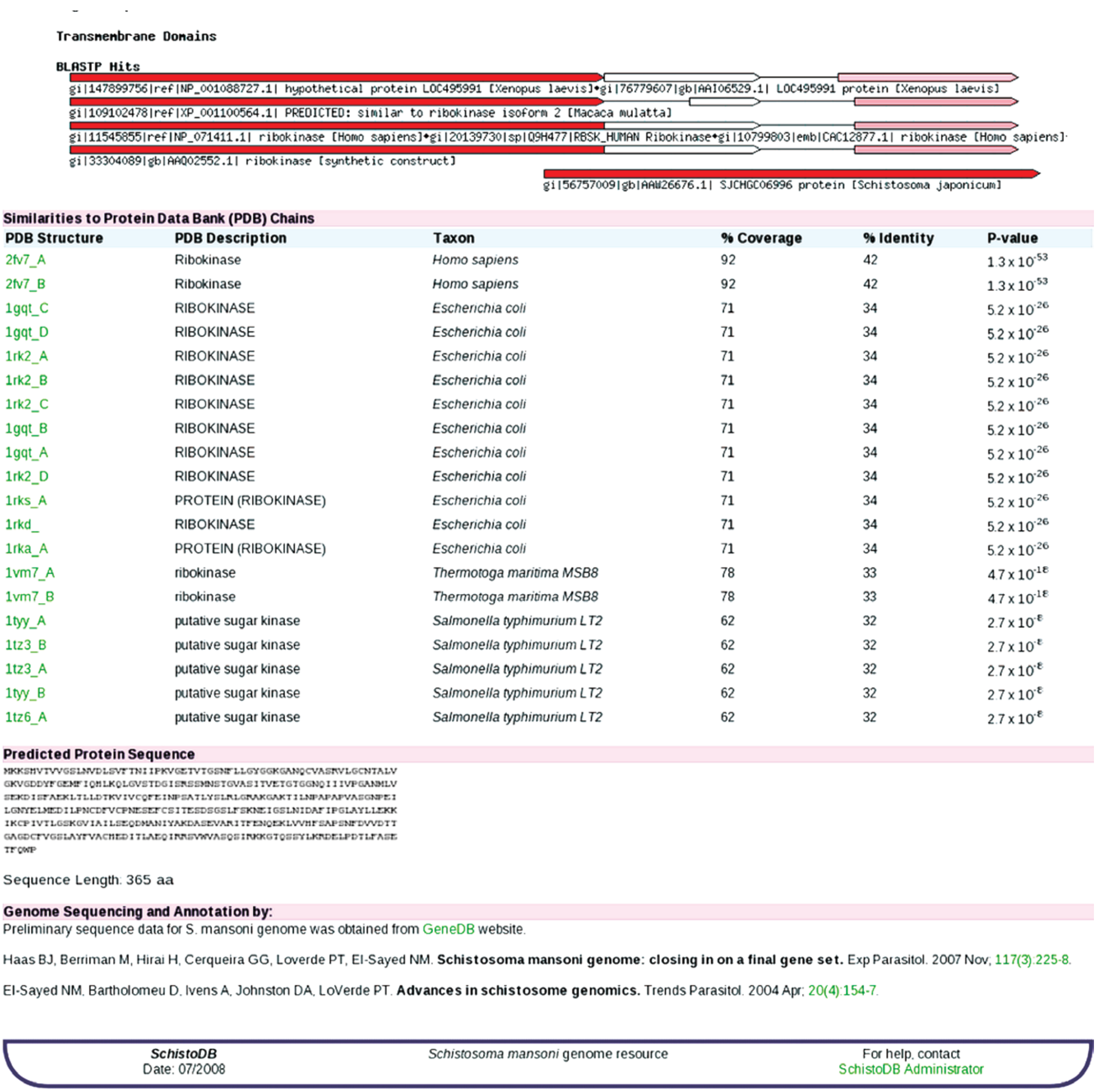
Kegg Drugs

Entry	Name	Synonyms	Activity	target	CAS	PubChem
D03736	Doramapimod (USAN)		Treatment of rheumatoid arthritis, Crohn's disease and psoriasis	mitogen-activated protein (MAP) kinase inhibitor [KO:K04441] [EC:2.7.11.24]	285983-48-4	17397825

Schistosoma mansoni Paralogs(OrthoMCL DB)

none
Find Smp_044850.2 in OrthoMCL DB

Predicted Protein Features



Transmembrane Domains

BLASTP Hits

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gi|147899756|ref|NP_001088727.1| hypothetical protein LOC495991 [Xenopus laevis]•gi|76779607|gb|AAI06529.1| LOC495991 protein [Xenopus laevis]
gi|109102478|ref|XP_001100564.1| PREDICTED: similar to ribokinase isoform 2 [Macaca mulatta]
gi|11545855|ref|NP_071411.1| ribokinase [Homo sapiens]•gi|20139730|sp|Q9H477|RBSK_HUMAN Ribokinase•gi|10799803|emb|CAC12877.1| ribokinase [Homo sapiens]·
gi|33304089|gb|AAQ02552.1| ribokinase [synthetic construct]
gi|56757009|gb|AAW26676.1| SJCHGC06996 protein [Schistosoma japonicum]
```

Similarities to Protein Data Bank (PDB) Chains

PDB Structure	PDB Description	Taxon	% Coverage	% Identity	P-value
2fv7_A	Ribokinase	*Homo sapiens*	92	42	1.3×10^{-53}
2fv7_B	Ribokinase	*Homo sapiens*	92	42	1.3×10^{-53}
1gqt_C	RIBOKINASE	*Escherichia coli*	71	34	5.2×10^{-26}
1gqt_D	RIBOKINASE	*Escherichia coli*	71	34	5.2×10^{-26}
1rk2_A	RIBOKINASE	*Escherichia coli*	71	34	5.2×10^{-26}
1rk2_B	RIBOKINASE	*Escherichia coli*	71	34	5.2×10^{-26}
1rk2_C	RIBOKINASE	*Escherichia coli*	71	34	5.2×10^{-26}
1gqt_B	RIBOKINASE	*Escherichia coli*	71	34	5.2×10^{-26}
1gqt_A	RIBOKINASE	*Escherichia coli*	71	34	5.2×10^{-26}
1rk2_D	RIBOKINASE	*Escherichia coli*	71	34	5.2×10^{-26}
1rks_A	PROTEIN (RIBOKINASE)	*Escherichia coli*	71	34	5.2×10^{-26}
1rkd_	RIBOKINASE	*Escherichia coli*	71	34	5.2×10^{-26}
1rka_A	PROTEIN (RIBOKINASE)	*Escherichia coli*	71	34	5.2×10^{-26}
1vm7_A	ribokinase	*Thermotoga maritima MSB8*	78	33	4.7×10^{-18}
1vm7_B	ribokinase	*Thermotoga maritima MSB8*	78	33	4.7×10^{-18}
1tyy_A	putative sugar kinase	*Salmonella typhimurium LT2*	62	32	2.7×10^{-8}
1tz3_B	putative sugar kinase	*Salmonella typhimurium LT2*	62	32	2.7×10^{-8}
1tz3_A	putative sugar kinase	*Salmonella typhimurium LT2*	62	32	2.7×10^{-8}
1tyy_B	putative sugar kinase	*Salmonella typhimurium LT2*	62	32	2.7×10^{-8}
1tz6_A	putative sugar kinase	*Salmonella typhimurium LT2*	62	32	2.7×10^{-8}

Predicted Protein Sequence

```
MKKSHVTVVGSLNVDLSVFTNIIPKVGETVTGSNFLLGYGGKGANQCVASRVLGCNTALV
GKVGDDYFGEMFIQHLKQLGVSTDGISRSSMNSTGVASITVETGTGGNQIIIVPGANMLV
SEKDISFAEKLTLLDTKVIVCQFEINPSATLYSLRLGRAKGAKTIILNPAPAPVASGNPEI
LGNYELMEDILPNCDFVCPNESEFCSITESDSGSLFSKNEIGSLNIDAFIPGLAYLLEKK
IKCPIVTLGSKGVIAILSEQDMANIYAKDASEVARITFENQEKLVVHFSAPSNFDVVDTT
GAGDCFVGSLAYFVACHEDITLAEQIRRSVWVASQSIRKKGTQSSYLKRDELPDTLFASE
TFQWP
```

Sequence Length: 365 aa

Genome Sequencing and Annotation by:

Preliminary sequence data for S. mansoni genome was obtained from GeneDB website.

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SchistoDB
Date: 07/2008

Schistosoma mansoni genome resource

For help, contact
SchistoDB Administrator

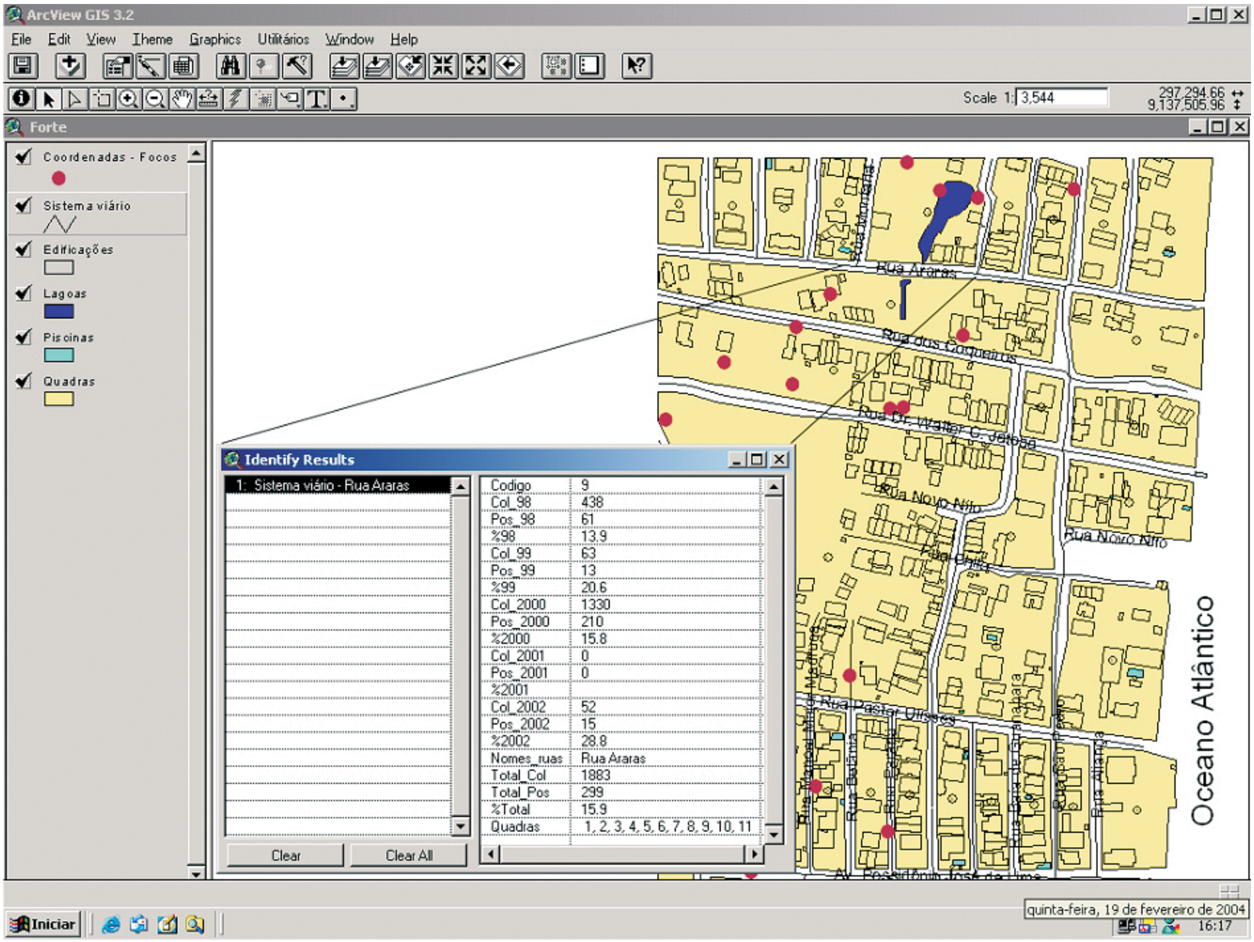
Screenshot from SchistoDB displaying the gene record page. In the example, the gene for ribokinase is displayed.

TABLE

Results of specific exams of 27 patients with presumptive diagnosis of schistosomal myeloradiculopathy examined in hospitals of Campinas, São Paulo (SP), Brazil between 1995-2005

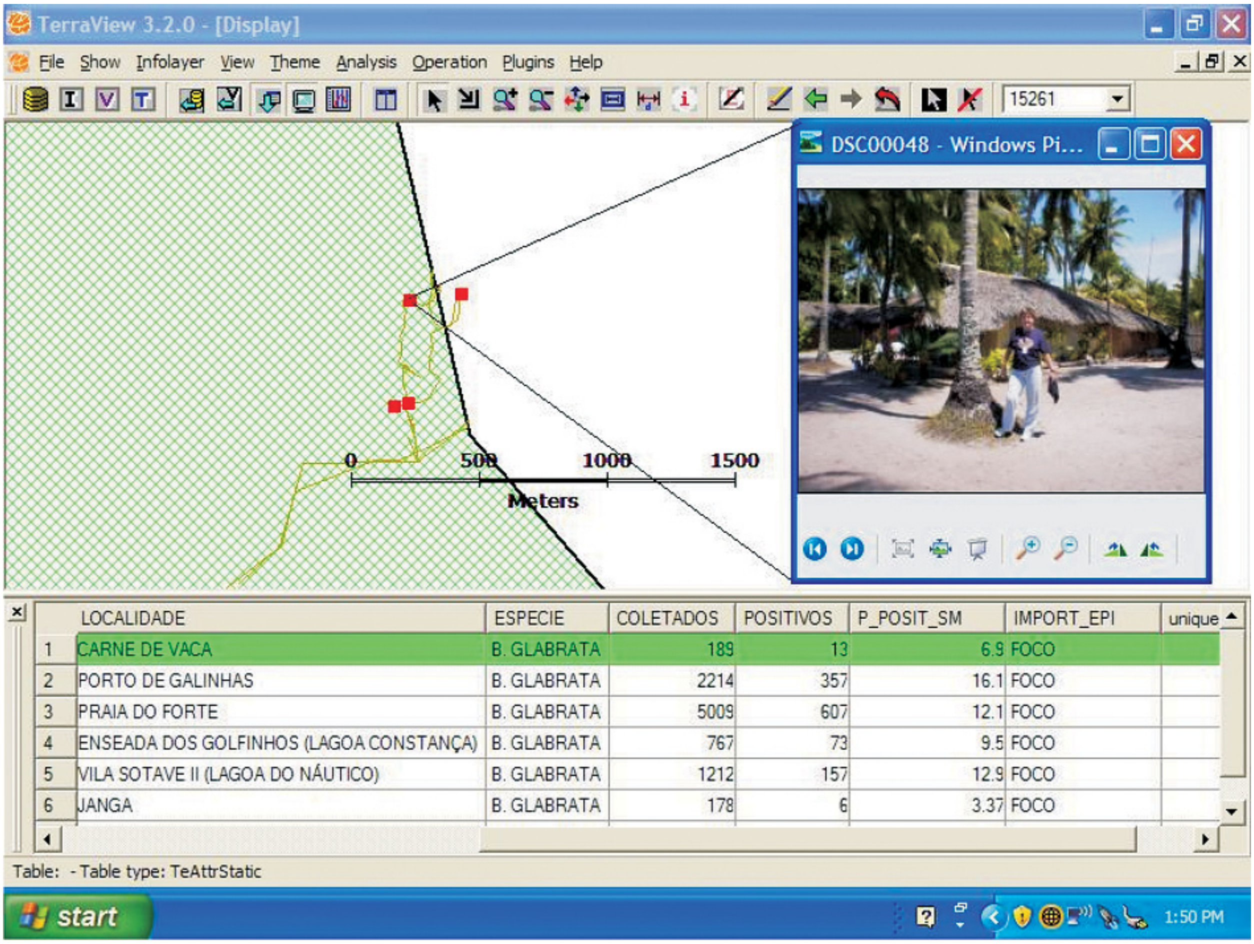
			Specific examinations				
Patient	Local where infection probably occurred	Time of follow-up	Stool examination	Number of samples	Immune reaction in serum	Immune reaction in CSF	Other examinations
1	Campinas (SP)	6 years	+	4	+	ND	Kato-Katz (8 EPG)
2	Campinas (SP)	8 years	+	1	ND	ND	Kato-Katz (48 EPG)
3	Amparo (SP)	6 years	-	1	ND	+	-
4	Campinas (SP)	5 years	-	3	+	ND	Rectal mucosa biopsy negative for *Schistosoma mansoni*
5	Campinas (SP)	4 years	+	1	ND	+	-
6	Limeira (SP)	2 years	ND	ND	ND	ND	Positive to spinal cord biopsy
7	Campinas (SP)	3 months	-	2	ND	+	-
8	Campinas (SP)	6 years 3 months	+	2	ND	ND	-
9	Campinas (SP)	5 years 8 months	+	3	ND	ND	Positive to spinal cord biopsy
10	Campinas (SP)	7 years 5 months	-	1	+	+	-
11	Campinas (SP)	10 years	-	3	ND	+	Positive rectal mucosa biopsy
12	Campinas (SP)	4 years	-	1	ND	+	-
13	Limeira (SP)	5 years 6 months	Ignored	Ignored	ND	+	-
14	Campinas (SP)	2 months	+	2	+	+	-
15	Minas Gerais (MG)	1 year	+	1	+	-	Kato-Katz (8 EPG)
16	Sergipe	2 months	+	2	ND	+	-
17	Nova Módica (MG)	1 year 3 months	-	2	ND	+	-
18	Porteirinha (MG)	3 years	-	3	ND	+	-
19	MG	1 year 5 months	+	2	ND	+	-
20	Guanambi (BA)	1 year 4 months	-	3	+	ND	-
21	MG	2 years 2 months	-	2	ND	+	-
22	No information	10 days	+	1	ND	ND	-
23	No information	6 years	-	1	ND	+	-
24	Caratinga (MG)	6 years	+	2	ND	ND	Kato-Katz (19 EPG)
25	Alagoas	1 year	-	1	-	+	-
26	Curvelo (MG)	12 years	-	3	ND	ND	Positive rectal mucosa biopsy
27	Lajinha (MG)	4 years	-	1	+	ND	-

EPG: eggs per gram; CSF: cerebrospinal fluid; ND: not done.



Codigo	9
Col_98	438
Pos_98	61
%98	13.9
Col_99	63
Pos_99	13
%99	20.6
Col_2000	1330
Pos_2000	210
%2000	15.8
Col_2001	0
Pos_2001	0
%2001	
Col_2002	52
Pos_2002	15
%2002	28.8
Nomes_ruas	Rua Araras
Total_Col	1883
Total_Pos	299
%Total	15.9
Quadras	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11

Fig. 5: application for monitoring the foci of schistosomiasis vectors at Forte beach, Itamaracá, Pernambuco, Brazil (KC Araújo, unpublished observations).



	LOCALIDADE	ESPECIE	COLETADOS	POSITIVOS	P_POSIT_SM	IMPORT_EPI	unique
1	CARNE DE VACA	B. GLABRATA	189	13	6.9	FOCO	
2	PORTO DE GALINHAS	B. GLABRATA	2214	357	16.1	FOCO	
3	PRAIA DO FORTE	B. GLABRATA	5009	607	12.1	FOCO	
4	ENSEADA DOS GOLFINHOS (LAGOA CONSTANÇA)	B. GLABRATA	767	73	9.5	FOCO	
5	VILA SOTAVE II (LAGOA DO NÁUTICO)	B. GLABRATA	1212	157	12.9	FOCO	
6	JANGA	B. GLABRATA	178	6	3.37	FOCO	

Table: - Table type: TeAttrStatic

Fig. 6: application for monitoring the foci of schistosomiasis vectors at Carne de Vaca, Goiana, Pernambuco, Brazil (KC Araújo, unpublished observations).

>SmBr18 (DQ137590.1)
ACTTACATGCATTACACACACTAGAACATCACAACGCACACAACCTGAACAACGGAAACATAACAGGGAACACCACTCCTCCCCA
TAACCATCATTCACCAAACATTCAAACACCACTATTACAACGAAAAACAATCAACACATAATCAACCCAACACACTATATCCCAC
ATT**CACACACACACACACACACA**AACACACTCCTTCATCAACATGTAGACAGAAAATGGAACACGACTACGCAATCAACATCGTC
GTCCAACGAGAAATCTGTCCAACCATCAATGTCAACTCTCATTACCACCCACACATATGTTAA*CAAACAACAA*GTGGACTTGGTT
GTAGATGTACTTACCATGCATCTA

NCBI:

DQ137590.1	Schistosoma mansoni clone 169AAT microsatellite sequence	673	673	100%	0.0	100%
DQ137504.1	Schistosoma mansoni clone 082AAT microsatellite sequence	538	538	99%	5e-150	93%
DQ137605.1	Schistosoma mansoni clone 016CA microsatellite sequence	534	534	99%	7e-149	93%
DQ137539.1	Schistosoma mansoni clone 118AAT microsatellite sequence	529	529	94%	3e-147	94%
DQ137489.1	Schistosoma mansoni clone 067AAT microsatellite sequence	514	514	90%	9e-143	94%
DQ137526.1	Schistosoma mansoni clone 105AAT microsatellite sequence	501	501	86%	7e-139	95%
DQ137525.1	Schistosoma mansoni clone 104AAT microsatellite sequence	496	496	91%	3e-137	93%
DQ137461.1	Schistosoma mansoni clone 038AAT microsatellite sequence	490	490	86%	2e-135	94%
DQ137520.1	Schistosoma mansoni clone 099AAT microsatellite sequence	481	481	99%	9e-133	91%
DQ137585.1	Schistosoma mansoni clone 164AAT microsatellite sequence	466	466	92%	3e-128	92%
DQ137567.1	Schistosoma mansoni clone 146AAT microsatellite sequence	457	457	94%	2e-125	90%
DQ137537.1	Schistosoma mansoni clone 116AAT microsatellite sequence	449	449	87%	3e-123	92%
DQ137466.1	Schistosoma mansoni clone 044AAT microsatellite sequence	366	366	66%	3e-98	93%

Alignment: NCBI

