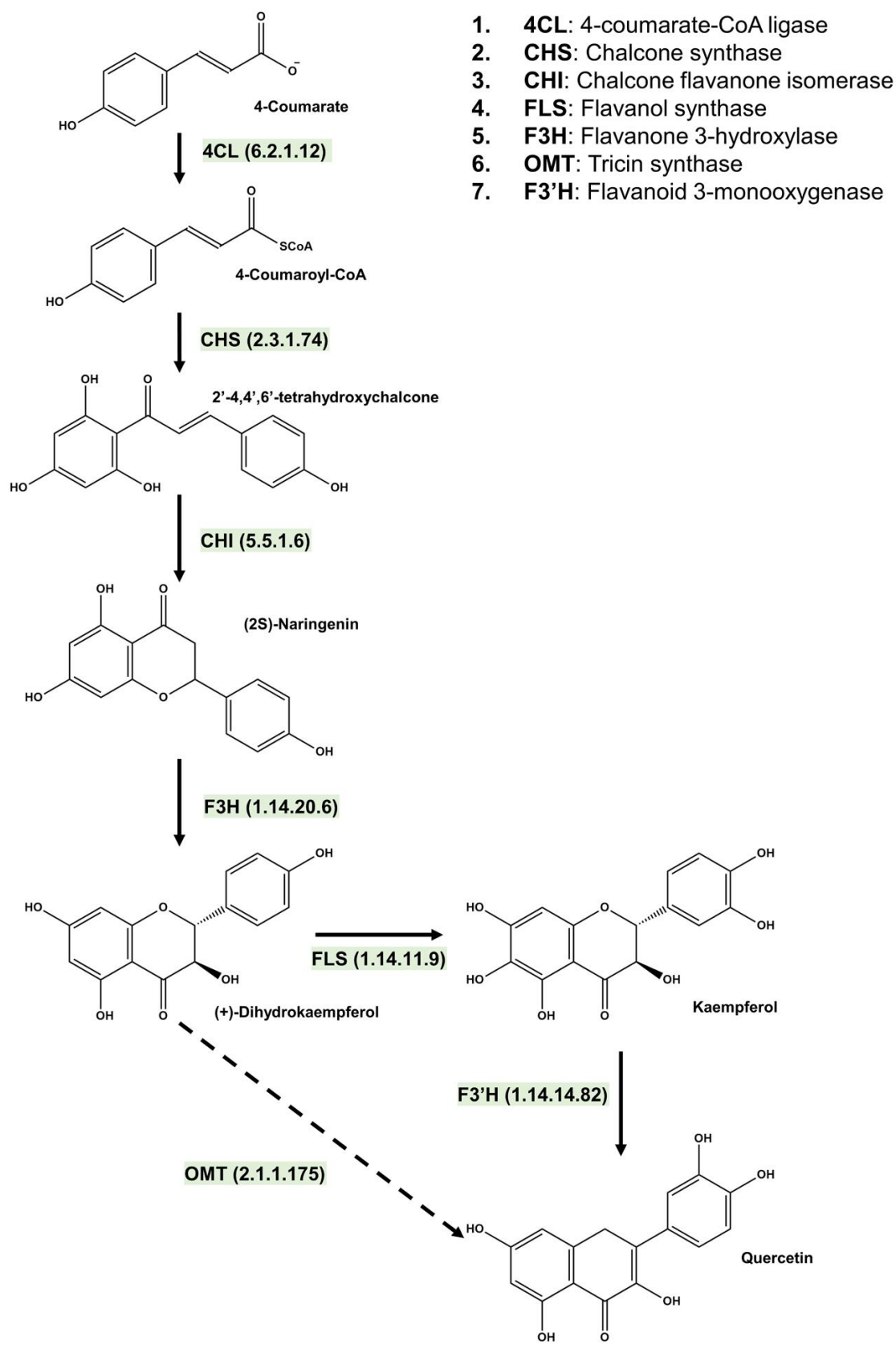


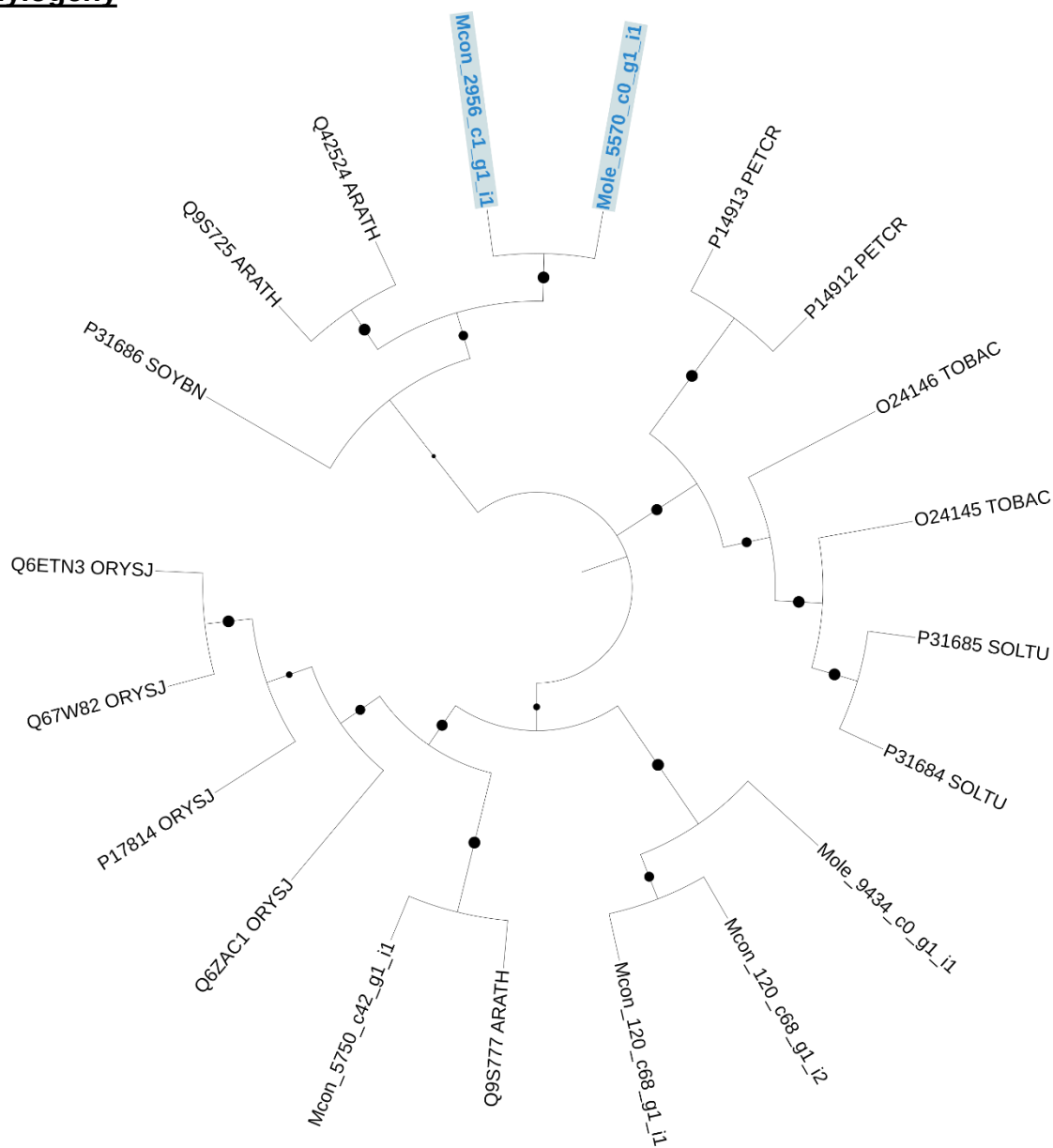
Quercetin biosynthesis

Pathway



1. 4-coumarate-CoA ligase (4CL)

Phylogeny



FIR mapping

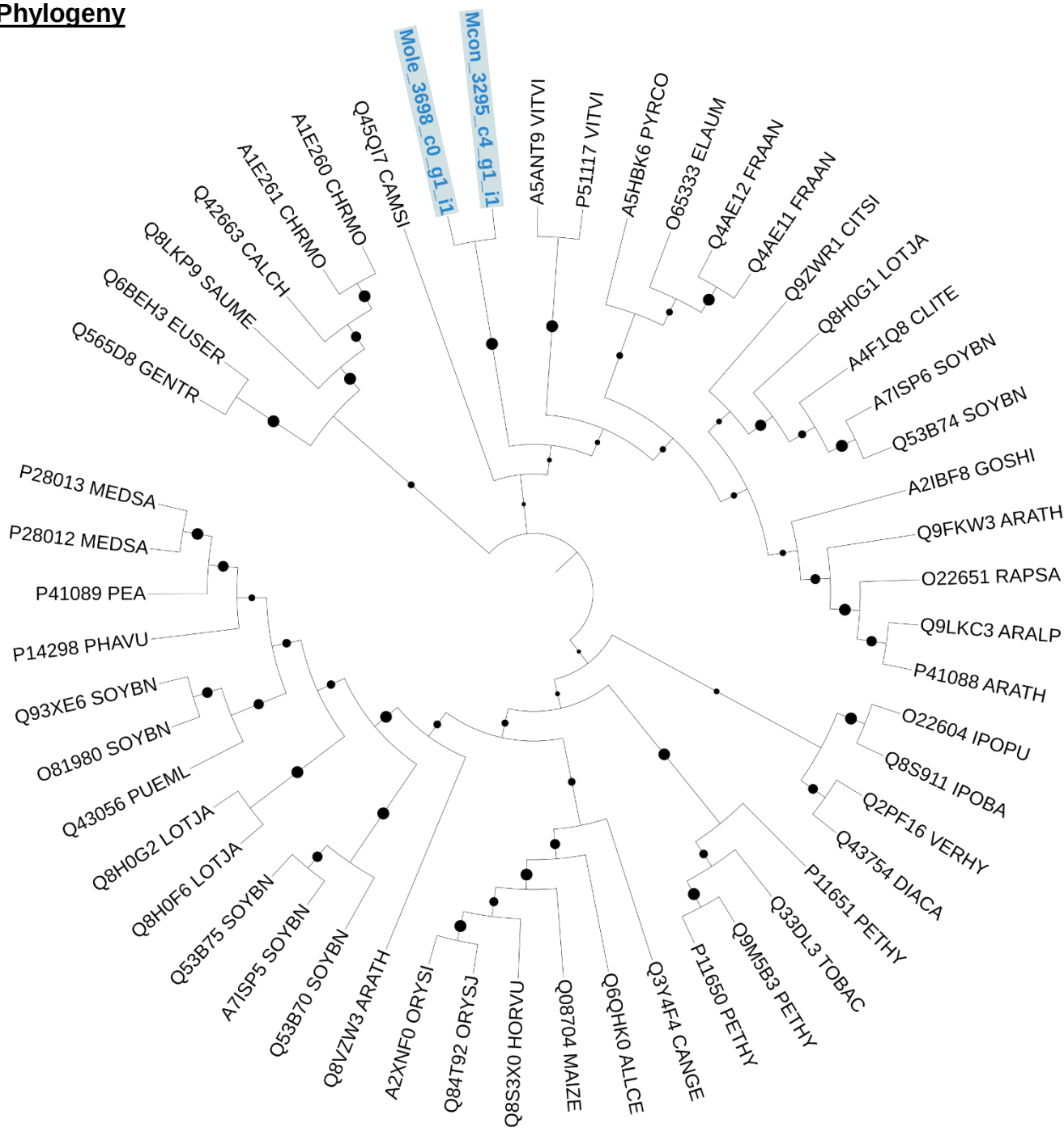
	190	200	210	390	400	410
Mole_5570_c0_g1_i1	NPDDVVALPYSSGTTGLPKGVMLTHK			SLPRNQPG	GEICIRGN	QIMKGYLND
Mcon_2956_c1_g1_i1	NPDDVVALPYSSGTTGLPKGVMLTHK			SLPRNQPG	GEICIRGN	QIMKGYLND
Q42524_ARATH	SPDDVVALPYSSGTTGLPKGVMLTHK			SLSRNQPG	GEICIRGH	QIMKGYLNN
P31684_SOLTU	QPDDVVALPYSSGTTGLPKGVMLTHK			SLPRNQPG	GEICIRGD	QIMKGYLND
O24145_TOBAC	QPDDVVALPYSSGTTGLPKGVMLTHK			SLPRNQPG	GEICIRGD	QIMKGYLND
Q67W82_ORYSJ	HPDDVVALPYSSGTTGLPKGVMLTHR			TLGRNQSG	GEICIRGE	QIMKGYLND

