

APPENDICES

Appendix A

Simpson's Index

The statistic, C is given by:

$$C = \sum_i^{Sobs} P_i^2$$

where, $Sobs$ is the number of observations but is usually approximated as:

$$P_i^2 = \left(\frac{N_i}{N_T} \right)^2$$

where N_i is the number of individuals in the i th species and N_T the total individuals in the sample. The index is:

$$D = \frac{1}{C}$$

The larger its value the greater the diversity.

Appendix B

Brillouin Index

The Brillouin index, HB, is calculated using:

$$HB = \frac{\ln N! - \sum_{i=1}^s \ln n_i!}{N}$$

where N is the total number of individuals in the sample, n_i is the number of individuals belonging to the i th species and s the species number.

Appendix C

The Components of 5X TBE (Tris Borate EDTA Buffer)

Components	JMR	Concentration	Amount Needed
Tris Base (Promega, USA)	121.14	445mM	1M = 121.14g in 1000ml 0.445M = 54g
Borate Acid (Promega, USA)	61.84	445mM	1M = 61.84g in 1000ml 0.445M = 27.52g
EDTA	372.20	10mM	500mM in 1000ml 10mM = 20ml

Appendix D

Plasmid Extraction

Solution I (50mM glucose, 10mM EDTA, 25mM tris-Cl)

Components	Volume
1M Tris-Cl (pH 8.0)	1.25ml
0.5M EDTA (pH 8.0)	1.00ml
Glucose	450mg
Distilled water	Up to 50ml

Solution II (0.2NaOH, 1% SDS, 500µl)

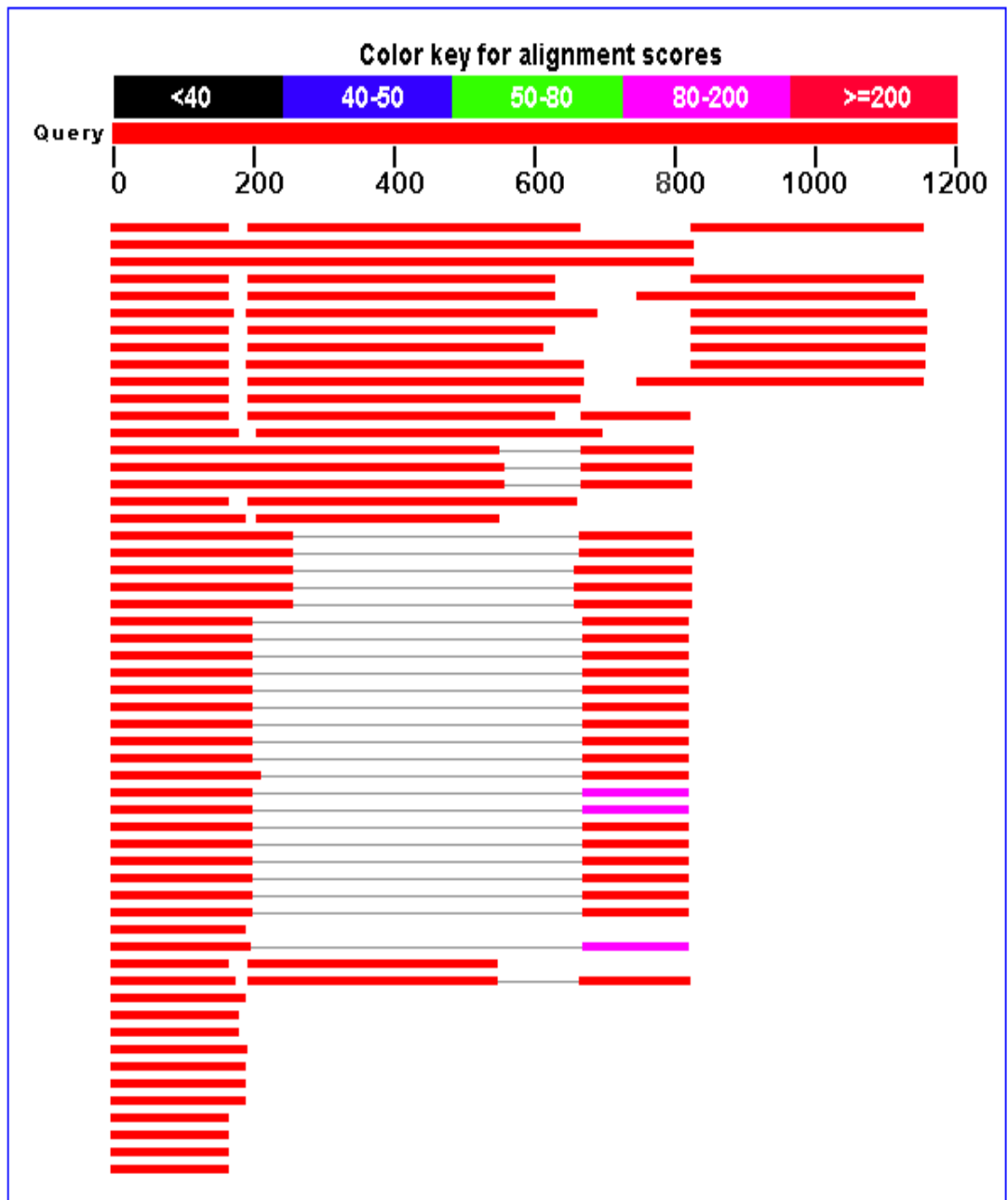
Components	Volume (µl)
NaOH (10N)	10
SDS (10%)	50
Distilled water	440