```
                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5          15         25         35         45         55         65
DQ137504        TGTGTGGGTT GAATATGTGG TGATAGTTGT TCGGTGTAAA AAGGGGTGTT TGAATGGTTG GTGAATGATG
DQ137520        .......... .......... .......... .......... .......... .......... ..........
DQ137590        .......... .......... .......... .......... .......... .......... ..........
DQ137605        .......... .......... .......... .......... .......... .......... ..........
DQ137537        .......... .......... .......... .......... .......... .......... ..........
DQ137526        .......... .......... .......... .......... .......... .......... ..........
DQ137585        .......... .......... .......... .......... .......... .......... ..........
DQ137489        .......... .......... .......... .......... .......... .......... ..........
DQ137461        .......... .......... .......... .......... .......... .......... ..........
DQ137466        .......... .......... .......... .......... .......... .......... ..........
DQ137525        .......... .......... .......... .......... .......... .......... ..........
DQ137539        .......... .......... .......... .......... .......... .......... ..........
CONTIG-0        TGTGTGGGTT GAATATGTGG TGATAGTTGT TCGGTGTAAA AAGGGGTGTT TGAATGGTTG GTGAATGATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     75         85         95        105        115        125        135
DQ137504        GGTTATGAGG AGGAGTGGTG TTCCCTGTTA TGTCTCCGTT GTTCAG-GTT GCGT-GTGTT GTGTG-TGTT
DQ137520        .......... .......... .......... .......... ......TGTT GTGTCGTGTT GTGTGGTGTT
DQ137590        .......... .......... .......... .......... .......... .......... ..........
DQ137605        .......... .......... .......... .......... .......... .......... ..........
DQ137537        .......... .......... .......... .......... .......... .......... ..........
DQ137526        .......... .......... .......... .......... .......... .......... ..........
DQ137585        .......... .......... .......... .......... .......... .......... ..........
DQ137489        .......... .......... .......... .......... .......... .......... ..........
DQ137461        .......... .......... .......... .......... .......... .......... ..........
DQ137466        .......... .......... .......... .......... .......... .......... ..........
DQ137525        .......... .......... .......... .......... .......... .......... ..........
DQ137539        .......... .......... .......... .......... .......... .......... ..........
CONTIG-0        GGTTATGAGG AGGAGTGGTG TTCCCTGTTA TGTCTCCGTT GTTCAGTGTT GCGTCGTGTT GTGTGGTGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    145        155        165        175        185        195        205
DQ137504        GTGATGTTCT AGTGTGTGTA -ATGCATG-T AAGTAC-TCT -CAACCA-GT CCACTTGTTG TTTGTTAACA
DQ137520        GTGATGTTCT AGTGTGTGTA -ATGCATG-T AA-TAC-TCT -CAACCA-GT CCACTTGTTG TTTGTTAACA
DQ137590        .......... ........TA GATGCATGGT AAGTACATCT ACAACCAAGT CCACTTGTTG TTTGTTAACA
DQ137605        .......... .......... .ATGCAAG-T AAGTAC-TCT -CAACCA-GT CCACTTGTTG TTTGTTAACA
DQ137537        .......... .......... .......... ....AC-TCT -CAACCA-GT CCACTTGTTG TTTGTTAACA
DQ137526        .......... .......... .......... ........CT -CAACCA-GT CCACTTGTTG TTTGTTAACA
DQ137585        .......... .......... .......... .......... ..AACCA-GT CCACTTGTTG TTTGTTAACA
DQ137489        .......... .......... .......... .......... .......... CCACTTGTTG TTTGTTAACA
DQ137461        .......... .......... .......... .......... .......... .......... ......AACA
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DQ137466       .......... .......... .......... .......... .......... .......... ..........
DQ137525       .......... .......... .......... .......... ........GT CCACTTGTTG TTTGTTAACA
DQ137539       .......... .......... .......... .....C-TCT -CAACCA-GT CCACTTTTTG TTTGTTAACA
CONTIG-0       GTGATGTTCT AGTGTGTGTA -ATGCATG-T AAGTAC-TCT -CAACCA-GT CCACTTGTTG TTTGTTAACA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  215        225        235        245        255        265        275
DQ137504       TATGT-GTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
DQ137520       TATGT-GTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
DQ137590       TATGT-GTGG GTGGTAATGA GAGTTGACAT TGATGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
DQ137605       TATGT-GTGG GTG-TAATGA GAGT-GACAT TGATGGTGGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
DQ137537       TATGT-GTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
DQ137526       TATGT-GTGG GTG-TAATGA GAGT-GACAT TGAAGGTTGG ACAGATTTCT CGTTGGACGA AGATGTTGAT
DQ137585       TATGT-GTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
DQ137489       TATGT-GTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
DQ137461       TATGTTGTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
DQ137466       .......... .......... .......... .......... .......... .......... ..........
DQ137525       TATGT-GTGG TTG-TAATGT GAGT-GACAT TGTTGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
DQ137539       TATGT-GTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT
CONTIG-0       TATGT-GTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT CGTTGGACGA CGATGTTGAT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  285        295        305        315        325        335        345
DQ137504       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGTTTGTGTG TGTGTGTG--
DQ137520       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGT--GTGT- --T-TGTG--
DQ137590       T-GCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGTTTGTGTG TGTGTGTGTG
DQ137605       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGTTTGTGTG TGTGTGTGTG
DQ137537       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATGGTTGA TGAAGGAGTG TGTTTGTGTG TGTGTGTGTG
DQ137526       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGTTTGTGTG TGTGTGTGTG
DQ137585       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGT--GTGT- --T-TGTG--
DQ137489       TTGCGTAG-T C-GTGTTCCA TTT-CTGTCT ACATG-TTGA TGAAGGAGCG TGTTTGTGTG TGTGTGTGTG
DQ137461       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGTTTGTGTG TGTGTGTGTG
DQ137466       ..GCGTAGAT CAGTGTTCCA ATTTCTGTCT ACATG-TTGA TGAAGGAGTG TGTTTGTGTG TGTGTGTGTG
DQ137525       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGTTTGTGTG TGTGTGT--G
DQ137539       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGTTTGTGTG TGTGTGTGTG
CONTIG-0       TTGCGTAG-T C-GTGTTCCA TTTTCTGTCT ACATG-TTGA TGAAGGAGTG TGTTTGTGTG TGTGTGTGTG

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  355        365        375        385        395        405        415
DQ137504       ----AATGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
DQ137520       ----AACGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
DQ137590       TGTGAATGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
DQ137605       ----AATGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
DQ137537       TG--AATGTG GGATATAGTG TGTTGGGTTG GTTATGTGTT GATTGTTTC- CGTTGTAATA TTGGTGTTGG
DQ137526       TG--AATGTG GGATATAGTG TGTTGGGTTG ATTATGTGTC GATTGTTTTT CGTTGTAATA GTGGCATTTG
DQ137585       ----AACGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
DQ137489       TG--AACGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
DQ137461       TG--AACGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
DQ137466       TG--AATGTG G-ATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
DQ137525       ----AATGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
DQ137539       ----AATGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG
CONTIG-0       TG--AATGTG GGATATAGTG TGTTGGGTTG ATTATGTGTT GATTGTTTTT CGTTGTAATA GTGGTGTTTG

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475        485
DQ137504       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137520       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137590       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137605       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137537       AATGTTTGGT GAATGATGGT TAATGGGGAG AATTGTGTGT CCCCTGTAA- GTTTCCCGT- GTGTCAGGTT
DQ137526       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCC-TGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137585       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137489       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137461       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137466       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137525       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
DQ137539       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT
CONTIG-0       AATGTTTGGT GAATGATGGT TA-TGGGGAG GAGTG-GTGT TCCCTGTTAT GTTTCC-GTT GT-TCAGGTT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  495        505        515        525        535        545        555
DQ137504       GTGTGTGTTG TGTGTGTTGT GATGTTCTAG TGTGTGTAAT GCATGTAAGT .......... ..........
DQ137520       GTGTGTGTTG TGTGTGTTGT GATGTTCTGG TGTGTGTAAT GCATGTAAGT .......... ..........
DQ137590       GTGT------ ---GCGTTGT GATGTTCTAG TGTGTGTAAT GCATGTAAGT .......... ..........
DQ137605       GTGTGTGTTG TGTGTGTTGT GATGTTCTAG TGTGTATAAT GCATGTAAGT .......... ..........
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DQ137537      GTGTGTGTTG TGTGTGTTG. .......... .......... .......... .......... ..........
DQ137526      GTGTGTGTTG TGTGTGTTGT GATGTTCTAG TG........ .......... .......... ..........
DQ137585      GTGTGTGTTG TGTGTGTTGT GATGTTCTAG TGTGTGTAAT GCATGT.... .......... ..........
DQ137489      GTGTGTGTTG TGTGTGTTGT GATGTTCTAG TGTGTGTAAT GCATGTAAAT .......... ..........
DQ137461      GTGTGTGTTG TGTGTGTTGT GATGTTATAG TGTGTGTAAT GCATGTAAGT .......... ..........
DQ137466      GTGTGTGTTG TGTGTGTTGT GATGTTCTAG TGTGTGTAAT GCATGTAAGT .......... ..........
DQ137525      GTGTGTGTTG TGTGTGTTGT GATGTTCTAG TGTGTGTAAT GCATGTAAGC A......... ..........
DQ137539      GTGTGTGTTG TGTGTGTTGT GATGTTCTAG TGTGTGTAAT GCATGTAAGT ACTCTCAACC AGTCCACTTG
CONTIG-0      GTGTGTGTTG TGTGTGTTGT GATGTTCTAG TGTGTGTAAT GCATGTAAGT ACTCTCAACC AGTCCACTTG

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 565        575        585        595        605        615        625
DQ137504      .......... .......... .......... .......... .......... .......... ..........
DQ137520      .......... .......... .......... .......... .......... .......... ..........
DQ137590      .......... .......... .......... .......... .......... .......... ..........
DQ137605      .......... .......... .......... .......... .......... .......... ..........
DQ137537      .......... .......... .......... .......... .......... .......... ..........
DQ137526      .......... .......... .......... .......... .......... .......... ..........
DQ137585      .......... .......... .......... .......... .......... .......... ..........
DQ137489      .......... .......... .......... .......... .......... .......... ..........
DQ137461      .......... .......... .......... .......... .......... .......... ..........
DQ137466      .......... .......... .......... .......... .......... .......... ..........
DQ137525      .......... .......... .......... .......... .......... .......... ..........
DQ137539      TTGTTTGCTA ACATATGTGT GGGTGTAATG AGAGTGTTCC CTGTTATGTT TCCGTTGTTC AGGTTGTGTG
CONTIG-0      TTGTTTGCTA ACATATGTGT GGGTGTAATG AGAGTGTTCC CTGTTATGTT TCCGTTGTTC AGGTTGTGTG

              ....|....| ....|....| ....|....| ....|....| ....|
                 635        645        655        665        675
DQ137504      .......... .......... .......... .......... .....
DQ137520      .......... .......... .......... .......... .....
DQ137590      .......... .......... .......... .......... .....
DQ137605      .......... .......... .......... .......... .....
DQ137537      .......... .......... .......... .......... .....
DQ137526      .......... .......... .......... .......... .....
DQ137585      .......... .......... .......... .......... .....
DQ137489      .......... .......... .......... .......... .....
DQ137461      .......... .......... .......... .......... .....
DQ137466      .......... .......... .......... .......... .....
DQ137525      .......... .......... .......... .......... .....
DQ137539      TGTTGTGTGT GTTGTGATGT TCTAGTGTGT GTAATGCATG TAAGT
CONTIG-0      TGTTGTGTGT GTTGTGATGT TCTAGTGTGT GTAATGCATG TAAGT
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geneDB:

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shisto4743c05.p1k                                              1482   7.9e-61    1
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***S. mansoni* predicted proteins [wublastx], for query: SmBr18**

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Sm02551                                                        249    2.1e-21    1
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***S. mansoni* predicted genes (coding sequences) [wublastn], for query: SmBr18**

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Sm02551                                                       1559    5.3e-66    1
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TIGR:

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s_mansoni|TC34704 homologue to UP|EGG3_SCHMA (P13396) Egg...  1491   2.0e-63    1
```

Alignment: Genedb-TIGR

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              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  5         15         25         35         45         55         65
4743c05.      .......... .......... .......... .......... .......... .......... ..........
Sm02551       .......... .......... .......... .......... .......... .......... ..........
TC34704       ACTATTACAG TGAAGAACAA TCAACACATA ATCAACCCAA CACACAATAT CCCACATTCA CACACACACA
Contig-0      ACTATTACAG TGAAGAACAA TCAACACATA ATCAACCCAA CACACAATAT CCCACATTCA CACACACACA

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  75         85         95        105        115        125        135
4743c05.      .......... .......... .......... .......... .......... .......... ..........
Sm02551       .......... .......... .......... .......... ...ACAC-AC -AC--AACA- CACACAACCT
TC34704       CACACAAACA CACTCCTTCA TCAACATGTA GACAGAAAAT GGAACACGAC TACGCAA-AT CA-ACATCGT
Contig-0      CACACAAACA CACTCCTTCA TCAACATGTA GACAGAAAAT GGAACACGAC TACGCAACAT CACACAACCT
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              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   145        155        165        175        185        195        205
4743c05.      .......... .......... .......... .......... .......... .......... ..........
Sm02551       -GAACAACG- GAAA-CA-T- -AAC-AGGGA A---CACTCT CATTACACCC ACACATATGT TAACAAACAA
TC34704       CGTCCAACGA GAAATCTGTC CAACCATC-A ATGTCACTCT CATTACACCC ACACATATGT TAACAAACAA
Contig-0      CGAACAACGA GAAATCAGTC CAACCAGCGA ATGTCACTCT CATTACACCC ACACATATGT TAACAAACAA

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   215        225        235        245        255        265        275
4743c05.      .......... .......... ......ATGC ATTACACACA CTAGAACATC ACAACACACC CATAGAGGCA
Sm02551       CAAGTGGACT GGTTGAGAGT ACTTACATGC ATTACACACA CTAGAACATC ACAACACAC- -A------CA
TC34704       CAAGTGGACT GGTTGAGAGT ACTTACATGC ATTACACACA CTAGAACATC ACAACACAC- -A------CA
Contig-0      CAAGTGGACT GGTTGAGAGT ACTTACATGC ATTACACACA CTAGAACATC ACAACACAC- -A------CA

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   285        295        305        315        325        335        345
4743c05.      AC-C------ ----GAACAA CGGAAACA-A ACAGGGAACA CC-CTACACG CCCATAACCA TCATTCACCA
Sm02551       ACACACACAA GCCTGAACAA CGGAAACATA ACAGGGAACA CCACTCCTC- CCCATAACCA TCATTCACCA
TC34704       AC-C------ ---TGAACAA CGGAAACATA ACAGGGAACA CCACTCCTC- CCCATAACCA TCATTCACCA
Contig-0      AC-C------ ---TGAACAA CGGAAACATA ACAGGGAACA CCACTCCTC- CCCATAACCA TCATTCACCA

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   355        365        375        385        395        405        415
4743c05.      AACATTCAAA CACCACGATT ACAACGAAAA ACAATCAACA CATAATCAAC CCAACACACT ATATCCCACA
Sm02551       AACATTCAAA CACCACTATT ACAACGAAAA ACAATCAACA CATAATCAAC CCAACACACT ATATCCCACA
TC34704       AACATTCAAA CACCACTATT ACAACGAAAA ACAATCAACA CATAATCAAC CCAACACACT ATATCCCACA
Contig-0      AACATTCAAA CACCACTATT ACAACGAAAA ACAATCAACA CATAATCAAC CCAACACACT ATATCCCACA

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475        485
4743c05.      TTCACACACA CACACACACA AACACACTCC TTCATCAACA TGTAGACAGA AAATGGAACA CGACTACGCA
Sm02551       TTCACACACA CACACACA-A A-CACACTCC TTCATCAACA TGTAGACAGA AAATGGAACA CGACTACGCA
TC34704       TTCACACACA CACACACACA AACACACTCC TTCATCAACA TGTAGACAGA AAATGGAACA CGACTACGCA
Contig-0      TTCACACACA CACACACACA AACACACTCC TTCATCAACA TGTAGACAGA AAATGGAACA CGACTACGCA

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   495        505        515        525        535        545        555
4743c05.      AATCAACATC GTCGTCCAAC GAGAAATCTG TCCAACCATC AATGTCACTC TCATTACACC CATACATATG
Sm02551       AATCAACATC GTCGTCCAAC GAGAAATCTG TCCAACCATC AATGTCACTC TCATTACACC CACACATATG
TC34704       AATCAACATC GTCGTCCAAC GAGAAATCTG TCCAACCATC AATGTCACTC TCATTACACC CACACATATG
Contig-0      AATCAACATC GTCGTCCAAC GAGAAATCTG TCCAACCATC AATGTCACTC TCATTACACC CACACATATG

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   565        575        585        595        605        615        625
4743c05.      TTAACAAACA ACAAGTGGAC TGGTTGAGAG TACTTACATG CATTACACAC ACTAGAACAT CACAA-----
Sm02551       TTAACAAACA ACAAGTGGAC TGGTTGAGAG TACTTACATG CATTACACAC ACTAGAACAT CACAACACAC
TC34704       TTAACAAACA ACAAGTGGAC TGGTTGAGAG TACTTACATG CATTACACAC ACTAGAACAT CACAACACAC
Contig-0      TTAACAAACA ACAAGTGGAC TGGTTGAGAG TACTTACATG CATTACACAC ACTAGAACAT CACAACACAC

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   635        645        655        665        675        685        695
4743c05.      ---------- ---CACACAC AACCTGAACA ACGGAAACAT AACAGGGAAC ACCACTCCTC CCCATAACCA
Sm02551       ACAACACACA CAAC-C---- ----TGAACA ACGGAAACAT AACAGGGAAC ACCACTCCTC CCCATAACCA
TC34704       ACAACACACA CAACACACAC AACCTGAACA ACGGAAACAT AACAGGGAAC ACCACTCCTC CCCATAACCA
Contig-0      ACAACACACA CAACACACAC AACCTGAACA ACGGAAACAT AACAGGGAAC ACCACTCCTC CCCATAACCA

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   705        715        725        735        745        755        765
4743c05.      TCATTCACCA AACATTCAAA CACCACGATT ACAACGAAAA ACAATCAACA CATAATCAAC CCAACACACT
Sm02551       TCATTCACCA AACATTCAAA CACCACTATT ACAACGAAAA ACAATCAACA CATAATCAAC CCAACACACT
TC34704       TCATTCACCA AACATTCAAA CACCACTATT ACAACGAAAA ACAATCAACA CATAATCAAC CCAACACACT
Contig-0      TCATTCACCA AACATTCAAA CACCACTATT ACAACGAAAA ACAATCAACA CATAATCAAC CCAACACACT

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   775        785        795        805        815        825        835
4743c05.      ATATCCCACA TTCACACACA CACACACACA AACACACTCC TTCATCAACA TGTAGACAGA AAATGGAACA
Sm02551       ATATCCCACA TTCACACACA CACACACACA AACACACTCC TTCATCAACA TGTAGACAGA AAATGGAACA
TC34704       ATATCCCACA TTCACACACA CACACACA-A A-CACACTCC TTCATCAACA TGTAGACAGA AAATGGAACA
Contig-0      ATATCCCACA TTCACACACA CACACACACA AACACACTCC TTCATCAACA TGTAGACAGA AAATGGAACA

              ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   845        855        865        875        885        895        905
4743c05.      CGACTACGCA AATCAACATC GTCGTCCAAC GAGAAATCTG TCCAACCATC AATGTCACTC TCATTACACC
Sm02551       CGACTACGCA AATCAACATC GTCGTCCAAC GAGAAATCTG TCCAACCATC AATGTCACTC TCATTACACC
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TC34704        CGACTACGCA AATCAACATC GTCGTCCAAC GAGAAATCTG TCCAACCATC AATGTCACTC TCATTACACC
Contig-0       CGACTACGCA AATCAACATC GTCGTCCAAC GAGAAATCTG TCCAACCATC AATGTCACTC TCATTACACC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   915        925        935        945        955        965        975
4743c05.       CACACATATG TTAACAAACA ACAAGTGGAC TGGTTGAGAG TACTTACATG CATTACACAC ACTAGAACAT
Sm02551        CACACATATG TTAACAAACA ACAAGTGGAC TGGTTGAGAG TACTTACATG CATTACACAC ACTAGAACAT
TC34704        CACACATATG TTAACAAACA ACAAGTGGAC TGGTTGAGAG TACTTACATG CATTACACAC ACTAGAACAT
Contig-0       CACACATATG TTAACAAACA ACAAGTGGAC TGGTTGAGAG TACTTACATG CATTACACAC ACTAGAACAT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   985        995       1005       1015       1025       1035       1045
4743c05.       CACAACACAC ACAACACACA CAACCTGAAC AACGGAAACA TAACAGGGAA CACCACTCCT --C-CCCATA
Sm02551        CACAACACAC ACAACACACA CAACCTGAAC AACGGAAACA TAACAGGGAA CACT-CTCAT TACACCCACA
TC34704        CACAACACAC ACAACACACA CAACCTGAAC AACGGAAACA TAACAGGGAA CACCACTCCT --C-CCCATA
Contig-0       CACAACACAC ACAACACACA CAACCTGAAC AACGGAAACA TAACAGGGAA CACCACTCCT --C-CCCATA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1055       1065       1075       1085       1095       1105       1115
4743c05.       A......... .......... .......... .......... .......... .......... ..........
Sm02551        -C-AT-ATGT TAACAAACAA -CAAGTGG-A CTGGTT--GA -GAGTA-C-- T-TACATGCA T--T-A---C
TC34704        ACCATCAT-T CACCAAACAT TCAAACACCA CTA-TTACAA CGAAAAACAA TCAACA--CA TAATCAACCC
Contig-0       ACCATCATGT CAACAAACAA TCAAACACCA CTAGTTACAA CGAAAAACAA TCAACATGCA TAATCAACCC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1125       1135       1145       1155       1165       1175       1185
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        A-CACACTAG A----ACAT- CACA-ACACA CACA-ACAC- ---ACA-A-- CCTGAA-CAA CG-G-AAACA
TC34704        AACACACTAT ATCCCACATT CACACACACA CACACACACA CACACACACT CCTTCATCAA CATGTAGACA
Contig-0       AACACACTAG ATCCCACATT CACACACACA CACACACACA CACACACACT CCTGAATCAA CATGTAAACA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1195       1205       1215       1225       1235       1245       1255
4743c05.      .......... .......... .......... .......... .......... .......... ..........
Sm02551        TAACAGGGAA CACCACT-C- C---TCCCC. .......... .......... .......... ..........
TC34704        GAAAATGGAA CACGACTACG CAAATCAACA TCGTCGTCCA ACGAGAAATC TGTCCAACCA TCAATGTCAC
Contig-0       GAAAAGGGAA CACCACTACG CAAATCAACA TCGTCGTCCA ACGAGAAATC TGTCCAACCA TCAATGTCAC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1265       1275       1285       1295       1305       1315       1325
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        TCTCATTACA CCCACACATA TGTTAACAAA CAACATGTGG ACTGGTTGAG AGTACTTACA TGCATTACAC
Contig-0       TCTCATTACA CCCACACATA TGTTAACAAA CAACATGTGG ACTGGTTGAG AGTACTTACA TGCATTACAC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1335       1345       1355       1365       1375       1385       1395
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        ACACTAGAAC ATCATCACAC CCAGTACAAC AACACCAACA ATTTGAAAAA CGAAACAGTC ACTCACACTC
Contig-0       ACACTAGAAC ATCATCACAC CCAGTACAAC AACACCAACA ATTTGAAAAA CGAAACAGTC ACTCACACTC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1405       1415       1425       1435       1445       1455       1465
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        GTCTTCTTAG TAGCCATTGG TTACGCCACC GCCTACACCA CATCACATGA CTATTCGGGT GGGTACGGTG
Contig-0       GTCTTCTTAG TAGCCATTGG TTACGCCACC GCCTACACCA CATCACATGA CTATTCGGGT GGGTACGGTG

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1475       1485       1495       1505       1515       1525       1535
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        GCGGTTGCTA TGGTAGCGAT TGTGATAGCG GTTATGGCCA TGGTGGAGGT TGCAGTGGTG GAGATTGTGG
Contig-0       GCGGTTGCTA TGGTAGCGAT TGTGATAGCG GTTATGGCCA TGGTGGAGGT TGCAGTGGTG GAGATTGTGG

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1545       1555       1565       1575       1585       1595       1605
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        TAATTACGGT GGTGGCTATG GTGGTGATTG CAATGGCGGA GATTGTGGTA ATTACCGCGG TGGCTATGGT
Contig-0       TAATTACGGT GGTGGCTATG GTGGTGATTG CAATGGCGGA GATTGTGGTA ATTACCGCGG TGGCTATGGT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1615       1625       1635       1645       1655       1665       1675
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4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        GGTGGGAATG GTGGACCCTG CTTTTTTGAC ACCCTCGCCC CGGCTTCGAT GAGGCCTTCC CTGCCCCCTA
Contig-0       GGTGGGAATG GTGGACCCTG CTTTTTTGAC ACCCTCGCCC CGGCTTCGAT GAGGCCTTCC CTGCCCCCTA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 1685       1695       1705       1715       1725       1735       1745
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        TGGCGGTGAT TATGGTAACG GTGGCAACGG CTTTGGAAAA GGTGGTAGTA AAGGCAACAA TTATGGAAAG
Contig-0       TGGCGGTGAT TATGGTAACG GTGGCAACGG CTTTGGAAAA GGTGGTAGTA AAGGCAACAA TTATGGAAAG

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 1755       1765       1775       1785       1795       1805       1815
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        GGTTATGGCG GTGGTAGCGG TAAGGGTAAG GGTGGTGGCA AAGGTGGCAA AGGCGGCAAA GGTGGCACTT
Contig-0       GGTTATGGCG GTGGTAGCGG TAAGGGTAAG GGTGGTGGCA AAGGTGGCAA AGGCGGCAAA GGTGGCACTT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 1825       1835       1845       1855       1865       1875       1885
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        ACAAACCCAG CCATTATGGA GGCGGTTACT GAGGCACCAG TTGAGTTGTG GATCATTCTA ATTTGTTTGT
Contig-0       ACAAACCCAG CCATTATGGA GGCGGTTACT GAGGCACCAG TTGAGTTGTG GATCATTCTA ATTTGTTTGT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                 1895       1905       1915       1925       1935       1945       1955
4743c05.       .......... .......... .......... .......... .......... .......... ..........
Sm02551        .......... .......... .......... .......... .......... .......... ..........
TC34704        GTCACACTCT CCACTGTCCT ATTTTTCTAC ACACCTCTCA ATTCAACTCA CTGTAATATA GTCGTGTTTG
Contig-0       GTCACACTCT CCACTGTCCT ATTTTTCTAC ACACCTCTCA ATTCAACTCA CTGTAATATA GTCGTGTTTG

               ....|....| ....|..
                 1965       1975
4743c05.       .......... .......
Sm02551        .......... .......
TC34704        AATTCGAGAT GAATAAA
Contig-0       AATTCGAGAT GAATAAA
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Alignment: NCBI/Genedb/Tiger

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               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5         15         25         35         45         55         65
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       ACTATTACAG TGAAGAACAA TCAACACATA ATCAACCCAA CACACAATAT CCCACATTCA CACACACACA
Contig-0       ACTATTACAG TGAAGAACAA TCAACACATA ATCAACCCAA CACACAATAT CCCACATTCA CACACACACA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   75         85         95        105        115        125        135
NCBI           .......... .....ACTTA CATGCATTAC AC--ACACTA GAACAT--CA CAAC-AC-AC ACAACA-CAC
GenedbTI       CACACAAACA CACTC-CTT- CAT-CA--AC ATGTAGAC-A GAAAATGGAA CA-CGACTAC GCAACATCAC
Contig-0       CACACAAACA CACTCACTTA CATGCATTAC ACGTACACTA GAAAATGGAA CAACGACTAC ACAACATCAC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  145        155        165        175        185        195        205
NCBI           ACAACCT-GA ACAACG-GAA A-CA-T--AA C-AGGGAA-- -CACTCTCAT TACACCCACA CATATGTTAG
GenedbTI       ACAACCTCGA ACAACGAGAA ATCAGTCCAA CCAGCGAATG TCACTCTCAT TACACCCACA CATATGTTAA
Contig-0       ACAACCTCGA ACAACGAGAA ATCAGTCCAA CCAGCGAATG TCACTCTCAT TACACCCACA CATATGTTAA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  215        225        235        245        255        265        275
NCBI           CAAACAACAA GTGGACTGGT TGAGAGTACT TACATGCATT ACACACACTA GAACATCACA ACACACACAA
GenedbTI       CAAACAACAA GTGGACTGGT TGAGAGTACT TACATGCATT ACACACACTA GAACATCACA ACACACACAA
Contig-0       CAAACAACAA GTGGACTGGT TGAGAGTACT TACATGCATT ACACACACTA GAACATCACA ACACACACAA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  285        295        305        315        325        335        345
NCBI           CACACACAAC CTGAACAACG GAAACATAAC AGGGAACACC ACTCCTCCCC ATAACCATCA TTCACCAAAC
GenedbTI       C-C------- -TGAACAACG GAAACATAAC AGGGAACACC ACTCCTCCCC ATAACCATCA TTCACCAAAC
Contig-0       CACACACAAC CTGAACAACG GAAACATAAC AGGGAACACC ACTCCTCCCC ATAACCATCA TTCACCAAAC
