Genetics and Molecular Biology

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Supplementary material to “Molecular evolution and diversification of phytoene synthase (PSY) gene family”

Table S1 - Detailed data of retrieved sequences and species used in this study.

Species	Acronymon	Score	Evalue	Transcript Name	CDS Acession Number	Location	Classification group	Order	Query
Anaeromyxobacter sp	*Asp*	*165*	*2,70E-39*	*ABS28258*	*ABS28258*	*Chromosome: 4,772,703-4,773,635 reverse strand*	*Prokariotae*	*Myxoccocales*	*Solyc03g031860.2.1*
Candidatus Parcubacteria bacterium	*Cpb*	*356*	*3,00E-118*	*MBC7822343*	*MBC7822343.1*		*Prokariotae*	*Candidatus parcubacteria*	*Solyc03g031860.2.1*
Cronobacter turicensis	*Ctu*	*333*	*2,00E-86*	*FN543093*	*FN543093.2*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*
Cronobacter universalis	*Cun*	*333*	*2,00E-86*	*CP012257*	*CP012257.1*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*
Erwinia gerundensis	*Ege*	*129*	*6,90E-32*	*CUU22454*	*CUU22454*	*Chromosome 1: 233,386-234,312 reverse strand.*	*Prokariotae*	*Enterobacteriales*	*Solyc03g031860.2.1*
Erwinia sp.	*Esp*	*162*	*6,70E-33*	*RRZ89314*	*RRZ89314*	*NODE_11_length_177429_cov_45.8436 17769 to 18209 (-)*	*Prokariotae*	*Enterobacteriales*	*Solyc03g031860.2.1*
Mixta calida	*Mca*	*345*	*3,00E-90*	*CP061511*	*CP061511.1*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*
Mixta gaviniae	*Mga*	*353*	*2,00E-92*	*CP026377*	*CP026377.1*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*

Species	Acronymon	Score	Evalue	Transcript Name	CDS Acession Number	Location	Classification group	Order	Query
Myxococcus fulvus	*Mfu*	*199*	*3,30E-31*	*SET01046*	*SET01046*	*SuperContig Ga0131203_101: 961,439-962,455 forward strand.*	*Prokariotae*	*Mixococcales*	*Solyc03g031860.2.1*
Myxococcus hansupus	*Mha*	*205*	*9,60E-50*	*AKQ69173*	*AKQ69173*	*Chromosome: 7,548,393-7,549,391 reverse strand.*	*Prokariotae*	*Mixococcales*	*Solyc03g031860.2.1*
Myxococcus macrosporus	*Mma*	*206*	*1,50E-50*	*ATB45335*	*ATB45335*	*Chromosome: 1,082,269-1,083,282 forward strand.*	*Prokariotae*	*Mixococcales*	*Solyc03g031860.2.1*
Myxococcus stipitatus	*Msi*	*204*	*2,50E-50*	*AGC42255*	*AGC42255*	*Chromosome: 1,121,269-1,122,288 forward strand.*	*Prokariotae*	*Mixococcales*	*Solyc03g031860.2.1*
Myxococcus virescens	*Mvi*	*201*	*3,90E-50*	*SDD40313*	*SDD40313*	*SuperContig Ga0070493_101: 905,667-906,677 reverse strand.*	*Prokariotae*	*Mixococcales*	*Solyc03g031860.2.1*
Myxococcus xanthus	*Mxa*	*202*	*5,10E-52*	*ABF86184*	*ABF86184*	*Chromosome: 1,021,919-1,022,929 forward strand*	*Prokariotae*	*Mixococcales*	*Solyc03g031860.2.1*
Pantoea agglomerans	*Pag*	*669*	*0.0*	*CP031650*	*CP031650.1*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*
Pantoea ananatis	*Pan*	*1678*	*0.0*	*D90087*	*D90087.2*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*