AMP-binding domain

Catalytic site

3. Chalcone flavanone isomerase (CHI)

Phylogeny



FIR mapping

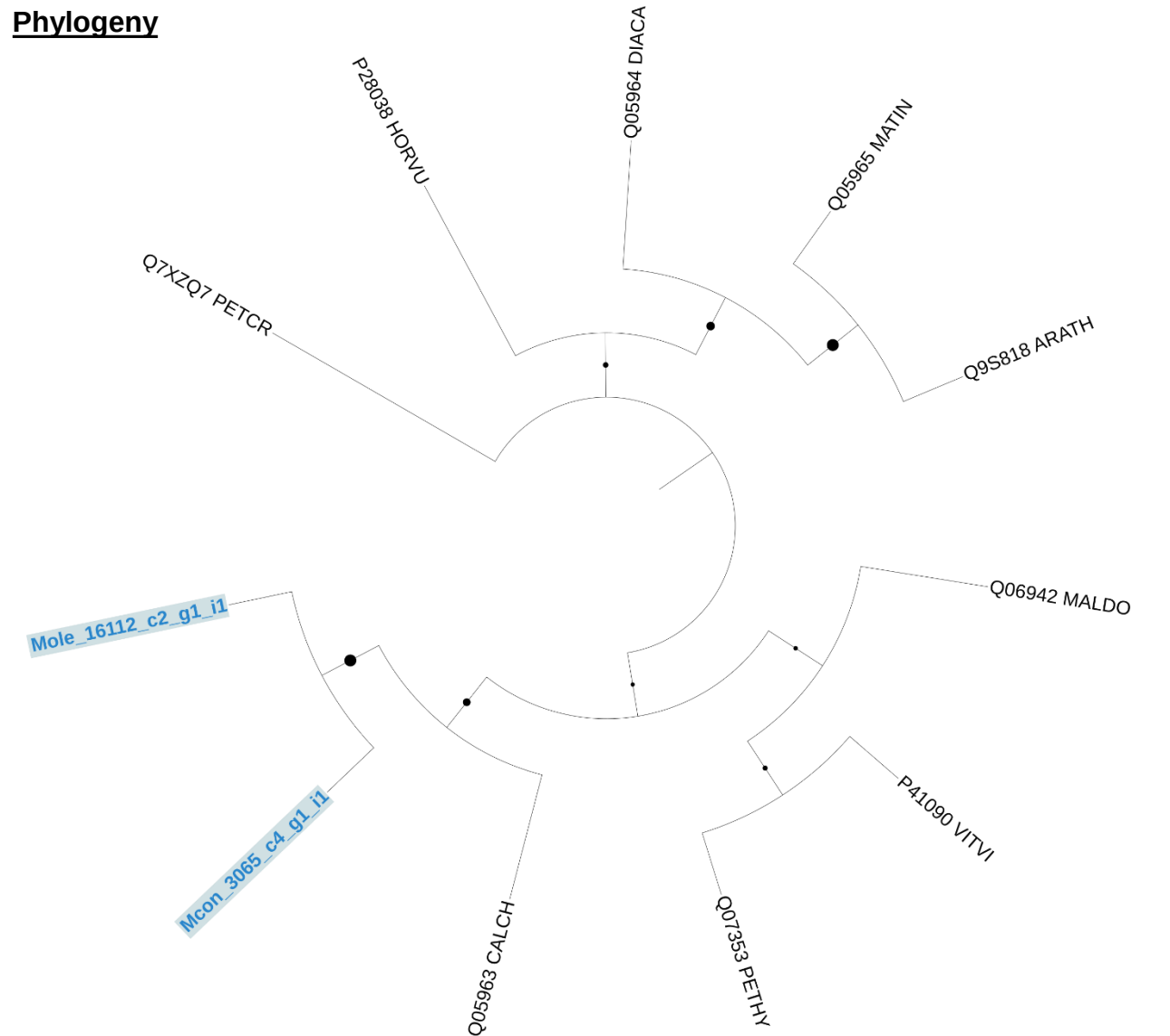
Mcon_3295_c4_g1_i1
Mole_3698_c0_g1_i1
P41088_ARATH
P51117_VITVI
Q84T92_ORYSJ
A7ISP6_SOYBN

50				60				70				120				130				210																																					
G	A	G	E	R	G	L	E	I	Q	Q	F	V	K	F	T	A	I	G	V	Y	L	M	I	L	P	L	T	G	Q	Y	S	E	K	V	A	E	N	C	V	K	Y	W	K	G	A	V	L	E	S	I	I	G	E	H	G	V	
G	A	G	E	R	G	L	E	I	Q	Q	F	V	K	F	T	A	I	G	V	Y	L	M	I	L	P	L	T	G	Q	Y	S	E	K	V	A	E	N	C	V	K	Y	W	K	G	A	V	L	E	S	I	I	G	E	H	G	V	
G	A	G	V	R	G	L	D	I	Q	G	F	V	I	F	T	V	I	G	V	Y	L	M	K	L	P	L	T	G	Q	Y	S	E	K	V	T	E	N	C	V	A	I	W	K	E	A	V	L	E	S	I	I	G	K	N	G	V	
G	A	G	V	R	G	L	E	I	Q	G	F	V	K	F	T	A	I	G	V	Y	L	T	I	L	P	L	T	G	R	Q	Y	S	E	K	V	T	E	N	C	V	A	F	W	K	E	A	V	L	E	S	I	I	G	K	H	G	V
G	A	G	V	R	G	V	E	I	A	G	N	F	I	K	F	T	A	I	G	V	Y	L	M	I	L	P	L	T	G	Q	Y	S	E	K	V	T	E	N	C	V	A	A	W	K	E	A	V	L	E	S	I	I	G	H	G	V	
G	A	G	V	R	G	L	Q	I	H	H	A	F	V	K	F	T	A	I	C	V	Y	L	M	I	K	P	L	T	G	Q	Y	S	E	K	V	A	E	N	C	V	A	I	W	R	E	A	V	L	E	S	M	I	G	K	N	G	V