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               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  355        365        375        385        395        405        415
NCBI           ATTCAAACAC CACTATTACA ACGAAAAACA ATCAACACAT AATCAACCCA ACACACTATA TCCCACATTC
GenedbTI       ATTCAAACAC CACTATTACA ACGAAAAACA ATCAACACAT AATCAACCCA ACACACTATA TCCCACATTC
Contig-0       ATTCAAACAC CACTATTACA ACGAAAAACA ATCAACACAT AATCAACCCA ACACACTATA TCCCACATTC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  425        435        445        455        465        475        485
NCBI           ACACACACAC ACACACAAAC ACACTCCTTC ATCAACATGT AGACAGAAAA TGGAACACGA CTACGCAAAT
GenedbTI       ACACACACAC ACACACAAAC ACACTCCTTC ATCAACATGT AGACAGAAAA TGGAACACGA CTACGCAAAT
Contig-0       ACACACACAC ACACACAAAC ACACTCCTTC ATCAACATGT AGACAGAAAA TGGAACACGA CTACGCAAAT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  495        505        515        525        535        545        555
NCBI           CAACATCGTC GTCCAACGAG AAATCTGTCC AACCATCAAT GTCACTCTCA TTACACCCAC ACATATGTTA
GenedbTI       CAACATCGTC GTCCAACGAG AAATCTGTCC AACCATCAAT GTCACTCTCA TTACACCCAC ACATATGTTA
Contig-0       CAACATCGTC GTCCAACGAG AAATCTGTCC AACCATCAAT GTCACTCTCA TTACACCCAC ACATATGTTA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  565        575        585        595        605        615        625
NCBI           ACAAACAACA AGTGGACTGG TTGAGAGTAC TTACATGCAT TACACACACT AGAACATCAC AACAC-CACA
GenedbTI       ACAAACAACA AGTGGACTGG TTGAGAGTAC TTACATGCAT TACACACACT AGAACATCAC AACACACACA
Contig-0       ACAAACAACA AGTGGACTGG TTGAGAGTAC TTACATGCAT TACACACACT AGAACATCAC AACACACACA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  635        645        655        665        675        685        695
NCBI           -CA-ACACGA CGCA-ACA-C -TGAACAACG GAGACATAAC AGGGAACACC ACTCCTCCTC ATAACCCATC
GenedbTI       ACACACACAA CACACACAAC CTGAACAACG GAAACATAAC AGGGAACACC ACTCCTCCCC ATAACC-ATC
Contig-0       ACACACACAA CACACACAAC CTGAACAACG GAAACATAAC AGGGAACACC ACTCCTCCCC ATAACCCATC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  705        715        725        735        745        755        765
NCBI           ATTCACCAAC CATTCAAACA CCCCTTTTTA CACCGAACAA CTATCACCAC ATATTCAACC CA-CACA...
GenedbTI       ATTCACCAAA CATTCAAACA CCACTATT-A CAACGAAAAA CAATCAACAC ATAATCAACC CAACACACTA
Contig-0       ATTCACCAAA CATTCAAACA CCACTATTTA CAACGAAAAA CAATCAACAC ATAATCAACC CAACACACTA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  775        785        795        805        815        825        835
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       TATCCCACAT TCACACACAC ACACACACAA ACACACTCCT TCATCAACAT GTAGACAGAA AATGGAACAC
Contig-0       TATCCCACAT TCACACACAC ACACACACAA ACACACTCCT TCATCAACAT GTAGACAGAA AATGGAACAC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  845        855        865        875        885        895        905
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       GACTACGCAA ATCAACATCG TCGTCCAACG AGAAATCTGT CCAACCATCA ATGTCACTCT CATTACACCC
Contig-0       GACTACGCAA ATCAACATCG TCGTCCAACG AGAAATCTGT CCAACCATCA ATGTCACTCT CATTACACCC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  915        925        935        945        955        965        975
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       ACACATATGT TAACAAACAA CAAGTGGACT GGTTGAGAGT ACTTACATGC ATTACACACA CTAGAACATC
Contig-0       ACACATATGT TAACAAACAA CAAGTGGACT GGTTGAGAGT ACTTACATGC ATTACACACA CTAGAACATC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  985        995        1005       1015       1025       1035       1045
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       ACAACACACA CAACACACAC AACCTGAACA ACGGAAACAT AACAGGGAAC ACCACTCCTC CCCATAACCA
Contig-0       ACAACACACA CAACACACAC AACCTGAACA ACGGAAACAT AACAGGGAAC ACCACTCCTC CCCATAACCA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1055       1065       1075       1085       1095       1105       1115
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       TCATGTCAAC AAACAATCAA ACACCACTAG TTACAACGAA AAACAATCAA CATGCATAAT CAACCCAACA
Contig-0       TCATGTCAAC AAACAATCAA ACACCACTAG TTACAACGAA AAACAATCAA CATGCATAAT CAACCCAACA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1125       1135       1145       1155       1165       1175       1185
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       CACTAGATCC CACATTCACA CACACACACA CACACACACA CACACTCCTG AATCAACATG TAAACAGAAA
Contig-0       CACTAGATCC CACATTCACA CACACACACA CACACACACA CACACTCCTG AATCAACATG TAAACAGAAA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1195       1205       1215       1225       1235       1245       1255
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NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       AGGGAACACC ACTACGCAAA TCAACATCGT CGTCCAACGA GAAATCTGTC CAACCATCAA TGTCACTCTC
Contig-0       AGGGAACACC ACTACGCAAA TCAACATCGT CGTCCAACGA GAAATCTGTC CAACCATCAA TGTCACTCTC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1265       1275       1285       1295       1305       1315       1325
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       ATTACACCCA CACATATGTT AACAAACAAC ATGTGGACTG GTTGAGAGTA CTTACATGCA TTACACACAC
Contig-0       ATTACACCCA CACATATGTT AACAAACAAC ATGTGGACTG GTTGAGAGTA CTTACATGCA TTACACACAC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1335       1345       1355       1365       1375       1385       1395
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       TAGAACATCA TCACACCCAG TACAACAACA CCAACAATTT GAAAAACGAA ACAGTCACTC ACACTCGTCT
Contig-0       TAGAACATCA TCACACCCAG TACAACAACA CCAACAATTT GAAAAACGAA ACAGTCACTC ACACTCGTCT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1405       1415       1425       1435       1445       1455       1465
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       TCTTAGTAGC CATTGGTTAC GCCACCGCCT ACACCACATC ACATGACTAT TCGGGTGGGT ACGGTGGCGG
Contig-0       TCTTAGTAGC CATTGGTTAC GCCACCGCCT ACACCACATC ACATGACTAT TCGGGTGGGT ACGGTGGCGG

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1475       1485       1495       1505       1515       1525       1535
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       TTGCTATGGT AGCGATTGTG ATAGCGGTTA TGGCCATGGT GGAGGTTGCA GTGGTGGAGA TTGTGGTAAT
Contig-0       TTGCTATGGT AGCGATTGTG ATAGCGGTTA TGGCCATGGT GGAGGTTGCA GTGGTGGAGA TTGTGGTAAT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1545       1555       1565       1575       1585       1595       1605
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       TACGGTGGTG GCTATGGTGG TGATTGCAAT GGCGGAGATT GTGGTAATTA CCGCGGTGGC TATGGTGGTG
Contig-0       TACGGTGGTG GCTATGGTGG TGATTGCAAT GGCGGAGATT GTGGTAATTA CCGCGGTGGC TATGGTGGTG

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1615       1625       1635       1645       1655       1665       1675
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       GGAATGGTGG ACCCTGCTTT TTTGACACCC TCGCCCCGGC TTCGATGAGG CCTTCCCTGC CCCCTATGGC
Contig-0       GGAATGGTGG ACCCTGCTTT TTTGACACCC TCGCCCCGGC TTCGATGAGG CCTTCCCTGC CCCCTATGGC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1685       1695       1705       1715       1725       1735       1745
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       GGTGATTATG GTAACGGTGG CAACGGCTTT GGAAAAGGTG GTAGTAAAGG CAACAATTAT GGAAAGGGTT
Contig-0       GGTGATTATG GTAACGGTGG CAACGGCTTT GGAAAAGGTG GTAGTAAAGG CAACAATTAT GGAAAGGGTT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1755       1765       1775       1785       1795       1805       1815
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       ATGGCGGTGG TAGCGGTAAG GGTAAGGGTG GTGGCAAAGG TGGCAAAGGC GGCAAAGGTG GCACTTACAA
Contig-0       ATGGCGGTGG TAGCGGTAAG GGTAAGGGTG GTGGCAAAGG TGGCAAAGGC GGCAAAGGTG GCACTTACAA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1825       1835       1845       1855       1865       1875       1885
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       ACCCAGCCAT TATGGAGGCG GTTACTGAGG CACCAGTTGA GTTGTGGATC ATTCTAATTT GTTTGTGTCA
Contig-0       ACCCAGCCAT TATGGAGGCG GTTACTGAGG CACCAGTTGA GTTGTGGATC ATTCTAATTT GTTTGTGTCA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                  1895       1905       1915       1925       1935       1945       1955
NCBI           .......... .......... .......... .......... .......... .......... ..........
GenedbTI       CACTCTCCAC TGTCCTATTT TTCTACACAC CTCTCAATTC AACTCACTGT AATATAGTCG TGTTTGAATT
Contig-0       CACTCTCCAC TGTCCTATTT TTCTACACAC CTCTCAATTC AACTCACTGT AATATAGTCG TGTTTGAATT

               ....|....| ...
                  1965
NCBI        .......... ...
GenedbTI    CGAGATGAAT AAA
Contig-0       CGAGATGAAT AAA
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>Smp_scaff000011
TTCCAGTATTTAAAATTCATCAGGGGAAATAATATATGTGGTCTTTTAATGCTACAGTTTGTATTGTATACTTAGGCTGACAATT
TTCAACTTGTTAGAATTTTTGCTTAAATTAGGAATAATTTGTTCTTGTTCTTGTGGTTGTGTGGTTTCATTCAGTTTCATATATA
TCTATTCTTTATTGGACTGAGCTTCAACCTTGCTAGTCGAATCCCAGTTATTTGGTAATTTAATCTGGGTCGCATTTGTTTCTTG
GTGTTTGTTAGTTGAAATTGGAAGCCACAAGTATTTGATTTATGTAATTCAGTATTATTTTGCAGTTTGGCATTGGTGCGAAATC
AGTGCATTCTTCAACAAAACCCACCTGTCGTTTCACCTGTTTCCTCAAGTCAGCACAATCCTTTGATTTCATCTCCGAGCGTTCG
TGGATTAATGTTACCAAATATCCAACCCAATGATTTATCTCTTTCCTCATACCTTTCACGTTTTCCTGTTCAACCAACAAATGCC
GAGTCTAAGCAGTCTGTTAGTCTGTCATCAACTATTATACCGTGTTCAAAACAACCATCAGGATTCGTCGCTTCACTCGAGGAAG
TGTCCACAGTTAAAGAAAGCGACCCAAACCGTGGTGGTTGGATGACAGATTATGAAGCAATTGGTGTGTTATTGATTCAGTTGCG
TCCTTTAATGGTATCTAATCCCTATGTCCAGGTCAGTTTCTTATTTTCTGAATGAGTTTCTAATTTACTACACTTTTAGTTGATT
ATGTGATTCTTAAGTAGCAGAGTTGCTTGAACATTAATGCCTCTGATCACTGAATGATTTTGTCGGCTGGATCGTTTATGTCTTT
TCATTCACTGTAAGTGAAACATAGGAGCTGTAGTTCTTAGCACTTGATGAAAATTAATCAAGGTTAATAGTTCCGTGATAAGTCA
CTTATTTACAGCAGTATGAAGCACCACATTATTAGGGCTATGCGGTAATAAAAATGTAGGTCAAACCTCTCCATATATCTGTTTA
GTGGATATAATTTGGGCGAAATTGCCTGTTTTGAAACGTCTTTTAATACAGTTTGAAAGTTGATACACCATATATTTATCATCAA
AATGATGGAATTCGACATCAAAATACTCGTTCTTTGAATTTCAGGTTCAATGAAATCCCACTTGTTTCGGATGATTTCCTTCAAG
AATAATTTGCTATAACTTCTGAGGATTTTGGCACAGTTGATAGTTTTTTCAACGGTTAATTGTAATAAATAGTTGTCTATTTATC
TCAAATTATGTATTCAAATTTCACATAACAAATAATCAAATTCTAACAAACAATTATTAGTTAGCCTATAATTTATTATGGGCAA
ATATGTATGGTTGTACAGCTTTGAAAATGAATTATTTGCTGAGTTAATCATTTTATTATTCAAGAAGTGTTTTTTAGAATTAATT
TCCGAGCTAATATAGATTGAATTTCATGTATGTGTCCTTAAGACCATGAATTTCCATGGCTTGTTTATTCATACTCAGATCAATG
TCTCTTTTGATTTTGAACTTTCTATGTAAAAGTGACCAGGAACTTCCGAGGCTTATTCATTTCTATCTTGAATAACCGAAATGCA
TCGGTGTCCATAACTGAGTAATACCCAGAATGTTGATTCTGTTACCAGTTGTTCCGTCATTTGACTTAAAATGCATTACTGCTTG
ATATACTGTAATTCAGTTAATTTCTGTGTCATGAGTGGAAAATGTAGTGGTTGTTTTATTCAGACAAATTTTTAGTTGTTAGTTT
AACGGTATAGTAGTTTCTCCATTTCGAGACATAATCTCACTGTTATAGTTGTTTTTAATCTCCCAGCTATACAACAAAATAAAAA
TAAATAACATCCGAAAATTGGCTAATTTCTAAGTTTGAATTTTGTTTAGGTATACGTTTATTGCTGTCAATGTACCTGAGCGTCT
TTCTTTTTGTCGTGAACAAGTCTAATAATGATATCGTACACTGACTAGTTATTCAAGGACTACTAACCATTATTTCTCTTGCCAG
GATTATTATTTTGCATCTCAATGGCTGCGACGAATGAATGCTATTCAAGCTAAGCATATTTCAAAACATAAAATGAACACTACAA
CTTCACCAGCAATAGTGCAGCTTCCTATTCCTATACCATTGGAAAGCTTGAGCGATTCCAATTCATCATATCAAGTAACTCTAAA
ACATAAACTTGTTATTCCGTTTCGTGCTGTGAATCGCAATCCTGGCTCTGACCAAAATGTGGATGAAAGCTGTGGCAGCTTAGAA
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GAGTGTGCGAAATGTTCAAGTCTTATCAGAACATGAATGAAGGATATTGTGTGTTGGGTTGATTATATGTTGATTGTTTTTCGTT
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TGTGTTGTGTGTGTTGTGTGTGTTGTGATGTTCTAGTGTGTGTAATGCATGTAAGTACTCTCGACCAGTCCACTTGTTGTTTGTT
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TCCATTTTCTGTCTACATGTTGATGAAGGAGTGTGTTTGTGTGTGTGTGTGTGTGTGCATGTGGGATATAGTGTGTTGGGTTGAT
TATGTGTTGATTGTTTTTCGTTGTAATAGTGGTGTTTGAATGTTTGGTGAATGATGGTTATGGGGAGGAGTGGTGTTCCCTGTTA
TGTTTCCGTTGTTCAGGTTGTGTGTGTTGTGTGTGTTGTGATGTTCTAGTGTGTGTAATGCATGTAAGTACTCTCAACCAGTCCA
CTTGTTGTTTGTTAACATATGTGTGGGTGTAATGAGAGTGACATTGATGGTTGGACAGATTTCTCGTTGGACGACGATGTTGATT
TGCGTAGTCGTGTTCCATTTTCTGTCTACATGTTGATGAAGGAGTGTGTTTGTGTGTGTGTGTGTGTGTGAATGTGGGATATTGT
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GTGTTCCCTGTTATGTTTCCGTTGTTCAGGTTGTGTGTGTTGTGTGTGTTGTGTGTGTTGTGATGTTCTAGTGTGTGTAATGCAT
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>Smp_scaff000068
TGTTGATTGTTTTTCGTTGTATAGTGGTGTTTGAATGTTTGGTGAATGATGGTTATGGGGAGGAGTGGTGTTCCCTGTTATGTTT
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TCCACTTGTTGTTTGTTAACATATGTGTGGGTGTAATGAGAGTGACATTGATGGTTGGACAGATTTCTCGTTGGACGACGATGTT
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AGTGGTGTTCCCTGTTATGTTTCCGTTGTTCAGGTTGTGTGTGTTGTGTGTGTTGTGTGTGTTGTGATGTTCTAGTGTGTGTAAT
GCATGTAAGTACTCTCAACCAGTCCACTTGTTGTTTGTTAACATATGTGTGGGTGTAATGAGAGTGACATTGATGGTTGGACAGA
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TCTTTTTTGTATTTTTGTTTGGTCTCTAATATTGTTATTAATTTATTTTCTTTTTTCGTGTTTTATTTGTTCTCTCTTTTAGGTT
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TTGTTTCTATTTTTTTGACAGATAATTCCCTTTTAAACATTCGAAATTAAAAATACGAAGTTGAGCGAAGAGATCTCATTTCAAC
GAATTTTTTATCAAGCTGTACAATCGTACTAATATGGAAAATTGTTTTTTTGTTAAAGTACTAATGGGAACACAAATAACCGAGA
TGATGGAAAATAATCTTTCTATTGAATCATCTTGGTTATTCGTGTGCACTTTAAGGGCTGAATTTATAACAGAAGTTTGCTGAAA
CGGCCTCAAATCATTTAGTTTTTCCCTTGTTAATAAATGGCAGTTCTGATAATTAACATAACCCATTGTGTTATTGGATAAGAAT
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AAAGAGAAGTCAGCGAAGAAAATTTTCTTTTCCACTAAATCGTTTACTTAAGCTGTACATTCTTGTTTATAATCATACGGAAAAT
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GGTAAGGAAGGAATATAACGATGAAAATAATAATTCACGGGTCAGATAATTGTCCAATTGACAGGTATGAAGAAAAATGACAAAC
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TCCCAAAGAGAATCTGTCGACGTCGAAGTAGTTCCTCATCTATTGTGTCAGTAGGACATACTCGCCTGATCCTTGAGGATAAAGA
GTGAATCAAGTTCCTCTTTCTACTCAGTGGTACCCGGCTATGGAAATTCGTTTACTGCCCATTCCAGGTCGCTTTTCTATACATC
AAAAAAAAGAAATTAATTGTTTGCCTCTGCTTCCAAAGTGAATTGAATAGAGGGGTGATAATTACTGAAACTTCAAAATTTCATT
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ATTGATAGTAAACTCATCTTTCATCTTCTTTAGGATTTTAATAAGCATCTGTTCCGTTTTTTTCAGTTGTCTTTTTGAACGGTTT
CTTTGGAGAATTTGACAGGATCATATAATATCGAACACAATTTGGTGACATAGTCAAGACGATCCACAAAGACGATTCTCAGACC
CTTGTCTAGGAGACACAACACTAAATCCTGATTTTTCGGAAGATCAGATAATTGAGATCTATGCTCTTTTGTGAGTAATCGACTA
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CTCAGAACACTATCCGACATGGCTTTTAAAAGGAGAATGTAAAACAATTACTAGTTCTATACAGGAGCATTTAATTAACTGTGAA
CACATCACTGCAAAAGAGTTTTCTCATAAAGTAATCTACACAGTCAAATGAATTGGATCGAAGGGAAATTGAATCAATATTTTAT
GCATTGCCGGAGCATTGGCAATCCACGAACTCAGACCCGAACTTTGTGTACAGAAACGACTGGTCCAACCCCTCTCATCCTTCCT
TGCCCCTGATTCTCTTTAGTGGTAGTTCTGATTTTCAAGGTAGCCCACTCTAATAACTTTCCAATTCATATTTGCTTACTGATCC
TTGTTGTTATTTGATTGATTGTTCTCGTTAGGTATTTTTTATCAAATGTCTCAAGTCCATTTTCTTGATTATTAACAGAATTGTC
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ATCCAAAACGTGAAAACATTTAAATAAAACACTCGAAAAATAAATCAAACCTAGTGACCAAATATGCAATGAAGACCATTCATAT
CACGATTCTGTTCCAGAAAGTAATAAAATCCAGGGTTTTATCACTGCGAAATGATCAGTATTGAACCCTTTAAAATCTTTAAAAT
TATTAGAGTGTTTGAGGTCAGTGTTTCAATACGTATATTTATTCATGGAAATGTCATCTACATGATGGTTGAGAGTGTATCATAT
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TTGATATTTACCCACCTCAAAAAACATTCCACTATTATTCGCTACTATTAAATTAGATAATCTGCATCTGCTTTTAGAAAAAGCT
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TAAAAAGTATTTGTGTATATATTCCTTGATTTGATTTCTTCTTCCCATAGACGTTCTCGACTGTTAGATTATCAACAAGAATTGA
TTAATCAACTAATCA