Pantoea ananatis	*Pan*	*1645*	*0.0*	*CP001875*	*CP001875.2*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*
Pantoea eucalypti	*Peu*	*625*	*2,00E-174*	*CP045721*	*CP045721.1*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*
Pantoea stewartii	*Pst*	*883*	*0.0*	*CP017591*	*CP017591.1*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*
Pantoea vagans	*Pva*	*662*	*0.0*	*KT156635*	*KT156635.1*		*Prokariotae*	*Enterobacteriales*	*Pantoeae ananatis D90087.2*
Ahnfeltiopsis flabelliformis	*Afl*	*312*	*2,00E-102*	*ATQ35976*	*ATQ35976*		*Rhodophyta*	*Gigartinales*	*Solyc03g031860.2.1*
Betaphycus gelatinus	*Bge*	*300*	*3,00E-98*	*ATQ35975*	*ATQ35975*		*Rhodophyta*	*Gigartinales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Chondrus crispus	*Cci*	*291*	*1,00E-95*	*ATQ35984*	*ATQ35984*		*Rhodophyta*	*Gigartinales*	*Solyc03g031860.2.1*
Cyanidioschyzon merolae	*Cme*	*317*	*4,00E-103*	*XP_005537057*	*XP_005537057*		*Rhodophyta*	*Cyanidiales*	*Solyc03g031860.2.1*
Dumontia simplex	*Dsi*	*306*	*3,00E-100*	*ATQ35978*	*ATQ35978*		*Rhodophyta*	*Gigartinales*	*Solyc03g031860.2.1*
Galdieria sulphuraria	*Gsu*	*498*	*1,70E-91*	*EME29253*	*EME29253*	*SuperContig scaf_26: 15,896-17,400 reverse strand*	*Rhodophyta*	*Cyanidiales*	*Solyc03g031860.2.1*
Gracilaria chouae	*Gco*	*295*	*1,00E-95*	*ATQ35977*	*ATQ35977*		*Rhodophyta*	*Gracilariales*	*Solyc03g031860.2.1*
Gracilariopsis chorda	*Gch*	*305*	*5,00E-100*	*PXF46860*	*PXF46860*		*Rhodophyta*	*Gracilariales*	*Solyc03g031860.2.1*
Gracilariopsis lemaneiformis	*Gle*	*305*	*1,00E-99*	*ATQ35980*	*ATQ35980*		*Rhodophyta*	*Gracilariales*	*Solyc03g031860.2.1*
Grateloupia catenata	*Gca*	*293*	*5,00E-95*	*ATQ35982*	*ATQ35982*		*Rhodophyta*	*Halymeniales*	*Solyc03g031860.2.1*
Grateloupia livida	*Gli*	*297*	*1,00E-96*	*ATQ35979*	*ATQ35979*		*Rhodophyta*	*Halymeniales*	*Solyc03g031860.2.1*
Grateloupia turuturu	*Gtu*	*298*	*7,00E-97*	*ATQ35985*	*ATQ35985*		*Rhodophyta*	*Halymeniales*	*Solyc03g031860.2.1*
Porphyridium purpureum	*Ppu*	*306*	*8,00E-99*	*KAA8491175*	*KAA8491175*		*Rhodophyta*	*Porphyridiales*	*Solyc03g031860.2.1*
Desmarestia viridis	*Dvi*	*290*	*6,00E-94*	*ATQ35993*	*ATQ35993*		*Ochrophyta*	*Desmarestiales*	*Solyc03g031860.2.1*
Dictyopteris undulata	*Dun*	*286*	*1,00E-92*	*ATQ35997*	*ATQ35997*		*Ochrophyta*	*Dictyotales*	*Solyc03g031860.2.1*
Ectocarpus siliculosus	*Esi*	*294*	*1,00E-94*	*CBJ31337*	*CBJ31337*	*scaffold sctg_244*	*Ochrophyta*	*Ectocarpales*	*Solyc03g031860.2.1*
Ishige okamurae	*Iok*	*293*	*6,00E-95*	*ATQ35992*	*ATQ35992*		*Ochrophyta*	*Ishigeales*	*Solyc03g031860.2.1*
Punctaria latifolia	*Pla*	*295*	*3,00E-95*	*ATQ35994*	*ATQ35994*		*Ochrophyta*	*Ectocarpales*	*Solyc03g031860.2.1*
Sargassum hemiphyllum	*She*	*295*	*1,00E-96*	*ATQ36002*	*ATQ36002*		*Ochrophyta*	*Fucales*	*Solyc03g031860.2.1*
Sargassum henslowianum	*Shn*	*295*	*2,00E-96*	*ATQ36001*	*ATQ36001*		*Ochrophyta*	*Fucales*	*Solyc03g031860.2.1*

