

Processed Data: Chapter 3 Tables and Figures

Table 1: The best-fit models according to the Bayesian information criterion (BIC) as performed in IQtree (Nguyen et al., 2015)

<b>Dataset</b>	<b>Number of sequences</b>	<b>Model</b>	<b>Model reference</b>	<b>The proportion of invariable sites (I)</b>	<b>Empirical base frequencies (F)</b>	<b>Gamma correction for among site rate variation</b>
<b>Het C</b>	4	VT	(Müller & Vingron, 2000)	Yes	Yes	No
<b>Het 6</b>	11	LG	(Le & Gascuel, 2008)	Yes	No	Yes
<b>Pin C</b>	11	LG	(Le & Gascuel, 2008)	Yes	Yes	Yes
<b>Het D</b>	21	VT	(Kalyaanamoorthy et al., 2017)	Yes	Yes	Yes
<b>Het E</b>	21	VT	(Müller & Vingron, 2000)	No	Yes	No
<b>Het R</b>	21	VT	(Müller & Vingron, 2000)	No	Yes	No
<b>HNWD1</b>	21	VT	(Müller & Vingron, 2000)	No	Yes	No
<b>HNWD2</b>	21	VT	(Müller & Vingron, 2000)	Yes	Yes	Yes
<b>HNWD3</b>	21	VT	(Müller & Vingron, 2000)	Yes	Yes	Yes
<b>Vic 6</b>	11	LG	(Le & Gascuel, 2008)	Yes	Yes	Yes
<b>Vic 7</b>	11	LG	(Le & Gascuel, 2008)	Yes	Yes	Yes
<b>AO404</b>	11	Blosum62	(Henikoff & Henikoff, 1992)	No	Yes	Yes
<b>AO370</b>	11	LG	(Le & Gascuel, 2008)	Yes	Yes	Yes

Table 2: Homologs in *F. circinatum* of the 14 HET-domain encoding *vic/het* genes previously characterized in model ascomycetes.

Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
<b><i>Neurospora crassa</i></b>	<i>het-C</i>	AAF08294.1	Fcirg_07624	0.00	64.62	21	3
			Fcirg_01689	9.21E-142	42.45	31	
			Fcirg_08454	9.91E-86	34.16	31	
	<i>het-6</i>	CAD37033.1	Fcirg_05558	1.90E-99	35.77	32	1
	<i>pin-C</i>	ABC46541.1	Fcirg_11570	1.29E-46	29.23	13	1
<b><i>Podospora anserina</i></b>	<i>het-D</i>	CAL30216.1	Fcirg_11350	0.00	43.33	30	20
			Fcirg_08680	4.17E-152	30.31	36	
			Fcirg_14595	2.13E-133	29.77	35	
			Fcirg_11141	2.70E-125	35.85	33	
			Fcirg_05581	5.14E-122	37.00	33	
			Fcirg_12012	1.16E-85	28.89	33	
			Fcirg_14567	1.06E-70	39.43	33	
			Fcirg_10819	1.33E-59	47.32	33	
			Fcirg_14677	5.66E-58	25.10	34	

Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
			Fcirg_05914	2.05E-56	45.49	38	
			Fcirg_14532	1.14E-55	48.23	34	
			Fcirg_12012	3.03E-55	35.99	34	
			Fcirg_02359	2.20E-54	48.00	33	
			Fcirg_04013	3.73E-54	31.31	37	
			Fcirg_08274	5.28E-54	47.09	33	
			Fcirg_06736	7.96E-54	45.13	36	
			Fcirg_12299	3.13E-51	32.28	33	
			Fcirg_04013	5.70E-51	38.06	38	
			Fcirg_07090	1.33E-50	45.19	35	
			Fcirg_12012	1.44E-50	39.18	33	
	<i>het-E</i>	CAL30215.1	Fcirg_11350	1.14E-154	51.45	32	19
			Fcirg_11141	4.79E-122	45.49	32	
			Fcirg_05581	3.63E-115	41.28	32	
			Fcirg_14595	3.15E-109	42.60	31	
			Fcirg_08680	4.93E-105	40.03	33	

Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
			Fcirg_14567	5.14E-90	44.91	33	
			Fcirg_10819	1.47E-61	50.88	33	
			Fcirg_07090	1.61E-55	45.70	35	
			Fcirg_05914	1.97E-55	44.49	38	
			Fcirg_12009	3.60E-55	48.51	33	
			Fcirg_14532	5.24E-55	42.80	32	
			Fcirg_02359	1.04E-53	47.53	33	
			Fcirg_08274	1.33E-52	45.26	34	
			Fcirg_12299	2.44E-52	46.15	33	
			Fcirg_01059	3.16E-50	44.13	34	
			Fcirg_09454	1.15E-49	46.38	37	
			Fcirg_02056	1.10E-47	38.77	36	
			Fcirg_11515	6.6E-46	41.33	40	
			Fcirg_05706	2.05E-43	43.50	33	
	<i>het-R</i>	ACM48730.1	Fcirg_11350	0.00	44.76	35	20
			Fcirg_08680	1.36E-162	31.22	37	

Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
			Fcirg_05581	1.00E-134	33.33	34	
			Fcirg_14595	2.39E-129	28.05	36	
			Fcirg_11141	7.56E-129	30.91	34	
			Fcirg_12012	4.51E-83	27.80	33	
			Fcirg_14567	1.85E-74	38.44	33	
			Fcirg_10819	6.49E-63	45.09	32	
			Fcirg_14677	4.36E-59	25.18	35	
			Fcirg_04013	6.38E-59	33.78	38	
			Fcirg_06736	5.16E-58	40.40	36	
			Fcirg_14755	1.42E-57	34.05	32	
			Fcirg_12009	3.97E-55	24.64	34	
			Fcirg_05914	5.65E-54	49.80	36	
			Fcirg_14532	1.12E-51	39.64	32	
			Fcirg_12299	1.46E-51	39.74	35	
			Fcirg_08274	6.85E-51	32.71	33	
			Fcirg_01059	2.43E-50	38.41	35	
			Fcirg_09454	2.85E-50	43.51	36	

Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
	<i>HNWD1</i>	CAL30203.1	Fcirg_11350	0.00	47.72	33	20
			Fcirg_08680	1.48E-158	33.06	30	
			Fcirg_14595	3.87E-147	32.36	32	
			Fcirg_05581	8.63E-129	32.59	33	
			Fcirg_11350	5.28E-124	43.00	36	
			Fcirg_11141	6.52E-122	30.27	35	
			Fcirg_14567	7.16E-87	44.06	32	
			Fcirg_14677	1.65E-82	24.48	33	
			Fcirg_12012	5.89E-71	26.91	32	
			Fcirg_10819	8.39E-62	49.78	32	
			Fcirg_06736	8.74E-61	40.13	33	
			Fcirg_05914	4.02E-59	39.40	35	
			Fcirg_12012	1.73E-57	38.51	33	
			Fcirg_09454	8.83E-57	47.06	32	
			Fcirg_14532	2.80E-56	40.40	30	
			Fcirg_04013	3.52E-56	35.87	35	
			Fcirg_02359				

Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
			Fcirg_12009	1.35E-55	50.43	32	
			Fcirg_12299	1.67E-55	40.07	33	
			Fcirg_07090	1.76E-55	47.56	36	
				4.47E-55	35.19	32	
	<i>HNWD2</i>	CAL30202.1	Fcirg_11350	0.00	46.97	32	20
			Fcirg_08680	8.45E-135	37.38	34	
			Fcirg_05581	1.52E-129	35.85	32	
			Fcirg_11141	2.06E-128	36.47	35	
			Fcirg_14595	6.00E-106	31.55	32	
			Fcirg_14567	9.00E-76	38.44	33	
			Fcirg_10819	1.27E-63	45.09	33	
			Fcirg_12009	3.32E-55	49.39	33	
			Fcirg_05914	1.81E-54	39.64	35	
			Fcirg_14532	7.13E-52	43.51	32	
			Fcirg_12299	7.97E-52	44.24	33	
			Fcirg_08274	3.60E-51	47.06	32	
			Fcirg_01059				



Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
			Fcirg_09454	1.61E-50	42.92	34	20
			Fcirg_07090	1.76E-50	44.09	33	
			Fcirg_02359	4.14E-50	39.45	32	
			Fcirg_02056	9.47E-50	42.92	33	
			Fcirg_12056	9.39E-47	36.94	32	
			Fcirg_12012	1.93E-45	24.37	34	
			Fcirg_11515	6.90E-45	38.64	35	
				2.91E-44	24.81	33	
			Fcirg_11350	0.00	45.58	33	
			Fcirg_08680	3.48E-172	32.42	32	
			Fcirg_14595	8.25E-156	35.49	34	
			Fcirg_05581	3.92E-151	33.91	34	
			Fcirg_11141	2.69E-148	35.41	33	
			Fcirg_14567	1.97E-92	43.42	33	
			Fcirg_12012	1.51E-80	28.15	32	
			Fcirg_10819	1.98E-65	53.88	33	

Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
			Fcirg_14677	8.91E-65	25.43	32	
			Fcirg_04013	2.87E-60	35.81	33	
			Fcirg_05914	1.17E-59	45.91	35	
			Fcirg_06736	1.78E-59	41.39	34	
			Fcirg_14532	1.52E-58	51.77	32	
			Fcirg_12009	3.67E-58	41.39	33	
			Fcirg_02359	5.50E-58	51.13	34	
			Fcirg_12299	3.79E-57	41.39	33	
			Fcirg_07090	1.95E-55	35.28	35	
			Fcirg_01221	1.64E-54	50.22	32	
			Fcirg_01059	1.28E-53	48.03	33	
			Fcirg_08274	3.30E-53	46.22	34	
<b><i>Cryphonectria</i> <i>parasitica</i></b>	<i>vic-6</i>	AET07139.1	Fcirg_11323	8.54E-57	33.33	35	10
			Fcirg_14134	1.55E-56	33.67	31	
			Fcirg_05676	2.80E-53	34.01	33	
			Fcirg_11997	5.93E-51	32.53	30	

Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
<i>Aspergillus oryzae</i>			Fcirg_13663	1.05E-50	34.45	33	
			Fcirg_14563	1.59E-49	31.28	32	
			Fcirg_11570	1.39E-48	28.54	34	
			Fcirg_13201	3.13E-46	31.31	32	
			Fcirg_15261	3.27E-46	32.12	32	
			Fcirg_05610	4.05E-43	29.66	31	
	<i>vic-7</i>	QHN64381.1	Fcirg_15095	3.31E-92	44.90	34	1
	<i>AO078</i>	AO090001000078	none	-	-	-	0
	<i>AO370</i>	AO090701000370	Fcirg_15261	5.94E-51	29.83	31	3
			Fcirg_13927	6.51E-43	29.41	31	
			Fcirg_11570	2.25E-40	27.06	33	
	<i>AO404</i>	AO090701000404	Fcirg_14532	3.60E-98	32.34	34	10
			Fcirg_12299	8.51E-54	34.94	40	

Species	<i>vic/het</i> gene	NCBI Accession number <sup>1</sup>	<i>F. circinatum</i> (FSP34) <sup>2</sup>	E-value	Identity (%) <sup>3</sup>	Query coverage (HSP/query) <sup>4</sup>	Number of hits
			Fcirg_08274	6.57E-50	41.16	44	
			Fcirg_09952	5.28E-47	44.70	34	
			Fcirg_09454	5.20E-45	40.08	46	
			Fcirg_07090	7.54E-44	38.08	45	
			Fcirg_12009	5.07E-42	31.81	40	
			Fcirg_10819	2.67E-41	36.56	52	
			Fcirg_01059	2.85E-41	38.52	41	
			Fcirg_02359	4.35E-41	36.92	45	

<sup>1</sup>

National Centre for Biotechnology Institute (<https://www.ncbi.nlm.nih.gov>) accession numbers.

<sup>2</sup> Identified using the *het/vic* gene in tblastn searches against the genome of *F. circinatum* isolate FSP34

<sup>3</sup> Percentage identity: the determinant of how similar the query and the hit sequence are.

<sup>4</sup> The percentage query coverage (High-scoring segment pair [HSP] length/query length \*100), the determinant of how much of the query sequence is covered by the hit sequence.

Table 3. Gene number and genome position for putative orthologs of the known HET domain-encoding *vic/het* genes identified in *F. circinatum*.

Model species	<i>vic/het</i> gene	<i>F. circinatum</i> gene <sup>1</sup>	Position in the genome FSP34 <sup>2</sup>
<b><i>N. crassa</i></b>	<i>het-C</i>	Fcirg_07624	Chromosome 4: 1580319-1582889
	<i>het-6</i>	Fcirg_05558	Chromosome 5: 15885-160826
	<i>pin-C</i>	Fcirg_11570	Chromosome 8: 895280-897626
<b><i>P. anserina</i></b>	<i>het-D, het-E, het-R, HNWD1, HNWD2, HNWD3</i>	Fcirg_11350	Chromosome 8: 359267-363902
		Fcirg_08680	Chromosome 6: 100512-105287
		Fcirg_14595	Chromosome 11: 334152-340394
		Fcirg_11141	Chromosome 7: 324973-3210650
		Fcirg_05581	Chromosome 5: 208037-211991
		Fcirg_12012	Chromosome 8: 2133397-2137752
		Fcirg_14677	Chromosome 11: 513905-519406`
<b><i>C. parasitica</i></b>	<i>vic-6</i>	Fcirg_05676	Chromosome 5: 430849-432451
		Fcirg_11997	Chromosome 8: 2096256-2098248
	<i>vic-7</i>	Fcirg_15095	Chromosome 11: 1644971-1647228
<b><i>A. oryzae</i></b>	<i>AO370</i>	Fcirg_05610	Chromosome 6: 2340225-2342183
	<i>AO404</i>	Fcirg_14532	Chromosome 11: 176925-179045

<sup>1</sup> Identified using a phylogeny-based approach (see Figures 2-9).

