SIG SUMMARY

Extracted SNP seqs for sigs from Tonys: full.table.sig1.rda, full.table.sig2.rda, full.table.sig3.rda

COORDS from JGI

SIG1 chr\_1 1537890 1540417 + gw1.1.74.1 12821

SIG2 chr\_7 1338802 1340055 - fgenesh1\_pg.C\_chr\_7000505 7122

SIG3 chr\_14 189795 190506 + fgenesh1\_pg.C\_chr\_14000069 9724

SIG3-like

Flagella chr 1667601 1668698 - fgenesh1\_pg.C\_chr\_1000629

SIG1: Protein ID 12821

[chr\_1:1537890-1540417](http://genome.jgi.doe.gov/cgi-bin/browserLoad?db=Thaps3&position=chr_1:1537890-1540417) (+)

Two introns; 95 and 87 bp long

SIG2: Protein ID 7122

[chr\_7:1338802-1340055 (-)](http://genome.jgi-psf.org/cgi-bin/browserLoad/?db=Thaps3&position=chr_7:1338802-1340055)

One intron of 99 bp

SIG 3

Protein ID: 9724

[chr\_14:189795-190506 (+)](http://genome.jgi-psf.org/cgi-bin/browserLoad/?db=Thaps3&position=chr_14:189795-190506)

1 intron 76 bp

SIG3-Like

Protein ID: [264161](http://genome.jgi-psf.org/cgi-bin/dispGeneModel?db=Thaps3&id=264161)

|  |  |
| --- | --- |
| [chr\_14:454581-455776 (+)](http://genome.jgi-psf.org/cgi-bin/browserLoad/?db=Thaps3&position=chr_14:454581-455776) |  |

 3 introns of 77, 66, 538 bp in length

Flagellar protofilament ribbon

Protein ID: 1495

[chr\_1:1667601-1668698 (-)](http://genome.jgi.doe.gov/cgi-bin/browserLoad/?db=Thaps3&position=chr_1:1667601-1668698)

no introns

Must be reverse complemented to count syn vs. Non-Syn

SIG1

Intron Snps Exon SNPs Syn Non-Syn

1007 0 0 0 0

1012 0 0 0 0

1013 0 3 1 2

1014 0 0 0 0

1015 0 0 0 0

3367 1 8 5 3

1335 0 0 0 0

\*\*Positions are not shared between IT and Wales

SIG2

Intron Snps Exon SNPs Syn Non-Syn

1007 0 0 0 0

1012 0 0 0 0

1013 0 1 0 1

1014 0 0 0 0

1015 0 0 0 0

3367 1 11 9 2

1335 0 0 0 0

Was reverse complemented in BioEdit to Count non-synonymous substitutions.

SIG3.264161

Intron Snps Exon SNPs Syn Non-Syn

1007 2 5 2 3

1012 2 5 2 3

1013 16 6 1 5

1014 2 2 1 1

1015 2 5 2 3

3367 5 7 4 3

1335 0 5 2 3

SIG3.9724

Intron Snps Exon SNPs Syn Non-Syn

1007 0 4 4 0

1012 0 4 4 0

1013 0 0 0 0

1014 0 4 4 0

1015 0 4 4 0

3367 1 0 0 0

1335 0 4 0 0

Protofilament

Intron Snps Exon SNPs Syn Non-Syn

1007 0 0 0 0

1012 0 0 0 0

1013 0 15 5 10

1014 0 0 0 0

1015 0 0 0 0

3367 0 14 5 9

1335 0 0 0 0

Sequences were reverse complemented (in BioEdit)

Non-synonymous snps were counted in BioEdit using sequence difference count matrix