

Supplementary Figure S1

Parrish et al. (2022), Metabolites

Translated peptide sequence alignment for selected monogalactosyldiacylglycerol synthases (MGDs) and digalactosyldiacylglycerol synthases (DGDs). Species abbreviations: A.t., *Arabidopsis thaliana*; E.a., *Equisetum arvense*; E.h., *Equisetum hyemale*; E.t., *Equisetum telmateia*.

A.t.MGD2	-----	0
A.t.MGD1	-----	0
E.t.MGD	-----	0
E.h.MGD	-----	0
A.t.DGD1	MVKETLIPSSSTMTGTSSSSSLMTLSSTNALSFLSKGWREVWDSADADLQIMRDRAN	60
A.t.DGD2	-----	0
E.h.DGD	-----MAP-----RGTDSHTTIPASAEKALSLISKSWFDVRKSANEDVKRMKDRAI	46
E.a.DGD	-----MAP-----WATDSHTTIPASAEKALSLISKSWFDVRKSANEDVKRMKDCAI	46
A.t.MGD2	-----	0
A.t.MGD1	-----	0
E.t.MGD	-----	0
E.h.MGD	-----	0
A.t.DGD1	SVKNLASTFDREIENFLNNSARSAFP-----VGSPSASS--FSNEIGIMKKLQ	106
A.t.DGD2	-----	0
E.h.DGD	SFSDLANSFDRELENFRKSSSLKIANNSSIAERFLQKFQNGETLLPSLSVSVPEEVNNKLR	106
E.a.DGD	SFSDLANSFDRELENFRKSSSLKIANNASIAERFLQKFQNGGTLPLSLNVSVPPEEVNNKLR	106
A.t.MGD2	-----	0
A.t.MGD1	-----MQ--NPSTV--TQESA-----AP-----VF-D	17
E.t.MGD	-----RVCGRGER-----ERMQ--RPSDA--LPQHS-----IPFTSAGDLEAPLIID	38
E.h.MGD	-----	0
A.t.DGD1	PKISEFRRVYSAPEISRK--VMERWGPAPARAKLGMDSLAIKKAIVSEMELDE--RQGV	160
A.t.DGD2	-----	0
E.h.DGD	ISFSGFSRSYSNPEFVKRRADFLHKWAPSKK--LDVSLIKKVLSPRIDEEDFYIKTGSE	163
E.a.DGD	ISFSGFSRSYSNPDFVKRQADFIHKWAPSKK--LDVSLIKKVLSPRIDEEDFYIKTGAE	163
A.t.MGD2	-----	0
A.t.MGD1	FFPRLR-GLTSRNRSPCSNSDGYA-----LSSSNALYF	49
E.t.MGD	HSCFLGGGGEASAGRPCVGDYSGR-----PRSVVVCCL	71
E.h.MGD	-----VGPIYGGP-----PRGVVHCL	16
A.t.DGD1	EMSRL-----RRRRNSDRVRFTEFF-----AEAERDGEAYFGDWEPIRSLKSRF-	204
A.t.DGD2	-----	0
E.h.DGD	VISSGKGHHGNHRNHTQRLVVKSWDKDNKNTKNEG-DGQGSILTQEWELLRRFKESWW	222
E.a.DGD	IISGKGHHGNCQNNCSQRVVVKSANNKHTKNEGDDGRGNLTQEWELLRRFKESWW	223
A.t.MGD2	-----MATTVMALA-----	9
A.t.MGD1	N-----GF-RTLPSRRMGKTLASL---SFNTKSSA--GSSL-----	79
E.t.MGD	RR-----CRGNAKPKPRPR-AKLILAMSASPWD-----RPPLSP-----	104
E.h.MGD	RR-----CVGNAKPKSFSR-AKAILAMSASPQDGFQFVNRSLSHSP-----	56
A.t.DGD1	KEFE-----KRSSLEILSGFKNSEFVEKLKTSF-KS---IYKETDEAKDVPLDVPPELLA	255
A.t.DGD2	-----	0
E.h.DGD	KDLETTAAVNRSPSDFDNM-RTEVFENIKKNL-RL---TVPRFEDGKDVAPLDVSELLA	277
E.a.DGD	KDLETTAVANKSPSDFDNITKTEIFENLKKNL-RL---TVPRFEDGKDVAPLDVSELLA	279
A.t.MGD2	-----EKVLERYGTSKSAVSVTSGDGKETHRTHHHIHKRIKS---YD	49
A.t.MGD1	--RRFISDFNSFIRFHCDKVVPESF-----ASVGGVGLSSDEN---GIREN-G---T	122
E.t.MGD	--PRGGAAFLASLGLRKDELL-----SSLANGDAKDCN---DAEAA-A---PP	144
E.h.MGD	--LRGGTAFLASLGLRQDEF-----SSLANDDIVKDCN---DGEAA-E---PP	95
A.t.DGD1	CLVRQSEPFLDQIGVRKDTCDRIVE-----SLCKCKSQQ-----L---WRLPSAQASD	300
A.t.DGD2	-----	0
E.h.DGD	ILIRQSESWLDHLGLKKDVVERVCD-----MLVKGRHKNKKE-QSHSIFNGNKEALAT	329
E.a.DGD	ILIRQSEPWLDYGLGLKKDVVERVCD-----MLVKGRHKNKKE-QSHSIFNGNKEVLAT	331