<sup>2</sup> Nucleotide position of the putative *vic/het* gene orthologs in the genome of strain FSP34 of *F.circinatum*.

Table 4: Number of homologs of the *F. circinatum* *het/vic* orthologs detected in genomes of four model fungi.

Reference fungi	<i>vic/het</i> gene	<i>F. circinatum</i> query <sup>2</sup>	Number of tblastn hits	Best hit information			
				Accession number	E-value	Identity (%)	Query coverage (%) <sup>3</sup>
<b><i>N. crassa</i></b>	<i>het-c</i>	Fcirg_07624	2	NC_026502	0.00	80.00	95.00
	<i>het-6</i>	Fcirg_05558	3	NC_026502	2.08E-101	36.98	51.45
	<i>pin-C</i>	Fcirg_08239	No hit	-	-	-	-
	<i>vic-6</i>	Fcirg_05676	1	NC_026506	7.73E-51	34.82	51.53
	<i>vic-6</i>	Fcirg_11997	4	NC_026507	1.96E-57	34.08	51.26
	<i>vic-7</i>	Fcirg_15095	No hit	-	-	-	-
	<i>AO370</i>	Fcirg_05610	1	NC_026503	8.83E-87	33.73	47.59
	<i>AO404</i>	Fcirg_14532	2	NC_026504	8.18E-82	51.08	70.56
	<i>HNWD</i> representative	Fcirg_11350	No hit	-	-	-	-
<b><i>P. anserina</i></b>	<i>het-c</i>	Fcirg_07624	2	NW_001914857	3.46E-121	52.72	69.39
	<i>het-6</i>	Fcirg_05558	2	NW_001914834	3.61E-147	39.05	56.90
	<i>pin-C</i>	Fcirg_08239	2	NW_001914834	1.82E-45	31.40	49.03
	<i>vic-6</i>	Fcirg_05676	1	NW_001914854	4.49E-48	30.70	45.63
	<i>vic-6</i>	Fcirg_11997	1	NW_001914857	6.99E-41	30.24	46.11

	<i>vic-7</i>	Fcirg_15095	No hit	-	-	-	-
	<i>AO370</i>	Fcirg_05610	2	NW_001914837	1.60e-46	32.07	46.56
	<i>AO404</i>	Fcirg_14532	12	NW_001914846	1.35E-80	52.72	69.39
	<i>HNWD</i> representative	Fcirg_11350	10	NW_001914858	0.00	100	57.36
<b><i>C. parasitica</i></b>	<i>het-c</i>	Fcirg_07624	2	NW_024468912	0.00	70.24	80.36
	<i>het-6</i>	Fcirg_05558	No hit	-	-	-	-
	<i>pin-C</i>	Fcirg_08239	2	NW_024468909	6.42E-45	33.42	48.77
	<i>vic-6</i>	Fcirg_05676	3	NW_024468911	3.07E-54	34.63	50.39
	<i>vic-6</i>	Fcirg_11997	2	NW_024468911	2.18E-47	32.48	49.00
	<i>vic-7</i>	Fcirg_15095	1	NW_024468914	8.23E-96	38.92	53.63
	<i>AO370</i>	Fcirg_05610	2	NW_024468912	1.80E-47	35.64	48.24
	<i>AO404</i>	Fcirg_14532	4	NW_024468911	2.41E-75	46.82	60.90
	<i>HNWD</i> representative	Fcirg_11350	4	NW_024468910	0.00	69.32	50.10
<b><i>A. oryzae</i></b>	<i>het-c</i>	Fcirg_07624	2	NC_036438	8.71E-163	61.97	78.87
	<i>het-6</i>	Fcirg_05558	1	NC_036440	6.03E-54	29.36	42.35
	<i>pin-C</i>	Fcirg_08239	2	NC_036438	5.20E-48	38.54	51.56
	<i>vic-6</i>	Fcirg_05676	No hit	-	-	-	-
	<i>vic-6</i>	Fcirg_11997	No hit	-	-	-	-

<i>vic-7</i>	Fcirg_15095	No hit	-	-	-	-
<i>AO370</i>	Fcirg_05610	No hit	-	-	-	-
<i>AO404</i>	Fcirg_14532	6	NC_036441	6.73E-159	50.84	68.23
<i>HNWD</i> representative	Fcirg_11350	8	NC_036440	2.05E-79	70.00	22.35

<sup>1</sup>The identified *het/vic* gene orthologs of *F. circinatum* isolate FSP34 used in the tblastn search sequences of the against fungi.

<sup>2</sup>National Centre for Biotechnology Institute (<https://www.ncbi.nlm.nih.gov>) accession numbers.