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Alignment: SmBr18/EST Contig/scaff000011/scaff000068 showing contig sequence

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                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     5          15         25         35         45         55         65
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      TTCCAGTATT TAAAATTCAT CAGGGGAAAT AATATATGTG GTCTTTTAAT GCTACAGTTT GTATTGTATA
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         TTCCAGTATT TAAAATTCAT CAGGGGAAAT AATATATGTG GTCTTTTAAT GCTACAGTTT GTATTGTATA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                     75         85         95        105        115        125        135
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      CTTAGGCTGA CAATTTTCAA CTTGTTAGAA TTTTTGCTTA AATTAGGAAT AATTTGTTCT TGTTCTTGTG
EST Contig       .......... .......... .......... .......... .......... .......... ..........
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scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       CTTAGGCTGA CAATTTTCAA CTTGTTAGAA TTTTTGCTTA AATTAGGAAT AATTTGTTCT TGTTCTTGTG

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   145        155        165        175        185        195        205
SmBr18         .......... .......... .......... .......... .......... .......... ..........
scaff000011    GTTGTGTGGT TTCATTCAGT TTCATATATA TCTATTCTTT ATTGGACTGA GCTTCAACCT TGCTAGTCGA
EST Contig     .......... .......... .......... .......... .......... .......... ..........
scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       GTTGTGTGGT TTCATTCAGT TTCATATATA TCTATTCTTT ATTGGACTGA GCTTCAACCT TGCTAGTCGA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   215        225        235        245        255        265        275
SmBr18         .......... .......... .......... .......... .......... .......... ..........
scaff000011    ATCCCAGTTA TTTGGTAATT TAATCTGGGT CGCATTTGTT TCTTGGTGTT TGTTAGTTGA AATTGGAAGC
EST Contig     .......... .......... .......... .......... .......... .......... ..........
scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       ATCCCAGTTA TTTGGTAATT TAATCTGGGT CGCATTTGTT TCTTGGTGTT TGTTAGTTGA AATTGGAAGC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   285        295        305        315        325        335        345
SmBr18         .......... .......... .......... .......... .......... .......... ..........
scaff000011    CACAAGTATT TGATTTATGT AATTCAGTAT TATTTTGCAG TTTGGCATTG GTGCGAAATC AGTGCATTCT
EST Contig     .......... .......... .......... .......... .......... .......... ..........
scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       CACAAGTATT TGATTTATGT AATTCAGTAT TATTTTGCAG TTTGGCATTG GTGCGAAATC AGTGCATTCT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   355        365        375        385        395        405        415
SmBr18         .......... .......... .......... .......... .......... .......... ..........
scaff000011    TCAACAAAAC CCACCTGTCG TTTCACCTGT TTCCTCAAGT CAGCACAATC CTTTGATTTC ATCTCCGAGC
EST Contig     .......... .......... .......... .......... .......... .......... ..........
scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       TCAACAAAAC CCACCTGTCG TTTCACCTGT TTCCTCAAGT CAGCACAATC CTTTGATTTC ATCTCCGAGC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   425        435        445        455        465        475        485
SmBr18         .......... .......... .......... .......... .......... .......... ..........
scaff000011    GTTCGTGGAT TAATGTTACC AAATATCCAA CCCAATGATT TATCTCTTTC CTCATACCTT TCACGTTTTC
EST Contig     .......... .......... .......... .......... .......... .......... ..........
scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       GTTCGTGGAT TAATGTTACC AAATATCCAA CCCAATGATT TATCTCTTTC CTCATACCTT TCACGTTTTC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   495        505        515        525        535        545        555
SmBr18         .......... .......... .......... .......... .......... .......... ..........
scaff000011    CTGTTCAACC AACAAATGCC GAGTCTAAGC AGTCTGTTAG TCTGTCATCA ACTATTATAC CGTGTTCAAA
EST Contig     .......... .......... .......... .......... .......... .......... ..........
scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       CTGTTCAACC AACAAATGCC GAGTCTAAGC AGTCTGTTAG TCTGTCATCA ACTATTATAC CGTGTTCAAA

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   565        575        585        595        605        615        625
SmBr18         .......... .......... .......... .......... .......... .......... ..........
scaff000011    ACAACCATCA GGATTCGTCG CTTCACTCGA GGAAGTGTCC ACAGTTAAAG AAAGCGACCC AAACCGTGGT
EST Contig     .......... .......... .......... .......... .......... .......... ..........
scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       ACAACCATCA GGATTCGTCG CTTCACTCGA GGAAGTGTCC ACAGTTAAAG AAAGCGACCC AAACCGTGGT

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   635        645        655        665        675        685        695
SmBr18         .......... .......... .......... .......... .......... .......... ..........
scaff000011    GGTTGGATGA CAGATTATGA AGCAATTGGT GTGTTATTGA TTCAGTTGCG TCCTTTAATG GTATCTAATC
EST Contig     .......... .......... .......... .......... .......... .......... ..........
scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       GGTTGGATGA CAGATTATGA AGCAATTGGT GTGTTATTGA TTCAGTTGCG TCCTTTAATG GTATCTAATC

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   705        715        725        735        745        755        765
SmBr18         .......... .......... .......... .......... .......... .......... ..........
scaff000011    CCTATGTCCA GGTCAGTTTC TTATTTTCTG AATGAGTTTC TAATTTACTA CACTTTTAGT TGATTATGTG
EST Contig     .......... .......... .......... .......... .......... .......... ..........
scaff000068    .......... .......... .......... .......... .......... .......... ..........
Contig-0       CCTATGTCCA GGTCAGTTTC TTATTTTCTG AATGAGTTTC TAATTTACTA CACTTTTAGT TGATTATGTG

               ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
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                   775        785        795        805        815        825        835
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     ATTCTTAAGT AGCAGAGTTG CTTGAACATT AATGCCTCTG ATCACTGAAT GATTTTGTCG GCTGGATCGT
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        ATTCTTAAGT AGCAGAGTTG CTTGAACATT AATGCCTCTG ATCACTGAAT GATTTTGTCG GCTGGATCGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   845        855        865        875        885        895        905
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     TTATGTCTTT TCATTCACTG TAAGTGAAAC ATAGGAGCTG TAGTTCTTAG CACTTGATGA AAATTAATCA
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        TTATGTCTTT TCATTCACTG TAAGTGAAAC ATAGGAGCTG TAGTTCTTAG CACTTGATGA AAATTAATCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   915        925        935        945        955        965        975
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     AGGTTAATAG TTCCGTGATA AGTCACTTAT TTACAGCAGT ATGAAGCACC ACATTATTAG GGCTATGCGG
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        AGGTTAATAG TTCCGTGATA AGTCACTTAT TTACAGCAGT ATGAAGCACC ACATTATTAG GGCTATGCGG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   985        995        1005       1015       1025       1035       1045
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     TAATAAAAAT GTAGGTCAAA CCTCTCCATA TATCTGTTTA GTGGATATAA TTTGGGCGAA ATTGCCTGTT
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        TAATAAAAAT GTAGGTCAAA CCTCTCCATA TATCTGTTTA GTGGATATAA TTTGGGCGAA ATTGCCTGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   1055       1065       1075       1085       1095       1105       1115
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     TTGAAACGTC TTTTAATACA GTTTGAAAGT TGATACACCA TATATTTATC ATCAAAATGA TGGAATTCGA
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        TTGAAACGTC TTTTAATACA GTTTGAAAGT TGATACACCA TATATTTATC ATCAAAATGA TGGAATTCGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   1125       1135       1145       1155       1165       1175       1185
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     CATCAAAATA CTCGTTCTTT GAATTTCAGG TTCAATGAAA TCCCACTTGT TTCGGATGAT TTCCTTCAAG
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        CATCAAAATA CTCGTTCTTT GAATTTCAGG TTCAATGAAA TCCCACTTGT TTCGGATGAT TTCCTTCAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   1195       1205       1215       1225       1235       1245       1255
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     AATAATTTGC TATAACTTCT GAGGATTTTG GCACAGTTGA TAGTTTTTTC AACGGTTAAT TGTAATAAAT
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        AATAATTTGC TATAACTTCT GAGGATTTTG GCACAGTTGA TAGTTTTTTC AACGGTTAAT TGTAATAAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   1265       1275       1285       1295       1305       1315       1325
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     AGTTGTCTAT TTATCTCAAA TTATGTATTC AAATTTCACA TAACAAATAA TCAAATTCTA ACAAACAATT
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        AGTTGTCTAT TTATCTCAAA TTATGTATTC AAATTTCACA TAACAAATAA TCAAATTCTA ACAAACAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   1335       1345       1355       1365       1375       1385       1395
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     ATTAGTTAGC CTATAATTTA TTATGGGCAA ATATGTATGG TTGTACAGCT TTGAAAATGA ATTATTTGCT
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        ATTAGTTAGC CTATAATTTA TTATGGGCAA ATATGTATGG TTGTACAGCT TTGAAAATGA ATTATTTGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   1405       1415       1425       1435       1445       1455       1465
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     GAGTTAATCA TTTTATTATT CAAGAAGTGT TTTTTAGAAT TAATTTCCGA GCTAATATAG ATTGAATTTC
EST Contig      .......... .......... .......... .......... .......... .......... ..........
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scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         GAGTTAATCA TTTTATTATT CAAGAAGTGT TTTTTAGAAT TAATTTCCGA GCTAATATAG ATTGAATTTC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1475       1485       1495       1505       1515       1525       1535
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      ATGTATGTGT CCTTAAGACC ATGAATTTCC ATGGCTTGTT TATTCATACT CAGATCAATG TCTCTTTTGA
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         ATGTATGTGT CCTTAAGACC ATGAATTTCC ATGGCTTGTT TATTCATACT CAGATCAATG TCTCTTTTGA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1545       1555       1565       1575       1585       1595       1605
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      TTTTGAACTT TCTATGTAAA AGTGACCAGG AACTTCCGAG GCTTATTCAT TTCTATCTTG AATAACCGAA
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         TTTTGAACTT TCTATGTAAA AGTGACCAGG AACTTCCGAG GCTTATTCAT TTCTATCTTG AATAACCGAA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1615       1625       1635       1645       1655       1665       1675
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      ATGCATCGGT GTCCATAACT GAGTAATACC CAGAATGTTG ATTCTGTTAC CAGTTGTTCC GTCATTTGAC
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         ATGCATCGGT GTCCATAACT GAGTAATACC CAGAATGTTG ATTCTGTTAC CAGTTGTTCC GTCATTTGAC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1685       1695       1705       1715       1725       1735       1745
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      TTAAAATGCA TTACTGCTTG ATATACTGTA ATTCAGTTAA TTTCTGTGTC ATGAGTGGAA AATGTAGTGG
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         TTAAAATGCA TTACTGCTTG ATATACTGTA ATTCAGTTAA TTTCTGTGTC ATGAGTGGAA AATGTAGTGG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1755       1765       1775       1785       1795       1805       1815
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      TTGTTTTATT CAGACAAATT TTTAGTTGTT AGTTTAACGG TATAGTAGTT TCTCCATTTC GAGACATAAT
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         TTGTTTTATT CAGACAAATT TTTAGTTGTT AGTTTAACGG TATAGTAGTT TCTCCATTTC GAGACATAAT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1825       1835       1845       1855       1865       1875       1885
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      CTCACTGTTA TAGTTGTTTT TAATCTCCCA GCTATACAAC AAAATAAAAA TAAATAACAT CCGAAAATTG
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         CTCACTGTTA TAGTTGTTTT TAATCTCCCA GCTATACAAC AAAATAAAAA TAAATAACAT CCGAAAATTG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1895       1905       1915       1925       1935       1945       1955
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      GCTAATTTCT AAGTTTGAAT TTTGTTTAGG TATACGTTTA TTGCTGTCAA TGTACCTGAG CGTCTTTCTT
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         GCTAATTTCT AAGTTTGAAT TTTGTTTAGG TATACGTTTA TTGCTGTCAA TGTACCTGAG CGTCTTTCTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    1965       1975       1985       1995       2005       2015       2025
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      TTTGTCGTGA ACAAGTCTAA TAATGATATC GTACACTGAC TAGTTATTCA AGGACTACTA ACCATTATTT
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         TTTGTCGTGA ACAAGTCTAA TAATGATATC GTACACTGAC TAGTTATTCA AGGACTACTA ACCATTATTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    2035       2045       2055       2065       2075       2085       2095
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      CTCTTGCCAG GATTATTATT TTGCATCTCA ATGGCTGCGA CGAATGAATG CTATTCAAGC TAAGCATATT
EST Contig       .......... .......... .......... .......... .......... .......... ..........
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         CTCTTGCCAG GATTATTATT TTGCATCTCA ATGGCTGCGA CGAATGAATG CTATTCAAGC TAAGCATATT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
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                   2105       2115       2125       2135       2145       2155       2165
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     TCAAAACATA AAATGAACAC TACAACTTCA CCAGCAATAG TGCAGCTTCC TATTCCTATA CCATTGGAAA
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        TCAAAACATA AAATGAACAC TACAACTTCA CCAGCAATAG TGCAGCTTCC TATTCCTATA CCATTGGAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   2175       2185       2195       2205       2215       2225       2235
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     GCTTGAGCGA TTCCAATTCA T-CATATCAA GTAACTCTAA AACATAAACT TGTTATTCC- GTTTCGTGCT
EST Contig      .......... ......TTTA TTCATCTC-- G-AA-T-TCA AACACGA-CT --ATATTACA GT---GAG-T
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        GCTTGAGCGA TTCCAATTCA TTCATATCAA GTAACTCTAA AACACAAACT TGATATTACA GTTTCGAGCT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   2245       2255       2265       2275       2285       2295       2305
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     GTGAATCGCA -ATCCTGGCT CTG-ACCAAA ATGTGGA--- TGAA-AGCTG TGGCAG---C ---TTAGAAA