Supplementary Figure S1 (continued)

Parrish et al. (2022), Metabolites

A.t.MGD2	DIDEDESSLE---LIQI-----GAERTKNVLILMSDTGGGHRA-----	84
A.t.MGD1	GGVLGEEGLP----LNGV-----EADRPKKVLILMSDTGGGHRA-----	157
E.t.MGD	ENMTVDGNAD---GAGV-----VPRRRKTVLILMSDTGGGHRA-----	179
E.h.MGD	ENVAVDENTN---EAGV-----VPRRRKTVLILMSDTGGGHRA-----	130
A.t.DGD1	LIENDNHGVDLDMRIASVLQSTGHHYDGGFWTDFVKPETPENKRHVAIVTTASLPWMTGT	360
A.t.DGD2	-----MTNQEQHIAIFTTASIPWLTGT	23
E.h.DGD	VKDTGKSMEELDFRLASVMQSTGYKYNGRTWGGQIKKEVESGMRNIAIFTTASLPWMTGT	389
E.a.DGD	MKDTGKNMEELDFRLASVMQSTGYNYNGRTRGGQSMKDVETGMRNIAIFTTASLPWMTGT	391
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A.t.MGD2	-SAEAIRDAFKIEFGDKYRVIVKDVWKEYT---GWPL-----NDMERSY	124
A.t.MGD1	-SAEAIRAAFNQEFGDEYQVFITDLWTDHT---PWPf-----NQLPRSY	197
E.t.MGD	-SAEAIKATFQLEFGDEYEVLTDLWKEHT---PWPf-----NQLPRSY	219
E.h.MGD	-SAEAIKATFQLEFGDEYEVLTDLWKEYT---PWPf-----NQLPRSY	170
A.t.DGD1	AVNPLFRAAYLAKAAKQ-SVTLVVPWLCESDQELVYPNNLTFSPEEQESYIRKWLEERI	419
A.t.DGD2	AVNPLFRAAYLANDGER-RVTLVIPWLTTLKHQKLVPNSITFSSPSEQEAYVRQWLEERV	82
E.h.DGD	AVNPLLRAYLAKNGKQ-NVTLLVPWLCKKEQKLVPNNMNFDSPEEQEAYVRNWLESRL	448
E.a.DGD	AVNPLLRAYLAKNGKQ-NVTLLVPWLCKKDQKFVYPNNMTFDSPEEQEGYVRNWLESRL	450
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A.t.MGD2	KFMVKHVQLWKVAFHSTSPKWIHSCYLAIAAYAKEVEAGLMEYKPEIIISVHPLMQHI	184
A.t.MGD1	NFLVKHGT LWKMTYYGTSPRIVHQSNAATSTFIAREIAQGLMKYQPDIIISVHPLMQHV	257
E.t.MGD	GFLVKHSTLWKATYHVTAPRIVHRTHFAVTSTFIARKVMQGLLKHKPDVIVSVHPLMQHI	279
E.h.MGD	GFLVRHSTLWKATYHVTAPRIVHRTHFAVTSTFIARKVMQGLLKHKPDVIVSVHPLMQHI	230
A.t.DGD1	GFK---ADFKISFYPGKFSKERRSIF-----PAGDTSQFISSKDADIAILEEPEHLNW	469
A.t.DGD2	SFR---LAFEIRFYPGKFAIDKRSIL-----PVGDISDAIPDEEADIAVLEEPEHLTW	132
E.h.DGD	GFK---SDFKIAFYPGKFSKQKRSIL-----ACGDISQFISDEEADIAVLEEPEHLTW	498
E.a.DGD	GFK---SDFKIAFYPGKFSKQKRSIL-----ACGDISQFVSDQEADIAVLEEPEHLTW	500