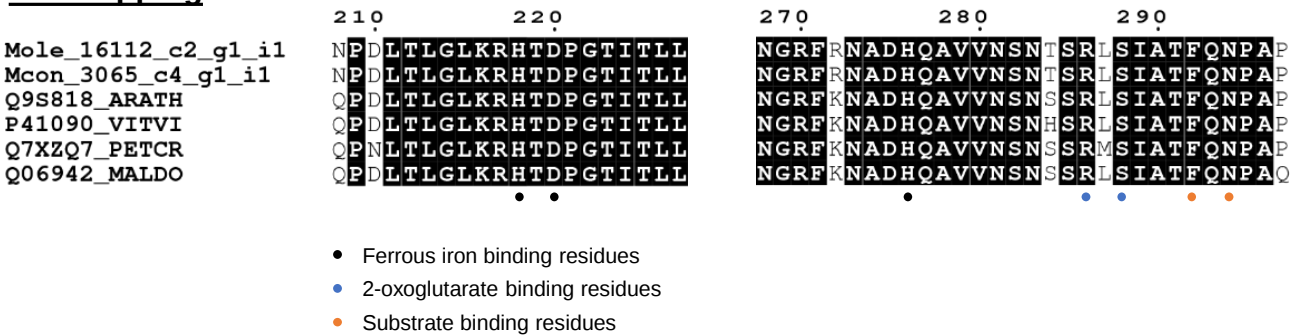
- Binding site residues

4. Flavanol synthase (FLS) / 5. Flavanone 3-hydroxylase (F3H)

Phylogeny

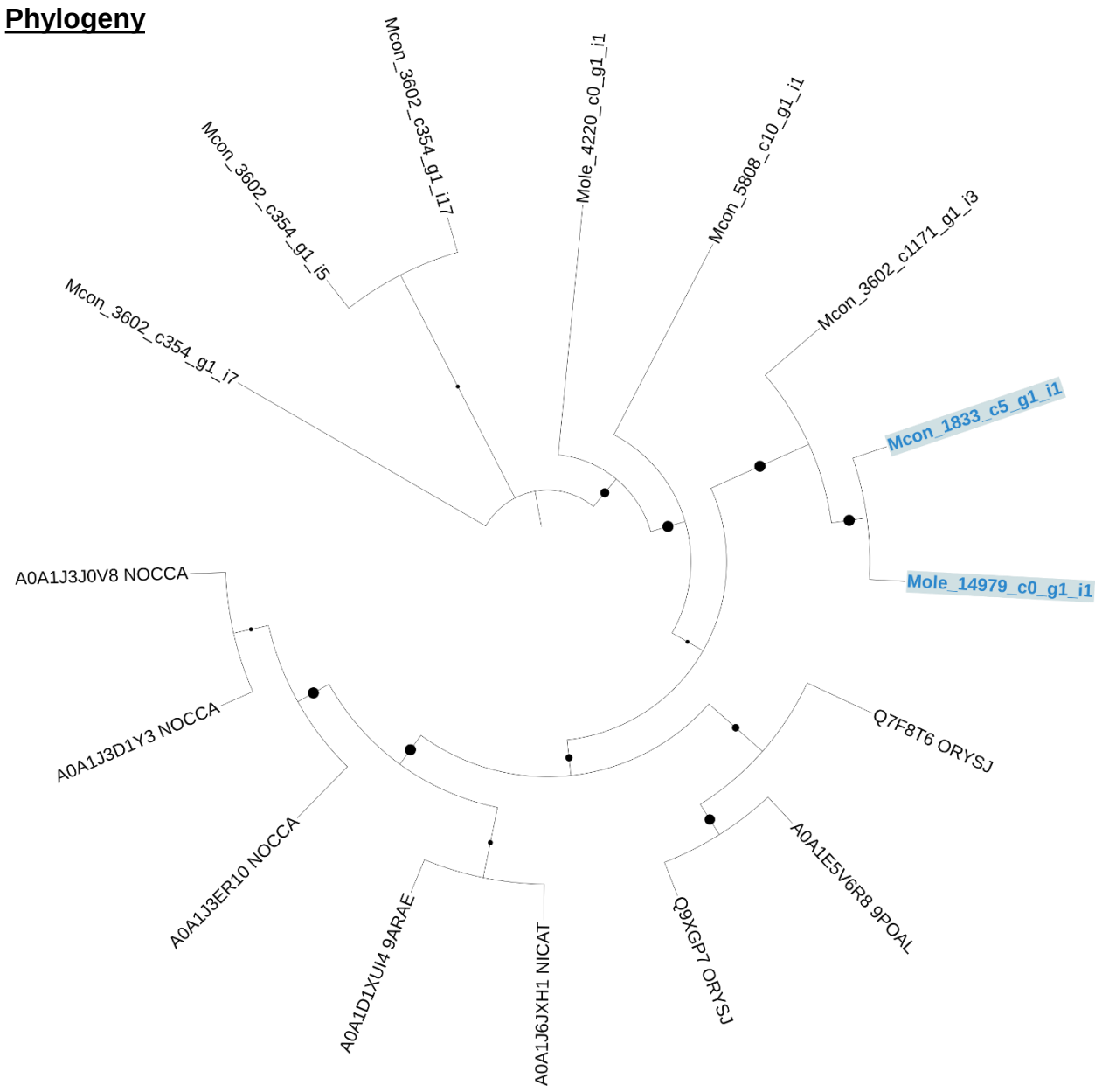


FIR mapping



5. Tricin synthase (OMT)

Phylogeny

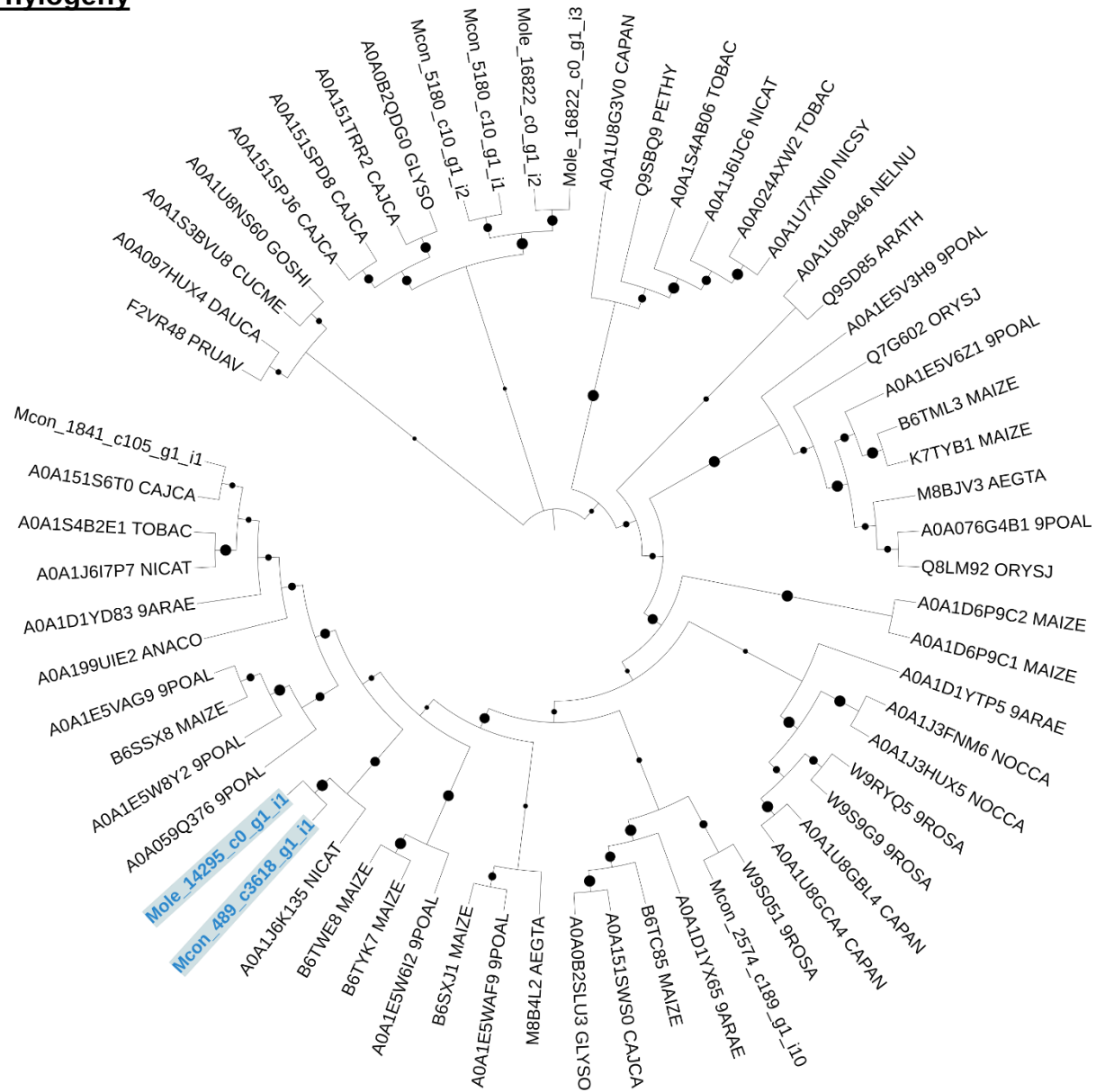


FIR mapping



6. Flavanoid 3-monooxygenase (F3'H)

Phylogeny



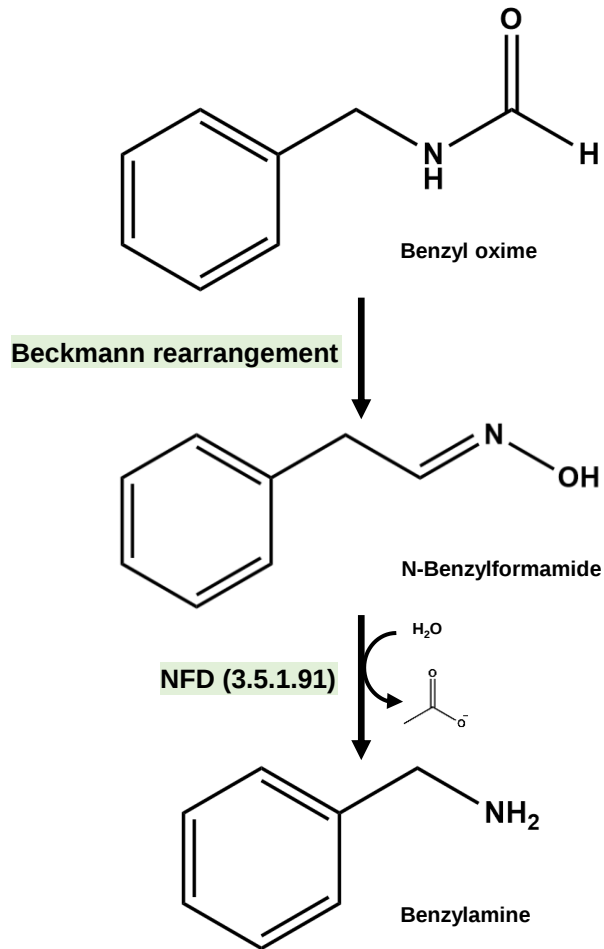
FIR mapping

	440	450	460	470
Mcon_489_c3618_g1_i1	GRSFE	LIPFGS	GRRMCPGYS	LGLKMIQSMLANLLHGFHW
Mole_14295_c0_g1_i1	GRSFE	LIPFGS	GRRMCPGYS	LGLKMIQSMLANLLHGFHW
M8B4L2_AEGTA	GQDME	LIPFGA	GRRMCPGYS	LGLKVVQLIVANLLHGFHW
B6TWE8_MAIZE	GHDFQ	LIPFGS	GRRMCPGIN	LALKVMALSLANLLHGFHW
A0A1J6K135_NICAT	GQNFT	LIPFGS	GRRRC	CPGHNLG
Q9SD85_ARATH	GSDFE	LIPFGA	GRRIC	AGLSLGLRTIQFLTATLVQGFHW