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Sargassum thunbergii	Sth	297	3,00E-96	ATQ35998	ATQ35998		Ochrophyta	Fucales	Solyc03g031860.2.1
Sargassum vachellianum	Sva	295	1,00E-95	ATQ36000	ATQ36000		Ochrophyta	Fucales	Solyc03g031860.2.1
Scytosiphon lomentaria	Slo	295	2,00E-95	ATQ35995	ATQ35995		Ochrophyta	Ectocarpales	Solyc03g031860.2.1
Undaria pinnatifida	Upi	291	4,00E-94	ATQ35996	ATQ35996		Ochrophyta	Laminariales	Solyc03g031860.2.1
Cyanobacteria bacterium	Cba	358	3,00E-121	DNME01000182.1	HBB31740.1		Cyanophyta	Chroococcales	Solyc03g031860.2.1
Cyanobacteria bacterium	Cba	357	1,00E-120	RFIF01000104.1	RMF69129.1		Cyanophyta	Chroococcales	Solyc03g031860.2.1
Cyanothece sp.	Csp	360	8,00E-120	NET36663	NET36663	JAAHFT010000438.1:6921-7850	Cyanophyta	Oscillatoriales	Solyc03g031860.2.1
Desertifilum sp.	Dsp	365	7,00E-122	NES97327	NES97327		Cyanophyta	Oscillatoriales	Solyc03g031860.2.1
Elainella sp.	Els	348	3,00E-115	MBF2049978	MBF2049978	JACYLO010000073.1:11222-12151	Cyanophyta	Synechococcales	Solyc03g031860.2.1
Hydrocoleum sp.	Hsp	348	5,00E-115	OZH53043	OZH53043	LGSU01001248.1:5456-6394	Cyanophyta	Oscillatoriales	Solyc03g031860.2.1
Leptolyngbyaceae cyanobacterium	Lcy	360	2,00E-119	NJR49961	NJR49961	JAAUOZ010000055.1:27289-28224	Cyanophyta	Synechococcales	Solyc03g031860.2.1
Nostocales cyanobacterium	Ncy	348	3,00E-115	TAE59201	TAE59201	RDXV01000048.1:21825-22757	Cyanophyta	Nostocales	Solyc03g031860.2.1
Okeania sp.	Osp	348	5,00E-115	NES03100	NES03100	JAAHGT010000113.1:11469-12407	Cyanophyta	Oscillatoriales	Solyc03g031860.2.1
Oscillatoriales cyanobacterium	Ocy	349	1,00E-117	OIP71133.1	OIP71133.1		Cyanophyta	Oscillatoriales	Solyc03g031860.2.1
Spirulinaceae cyanobacterium	Scy	348	4,00E-115	NJK99192	NJK99192	JAAUTY010000001.1:236214-237143	Cyanophyta	Spirulinales	Solyc03g031860.2.1
Synechococcus elongatus	Sel	365	1,00E-123	QFZ92142.1	QFZ92142.1		Cyanophyta	Synechococcales	Solyc03g031860.2.1
Thermosynechococcus elongatus	Tel	352	7,00E-119	AXY68520.1	AXY68520.1		Cyanophyta	Synechococcales	Solyc03g031860.2.1
Chlamydomonas reinhardtii	Cre	402.1	3.3E-137	Cre02.g095092.t1.1 (primary)	Cre02.g095092.t1.1	chromosome_2:3336147..3340314 reverse	Chlorophyta	Volvocales	Solyc03g031860.2.1

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Coccomyxa subellipsoidea	*Csu*	*387.9*	*1,00E-132*	*52083 (primary)*	*52083*	*scaffold_1:571729..575130 forward*	*Chlorophyta*	*Incertae sedis*	*Solyc03g031860.2.1*
Dunaliella salina	*Das*	*404.8*	*6.3E-138*	*Dusal.0943s00001.1 (primary)*	*Dusal.0943s00001.1*	*scaffold943:9490..19698 reverse*	*Chlorophyta*	*Chlamydomonadales*	*Solyc03g031860.2.1*
Dunaliella salina	*Das*	*374.0*	*6.3E-126*	*Dusal.0031s00032.1 (primary)*	*Dusal.0031s00032.1*	*scaffold31:479535..492555 forward*	*Chlorophyta*	*Chlamydomonadales*	*Solyc03g031860.2.1*