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A.t.MGD2	PLWLKQWELQKRVLf---VT---VIT---DLNTCHPTWFHpgVNRcyCPSQE-----	228
A.t.MGD1	PLRVLRSKGLLKKIVf---TT---VIT---DLSTCHPTWFHKLVTRCYCpSTE-----	301
E.t.MGD	PLRILKARGLLKKIPf---TT---VIT---DLSTCHPTWFHRLVTRCFCpTKE-----	323
E.h.MGD	PLRILKARGLLKKIPf---TT---VIT---DLSTCHPTWFHRLVTRCFCpTKE-----	274
A.t.DGD1	YYHGKRWTDKFNHVVGIVHTNYLEYIKREKNGALQAFFVNHVNNWVTRAYCDKVLRLSAA	529
A.t.DGD2	FHHGQKWTKFNYVIGIVHTNYLEYVVKREKQGRVKAFFLKYLNWVVGIVYCHKVIRLSAA	192
E.h.DGD	YFHGKRWTDKFNHVVGIVHTNYLEYVVKREKNGALQAFLLKHVNNWVTRIYCHKVIRLSAA	558
E.a.DGD	YFHGKRWTDKFKYVVGIVHTNYLEYVVKREKNGALQAFLLKHVNNWVTRIYCDKVLRLSAA	560
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A.t.MGD2	-----VAKRALFDGLDESQVRVFGLP-----VRPSFARAVLVKDDLR	265
A.t.MGD1	-----VAKRAQKAGLETSQIKVYGLP-----VRPSFVKPVRPKVELR	338
E.t.MGD	-----VAEKALKAGLKTTQIRVYGLP-----IRPSFCKDIPPKVDLR	360
E.h.MGD	-----VAEKALKAGLKTTQIRVYGLP-----IRPSFCKDIPPKVELR	311
A.t.DGD1	TQDLPKSVVCNVHGVNPKFLMIGEKIAEERSRGEQAFSGAYFLGKMVWAKGYRELIDLm	589
A.t.DGD2	TQEYPKSIVCNVHGVNPKFLEIGLRKLEQQKLQEQPFTKGAYYIGKMVWSKGYKELLKLL	252
E.h.DGD	TQELPRsIVCNVHGVNPKFLEIGEKMAQDGKGSQDTFSKGAYFLGKMVWGKGYRELVDLL	618
E.a.DGD	TQELPRsIVCNVHGVNPKFLEIGEKMVQEGEGSQDTFSKGAYFLGKMVWGKGYRELVDLL	620
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A.t.MGD2	KELEMDQDLRAVLLMGGGEGMGpVketAKALEEFlyDKENRKPIGQMVICGRNKKLASA	325
A.t.MGD1	RELGMdENLPAVLLMGGGEGMGpIEATARALADALYDKNLGEAVGQVLIICGRNKKLQSK	398
E.t.MGD	RSLGMNEELPAVLLMGGGEGMGpVESTAKALGESLFCQQSGEaIGQLVVICGRNtkLVKN	420
E.h.MGD	RALGMNEELPAVLLMGGGEGMGpVESTAKALGESLFCQQSGEaIGQLVVICGRNMkLVKN	371
A.t.DGD1	AKHKSELGSFNLDVYNGEDAVEVQRAAKKHDLNlnFLKGRDHADdAL-----	637
A.t.DGD2	EKHQKELAELEVDLYGDGEDSEEIKEAARKLDLTvNVYPGRDHADSLF-----	300
E.h.DGD	AKHKSDLGSLKIDVFGTGEDSEEVKATAKKLGldLnFNHQGRDHADdCL-----	666
E.a.DGD	AKHKSDLGSLKIDVFGTGEDSEEVKATAKKLGldLnFNQGRDHADdSL-----	668
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Supplementary Figure S1 (continued)