EST Contig      -TGAATTG-A GA----GG-T GTGTAGAAAA ATA-GGACAG TGGAGAG-TG TGACACAAAC AAATTAGAAT
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        GTGAATCGCA GATCCTGGCT CTGTACAAAA ATATGGACAG TGAAGAGCTG TGACACAAAC AAATTAGAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   2315       2325       2335       2345       2355       2365       2375
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     -A---A-AA- --AAGTGTAT GT-TCAGAAA C----TCC-T ACAT--CTGA ATCAAGTAA- TGC-AC-TGG
EST Contig      GATCCACAAC TCAACTGG-T GCCTCAGTAA CCGCCTCCAT A-ATGGCTGG GTTT-GTAAG TGCCACCTTT
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        GATCCACAAC TCAACTGGAT GCCTCAGAAA CCGCCTCCAT ACATGGCTGA ATCAAGTAAG TGCCACCTGG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   2385       2395       2405       2415       2425       2435       2445
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     GTCGTCCTAC TAG--ATCTA ATGTTCATCG ACCC---CG- TGTA--G-TA GCA--G--AG TTATCTCTGG
EST Contig      GCCG-CCTT- T-GCCACCTT -TGC-CACC- ACCCTTACCC T-TACCGCTA CCACCGCCA- TAACC-CT--
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        GCCGTCCTAC TAGCCACCTA ATGCTCACCG ACCCTTACCC TGTACCGCTA CCACCGCCAG TAACCTCTGG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   2455       2465       2475       2485       2495       2505       2515
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     CGTCCGCGAT T-TCAT-CTA CTTCAGAAA- ACTCTTATCC AATGA--TA- CACATCGATA ACCAT--TCA
EST Contig      T-TCCATAAT TGT--TGC-- CTTTACTACC AC-CTTTTCC AAAGCCGTTG C-CACCGTTA -CCATAATCA
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        CGTCCACAAT TGTCATGCTA CTTCACAAAC ACTCTTATCC AAAGACGTAG CACACCGATA ACCATAATCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   2525       2535       2545       2555       2565       2575       2585
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     CTGA-ATAGA AA--AGT-AA GTCA-CA-C- AAT------- -A---TAATA CAAAATA--A ---TC-A--A
EST Contig      CCGCCATAGG GGGCAGGGAA GGCCTCATCG AAGCCGGGGC GAGGGTG-T- CAAAAAAGCA GGGTCCACCA
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        CCGACATAGA AAGCAGGGAA GGCATCATCG AAGCCGGGGC GAGGGTAATA CAAAAAAGCA GGGTCCACCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   2595       2605       2615       2625       2635       2645       2655
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     TACA-AT-A- -ATAAACAC- G-GAAAATG- CGCATCAATT TCTC-CCGGA GTG---TGCG A--A--AT-G
EST Contig      TTCCCACCAC CATAGCCACC GCGGTAATTA C-CA-CAATC TC-CGCC--A TTGCAAT-C- ACCACCATAG
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        TACACACCAC CATAAACACC GCGAAAATGA CGCATCAATC TCTCGCCGGA GTGCAATGCG ACCACCATAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   2665       2675       2685       2695       2705       2715       2725
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     TTCA--A--G TC-TTATCAG AA-C---A-- --TG-AA--T G-A--A-GG- -ATATT-G-T GTGT---TGG
EST Contig      C-CACCACCG TAATTACCAC AATCTCCACC ACTGCAACCT CCACCATGGC CATAACCGCT ATCACAATCG
scaff000068     .......... .......... .......... .......... .......... .......... ..........
Contig-0        CTCACCACCG TAATTACCAC AATCTCCACC ACTGCAACCT CCACCATGGC CATAACCGCT ATCACAATCG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   2735       2745       2755       2765       2775       2785       2795
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     GTTGATTATA TGTT---G-- ATTGTTTTT- CGTTGTAATA GTGGTGTTTG AATGT--T-T -GG---TG--
EST Contig      CT--ACCATA -GCAACCGCC ACCGTACCCA CCC-G-AATA GTCATG--TG A-TGTGGTGT AGGCGGTGGC
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scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         CTTGACCATA TGCAACCGCC ACCGTACCCA CCCTGTAATA GTCATGTTTG AATGTGGTGT AGGCGGTGGC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    2805       2815       2825       2835       2845       2855       2865
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      --AATGA-TG GTTA-TGGGG AG--GAGTGG TGTTCCCTGT TA-TGTTTCC GTTGTTCAGG TTGT-GTGTG
EST Contig       GTAACCAATG GCTACTAAGA AGACGAGTG- TGAG---TG- -ACTGTTTC- GTTTTTCAAA TTGTTG-GTG
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         GTAACCAATG GCTACTAAGA AGACGAGTGG TGAGCCCTGT TACTGTTTCC GTTGTTCAAA TTGTTGTGTG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    2875       2885       2895       2905       2915       2925       2935
SmBr18           .......... .......... .......... .........T AGATGCATGG TAAGTACATC TACAACCAAG
scaff000011      TTGTGTGTGT TGTGTGTGTT G-TGATGTTC TAGTGTGTGT A-ATGCATG- TAAGTAC-TC T-CGACCA-G
EST Contig       TTGT-TGTAC TG-G-GTGT- GATGATGTTC TAGTGTGTGT A-ATGCATG- TAAGTAC-TC T-CAACCA-G
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         TTGTGTGTAC TGTGTGTGTT GATGATGTTC TAGTGTGTGT A-ATGCATG- TAAGTAC-TC T-CAACCA-G

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    2945       2955       2965       2975       2985       2995       3005
SmBr18           TCCACTTGTT GTTTGTTAAC ATATGTGTGG GTGGTAATGA GAGTTGACAT TGATGGTTGG ACAGATTTCT
scaff000011      TCCACTTGTT GTTTGTTAAC ATATGTGTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT
EST Contig       TCCACATGTT GTTTGTTAAC ATATGTGTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         TCCACTTGTT GTTTGTTAAC ATATGTGTGG GTG-TAATGA GAGT-GACAT TGATGGTTGG ACAGATTTCT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    3015       3025       3035       3045       3055       3065       3075
SmBr18           CGTTGGACGA CGATGTTGAT T-GCGTAGTC GTGTTCCATT TTCTGTCTAC ATGTTGATGA AGGAGTGTGT
scaff000011      CGTTGGACGA CGATGTTGAT TTGCGTAGTC GTGTTCCATT TTCTGTCTAC ATGTTGATGA AGGAGTGTGT
EST Contig       CGTTGGACGA CGATGTTGAT TTGCGTAGTG GTGTTCCCTT TTCTGTTTAC ATGTTGATTC AGGAGTGTGT
scaff000068      .......... .......... .......... .......... .......... .......... ..........
Contig-0         CGTTGGACGA CGATGTTGAT TTGCGTAGTC GTGTTCCATT TTCTGTCTAC ATGTTGATGA AGGAGTGTGT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    3085       3095       3105       3115       3125       3135       3145
SmBr18           -T-TGTGTGT GTGTGTGTGT GTGAATGTGG GATATAGTGT GTTGGGTTGA TTATG--TGT TGATTGTTTT
scaff000011      -T-TGTGTGT GTGTGTGTGT GTGCATGTGG GATATAGTGT GTTGGGTTGA TTATG--TGT TGATTGTTTT
EST Contig       GTGTGTGTGT GTGTGTGTGT GTGAATGTGG GATCTAGTGT GTTGGGTTGA TTATGCATGT TGATTGTTTT
scaff000068      .......... .......... .......... .......... .......... .......TGT TGATTGTTTT
Contig-0         -T-TGTGTGT GTGTGTGTGT GTGAATGTGG GATATAGTGT GTTGGGTTGA TTATG--TGT TGATTGTTTT

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    3155       3165       3175       3185       3195       3205       3215
SmBr18           TCGTTGTAA- TAGTGGTGTT TGAATGTTTG GTGA-ATGAT GGTTATGGGG AGGAGTGGTG TTCCCTGTTA
scaff000011      TCGTTGTAA- TAGTGGTGTT TGAATGTTTG GTGA-ATGAT GGTTATGGGG AGGAGTGGTG TTCCCTGTTA
EST Contig       TCGTTGTAAC TAGTGGTGTT TGATTGTTTG TTGACATGAT GGTTATGGGG AGGAGTGGTG TTCCCTGTTA
scaff000068      TCGTTGTA-- TAGTGGTGTT TGAATGTTTG GTGA-ATGAT GGTTATGGGG AGGAGTGGTG TTCCCTGTTA
Contig-0         TCGTTGTAA- TAGTGGTGTT TGAATGTTTG GTGA-ATGAT GGTTATGGGG AGGAGTGGTG TTCCCTGTTA

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    3225       3235       3245       3255       3265       3275       3285
SmBr18           TGTTTCCGTT GTTCAGGTTG TGT------- --GCGTTGTG ---------A TGTTCTAGTG TGTGTAATGC
scaff000011      TGTTTCCGTT GTTCAGGTTG TGTGTGTTGT GTGTGTTGTG ---------A TGTTCTAGTG TGTGTAATGC
EST Contig       TGTTTCCGTT GTTCAGGTTG TGTGTGTTGT GTGTGTTGTG ---------A TGTTCTAGTG TGTGTAATGC
scaff000068      TGTTTCCGTT GTTCAGGTTG TGTGTGTTGT GTGTGTTGTG TGTGTTGTGA TGTTCTAGTG TGTGTAATGC
Contig-0         TGTTTCCGTT GTTCAGGTTG TGTGTGTTGT GTGTGTTGTG ---------A TGTTCTAGTG TGTGTAATGC

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    3295       3305       3315       3325       3335       3345       3355
SmBr18           ATGTAAGT.. .......... .......... .......... .......... .......... ..........
scaff000011      ATGTAAGTAC TCTCAACCAG TCCACTTGTT GTTTGTTAAC ATATGTGTGG GTGTAATGAG AGTGACATTG
EST Contig       ATGTAAGTAC TCTCAACCAG TCCACTTGTT GTTTGTTAAC ATATGTGTGG GTGTAATGAG AGTGACATTG
scaff000068      ATGTAAGTAC TCTCAACCAG TCCACTTGTT GTTTGTTAAC ATATGTGTGG GTGTAATGAG AGTGACATTG
Contig-0         ATGTAAGTAC TCTCAACCAG TCCACTTGTT GTTTGTTAAC ATATGTGTGG GTGTAATGAG AGTGACATTG

                 ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                    3365       3375       3385       3395       3405       3415       3425
SmBr18           .......... .......... .......... .......... .......... .......... ..........
scaff000011      ATGGTTGGAC AGATTTCTCG TTGGACGACG ATGTTGATTT GCGTAGTCGT GTTCCATTTT CTGTCTACAT
EST Contig       ATGGTTGGAC AGATTTCTCG TTGGACGACG ATGTTGATTT GCGTAGTCGT GTTCCATTTT CTGTCTACAT
scaff000068      ATGGTTGGAC AGATTTCTCG TTGGACGACG ATGTTGATTT GCGTAGTCGT GTTCCATTTT CTGTCTACAT
Contig-0         ATGGTTGGAC AGATTTCTCG TTGGACGACG ATGTTGATTT GCGTAGTCGT GTTCCATTTT CTGTCTACAT
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                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        3435       3445       3455       3465       3475       3485       3495
SmBr18               .......... .......... .......... .......... .......... .......... ..........
scaff000011          GTTGATGAAG GAGTGTGTTT GTGTGTGTGT GTGTGTGTG- -AATGTGGGA TATTGTGTGT TGGGTTGATT
EST Contig           GTTGATGAAG GAGTGTGTTT GTGTGTGTGT GTGTGT--G- -AATGTGGGA TATAGTGTGT TGGGTTGATT
scaff000068          GTTGATGAAG GAGTGTGTTT GTGTGTGTGT GTGTGT--GT GAATGTGGGA TATAGTGTGT TGGGTTGATT
Contig-0             GTTGATGAAG GAGTGTGTTT GTGTGTGTGT GTGTGT--G- -AATGTGGGA TATAGTGTGT TGGGTTGATT

                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        3505       3515       3525       3535       3545       3555       3565
SmBr18               .......... .......... .......... .......... .......... .......... ..........
scaff000011          ATGTGTTGAT TGTTTTTCGT TGTAA-TAGT GGTGTTTGAA TGTTTGGTGA ATGATGG-TT ATGGGGAGGA
EST Contig           ATGTGTTGAT TGTTTTTCGT TGTAAATAGT GGTGTTTGAA TGTTTGGTGA ATGATGGGTT ATGGGGAGGA
scaff000068          ATGTGTTGAT TGTTTTTCGT TGTAA-TCGT GGTGTTTGAA TGTTTGGTGA ATGATGG-TT ATGGGGAGGA
Contig-0             ATGTGTTGAT TGTTTTTCGT TGTAA-TAGT GGTGTTTGAA TGTTTGGTGA ATGATGG-TT ATGGGGAGGA

                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        3575       3585       3595       3605       3615       3625       3635
SmBr18               .......... .......... .......... .......... .......... .......... ..........
scaff000011          GTGGTGTTCC CTGTTATGTT TCCGTTGTTC AGGTTGTGTG TGTTGTGTGT GTTGTGTGTG TTGTGATGTT
EST Contig           GTGGTGTTCC CTGTTATGTT TCCGTTGTTC AGGTTGTGTG TGTTGTGTGT GTTGTGTGTG TTGTGATGTT
scaff000068          GTGGTGTTCC CTGTTATGTT TCCGTTGTTC AGGTTGTGTG TGTTGTGTGT GTTGTGTGTG TTGTGATGTT
Contig-0             GTGGTGTTCC CTGTTATGTT TCCGTTGTTC AGGTTGTGTG TGTTGTGTGT GTTGTGTGTG TTGTGATGTT

                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        3645       3655       3665       3675       3685       3695       3705
SmBr18               .......... .......... .......... .......... .......... .......... ..........
scaff000011          CTAGTGTGTG TAATGCATGT AAGTACTCTC AACCAGTCCA ATTGTTGTTT GTTAACATAT GTGTGGGTGT
EST Contig           CTAGTGTGTG TAATGCATGT AAGTACTCTC AACCAGTCCA CTTGTTGTTT GTTAACATAT GTGTGGGTGT
scaff000068          CTAGTGTGTG TAATGCATGT AAGTACTCTC AACCAGTCCA CTTGTTGTTT GTTAACATAT GTGTGGGTGT
Contig-0             CTAGTGTGTG TAATGCATGT AAGTACTCTC AACCAGTCCA CTTGTTGTTT GTTAACATAT GTGTGGGTGT

                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        3715       3725       3735       3745       3755       3765       3775
SmBr18               .......... .......... .......... .......... .......... .......... ..........
scaff000011          AATGAGAGTG ACATTGATGG TTGGACAGAT TTCTCGTTGG ACGACGATGT TGATTTGCGT AGTCGTGTTC
EST Contig           AATGAGAGTG ACATTGATGG TTGGACAGAT TTCTCGTTGG ACGACGATGT TGATTTGCGT AGTCGTGTTC
scaff000068          AATGAGAGTG ACATTGATGG TTGGACAGAT TTCTCGTTGG ACGACGATGT TGATTTGCGT AGTCGTGTTC
Contig-0             AATGAGAGTG ACATTGATGG TTGGACAGAT TTCTCGTTGG ACGACGATGT TGATTTGCGT AGTCGTGTTC

                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        3785       3795       3805       3815       3825       3835       3845
SmBr18               .......... .......... .......... .......... .......... .......... ..........
scaff000011          CATTTTCTGT CTACATGTTG ATGAAGGAGT GTGT--GTGT GTGTGTGTG- ---AATGTGG GATATAGTGT
EST Contig           CATTTTCTGT CTACATGTTG ATGAAGGAGT GTGTTTGTGT GTGTGTGTGT GTGAATGTGG GATATAGTGT
scaff000068          CATTTTCTGT CTACATGTTG ATGAAGGAGT GTGTTTGTGT GTGTGTGTGT G--AATGTGG GATATAGTGT
Contig-0             CATTTTCTGT CTACATGTTG ATGAAGGAGT GTGTTTGTGT GTGTGTGTGT G--AATGTGG GATATAGTGT

                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        3855       3865       3875       3885       3895       3905       3915
SmBr18               .......... .......... .......... .......... .......... .......... ..........
scaff000011          GTTGGGTTGA TTATGTGTTG ATTGTTTTTC GTTGTAATAG TGGTGTTTGA ATGTTTGGTG AATGATGGTT
EST Contig           GTTGGGTTGA TTATGTGTTG ATTGTTTTTC GTTGTAATAG TGGTGTTTGA ATGTTTGGTG AATGATGGTT
scaff000068          GTTGGGTTGA TTATGTGTTG ATTGTTTTTC GTTGTAATAG TGGTGTTTGA ATGTTTGGTG AATGAAGGCT
Contig-0             GTTGGGTTGA TTATGTGTTG ATTGTTTTTC GTTGTAATAG TGGTGTTTGA ATGTTTGGTG AATGATGGTT

                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        3925       3935       3945       3955       3965       3975       3985
SmBr18               .......... .......... .......... .......... .......... .......... ..........
scaff000011          ATGGGGAGGA GTGGTGTTCC CTGT-TAT-G TTTCCG-TTG TTCAGGTTGT GTGTGTTGTG TGTGTTGTGA
EST Contig           ATGGGGAGGA GTGGTGTTCC CTGT-TAT-G TTTCCG-TTG TTCAGGTTGT GTGTGTTGTG TGTGTTGTGA
scaff000068          GTGGGTTTCT TTG-T-TTTC TTGTATTTAG TT-CTGATT- TT-A--TT-T CTGT-TTGTC TTT-TTTTTA
Contig-0             ATGGGGAGGA GTGGTGTTCC CTGT-TAT-G TTTCCG-TTG TTCAGGTTGT GTGTGTTGTG TGTGTTGTGA

                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        3995       4005       4015       4025       4035       4045       4055
SmBr18               .......... .......... .......... .......... .......... .......... ..........
scaff000011          TGTT--CT-A GTGTGTGTAA TGCATGTAAG TACTCTCAAC CAGTCCACTT GTTGTTTG-T -TA-ACATAT
EST Contig           TGTT--CT-A GTGTGTGTAA TGCATGTAAG TACTCTCAAC CAGTCCACTT GTTGTTTG-T -TA-ACATAT
scaff000068          TGTTTGCGGA GTGT-T-T-- T-C-T-T--- TT-T-T---- --GT--A-TT TTTGTTTGGT CTCTA-ATAT
Contig-0             TGTT--CT-A GTGTGTGTAA TGCATGTAAG TACTCTCAAC CAGTCCACTT GTTGTTTG-T -TA-ACATAT

                     ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                        4065       4075       4085       4095       4105       4115       4125
SmBr18               .......... .......... .......... .......... .......... .......... ..........