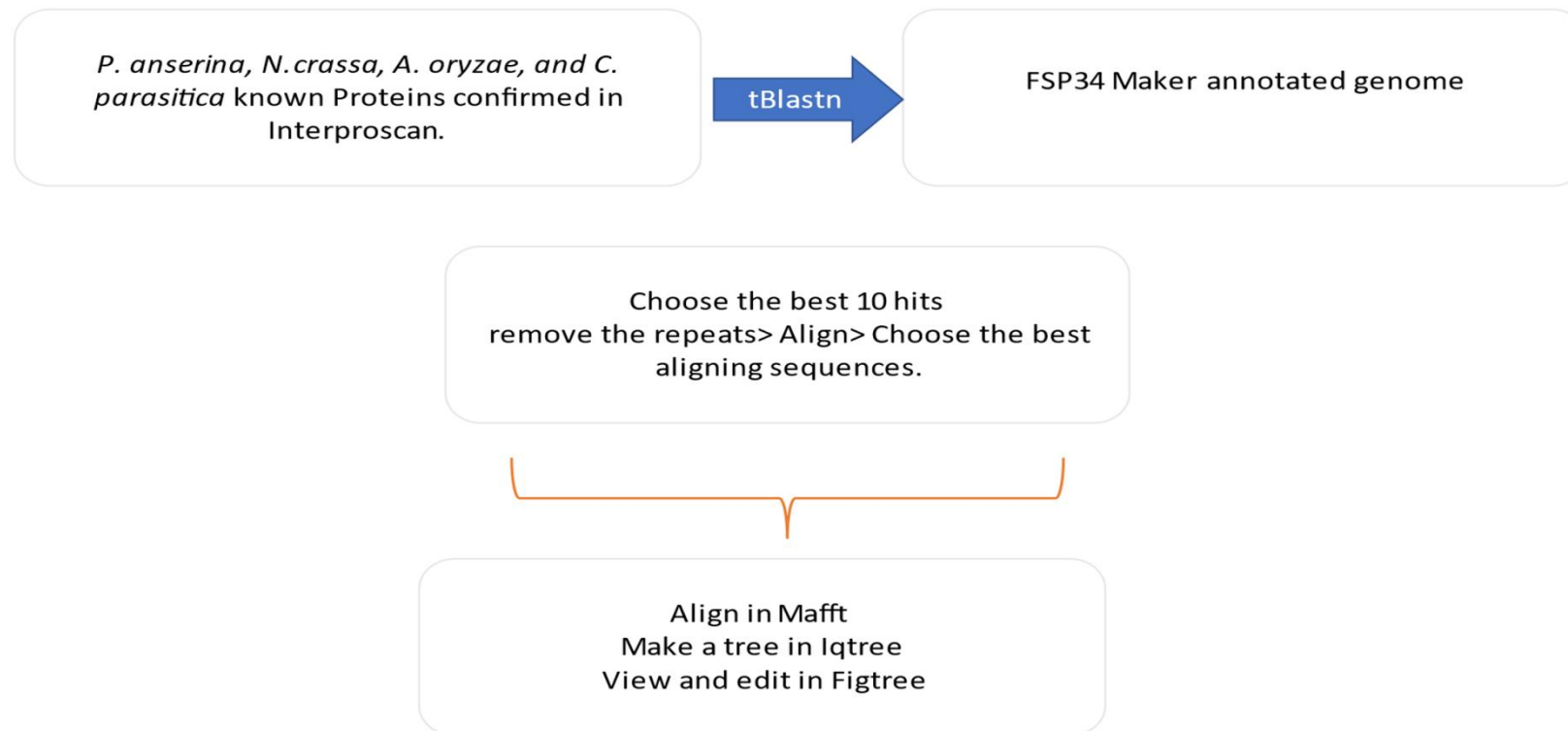


Figure 1: Overview of the methodology used to identify orthologs of the known HET-domain containing het/vic genes from four model fungi.

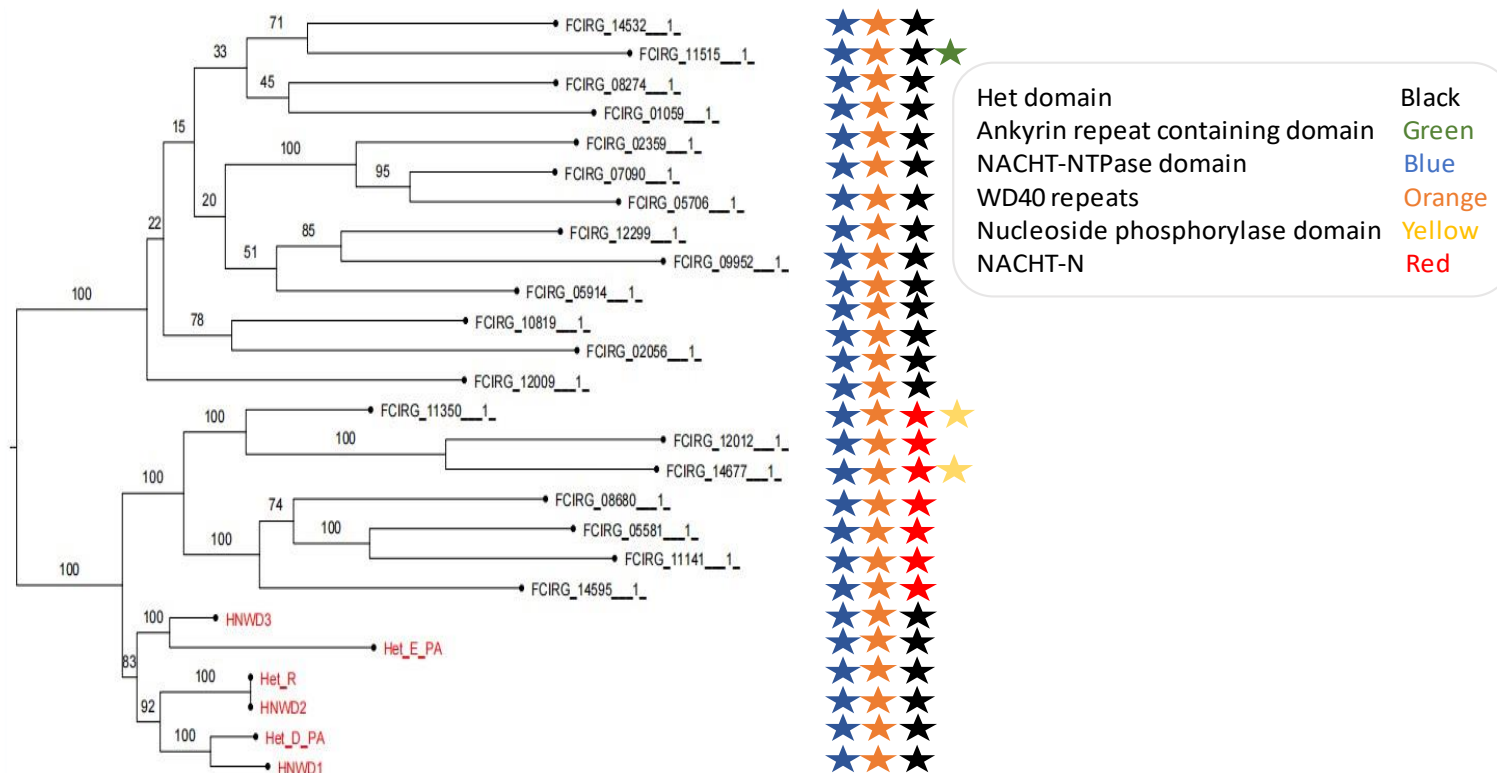


Figure 2: Phylogenetic tree showing the relationships among the *Podospira anserina* het domain coding genes such as *Het-D*, *Het-R*, *Het-E*, *HNWD1*, *HNWD2*, *HNWD3* and their blast hits and domains they code for in *F. circinatum* FSP34 isolate. Each coloured star represents a different protein domain that was identified using the InterProScan per gene in the phylogenetic tree.