Parrish et al. (2022), Metabolites

A.t.MGD2	LEAIDWKIPVKVRFETQMEKWMGACDCIITKAGPGTIAESLIRSLPIILNDYIPGQKEG	385
A.t.MGD1	LSSLDWKIPVQVKGFITKMEECMGACDCIITKAGPGTIAEAMIRGLPIILNGYIAGQEAG	458
E.t.MGD	LQSINWSMPVQIRGFEKNIEEWMGACDCLITKAGPGTIAEAMIRGLPLILSDYIAGQEVG	480
E.h.MGD	LQSINWSIPVQIRGFEKNIEEWMGACDCLITKAGPGTIAEAMIRGLPLILSDYIAGQEVG	431
A.t.DGD1	-----HKYKVFINPSISDVLC-----TATAEALAMGKFVVCADHPSNEFFR	678
A.t.DGD2	-----HNYKVFLNPSTTDVVC-----TTTAEALAMGKIVVCANHISNKFFK	341
E.h.DGD	-----HGYKVFINPSISDVVC-----TTTAEALAMGKIVVCADHPSNEFFR	707
E.a.DGD	-----HGYKVFINPSISDVVC-----TTTAEALAMGKIVVCADHPSNDFFR	709
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A.t.MGD2	NVPYVVENGAGVFTRSPKETARIVGEWFSTKTDELEQTSNARKLAQPEAVFDIVKDIDE	445
A.t.MGD1	NVPYVVENGCGKFSKSPKEISKIVADWFGPASKELEIMSQNALRLAKPEAVFKIVHDMHE	518
E.t.MGD	NVPFVVDNGAGKFLKEPKKIAQTVADWFGPKREELHTMSRNALKLARPDVFKIVHDLDR	540
E.h.MGD	NVPFVVDNGAGKFLKEPKKIAQTVADWFGPKREELHMSRNALKLARPDVFKIVHDLDR	491
A.t.DGD1	SFPN-----CLTYKTS-EDFVSKVQEAMTKEPLPLTPEQMYNLSWEAATQRFMEYSDDLK	732
A.t.DGD2	QFPN-----CRTYDDG-QGFVRATLKALGEQPSQLTEQQRHELSEWEAATQRFKIVSDLN	395
E.h.DGD	SFPN-----CLTYKDS-REFVEKVKEAMADPAPLTLEQRHLLSWEAATERFIEYAEIDK	761
E.a.DGD	SFPN-----CLTYKDS-REFVEKVKEAMDIDPVPLTPEQRHLLSWEAATERFIEYAEIDK	763
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A.t.MGD2	LSEQRGRL-----ASVSYNLTSSF--ASLV-----	468
A.t.MGD1	LVRKKNSL-----PQLSCTA-----	533
E.t.MGD	LARRKVFL-----EENRTLVP-----	557
E.h.MGD	LARRKVFL-----EENRTLVP-----	508
A.t.DGD1	ILNNGEGG-----RKMRKRSRSPFNEVDGGLAFSHYVLTGNDFLRLCTGATPR	782
A.t.DGD2	LSRADSN--LSKRVSFASSISV-----GKNLEDMSAYIHFLASGFASRTAFGAIPG	446
E.h.DGD	PFIKQGGESVTPEKVVQKKAMALSMAMPNPFELVDNSLAAAHYCLTGIEAARFISGALPG	821
E.a.DGD	PFIKQGGESVTPEKVVQKKAMALSMAMPNPFELVDNSLAAAHYCLTGIEAARLISGALPG	823
A.t.MGD2	-----	468
A.t.MGD1	-----	533
E.t.MGD	-----	557
E.h.MGD	-----	508
A.t.DGD1	TKDYDNQHCKDLNLVP--PHVHKPIFGW	808
A.t.DGD2	SLQPDEELCRDLGLSLNTPSPNTRKQD-	473
E.h.DGD	SINYDSQHSKDLHLQP--PSVEKPVYGW	847
E.a.DGD	SSNYDSQHSKDLHLQP--PSVERPVYGW	849