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scaff000011     GTGTGGGTGT AATGAGAGTG ACATT----G ATGGT-GGAC A-GA...... .......... ..........
EST Contig      GTGTGGGTGT AATGAGAGTG ACATT---CG CTGGTTGGAC T-GATT-TCT CGTTGTTCGA GGTTGTGTGA
scaff000068     -TGTTA-T-T AATTT-ATTT TCTTTTTTCG -TG-TTTTAT TTG-TTCTCT C-TT-TT--A GGTTGA-TGA
Contig-0        GTGTGGGTGT AATGAGAGTG ACATT---CG ATGGTTGGAC T-GATTCTCT CGTTGTTCGA GGTTGAGTGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4135       4145       4155       4165       4175       4185       4195
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      TGTTG-TGTA GTCGTTGTTC CATTTTCTAG TGTACGTGTA ---AT--GCA TGT-AAGTG- A---GT-GT-
scaff000068     TGAAGAT-TA --CATT---C C-TT--CTCG T-T-C-TG-A GCCATCTG-A TGTGAAGTAC AATCGTCGTC
Contig-0        TGAAGATGTA GTCATTGTTC CATTTTCTAG TGTACGTGTA GCCATCTGCA TGTGAAGTAC AATCGTCGTC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4205       4215       4225       4235       4245       4255       4265
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      GTTTG-TGTG TGTGTGTGTG TGAATGTGGG ATAT-TGTGT GTTGGGTTGA T-TATGTGT- T-G-A-TTGT
scaff000068     GTTTGCT-TA T-TCT-TGC- TCAA-GTGG- A-ACGTGTAT GTT---TTTT TCTAT-TGTA TAGTACTTGT
Contig-0        GTTTGCTGTA TGTCTGTGCG TCAATGTGGG ATACGTGTAT GTTGGGTTGA TCTATGTGTA TAGTACTTGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4275       4285       4295       4305       4315       4325       4335
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      TCTTCACTGT AATAGT.... .......... .......... .......... .......... ..........
scaff000068     TAT--A-TAT A-TA-TTTTT TATCGTGTTT GTGTCGTAGA TCGTTTTTCA TTTGTTGTAA CTTTGTAGGT
Contig-0        TATTCACTAT AATAGTTTTT TATCGTGTTT GTGTCGTAGA TCGTTTTTCA TTTGTTGTAA CTTTGTAGGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4345       4355       4365       4375       4385       4395       4405
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CAAAAATGAT CCTCTCTCCG TCGTTTTATT CGTTGCTTTG TTAATTACAC TTTTGACTTT TCTTTTACGA
Contig-0        CAAAAATGAT CCTCTCTCCG TCGTTTTATT CGTTGCTTTG TTAATTACAC TTTTGACTTT TCTTTTACGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4415       4425       4435       4445       4455       4465       4475
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TTGTTTCTAT TTTTTTGACA GATAATTCCC TTTTAAACAT TCGAAATTAA AAATACGAAG TTGAGCGAAG
Contig-0        TTGTTTCTAT TTTTTTGACA GATAATTCCC TTTTAAACAT TCGAAATTAA AAATACGAAG TTGAGCGAAG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4485       4495       4505       4515       4525       4535       4545
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AGATCTCATT TCAACGAATT TTTTATCAAG CTGTACAATC GTACTAATAT GGAAAATTGT TTTTTTGTTA
Contig-0        AGATCTCATT TCAACGAATT TTTTATCAAG CTGTACAATC GTACTAATAT GGAAAATTGT TTTTTTGTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4555       4565       4575       4585       4595       4605       4615
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AAGTACTAAT GGGAACACAA ATAACCGAGA TGATGGAAAA TAATCTTTCT ATTGAATCAT CTTGGTTATT
Contig-0        AAGTACTAAT GGGAACACAA ATAACCGAGA TGATGGAAAA TAATCTTTCT ATTGAATCAT CTTGGTTATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4625       4635       4645       4655       4665       4675       4685
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CGTGTGCACT TTAAGGGCTG AATTTATAAC AGAAGTTTGC TGAAACGGCC TCAAATCATT TAGTTTTTCC
Contig-0        CGTGTGCACT TTAAGGGCTG AATTTATAAC AGAAGTTTGC TGAAACGGCC TCAAATCATT TAGTTTTTCC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4695       4705       4715       4725       4735       4745       4755
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CTTGTTAATA AATGGCAGTT CTGATAATTA ACATAACCCA TTGTGTTATT GGATAAGAAT AAAGAGAAGT
Contig-0        CTTGTTAATA AATGGCAGTT CTGATAATTA ACATAACCCA TTGTGTTATT GGATAAGAAT AAAGAGAAGT
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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4765       4775       4785       4795       4805       4815       4825
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CAGCGAAGAA AATTTTCTTT TCCACTAAAT CGTTTACTTA AGCTGTACAT TCTTGTTTAT AATCATACGG
Contig-0        CAGCGAAGAA AATTTTCTTT TCCACTAAAT CGTTTACTTA AGCTGTACAT TCTTGTTTAT AATCATACGG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4835       4845       4855       4865       4875       4885       4895
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AAAATACATG TCTAGAGAAG GATAGAAAAG ATTGCATTAT AAATGGATTC GAGACTCTTA TTATCAAATG
Contig-0        AAAATACATG TCTAGAGAAG GATAGAAAAG ATTGCATTAT AAATGGATTC GAGACTCTTA TTATCAAATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4905       4915       4925       4935       4945       4955       4965
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AGGTTTCGCA ATAACCAATG GGTAAGGAAG GAATATAACG ATGAAAATAA TAATTCACGG GTCAGATAAT
Contig-0        AGGTTTCGCA ATAACCAATG GGTAAGGAAG GAATATAACG ATGAAAATAA TAATTCACGG GTCAGATAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   4975       4985       4995       5005       5015       5025       5035
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TGTCCAATTG ACAGGTATGA AGAAAAATGA CAAACATGAA GGTCATAATA AAAACTGAAT AATAATCATG
Contig-0        TGTCCAATTG ACAGGTATGA AGAAAAATGA CAAACATGAA GGTCATAATA AAAACTGAAT AATAATCATG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5045       5055       5065       5075       5085       5095       5105
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AAAACTTGTA ATAATAATAA TAATAATAAC TGATTAGAGT TTAAAATTAC AAAACAGTTA TCTAAAAAAT
Contig-0        AAAACTTGTA ATAATAATAA TAATAATAAC TGATTAGAGT TTAAAATTAC AAAACAGTTA TCTAAAAAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5115       5125       5135       5145       5155       5165       5175
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CAATAATAAC CGAAGAAAAA CGAAGAAAAA AGGGAGAAAA ACCGAAACAT ACTACTAAAG AGAATCAGGG
Contig-0        CAATAATAAC CGAAGAAAAA CGAAGAAAAA AGGGAGAAAA ACCGAAACAT ACTACTAAAG AGAATCAGGG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5185       5195       5205       5215       5225       5235       5245
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     GCAAGGAAGG ATGAGAGGGG TTGGACCAGT CGTTTCTGTA CACAAAGTTC GGGTCTGAGT TCGTGGATTG
Contig-0        GCAAGGAAGG ATGAGAGGGG TTGGACCAGT CGTTTCTGTA CACAAAGTTC GGGTCTGAGT TCGTGGATTG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5255       5265       5275       5285       5295       5305       5315
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CCAATGCTCC GGCAATGCAT AAAATATTGA TTCAATTTCC CTTCGATCCA ATTCATTTGA CTGTGTAGAT
Contig-0        CCAATGCTCC GGCAATGCAT AAAATATTGA TTCAATTTCC CTTCGATCCA ATTCATTTGA CTGTGTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5325       5335       5345       5355       5365       5375       5385
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TACTTTATGA GAAAACTCTT TTGCAGTGAT GTGTTCACAG TTAATTAAAT GCTCCTGTAT AGAACTAGTA
Contig-0        TACTTTATGA GAAAACTCTT TTGCAGTGAT GTGTTCACAG TTAATTAAAT GCTCCTGTAT AGAACTAGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5395       5405       5415       5425       5435       5445       5455
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
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EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     ATTGTTTTAC ATTCTCCTTT TAAAAGCCAT GTCGGATAGT GTTCTGAGAT GCGTTTTGGA AAGTGCTCGC
Contig-0        ATTGTTTTAC ATTCTCCTTT TAAAAGCCAT GTCGGATAGT GTTCTGAGAT GCGTTTTGGA AAGTGCTCGC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5465       5475       5485       5495       5505       5515       5525
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TTTGTGCGGC CAATGTAGCC TGCCCCACAC TAGCAAGTAA ATTTATAGAT ACACGTTGAT GTGGCCCAAA
Contig-0        TTTGTGCGGC CAATGTAGCC TGCCCCACAC TAGCAAGTAA ATTTATAGAT ACACGTTGAT GTGGCCCAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5535       5545       5555       5565       5575       5585       5595
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     GAGGAAGTTT ATACTTAACA CATCGGAGAA TGGTGGGCCG GCTAGAGAAA ACAATTCTGA GCTTAGCTGA
Contig-0        GAGGAAGTTT ATACTTAACA CATCGGAGAA TGGTGGGCCG GCTAGAGAAA ACAATTCTGA GCTTAGCTGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5605       5615       5625       5635       5645       5655       5665
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     GTAGAACGTT TTATTCAACG ATTTTGAAAT ACGTTTATTT AAGATTTCAG CAGTCGTATC TCCCTTAAAT
Contig-0        GTAGAACGTT TTATTCAACG ATTTTGAAAT ACGTTTATTT AAGATTTCAG CAGTCGTATC TCCCTTAAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5675       5685       5695       5705       5715       5725       5735
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TCCATATTCA TAAATAGAAT TTTCTTTTGT ACTGTTGGTG CTTTGTCAGG ATGACGTCTA GCTGTTAAGT
Contig-0        TCCATATTCA TAAATAGAAT TTTCTTTTGT ACTGTTGGTG CTTTGTCAGG ATGACGTCTA GCTGTTAAGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5745       5755       5765       5775       5785       5795       5805
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TGCTACCGAC GAATCTAGGT GGATAACCAT TCCCAAAGAG AATCTGTCGA CGTCGAAGTA GTTCCTCATC
Contig-0        TGCTACCGAC GAATCTAGGT GGATAACCAT TCCCAAAGAG AATCTGTCGA CGTCGAAGTA GTTCCTCATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5815       5825       5835       5845       5855       5865       5875
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TATTGTGTCA GTAGGACATA CTCGCCTGAT CCTTGAGGAT AAAGAGTGAA TCAAGTTCCT CTTTCTACTC
Contig-0        TATTGTGTCA GTAGGACATA CTCGCCTGAT CCTTGAGGAT AAAGAGTGAA TCAAGTTCCT CTTTCTACTC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5885       5895       5905       5915       5925       5935       5945
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AGTGGTACCC GGCTATGGAA ATTCGTTTAC TGCCCATTCC AGGTCGCTTT TCTATACATC AAAAAAAAGA
Contig-0        AGTGGTACCC GGCTATGGAA ATTCGTTTAC TGCCCATTCC AGGTCGCTTT TCTATACATC AAAAAAAAGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   5955       5965       5975       5985       5995       6005       6015
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AATTAATTGT TTGCCTCTGC TTCCAAAGTG AATTGAATAG AGGGGTGATA ATTACTGAAA CTTCAAAATT
Contig-0        AATTAATTGT TTGCCTCTGC TTCCAAAGTG AATTGAATAG AGGGGTGATA ATTACTGAAA CTTCAAAATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6025       6035       6045       6055       6065       6075       6085
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TCATTGAGGT TTATATCTTC TTCACAAATA ATGAAAGTAT CATCCATAGA TCACCTATAT AAGTGAAATC
Contig-0        TCATTGAGGT TTATATCTTC TTCACAAATA ATGAAAGTAT CATCCATAGA TCACCTATAT AAGTGAAATC
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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6095       6105       6115       6125       6135       6145       6155
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TCTCAATTAT TGGTCGAAGT TAGGTATTTT CTAGATTGGC CATGAAACAA TCAGCCAAGA GGAGAACCAA
Contig-0        TCTCAATTAT TGGTCGAAGT TAGGTATTTT CTAGATTGGC CATGAAACAA TCAGCCAAGA GGAGAACCAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6165       6175       6185       6195       6205       6215       6225
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TAGAGAACCC ATTGCAACTC TATCCATTTG TCTGTAGGAA TCATCATTAA ATCTAAGTTG CACGTTGAGA
Contig-0        TAGAGAACCC ATTGCAACTC TATCCATTTG TCTGTAGGAA TCATCATTAA ATCTAAGTTG CACGTTGAGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6235       6245       6255       6265       6275       6285       6295
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     GTACTTCGTA GAAGTAGCTC TTCTAGATAA TGTTTTGGGA TACAAATATC AAGGTTATTG TTTTCAATAT
Contig-0        GTACTTCGTA GAAGTAGCTC TTCTAGATAA TGTTTTGGGA TACAAATATC AAGGTTATTG TTTTCAATAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6305       6315       6325       6335       6345       6355       6365
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AGTTACATAA AAAACATAGT TTCTGTGAGA GGAACATTTG TAGAAAGAGA AGTAACATCC AGTGAAATCA
Contig-0        AGTTACATAA AAAACATAGT TTCTGTGAGA GGAACATTTG TAGAAAGAGA AGTAACATCC AGTGAAATCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6375       6385       6395       6405       6415       6425       6435
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TTTTCCTATC ATTTATATTG ACATTTTTAA TTGAGTCGAC AAAGTCAAAG GAATCAAGAG AATTGTATTT
Contig-0        TTTTCCTATC ATTTATATTG ACATTTTTAA TTGAGTCGAC AAAGTCAAAG GAATCAAGAG AATTGTATTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6445       6455       6465       6475       6485       6495       6505
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     ATTGATATGA TTTTTAACGG ATTGTAAAAT ATCAACTGGC CATTTAGCAA TCAGATGATA CAGAGAGTCG
Contig-0        ATTGATATGA TTTTTAACGG ATTGTAAAAT ATCAACTGGC CATTTAGCAA TCAGATGATA CAGAGAGTCG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6515       6525       6535       6545       6555       6565       6575
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TCCATATCGA GCATAGGATG TAGAGGGACA TTATAACTAT GAACTTTTGT GAGTCCATAT AGTCTTGGTA
Contig-0        TCCATATCGA GCATAGGATG TAGAGGGACA TTATAACTAT GAACTTTTGT GAGTCCATAT AGTCTTGGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6585       6595       6605       6615       6625       6635       6645
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TAACGGAACC CGATGGTCTA ATATGTTCAT AGAGGTCACA ATTGATAGTA AACTCATCTT TCATCTTCTT
Contig-0        TAACGGAACC CGATGGTCTA ATATGTTCAT AGAGGTCACA ATTGATAGTA AACTCATCTT TCATCTTCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6655       6665       6675       6685       6695       6705       6715
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TAGGATTTTA ATAAGCATCT GTTCCGTTTT TTTCAGTTGT CTTTTTGAAC GGTTTCTTTG GAGAATTTGA
Contig-0        TAGGATTTTA ATAAGCATCT GTTCCGTTTT TTTCAGTTGT CTTTTTGAAC GGTTTCTTTG GAGAATTTGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6725       6735       6745       6755       6765       6775       6785
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
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EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CAGGATCATA TAATATCGAA CACAATTTGG TGACATAGTC AAGACGATCC ACAAAGACGA TTCTCAGACC
Contig-0        CAGGATCATA TAATATCGAA CACAATTTGG TGACATAGTC AAGACGATCC ACAAAGACGA TTCTCAGACC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6795       6805       6815       6825       6835       6845       6855
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CTTGTCTAGG AGACACAACA CTAAATCCTG ATTTTTCGGA AGATCAGATA ATTGAGATCT ATGCTCTTTT
Contig-0        CTTGTCTAGG AGACACAACA CTAAATCCTG ATTTTTCGGA AGATCAGATA ATTGAGATCT ATGCTCTTTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6865       6875       6885       6895       6905       6915       6925
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     GTGAGTAATC GACTAATTGT AGGTATTTTC TTCACATATT GATAACAACA GTCTACAAGA GTTGTTTTGA
Contig-0        GTGAGTAATC GACTAATTGT AGGTATTTTC TTCACATATT GATAACAACA GTCTACAAGA GTTGTTTTGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   6935       6945       6955       6965       6975       6985       6995
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AATGCTCATA ATCTTTATTA GATACTGGAA TAAAGTCACT TGTCTGATGA ATGAGGCTTT CAACCTAGAT