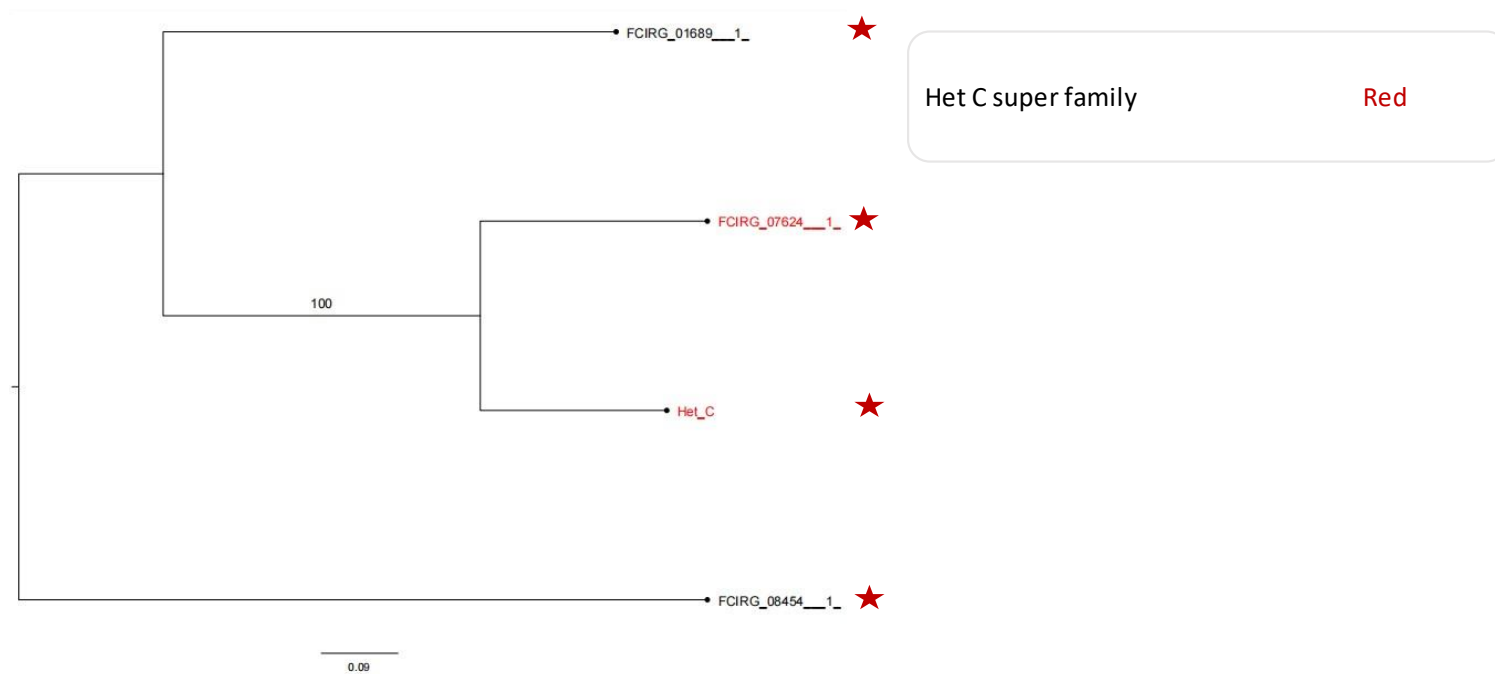


Figure 3: Phylogenetic tree showing the *het-C* homolog and domains they code for in *F. circinatum* FSP34 isolate. Each coloured star represents a different protein domain that was identified using the InterProScan per gene in the phylogenetic tree.

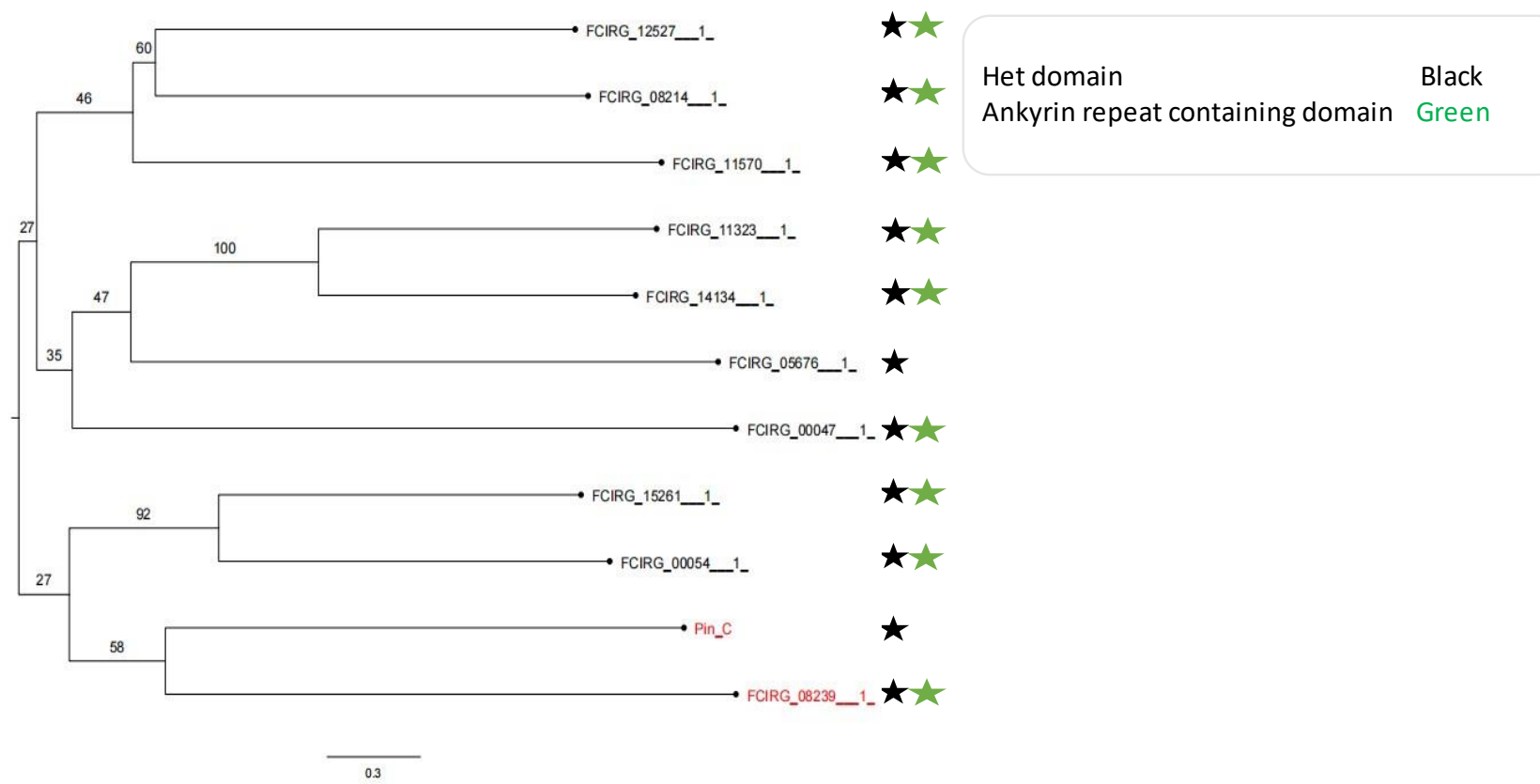


Figure 4: Phylogenetic tree showing the *Pin-C* homolog and domains they code for in *F. circinatum* FSP34 isolate. Stars represent a different protein domain that was identified using the InterProScan per gene in the phylogenetic tree.