Micromonas pusilla	*Mpu*	*385.6*	*1.5E-130*	*32317 (primary)*	*32317*	*scaffold_3:822114..824691 reverse*	*Chlorophyta*	*Mamiellales*	*Solyc03g031860.2.1*
Micromonas sp	*M*	*387.1*	*2.7E-132*	*85839 (primary)*	*85839*	*Chr_10:705277..706335 forward*	*Chlorophyta*	*Mamiellales*	*Solyc03g031860.2.1*
Ostreococcus lucimarinus	*Olu*	*349.7*	*7,00E-119*	*12559 (primary)*	*12559*	*Chr_5:565049..565870 reverse*	*Chlorophyta*	*Mamiellales*	*Solyc03g031860.2.1*
Volvox carteri	*Vca*	*402.5*	*2.2E-137*	*Vocar.0027s0175.1*	*Vocar.0027s0175.1*	*scaffold_27:1630403..1637580 reverse*	*Chlorophyta*	*Volvocales*	*Solyc03g031860.2.1*
Marchantia polymorpha	*Mpo*	*532.7*	*0.0*	*Mapoly0040s0104.1 (primary)*	*Mapoly0040s0104.1*	*scaffold_40:1067130..1071400 forward*	*Bryophyta*	*Marchantiales*	*Solyc03g031860.2.1*
Physcomitrella patens	*Ppa*	*531.6*	*0.0*	*Pp3c24_10180V3.1 (primary)*	*Pp3c24_10180V3.1*	*Chr24:6938725..6942585 forward*	*Bryophyta*	*Funariales*	*Solyc03g031860.2.1*
Physcomitrella patens	*Ppa*	*520*	*0.0*	*Pp3c8_21760V3.1 (primary)*	*Pp3c8_21760V3.1*	*Chr08:14919012..14922846 forward*	*Bryophyta*	*Funariales*	*Solyc03g031860.2.1*
Physcomitrella patens	*Ppa*	*518.9*	*0.0*	*Pp3c24_16380V3.1 (primary)*	*Pp3c24_16380V3.1*	*Chr24:10757319..10761131 forward*	*Bryophyta*	*Funariales*	*Solyc03g031860.2.1*
Sphagnum fallax	*Sfa*	*521.9*	*0.0*	*Sphfalx0049s0098.1 (primary)*	*Sphfalx0049s0098.1*	*super_49:1449572..1454449 reverse*	*Bryophyta*	*Sphagnales*	*Solyc03g031860.2.1*
Aspergillus costaricaensis	*Acs*	*82*	*7,00E-14*	*XP_025539973*	*XP_025539973*		*Fungi*	*Eurotiales*	*Solyc03g031860.2.1*
Aspergillus luchuensis	*Alu*	*83,2*	*5,00E-15*	*GAT30047*	*GAT30047*	*map: 6-6 F, contig: AA1_SCon_033*	*Fungi*	*Eurotiales*	*Solyc03g031860.2.1*
Aspergillus neoniger	*Ane*	*80,9*	*2,00E-13*	*XP_025475515*	*XP_025475515*		*Fungi*	*Eurotiales*	*Solyc03g031860.2.1*
Aspergillus piperis	*Api*	*83,2*	*5,00E-15*	*XP_025516982*	*XP_025516982*		*Fungi*	*Eurotiales*	*Solyc03g031860.2.1*
Colletotrichum higginsianum	*Chi*	*75,1*	*8,00E-12*	*CCF46103*	*CCF46103*	*contig cont1.829*	*Fungi*	*Glomerellales*	*Solyc03g031860.2.1*
Fusarium albosuccineum	*Fal*	*77*	*1,00E-12*	*KAF4458563*	*KAF4458563*		*Fungi*	*Hypocreales*	*Solyc03g031860.2.1*

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Nannizzia gypsea	*Ngy*	*80,9*	*2,00E-13*	*XP_003174566*	*XP_003174566*		*Fungi*	*Onygenales*	*Solyc03g031860.2.1*
Pyrenophora seminiperda	*Pse*	*94,4*	*9,00E-18*	*RMZ72926*	*RMZ72926*	*scaffold00043*	*Fungi*	*Pleosporales*	*Solyc03g031860.2.1*
Pyrenophora tritici-repentis	*Pti*	*89*	*2,00E-16*	*KAA8614953*	*KAA8614953*	*V1_contig_00009*	*Fungi*	*Pleosporales*	*Solyc03g031860.2.1*
Rosellinia necatrix	*Rne*	*76,3*	*5,00E-12*	*GAP92111*	*GAP92111*	*scaffold: Contig75*	*Fungi*	*Xylariales*	*Solyc03g031860.2.1*
Acyrthosiphon pisum	*Aps*	*64,7*	*1,00E-08*	*XP_003241668*	*XP_003241668*		*Arthropoda*	*Hemiptera*	*Solyc03g031860.2.1*