Supplementary Figure S1 (continued)

Parrish et al. (2022), Metabolites

Translated peptide sequence alignment for a styrylpyrone synthase (SPS), a p-coumaroyltriatic acid synthase (CTAS), selected chalcone synthases (CHSs), and a contig of transcriptome data for Equisetum telmateia (DN52675). Species abbreviations: C.p., Cyclosorus parasiticus; E.a., Equisetum arvense; E.h., Equisetum hyemale; E.t., Equisetum telmateia; P.M., Piper methysticum.

P.m.SPS	-----MSKTVEDRAAQRAGPATVLAIGTATPANVVYQTDYPDYFRVTKSEHMTKLKN	54
E.h.CTAS	-----PLTAYEQANYPDFYFGITNSNHMTDLKE	28
E.t.DN52675	-----	0
C.p.CHS	MPVPNGATFPPCARKMERADGPATVLAIGTANPPNVFDQSTYPDFYFNITNSNHMTDLKT	60
E.a.CHS	MTVLEESADASSRRLAQRANGPATVLAIGTANPANVFEQSSYPDFYFDITNSQHMTLKL	60
P.m.SPS	KFQRMCDRSTIKKRYMVLTEELLEKNLSLCTYMEPSLDARQDILVPEVPKLGKEAADEAI	114
E.h.CTAS	KFSRMCEKSGIKKRYLHLTEELKANPSCGYWEKSLDVRQDIVVVEVPMLARQASIKAI	88
E.t.DN52675	-----VVVEVPKLAKEASLKVI	17
C.p.CHS	KFQRMCDKSGITKRYMYLNEEILKANPNMCAYWEKSLDVRQDMVVVEVPKLGKEAATKAI	120
E.a.CHS	KFSRMCKSGIKKRYMHLNSEILKANPSLCAYWEKSLDVRQDIATVVEVPKLGKEASLKAI	120
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P.m.SPS	AEWGRPKSEITHLIFCTTCGVDMPGADYQLTKLLGLRSSVRRTMLYQQGCFGGGTVLRRLA	174
E.h.CTAS	KEWGQPKSKITHLVFCTTNGLDMPGADWKLTKLLGLHPNVKRLMIYQQGCFAGGTVMRIA	148
E.t.DN52675	KEWGQPKSKITHLIFCSTSGVDIPGADWQLTKILGLCPSVKRLMMYQQGCFAGGTVLRRIA	77
C.p.CHS	KEWGQPKSKITHVVFCTTSGVDMPGADWALTLLGLRPSVKRLMMYQQGCFAGGTVMRVA	180
E.a.CHS	KEWGQPKSKITHLVFCTTSGVDMPGADWALTLLGLRPSVKRLMMYQQGCFAGGTVLRVA	180
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P.m.SPS	KDLAENNAGARVLVVCSEITTAVERNFRGPSDTHLDLLVGLALFGDGAAAVIVGADPDPTLE	234
E.h.CTAS	KDLAENNKDARVLVVCSEIN-LSTFRGPSDIHLDSLVGQALIGDGASAMIGSDPIPKVE	207
E.t.DN52675	KDLAENNKDARVLVVCSEIT-VVTFRGPSETNFANLVGQALFGDGVSAVIGSDPIQVE	136
C.p.CHS	KDLAENNKGARVLVVCSELT-AVTFRGPSETHLDSLVGQALFGDGASAIIVGADPIPEVE	239
E.a.CHS	KDVAENNKGARVLVVCSEIT-CVTFRGPSETHLDSLVGQALFGDGAAAVILGSDPLPE-E	238
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P.m.SPS	RPLFQIVSGAQTIIPDSEGAINGHLREVGLTIRLLKDVPLVSMNIEKCLMEAFAPM---	291
E.h.CTAS	TPWFELHWSGSTILPESNGAIDGHLREVGLIFHLSKDVPRIISKNIQVLLTDAFEKAFL-	266
E.t.DN52675	TPWFELHWSGSTILPDSGDAIDGHLREVGLTFHLREDVPRIISKNIQVVLNDAFDKVPF-	195
C.p.CHS	RPWFELHWSGSTILPDSGDAIDGHLREVGLTFHLMKDVPPIISKNIQVTLKDAFEKVF-	298
E.a.CHS	NPCFELHWSGSNILPDSGDAIDGHLREVGLTFHLMKDVPPIISKNIQVVLNDAFRSAFDE	298
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P.m.SPS	-----GIHDWNSIFWIAHPGGPTILDQVEAKLGLKEEKLKSTRAVLREYGNMSSACVLF	345
E.h.CTAS	--GGKEAPPSYNDVFWIAHPGGPAILDQIEAKLQLKMEKMHASRSILSEYGNMSSASVIF	324
E.t.DN52675	--SGEGAPLSYNDVFWIAHPGGPAILDQIEEKLKLIPIKKMQASRAILYEGNMSSASVFF	253
C.p.CHS	--NEEGEVPSYNDVFWIAHPGGPAILDQVEQKLQKTEKMAASRQVLSYGNMSSACVLF	356
E.a.CHS	SGNAEDRPASVNDIFWIAHPGGPAILDQVEEKMMLAPEKMRATRDVLSEYGNMSSACVLF	358
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P.m.SPS	ILDEVKRKSMEEGKTTTGEGLDWGVLFVFGPGFTVETVVLHSMPIPKADEGR	397
E.h.CTAS	IMDYMRQQAWEKKLATTEGLDWGVLLGFGPGLTVETILLKSVNLN-----	371
E.t.DN52675	IMDYLRKQSLENKLPTTGDGFDWGLLLGFGPGLTITETIVLKSVPINN-----	300
C.p.CHS	IMDHLRKKSVEQKLATSGEGYEWGLLLGFGPGLTCTETVVLRSVPLATE----	404
E.a.CHS	IMDHMRMSAQNKLTTEGLDWGVLLGFGPGLTETVVLKSIRLAC-----	405
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Supplementary Figure S1 (continued)

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Translated peptide sequence alignment for phenylalanine ammonia lyases (PALs). Species abbreviations: E.a., Equisetum arvense; P.a., Pteridium aquilinum; P.e., Peltia epiphylla; 56P.n., Psilotum nudum.