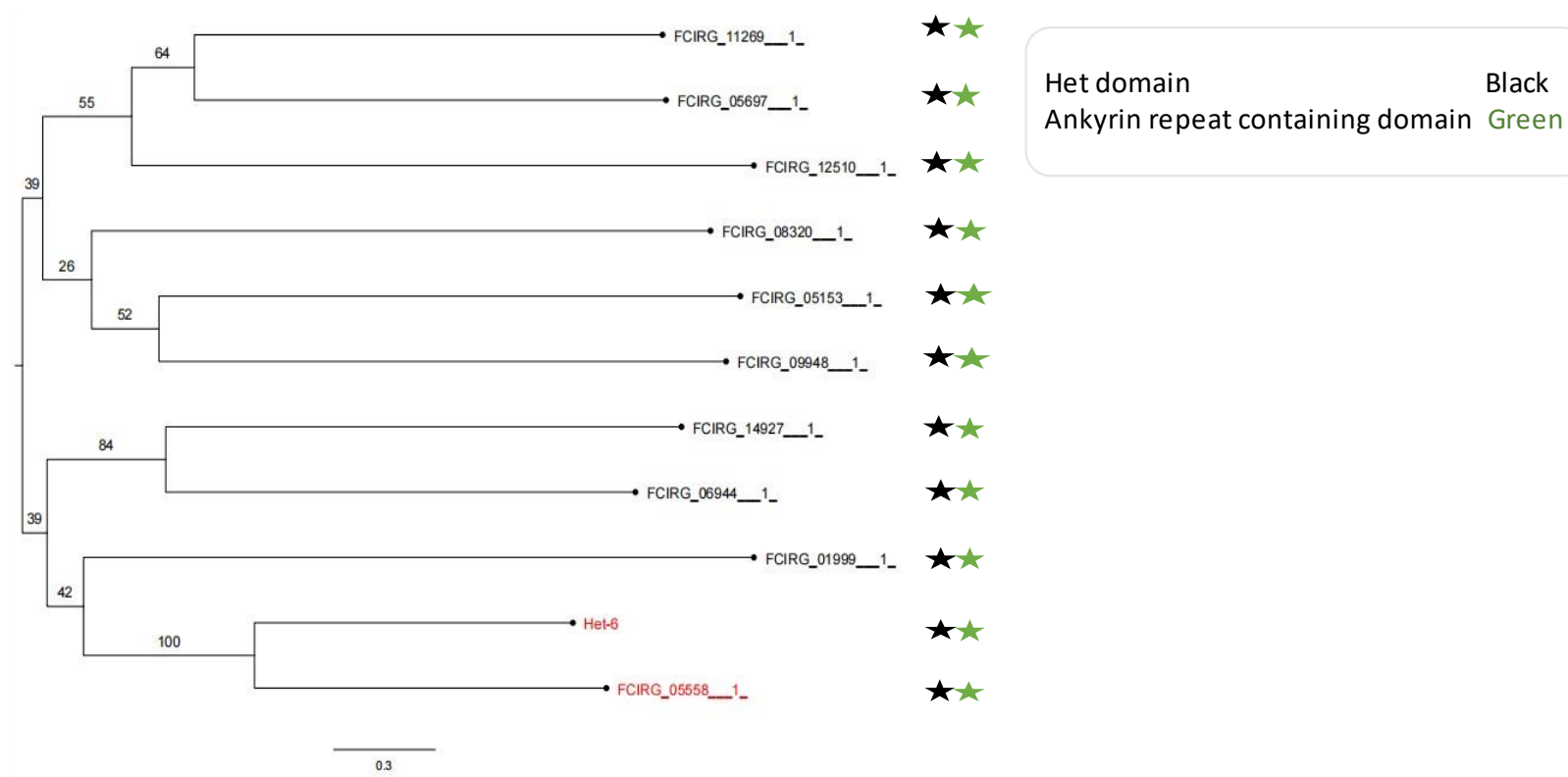


Figure 5: Phylogenetic tree showing the *het-6* homolog and domains they code for in *F. circinatum* FSP34 isolate. Each coloured star represents a different protein domain that was identified using the InterProScan per gene in the phylogenetic tree.