Solution III

Components	Volume
5M Potassium acetate	60ml
Glacial acetic acid	11.5ml
Distilled water	28.5ml

Appendix E

Distribution of 129 Blast Hits on the Query Sequence



Appendix F

Sequences producing significant alignment

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
AJ002438.1	Toxocara cf. canis first internal transcribed spacer ribosomal DNA	861	861	39%	0.0	99%	
AF411203.1	Contracaecum osculatum 18S ribosomal RNA gene, partial sequence;	695	695	68%	0.0	82%	
AB277825.1	Contracaecum osculatum genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2	678	678	68%	0.0	82%	
AJ002440.1	Toxocara cf. canis second internal transcribed spacer ribosomal DNA	604	604	27%	2e-169	99%	
AM231609.1	Toxocara malaysiensis internal transcribed spacer 2	569	569	27%	8e-159	97%	
EU220233.1	Toxocara vitulorum isolate 1d internal transcribed spacer 1, partial se	556	556	36%	6e-155	89%	
AJ007455.1	Toxocara vitulorum DNA for internal transcribed spacer 1, ITS1	556	556	36%	6e-155	89%	
AB110024.1	Toxocara canis genes for internal transcribed spacer 1, 5.8S ribosom	553	553	41%	8e-154	86%	
EU220232.1	Toxocara vitulorum isolate 1c internal transcribed spacer 1, partial se	551	551	36%	3e-153	89%	
EU220231.1	Toxocara vitulorum isolate 1b internal transcribed spacer 1, partial se	551	551	35%	3e-153	90%	
AB110025.1	Toxocara cati genes for internal transcribed spacer 1, 5.8S ribosomal	551	551	39%	3e-153	87%	
AJ002436.1	Toxocara cati (Australia) first internal transcribed spacer ribosomal DI	551	551	39%	3e-153	87%	
AJ002437.1	Toxocara cati (Malaysia) first internal transcribed spacer ribosomal DI	549	549	39%	1e-152	87%	
EU220230.1	Toxocara vitulorum isolate 1a internal transcribed spacer 1, partial se	545	545	36%	1e-151	89%	
AB110026.2	Toxocara canis genes for internal transcribed spacer 1, 5.8S ribosom	545	545	41%	1e-151	86%	
AF411204.1	Contracaecum rudolphii 18S ribosomal RNA gene, partial sequence; ir	534	787	59%	3e-148	95%	
AB110033.1	Toxocara cati genes for internal transcribed spacer 2, 5.8S ribosomal	527	527	33%	5e-146	90%	
AB277826.1	Hysterothylacium aduncum genes for 18S rRNA, ITS1, 5.8S rRNA, ITS	523	781	59%	6e-145	96%	
AF115571.1	Hysterothylacium auctum ribosomal RNA intergenic spacer region and	514	770	59%	4e-142	96%	
AJ002435.1	Toxocara canis first internal transcribed spacer ribosomal DNA	505	505	39%	2e-139	86%	
AJ002441.1	Toxocara cati (Malaysia) second internal transcribed spacer ribosoma	416	416	27%	1e-112	89%	
Y09493.1	Toxocara cati rRNA gene, partial	407	407	27%	6e-110	88%	
AB053231.1	Toxocara tanuki DNA, ITS1	398	398	28%	4e-107	87%	
AB277824.1	Pseudoterranova decipiens genes for 18S rRNA, ITS1, 5.8S rRNA, ITS	383	630	34%	1e-102	94%	
AB277821.1	Anisakis physeteris genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S	364	620	35%	4e-97	94%	
AB277823.1	Anisakis peqreffii genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rR	359	607	35%	2e-95	93%	
AB277822.1	Anisakis simplex genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 28S rR	359	607	35%	2e-95	93%	