P.e. PAL	-----RLHGKNNLFVD--GPVAKPPHWAKAAEALQTSHYEEVR	36
E.a. PAL	MAAEFQNKQLAELHRPPTLPLPVQGNPLFVDSKEPVAKPPHWQKAAEALQSSHYEEIR	60
P.a. PAL	-----GGSFLLDDIK	9
P.n. PAL	MTADLVLPVLGIGSKPLGLAHTVCGRLLP---HKSEGDLKLVESAQSECSHLDDEV	
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P.e. PAL	RMIRQFYESEKVLGRSSSLTVGQVTAQTQRASVIVQLDEAEAKSRVDESSNWVLNRTLTG	96
E.a. PAL	RMIRQFLETEKVVVLQGSSTLVGQVTAQTQRSEVAVELDEATAKARVDESSNWVLNNILKG	120
P.a. PAL	QMISTFTAEEELKIEGKTLTVAEVAFAFARKSEKVLCLDEAAAKQRVDESALWVQNKIMKG	69
P.n. PAL	RMVKEFSDGNVVSQGLNLTVAQVAARPDVKVELDSAVARRRVDESSEWVNVHIMKG	116
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P.e. PAL	TDTYGVTTGFGATSHRRTNQVVDLQRELIRFLNAGVIGR-DSDGCSLPLKYARAAMLVRT	155
E.a. PAL	TDTYGVTTGFGATSHRRTTQAHDQLRELIRFLNAGVITAGKGANCTLPLPYAKAAMLVRT	180
P.a. PAL	CDVYGVTTGFGATSHRRTNQGIIDLQRELIRFLNAGIFG--KSQANALPLDARAAMLVRT	127
P.n. PAL	TDTYGVTTGFGATSHRRTNQGIELQKELIRFLNAGILTGDKEECNSLPTPAVRAAILVRT	176
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P.e. PAL	NTLMQGYSGIRWDILDAMRKLMCANVPIKPLPLRGTTITASGDLVPLSYIAGLLTGRSNSKA	215
E.a. PAL	NTLMQGYSGIRWAILNGFEKLMNGNIIPKMPPLRGTTITASGDLVPLSYIAGLLTARENSRA	240
P.a. PAL	NTLMQGYSGIRWEILQTIKLLNANITPLPLPLRGTTITASGDLVPLSYLAGVLTGRPNska	187
P.n. PAL	NTLMQGYSGIRWAILLEAMEKLLNSQITPRPLPLRGTTITASGDLVPLSYIAGLLTARENSRA	236
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P.e. PAL	ITPEGKEVSAAEALKIAGIDGPFELQPKLGLVNGTSGAAVAANVCFDANVLALLSEV	275
E.a. PAL	ITPSGEEIPAAEALKLVGIEEPFVLQPKLGLVNGTSGAAVAANVCFDANVLALLAEV	300
P.a. PAL	VTAEGKVVSAGAEALKMVGVEKPFELQPKLGLVNGTAVGAGLASMVCDAHILALLSVV	247
P.n. PAL	VTAEGKEVTGEEALKLAGIQEPFDLQPKLGLVNGTAVGAGLAHVVCYDANIFALLAEV	296
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P.e. PAL	LSAFFCEVMQKGKPEFTDPLTHQLKHHPGQIEAAAVMEFLLEGSSYMKAALKHETDPLSK	335