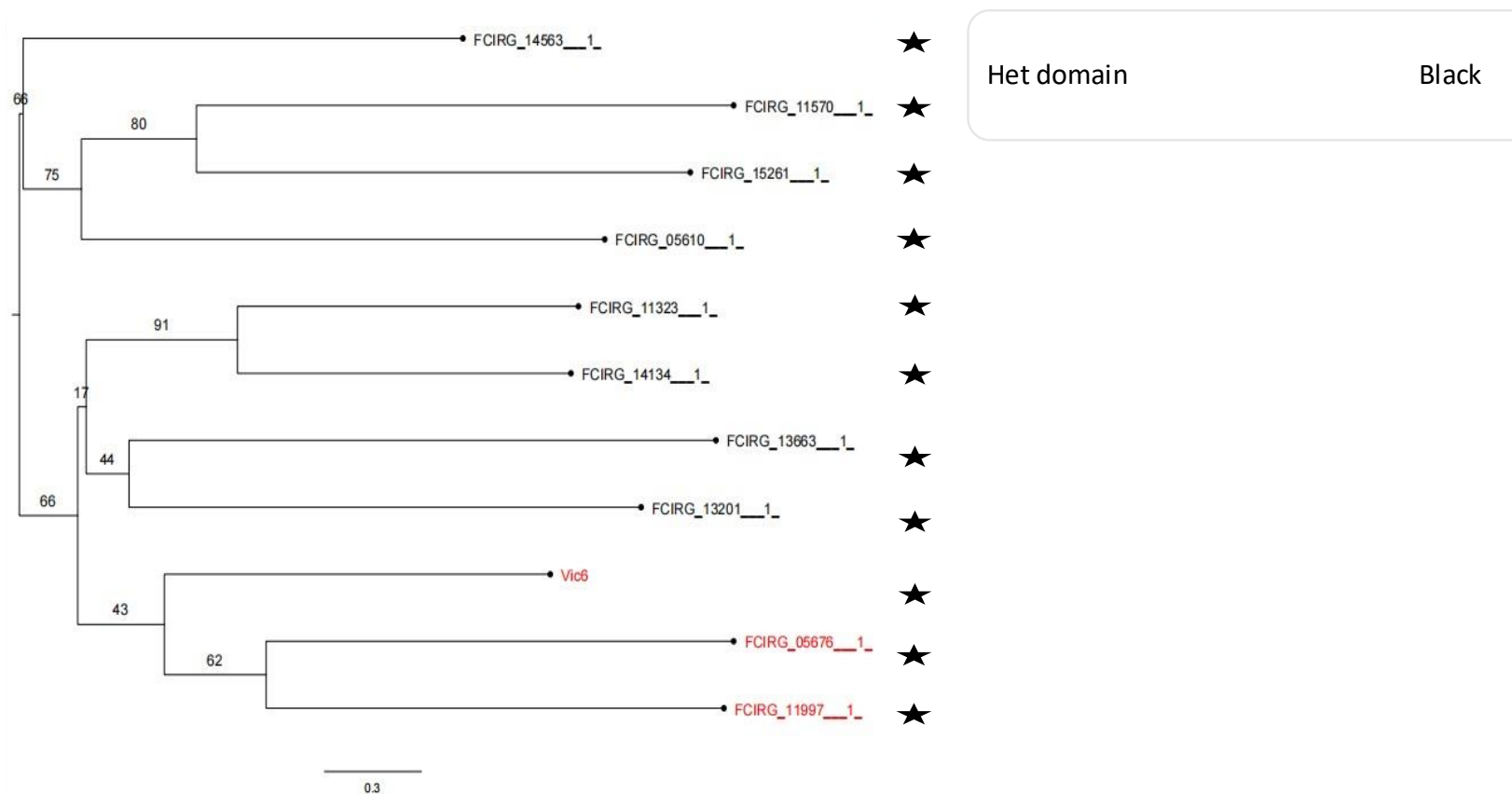


Figure 6: Phylogenetic tree showing the *vic-6* hits and domains they code for in *F. circinatum* FSP34 isolate. Each coloured star represents a different protein domain that was identified using the InterProScan per gene in the phylogenetic tree.

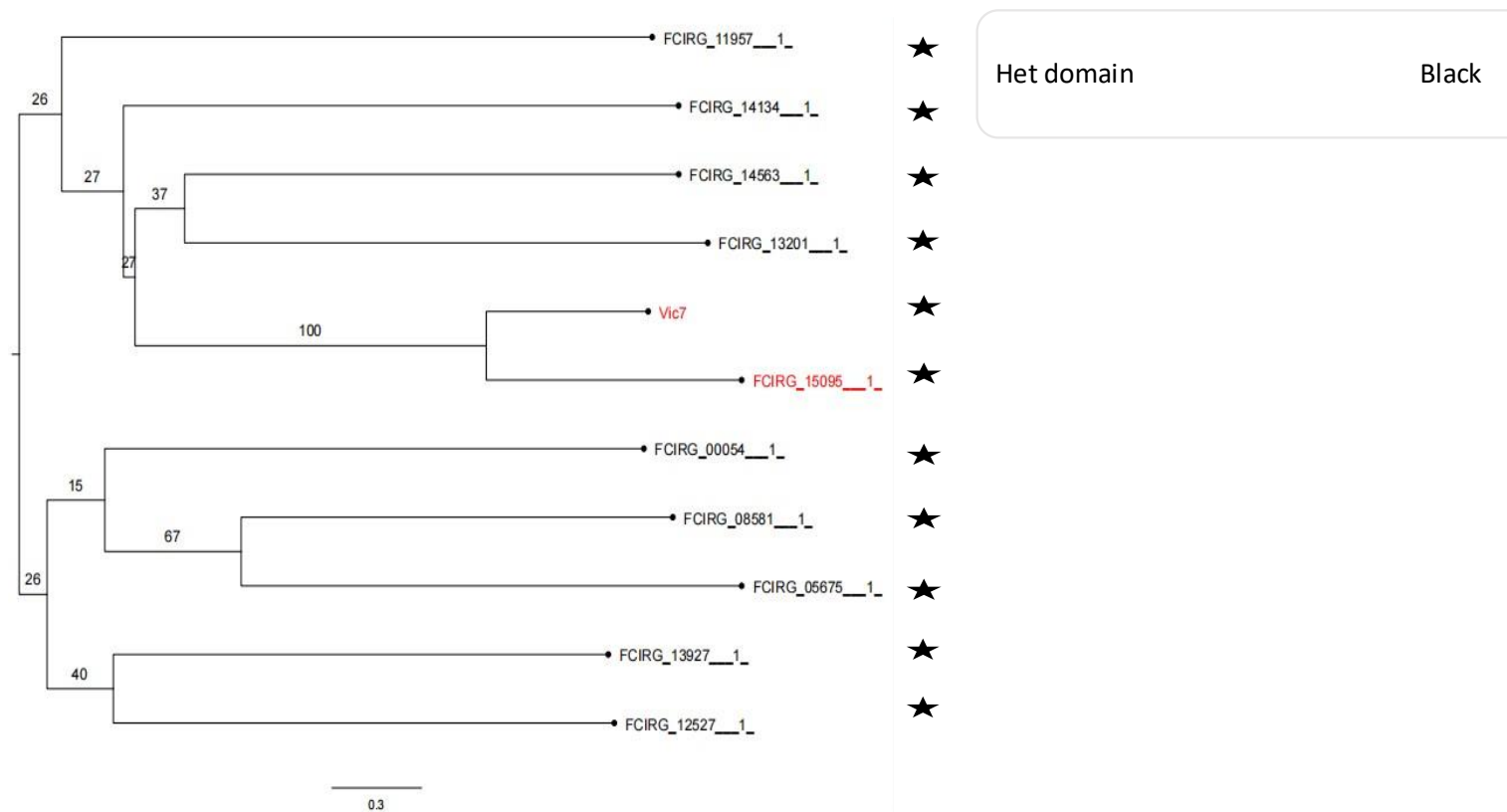


Figure 7: Phylogenetic tree showing the *vic-7* homolog and other close hits, and domains they code for in *F. circinatum* FSP34 isolate. Each coloured star represents a different protein domain that was identified using the InterProScan per gene in the phylogenetic tree.