Heme binding region

Benzylamine biosynthesis

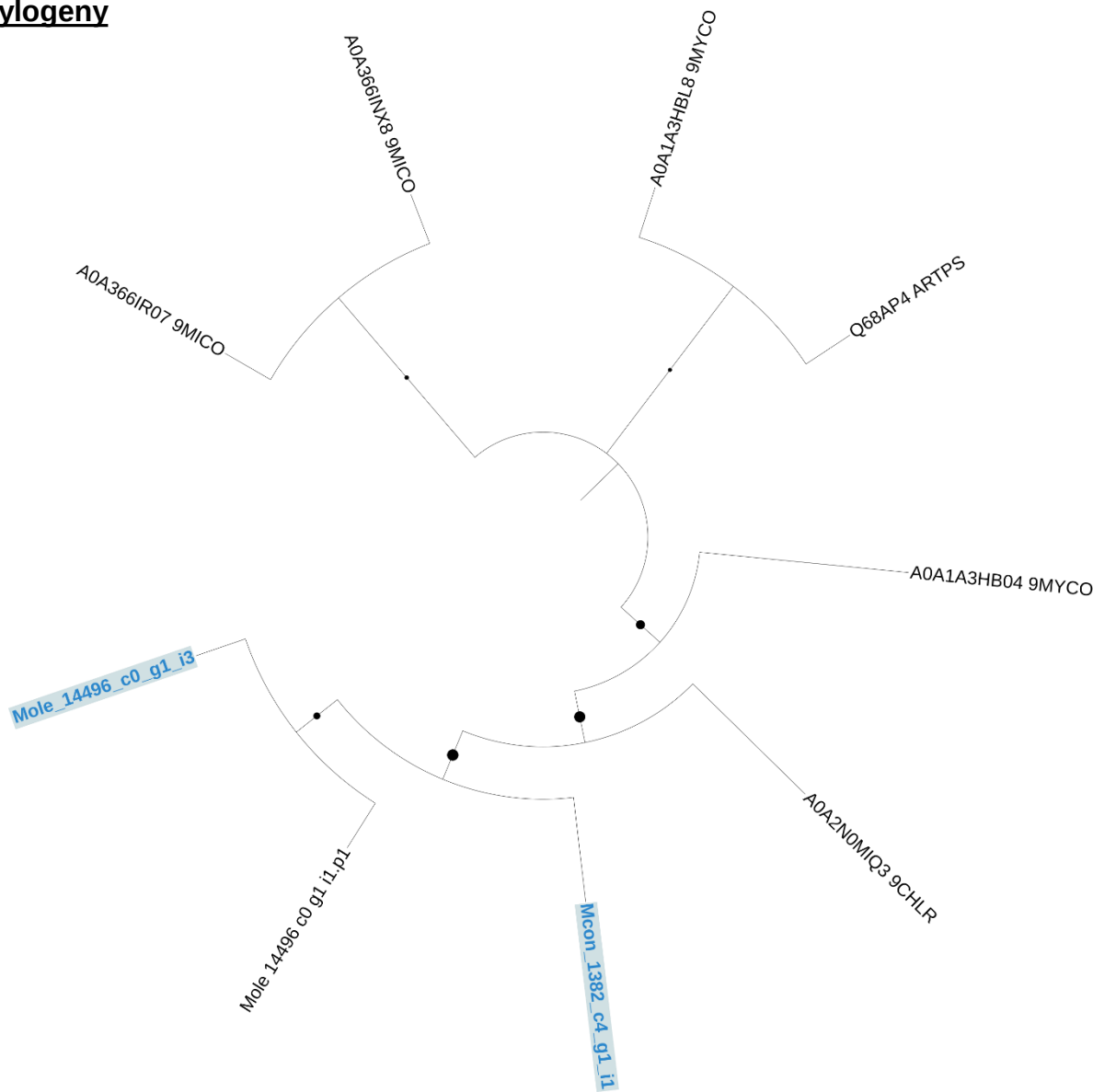
Pathway



1. **NFD**: N-substituted formamide deformylase

1. N-substituted formamide deformylase (NFD)

Phylogeny



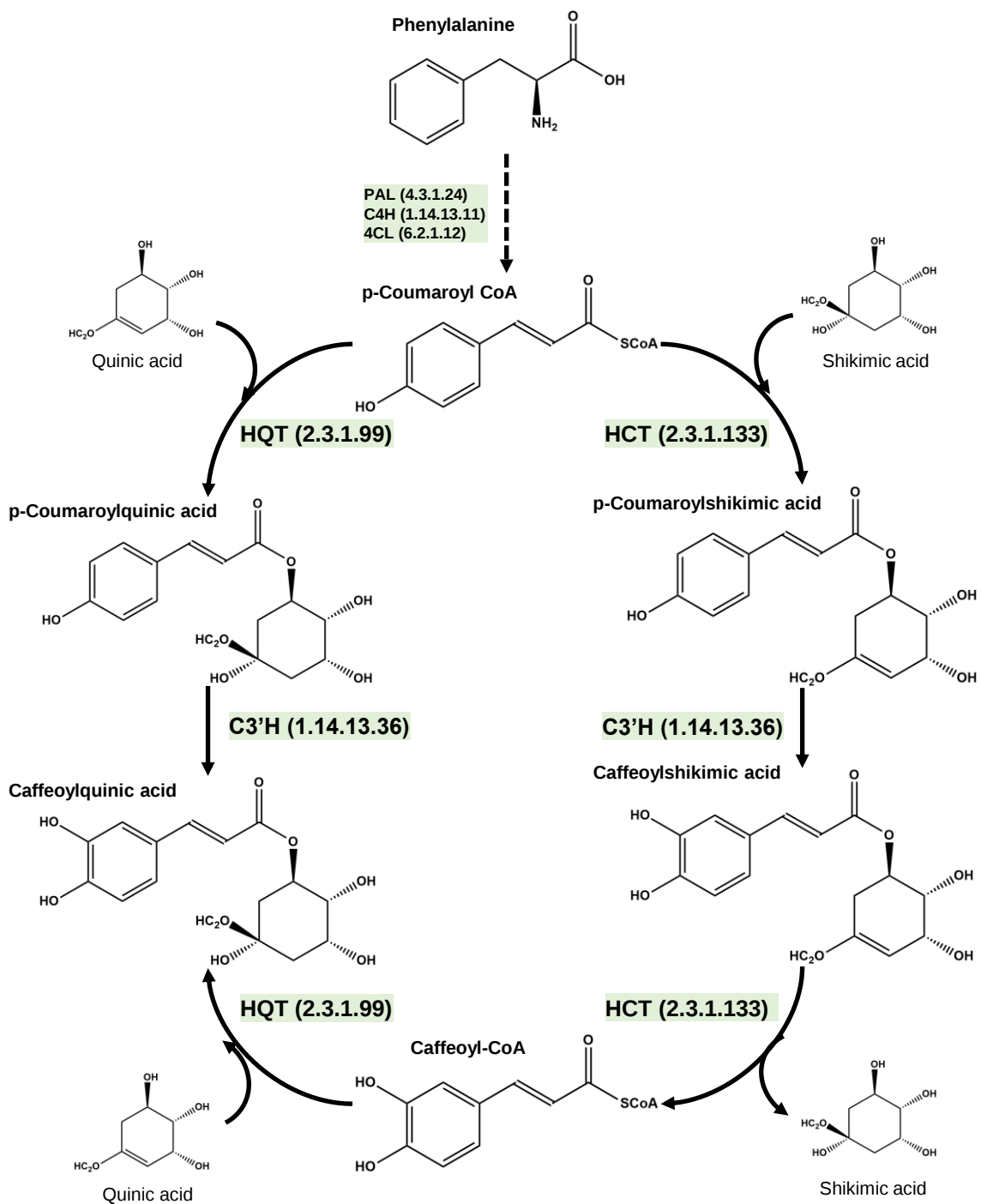
FIR mapping

	100	110	380	410	420	470	480
Mole_14496_c0_g1_i3	RKVVV	PGFIDSHVHLIFGGGL	ASDESGLQVAIH	QDRRFRIEHAQHLAPG	SRGALLALGSDW	FVVDI	
Mcon_1382_c4_g1_i1	RKVVV	PGFIDSHVHLIFGGGL	ASDESGLQVAIH	QDRRFRIEHAQHLAPG	SRGALLALGSDW	FVVDI	
A0A2N0MIQ3_9CHLR	GRTLL	PAFSDPHNHFSINTL	QAHKRGMQVAIH	EEPRFRTEHFTITSIA	DQGLTVSGSDY	PCGFL	
A0A366INX8_9MICO	GRAVV	PGFIDAHNHMSIAAF	TAAAGCIDLAIH	DDPTDRLIEHAFIAEKA	DAGVRVSFASDH	PCGTY	
Q68AP4_ARTPS	GKTVV	PGFIDAHNHLSVAAF	RASKLGINLAIH	ADTVLRLEHAFIAETG	DAGVRVSLASDH	PCGTY	
A0A1A3HBL8_9MYCO	GRIVV	PGFIDVHNHLSISAF	AAGDLCIGTGAIH	IDSVLRMEHAFIAAPE	DAGVRVTLASDH	PCGPF	
		●		●			