E.a. PAL	ISALFCEVMQKGKPEFTDPLTHQLKHHPGQIEAAAVMEYLLLEGSSYMQAALKHETDPLSK	360
P.a. PAL	TSAMFCEVMQKGKPEFTDPLTHRLKHHPGQIEAAAVMEYLLLEGSSALVKAASKLHGVDAKK	307
P.n. PAL	LSALFCEVMQKGKPEFTDHLTHRLKHHPGQIEAAAVMEWLLDGSSYMKAALKHETDPLKK	356
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P.e. PAL	PKQDRYALRTSPQWLGPQIEVIRSATHSIEREINSVNDNPLIDVSRDMALHGGNFQGTPI	395
E.a. PAL	PKQDRYALRTSPQWLGPQAEVIRAAATHCIEREINSVNDNPLIDVSRDMALHGGNFQGTPI	420
P.a. PAL	PKQDRYALRTSPQWLGPQIEVIRFATQLIQREINSVNDNPLIDVSRDLALHGGNFQGTPI	367
P.n. PAL	PKQDRYALRTSPQWLGPQIEVIRLATHAIQREINSVNDNPLIDVARDKALHGGNFQGTPI	416
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P.e. PAL	GVSMNDMRLAIAIGKLMFAQFSELVCDYNSGLPSNLSGGPNPSLDYGFKGAEIAMAAY	455
E.a. PAL	GVSMNDMRLAIAIGKLMFAQFSELVCDHYNSGLPSNLSGGPNPSLDYGFKGAEIAMAAY	480
P.a. PAL	GTAMDNIRLALAAIGKLMFAQFSELVNDYFNNGLPSNLSAGPNPSLDYGLKGGEIAMASY	427
P.n. PAL	GVSMNDMRLAIAIAIGKLMFAQFSELVNDLYNGLPSNLSGSPNPSLDYGFKGAEIALASY	476
	*.:***:*.*:***** **:****** **:****** **:******:***:***:***:***:***: *	
P.e. PAL	CSELQYLANPVTTHVQSAEQHNQDVNSLGLIAARKTAEAEIILKLMSSTYMVALCQAVDL	515
E.a. PAL	CSELQYLANPVTTHVQSAEQHNQDVNSLGLISARKTAEAEIILKLMSASYLVALCQAVDL	540
P.a. PAL	TSELYLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAEVVLKMCATYLVGICQAVDL	487
P.n. PAL	TSEMQYLANPVTTHVQSAEQHNQDVNSLGLISARKTAEADILKLMIISTYIVALCQAVDL	536
	:*:***.* *****:***** **:*:***** :*:*.:***:***:***:***: *	
P.e. PAL	RHLEENMQAVVKRLVESATKSTLYTENG-SLFPTRFSEKDLLQVVDHQPVFSYIDNASNP	574
E.a. PAL	RHLEENMQAIVKHVVKVKKSLYNVEGESLLPWAGAEKELLSIIDHQPVFSYIDNASNP	600
P.a. PAL	RHLEENLQAAVKQVVSQAAKKTLTGGNGVLLAARFCEKDLLQVVDNEHVFTYADDPVSP	547
P.n. PAL	RHLEENMKAIAKHMVCQVARRTLYFDHNGLLPSRFCEKELLHVVEHEPIFLYIDNASNP	596
	*****:*. :*:*. :*. :*. :*. :*. :*. :*. :*. :*. :*. :*. :*. :*. :*. :*	