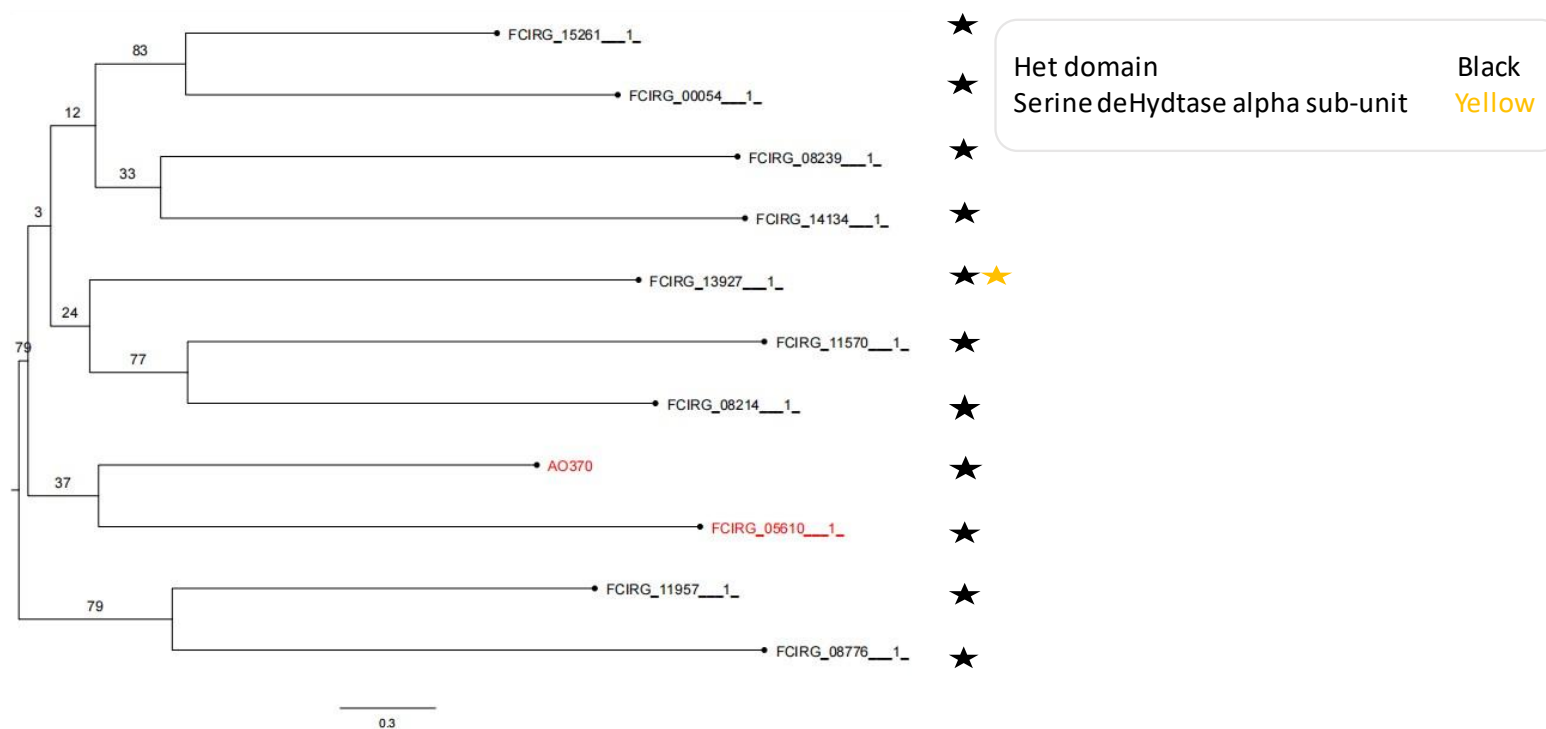


Figure 8: Phylogenetic tree showing the *AO370* homolog and other close hits, and domains they code for in *F. circinatum* FSP34 isolate. Each coloured star represents a different protein domain that was identified using the InterProScan per gene in the phylogenetic tree.



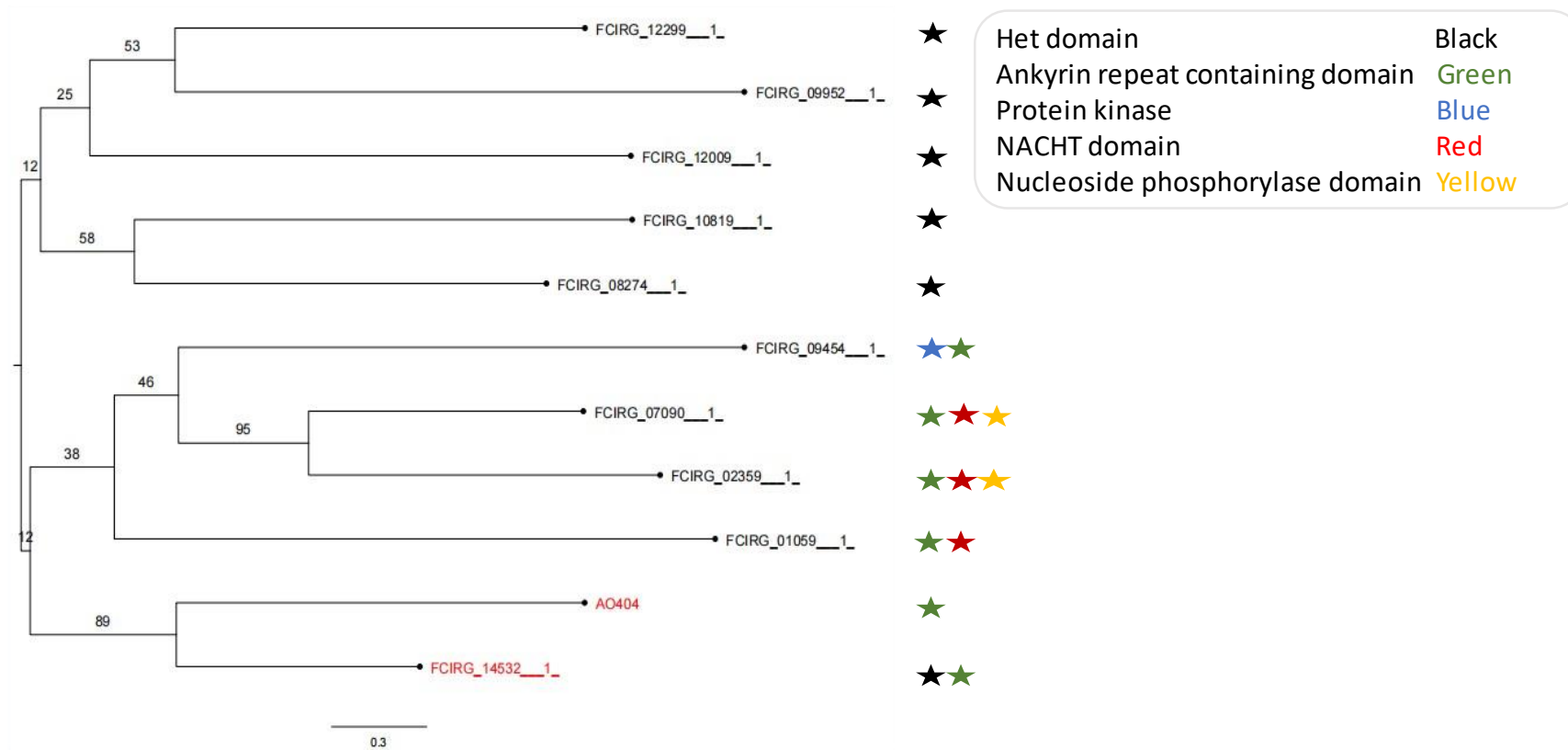


Figure 9: Phylogenetic tree showing the AO404 hits and domains they code for in *F. circinatum* FSP34 isolate. Each coloured star represents a different protein domain that was identified using the InterProScan per gene in the phylogenetic tree.