Contig-0        AATGCTCATA ATCTTTATTA GATACTGGAA TAAAGTCACT TGTCTGATGA ATGAGGCTTT CAACCTAGAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7005       7015       7025       7035       7045       7055       7065
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TTTAGCGTTG AGTTCATTAA TGTTAGTTGA AGTACTACAA AATTTAGGAA CAACATTTAT CTATAAATTT
Contig-0        TTTAGCGTTG AGTTCATTAA TGTTAGTTGA AGTACTACAA AATTTAGGAA CAACATTTAT CTATAAATTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7075       7085       7095       7105       7115       7125       7135
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     ACTTGCTAGT GTGGGGCAGG CTACATTGGC CGCACAAAGC GAGCACTTTC CAAAACGCAT CTCAGAACAC
Contig-0        ACTTGCTAGT GTGGGGCAGG CTACATTGGC CGCACAAAGC GAGCACTTTC CAAAACGCAT CTCAGAACAC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7145       7155       7165       7175       7185       7195       7205
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TATCCGACAT GGCTTTTAAA AGGAGAATGT AAAACAATTA CTAGTTCTAT ACAGGAGCAT TTAATTAACT
Contig-0        TATCCGACAT GGCTTTTAAA AGGAGAATGT AAAACAATTA CTAGTTCTAT ACAGGAGCAT TTAATTAACT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7215       7225       7235       7245       7255       7265       7275
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     GTGAACACAT CACTGCAAAA GAGTTTTCTC ATAAAGTAAT CTACACAGTC AAATGAATTG GATCGAAGGG
Contig-0        GTGAACACAT CACTGCAAAA GAGTTTTCTC ATAAAGTAAT CTACACAGTC AAATGAATTG GATCGAAGGG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7285       7295       7305       7315       7325       7335       7345
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AAATTGAATC AATATTTTAT GCATTGCCGG AGCATTGGCA ATCCACGAAC TCAGACCCGA ACTTTGTGTA
Contig-0        AAATTGAATC AATATTTTAT GCATTGCCGG AGCATTGGCA ATCCACGAAC TCAGACCCGA ACTTTGTGTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7355       7365       7375       7385       7395       7405       7415
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CAGAAACGAC TGGTCCAACC CCTCTCATCC TTCCTTGCCC CTGATTCTCT TTAGTGGTAG TTCTGATTTT
Contig-0        CAGAAACGAC TGGTCCAACC CCTCTCATCC TTCCTTGCCC CTGATTCTCT TTAGTGGTAG TTCTGATTTT
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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7425       7435       7445       7455       7465       7475       7485
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CAAGGTAGCC CACTCTAATA ACTTTCCAAT TCATATTTGC TTACTGATCC TTGTTGTTAT TTGATTGATT
Contig-0        CAAGGTAGCC CACTCTAATA ACTTTCCAAT TCATATTTGC TTACTGATCC TTGTTGTTAT TTGATTGATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7495       7505       7515       7525       7535       7545       7555
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     GTTCTCGTTA GGTATTTTTT ATCAAATGTC TCAAGTCCAT TTTCTTGATT ATTAACAGAA TTGTCCCATT
Contig-0        GTTCTCGTTA GGTATTTTTT ATCAAATGTC TCAAGTCCAT TTTCTTGATT ATTAACAGAA TTGTCCCATT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7565       7575       7585       7595       7605       7615       7625
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AAATTTTCGA TTTCATCGAA TGACAATTTT TTTCCTGAGT TCTACACTTT TTCTCATCAA TCAAGGATTA
Contig-0        AAATTTTCGA TTTCATCGAA TGACAATTTT TTTCCTGAGT TCTACACTTT TTCTCATCAA TCAAGGATTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7635       7645       7655       7665       7675       7685       7695
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TTCTTGAACT ATCGTGTATA TGTCGTACGG ATTTGTTCGC GTGAATTGCA TTTCGCCCTA AAAACAGCTT
Contig-0        TTCTTGAACT ATCGTGTATA TGTCGTACGG ATTTGTTCGC GTGAATTGCA TTTCGCCCTA AAAACAGCTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7705       7715       7725       7735       7745       7755       7765
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     GCTGTCGTTC GTAATTCTTA ATTATCATAG CTTTCACAAA AGTGAACGAG ACTGTTGGGA AGCTTTGAAA
Contig-0        GCTGTCGTTC GTAATTCTTA ATTATCATAG CTTTCACAAA AGTGAACGAG ACTGTTGGGA AGCTTTGAAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7775       7785       7795       7805       7815       7825       7835
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TTATGTAAAT AATATCATTA TATACATTAT CTATATATAT ATGAAGATGG TTATTTATAG TGTTTAGTGA
Contig-0        TTATGTAAAT AATATCATTA TATACATTAT CTATATATAT ATGAAGATGG TTATTTATAG TGTTTAGTGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7845       7855       7865       7875       7885       7895       7905
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TTTTTATGTT TTCTCTATTT TTTCCTCTCA TATCTGTTTA GATGTTTTCA ATATTATTGA TCTTAGATGA
Contig-0        TTTTTATGTT TTCTCTATTT TTTCCTCTCA TATCTGTTTA GATGTTTTCA ATATTATTGA TCTTAGATGA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7915       7925       7935       7945       7955       7965       7975
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AGTTTCCTTA TCTCTCAAAA GAGTTGTTGT TCAAAATGAC GCGTAAGTGT ACCCTATACT TTTTGTAGAA
Contig-0        AGTTTCCTTA TCTCTCAAAA GAGTTGTTGT TCAAAATGAC GCGTAAGTGT ACCCTATACT TTTTGTAGAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   7985       7995       8005       8015       8025       8035       8045
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CTATGACTTT TTGACTTTCG GGTCTGATTT TTCACTTGAG AGCTGTACTG TTTTGTATTG TATCGCTCTA
Contig-0        CTATGACTTT TTGACTTTCG GGTCTGATTT TTCACTTGAG AGCTGTACTG TTTTGTATTG TATCGCTCTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8055       8065       8075       8085       8095       8105       8115
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
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EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AAGTTCCCGT TTATAATCCA AAACGTGAAA ACATTTAAAT AAAACACTCG AAAAATAAAT CAAACCTAGT
Contig-0        AAGTTCCCGT TTATAATCCA AAACGTGAAA ACATTTAAAT AAAACACTCG AAAAATAAAT CAAACCTAGT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8125       8135       8145       8155       8165       8175       8185
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     GACCAAATAT GCAATGAAGA CCATTCATAT CACGATTCTG TTCCAGAAAG TAATAAAATC CAGGGTTTTA
Contig-0        GACCAAATAT GCAATGAAGA CCATTCATAT CACGATTCTG TTCCAGAAAG TAATAAAATC CAGGGTTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8195       8205       8215       8225       8235       8245       8255
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TCACTGCGAA ATGATCAGTA TTGAACCCTT TAAAATCTTT AAAATTATTA GAGTGTTTGA GGTCAGTGTT
Contig-0        TCACTGCGAA ATGATCAGTA TTGAACCCTT TAAAATCTTT AAAATTATTA GAGTGTTTGA GGTCAGTGTT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8265       8275       8285       8295       8305       8315       8325
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TCAATACGTA TATTTATTCA TGGAAATGTC ATCTACATGA TGGTTGAGAG TGTATCATAT TATTACATCA
Contig-0        TCAATACGTA TATTTATTCA TGGAAATGTC ATCTACATGA TGGTTGAGAG TGTATCATAT TATTACATCA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8335       8345       8355       8365       8375       8385       8395
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TTACTAGTAA GTTAATTCTA CATTTGTTCC AGGTCAATCC ATTCTTCTAG ATATTCTTTA AAATTGTTAA
Contig-0        TTACTAGTAA GTTAATTCTA CATTTGTTCC AGGTCAATCC ATTCTTCTAG ATATTCTTTA AAATTGTTAA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8405       8415       8425       8435       8445       8455       8465
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     AAGGCTTGAT ATTTACCCAC CTCAAAAAAC ATTCCACTAT TATTCGCTAC TATTAAATTA GATAATCTGC
Contig-0        AAGGCTTGAT ATTTACCCAC CTCAAAAAAC ATTCCACTAT TATTCGCTAC TATTAAATTA GATAATCTGC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8475       8485       8495       8505       8515       8525       8535
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     ATCTGCTTTT AGAAAAAGCT ACAGGATTCT GTCACTTCCA TCTATTTAAA CCTTAATTAT TACTAATATC
Contig-0        ATCTGCTTTT AGAAAAAGCT ACAGGATTCT GTCACTTCCA TCTATTTAAA CCTTAATTAT TACTAATATC

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8545       8555       8565       8575       8585       8595       8605
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CCTAATATCT TATATGAATT TTTGTGCAAG TTTTCATGTC ATGGACCTAG GCATACAAAA GTTTTATAAT
Contig-0        CCTAATATCT TATATGAATT TTTGTGCAAG TTTTCATGTC ATGGACCTAG GCATACAAAA GTTTTATAAT

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8615       8625       8635       8645       8655       8665       8675
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TCAATAAAAC AGAACGATCT TTAAGAAATA GAAACTCCAC AATTGCATTG TGTTTATAGG TGTTGCTTTG
Contig-0        TCAATAAAAC AGAACGATCT TTAAGAAATA GAAACTCCAC AATTGCATTG TGTTTATAGG TGTTGCTTTG

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8685       8695       8705       8715       8725       8735       8745
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     ACGTTTTGTG AATTCGTATA CTACTTGGAT AGTTTTTTTC TTCTTCATAG TATCTTGTGA CTTCAATTAA
Contig-0        ACGTTTTGTG AATTCGTATA CTACTTGGAT AGTTTTTTTC TTCTTCATAG TATCTTGTGA CTTCAATTAA
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                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8755       8765       8775       8785       8795       8805       8815
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     TGTTATTCCA AACTTTTCGG CATATTGACA AACATATTTG AATATAGAGC CTATTTGGAT TTATTTTTTA
Contig-0        TGTTATTCCA AACTTTTCGG CATATTGACA AACATATTTG AATATAGAGC CTATTTGGAT TTATTTTTTA

                ....|....| ....|....| ....|....| ....|....| ....|....| ....|....| ....|....|
                   8825       8835       8845       8855       8865       8875       8885
SmBr18          .......... .......... .......... .......... .......... .......... ..........
scaff000011     .......... .......... .......... .......... .......... .......... ..........
EST Contig      .......... .......... .......... .......... .......... .......... ..........
scaff000068     CAAAAAAATA TAAAAAGTAT TTGTGTATAT ATTCCTTGAT TTGATTTCTT CTTCCCATAG ACGTTCTCGA
Contig-0        CAAAAAAATA TAAAAAGTAT TTGTGTATAT ATTCCTTGAT TTGATTTCTT CTTCCCATAG ACGTTCTCGA

                ....|....| ....|....| ....|....| ....|....|
                   8895       8905       8915       8925
SmBr18          .......... .......... .......... ..........
scaff000011     .......... .......... .......... ..........
EST Contig      .......... .......... .......... ..........
scaff000068     CTGTTAGATT ATCAACAAGA ATTGATTAAT CAACTAATCA
Contig-0        CTGTTAGATT ATCAACAAGA ATTGATTAAT CAACTAATCA
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Yellow squared letters = CA88 nuclear repetitive DNA sequence end.
Squared letters = CA88 nuclear repetitive DNA sequence begin.
Underlined italic = SmBr18 microsatellite.
Underlined = GT rich region.
In red forward and reverse primers sites.

TABLE

Predictive variables

Group 1 - Socioeconomic and demographic features

Variable	Description[a]
HDI-91	Human development index in year 1991
HDI-00	Human development index in year 2000
HDII-91	Income human development index in year 1991
HDII-00	Income human development index in year 2000
HDIL-91	Longevity human development index in year 1991
HDIL-00	Longevity human development index in year 2000
HDIE-91	Education human development index in year 1991
HDIE-00	Education human development index in year 2000
Inc without	Families without income (%)
Inc 1 wage	Families with income lower than 1 monthly minimum wage (%)
Inc 1-5 wages	Families with income from 1-5 monthly minimum wage (%)
Inc 5-10 wages	Families with income from 5-10 monthly minimum wage (%)[b]
Inc 10-15 wages	Families with income from 10-15 monthly minimum wage (%)
Inc above 15	Families with income higher than 15 monthly minimum wage (%)
Ed 1	Family heads with less than 1 year of instruction or without an education (%)
Ed 1-3	Family heads with 1-3 study years of literacy level (%)
Ed 4-7	Family heads with 4-7 study years of literacy level (%)
Ed 8-10	Family heads with 8-10 study years of literacy level (%)
Ed 11-15	Family heads with 11-15 study years of literacy level (%)
DAbove15E	Family heads with more than 15 study years of literacy level (%)
EdNonDet 7	Family heads with non determined study (%)
Urb	Residence in urban area (%)
Rural	Residence in rural area (%)

a: source: SNIU(2005); *b*: legislation in Brazil establishes a value for a monthly minimum wage, which corresponds nowadays to a value of about U$ 200.00.

Group 2 - Basic sanitation

Variable	Description[a]
WaterPubServ	Residence with access to water supply provided by public service (%)
WaterWells	Residence with access to water supply by means of wells (%)
WaterAnother	Residence with another type of access to water (%)
SewRiverLake	Residence with sewage pumped straight into the sea, rivers or lakes (%)
SewTrench	Residence with sewage connected to trench (%)
SewRudCesspit	Residence with sewage connected to rudimentary cesspit (%)
SewSepCesspit	Residence with sewage connected to septic cesspit (%)
Sew	Residence with sewage connected to general network (%)
SewAnother	Residence with another type sewage (%)
WithSan	Residence with toilets (%)
WithoutSan	Residence with no toilets (%)

a: source: SNIU(2005).

Group 3 - Presence of water collections and dense vegetation in the summer

Variable	Description[a]
BlueS	Blue band in the summer
EVIS	Enhanced vegetation index in the summer
MirS	Middle infrared band in the summer
NDVIS	Normalized difference vegetation index in the summer
NirS	Near infrared band in the summer
VegS	Linear mixture model - vegetation in the summer
RedS	Red band in the summer
SoilS	Linear mixture model - soil in the summer
ShadeS	Linear mixture model - shade in the summer

a: source: MODIS.

↳

Group 4 - Presence of water collections and dense vegetation in the winter

Variable	Description[a]
BlueW	Blue band in the winter
EVIW	Enhanced vegetation index in the winter
MirW	Middle infrared band in the winter
NDVIW	Normalized difference vegetation index in the winter
NirW	Near infrared band in the winter
VegW	Linear mixture model - vegetation in the winter
RedW	Red band in the winter
SoilW	Linear mixture model - soil in the winter
ShadeW	Linear mixture model - shade in the winter

a: source: MODIS.

Group 5 - Climate

Variable	Description[a]
PrecW	Average of accumulated precipitation in the winter
PrecS	Average of accumulated precipitation in the summer
TmaxW	Average of daily maximum temperature in the winter
TmaxS	Average of daily maximum temperature in the summer
TminW	Average of daily minimum temperature in the winter
TminS	Average of daily minimum temperature in the summer

a: source: CPTEC/INPE.

Group 6 - Terrain

Variable	Description[a]
AWater1	Average of accumulated water - amount of water that may exist in the municipality, calculated from the Dem
AWater2	Median of accumulated water - amount of water that may exist in the municipality, calculated from the Dem
Dem	Digital elevation model of terrain
Dec	Slope declivity

a: source: SRTM.

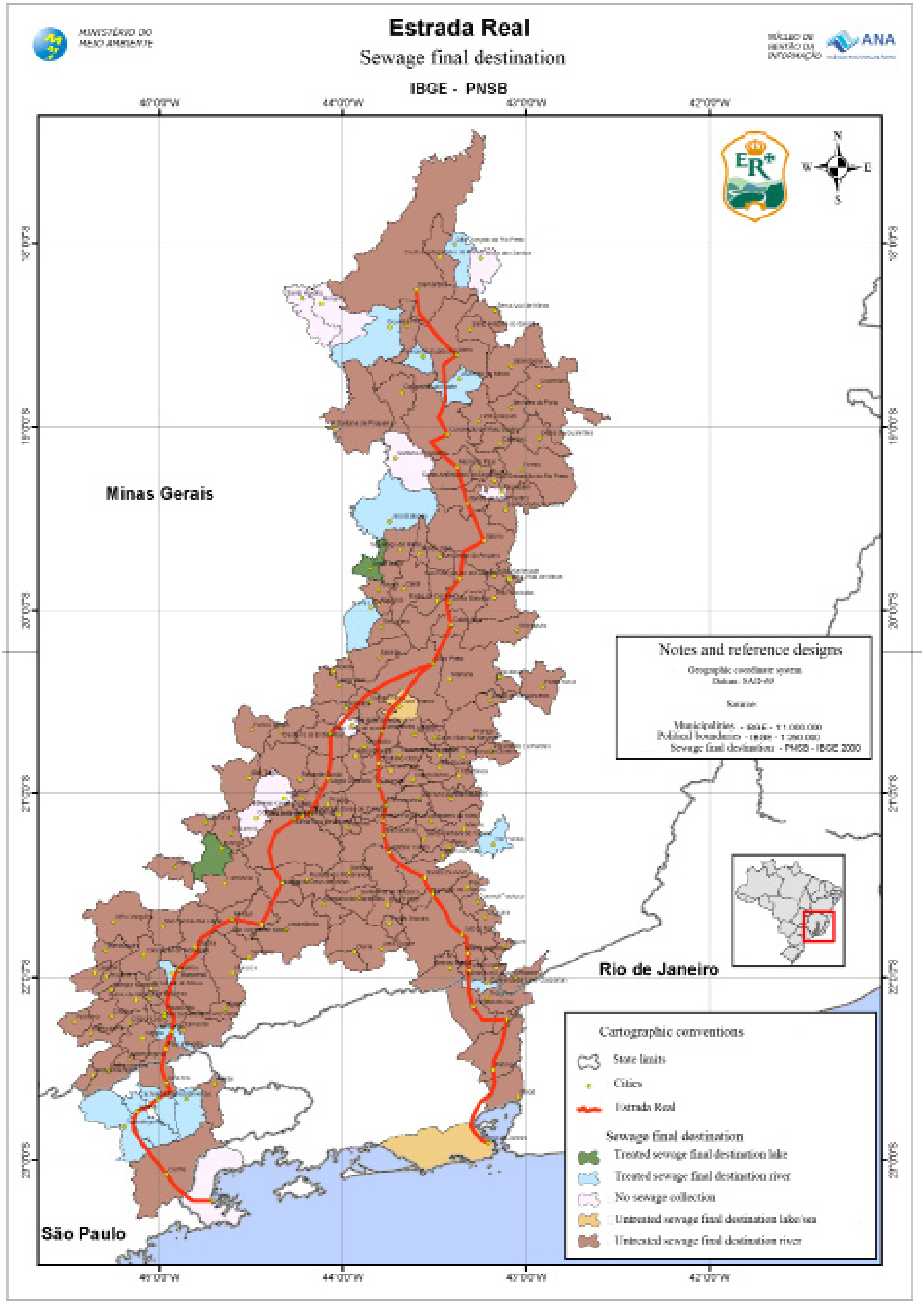

Fig. 1: map showing the municipalities of the Estrada Real project in Minas Gerais, Rio de Janeiro and São Paulo, Brazil and sewage destination (Brazilian Ministry of Environment).