Supplementary Figure S1 (continued)

Parrish et al. (2022), Metabolites

P.e.PAL	SYALMLQLREVLVEQALKTPQDEDC-----KEVTPLFTTIPKFEAELKKLLDAEVPKARD	629
E.a.PAL	DYALMLQLRQILVEQTFKVPADSEDESGANSQMPVLFNAIPVFEQALKEALDKEIPKARE	660
P.a.PAL	GYPLMQRLRQVLVEHAIKNPSNERD--EAT----SVMTRIPLFEDELHSQLPaelVNVRA	601
P.n.PAL	ASILMQKLKRLVLDQAMKNVEKEKEKLGAA---STLNRILLFEEELKNLFDSEIPRARE	652
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P.e.PAL	RYDGGDYAVPNRIKNCRTYPIYKFVRGELGTELLRGTATKSPGEDIEKVFTAILDGKLLL	689
E.a.PAL	SYDSGDFAVPNRINNCRTYPLYKFVRSELGTNLLRGTAPRSPGEDIEKVFNIMEGKLAI	720
P.a.PAL	SFDKGCPIASKVEECRSFPLYQFVRAQLGTQLLAGTRNQSPGQDFEVVFDAlSDGLLMC	661
P.n.PAL	RFDRGQFAVLNRIQNCRTYPLYRFVRDDLGTQLLSGTQTHSPGQDFQKVLDAISEGKLVA	712
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P.e.PAL	PLLKCLEGWGRGSAGPFTPRTPV---ASPAAYNPAYWAWFDNVRSPSAT-AGKGYWSLTG-	744
E.a.PAL	PLLRCLEGWGRGSAGPFTPRPVP---ASPAAFNPAYWAWFDNIRSPAAM-AGKGSWSSSAF	776
P.a.PAL	PLLQCLEGWTSQSPITTC-----	678
P.n.PAL	PLLKCIEGWSGHPGPFSC TQQQESADIEMCNPSSWIWFDQLHCFKAQGGGKGYFMLSVM	772
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P.e.PAL	-- 744	
E.a.PAL	GM 778	
P.a.PAL	-- 678	
P.n.PAL	-- 772	