- Metal binding residues

Chlorogenic acid biosynthesis

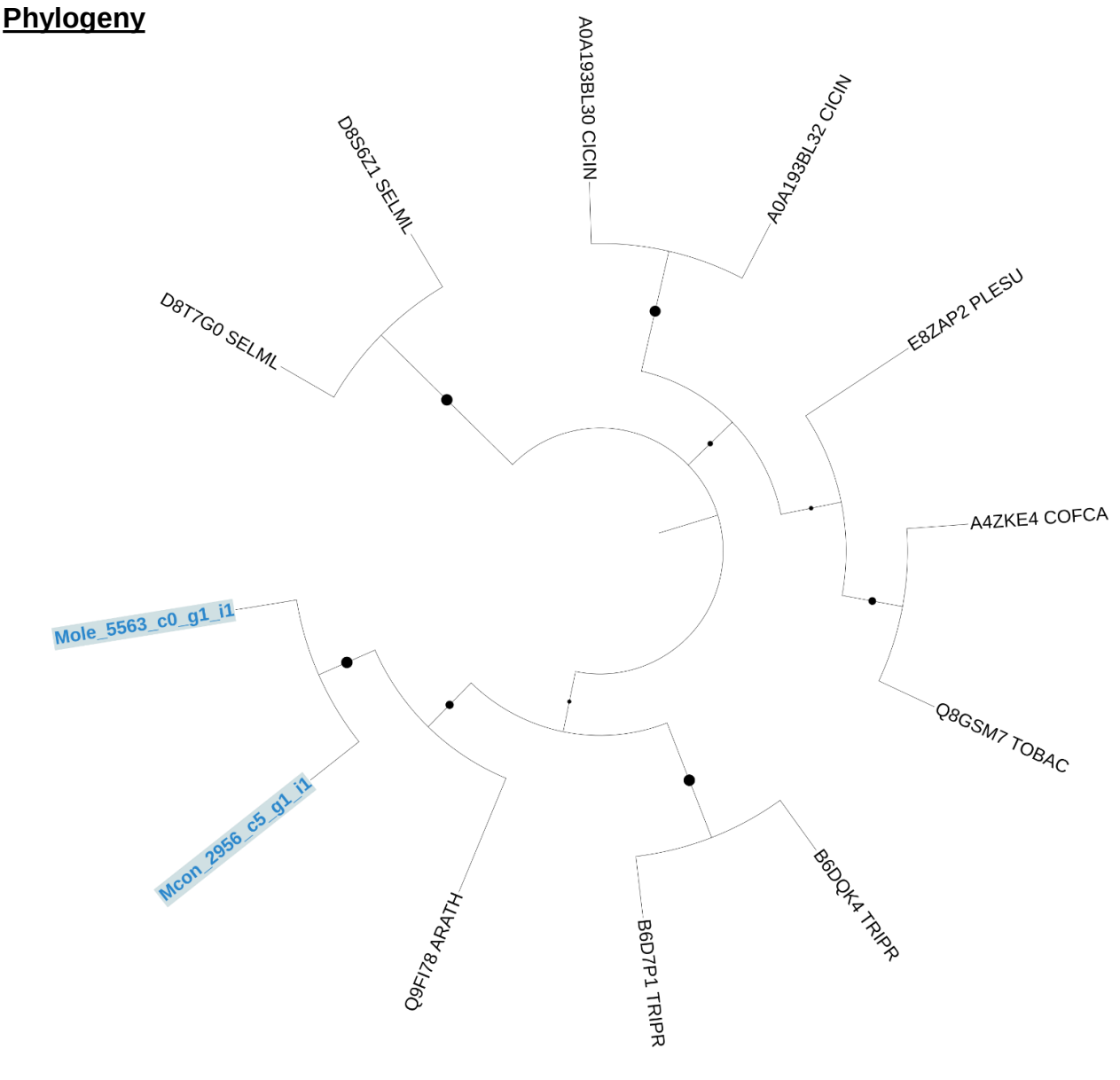
Pathway



1. **HCT**: Hydroxycinnamoyl-CoA shikimate/quinic acid hydroxycinnamoyl transferase
2. **HQT**: Hydroxycinnamoyl-CoA quinate hydroxycinnamoyl transferase
3. **C3'H**: *p*-coumaroyl ester 3-hydroxylase

1. Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase (HCT)

Phylogeny

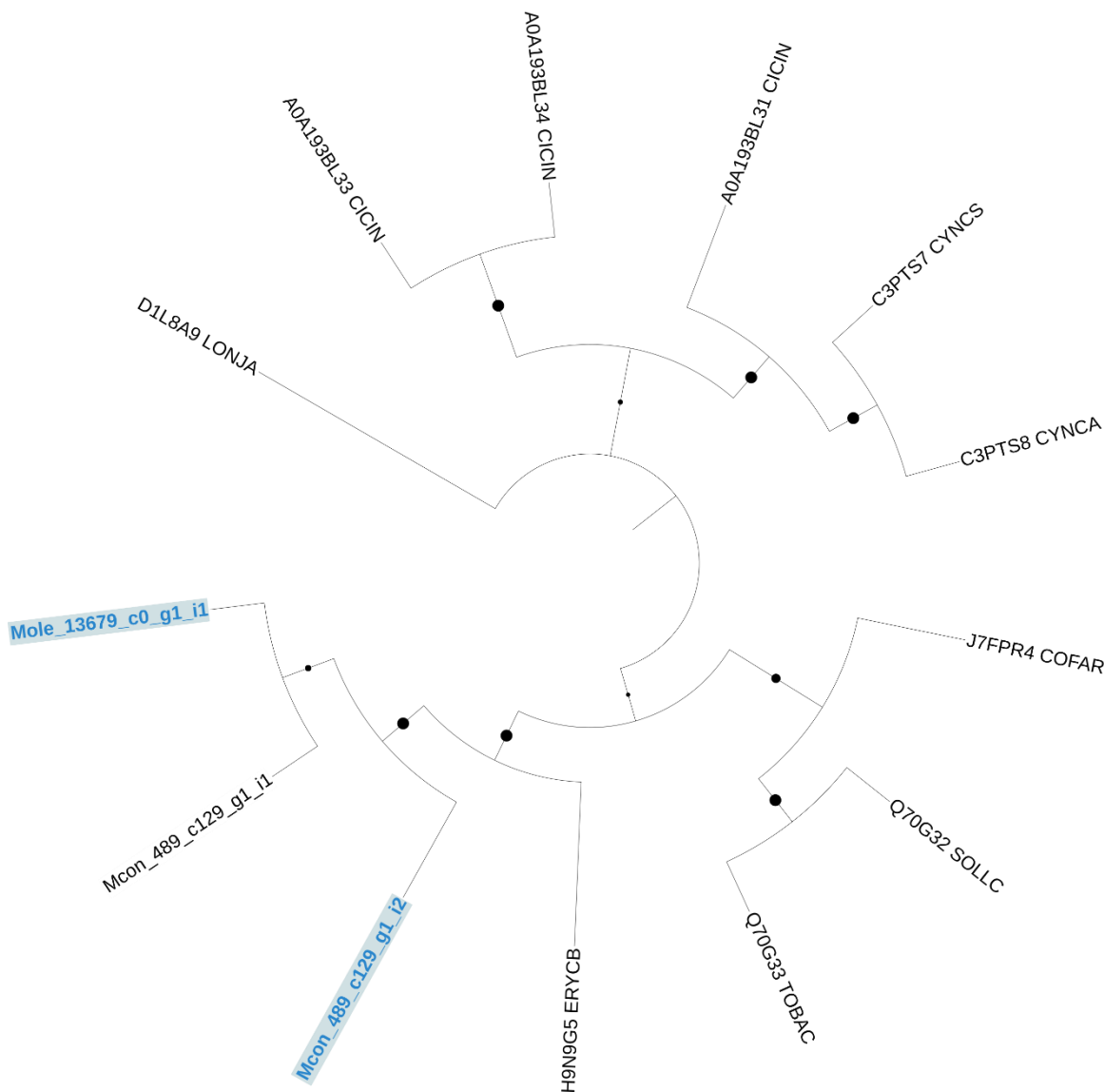


FIR mapping



2. Hydroxycinnamoyl-CoA quinate hydroxycinnamoyl transferase (HQT)

Phylogeny

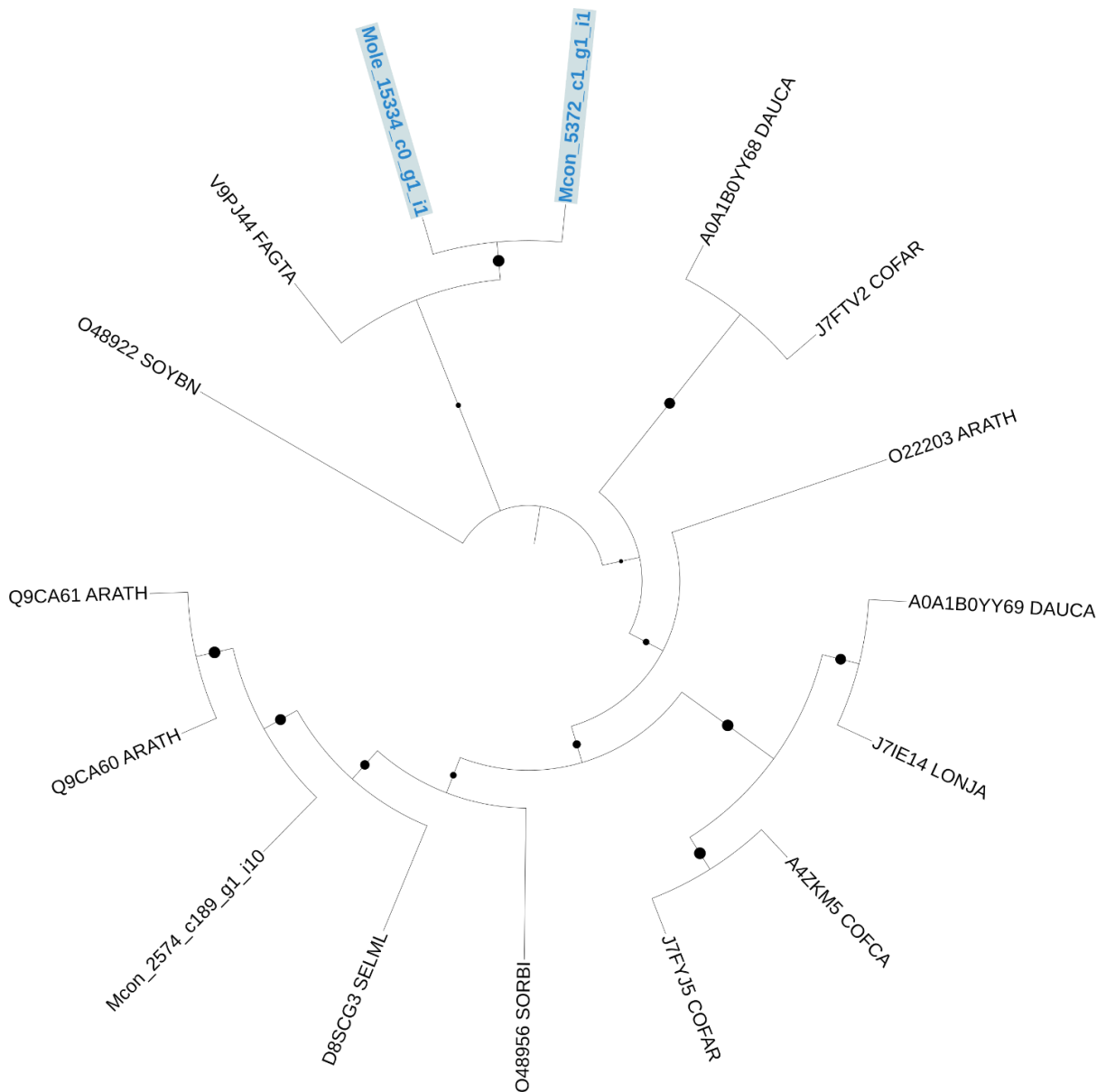


FIR mapping

Mole_13679_c0_g1_i1	150	160	370	380
Mcon_489_c129_g1_i2	LGVGLHHTLADGTSALHF	MRLPIHDA	DFGWGRP	IFMGP
C3PTS8_CYNCA	LGVGLHHTLADGTSALHF	MRLPIHDA	DFGWGRP	IFMGP
Q70G33_TOBAC	LGCGLHHTLSDGLSSLHF	TRLPIYES	DFGWGRP	IFMGP
Q70G32_SOLLC	LGCGVVFHTLSDGLSSLHF	TRLPVHDS	DFGWGRP	IFMGP
	LGCGVVFHTLSDGLSSLHF	TRLPVHEC	DFGWGRP	IFMGP
	HXXXDG	DFGWG		
	Conserved BAHD acyltransferase domains			

3. *p*-coumaroyl ester 3-hydroxylase (C3'H)

Phylogeny



FIR mapping