Drosophila bipectinata	*Dbi*	*93,6*	*6,00E-19*	*XP_017095802*	*XP_017095802*		*Arthropoda*	*Diptera*	*Solyc03g031860.2.1*
Drosophila elegans	*Del*	*93,2*	*8,00E-19*	*XP_017118015*	*XP_017118015*		*Arthropoda*	*Diptera*	*Solyc03g031860.2.1*
Drosophila eugracilis	*Deu*	*108*	*3,00E-24*	*XP_017070630*	*XP_017070630*		*Arthropoda*	*Diptera*	*Solyc03g031860.2.1*
Drosophila ficusphila	*Dfi*	*109*	*7,00E-25*	*XP_017040643*	*XP_017040643*		*Arthropoda*	*Diptera*	*Solyc03g031860.2.1*
Drosophila kikkawai	*Dki*	*93,2*	*7,00E-19*	*XP_017032848*	*XP_017032848*		*Arthropoda*	*Diptera*	*Solyc03g031860.2.1*
Tetranychus urticae	*Tut*	*56*	*0.00035*	*tetur01g11260*	*DAA34969.1*	*SuperContig HE587301: 5,209,423-5,213,678 reverse strand*	*Arthropoda*	*Trombidiformes*	*Tetranychus urticae ASM23943v1*
Klebsormidium nitens	*Kni*	*448*	*3,00E-154*	*kfl00019_0320_v1.1*	*kfl00019_0320*		*Charophyta*	*Klebsormidiales*	*Solyc03g031860.2.1*
Selaginella moellendorffii	*Smo*	*523.1*	*0.0*	*233658 (primary)*	*233658*	*scaffold_47:782646..784025 forward*	*Lycophytes*	*Selaginellales*	*Solyc03g031860.2.1*
Picea abies	*Pab*	*567,38*	*0.0*	*MA_86494g0010*	*MA_86494g0010*	*MA_86494:2318..6959*	*Gymnosperm*	*Pinales*	*Solyc03g031860.2.1*
Picea abies	*Pab*	*236,5*	*0.0*	*MA_407452g0010*	*MA_407452g0010*	*MA_407452:1629..2244*	*Gymnosperm*	*Pinales*	*Solyc03g031860.2.1*
Pinus taeda	*Pta*	*539,26*	*0.0*	*PITA_000050116*	*PITA_000050116*	*Scaffold 880084.2:2751..7208*	*Gymnosperm*	*Pinales*	*Solyc03g031860.2.1*
Pinus taeda	*Pta*	*480,71*	*9,83E-170*	*PITA_000002541*	*PITA_000002541*	*tscaffold 4861:26078..42463*	*Gymnosperm*	*Pinales*	*Solyc03g031860.2.1*

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Amborella trichopoda	*Atr*	*562*	*0.0*	*evm_27.model.AmTr_v1.0_scaffold00032.92 (primary)*	*evm_27.model.AmTr_v1.0_scaffold00032.92*	*AmTr_v1.0_scaffold00032:1823840..1832740 reverse*	*Early angiosperm*	*Amborellales*	*Solyc03g031860.2.1*
Amborella trichopoda	*Atr*	*537.3*	*0.0*	*evm_27.model.AmTr_v1.0_scaffold00044.14 (primary)*	*evm_27.model.AmTr_v1.0_scaffold00044.14*	*AmTr_v1.0_scaffold00044:320296..333892 reverse*	*Early angiosperm*	*Amborellales*	*Solyc03g031860.2.1*
Spirodela polyrhiza	*Spo*	*602.4*	*0.0*	*Spipo1G0051600 (primary)*	*Spipo1G0051600*	*pseudo1:3342204..3344393 forward*	*Monocots*	*Alismatales*	*Solyc03g031860.2.1*
Spirodela polyrhiza	*Spo*	*546.6*	*0.0*	*Spipo8G0020300 (primary)*	*Spipo8G0020300*	*pseudo8:2050614..2052383 reverse*	*Monocots*	*Alismatales*	*Solyc03g031860.2.1*
Zostera marina	*Zmr*	*569.7*	*0.0*	*Zosma16g00900.1*	*Zosma16g00900.1*	*scaffold_16:567834..570010 reverse*	*Monocots*	*Alismatales*	*Solyc03g031860.2.1*
Aegilops tauschii	*Ata*	*1276*	*3,00E-168*	*AET7Gv21342500.2*	*AET7Gv21342500*	*Chromosome 7D: 639,162,008-639,167,161 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Aegilops tauschii	*Ata*	*1254*	*3,40E-165*	*AET5Gv20068500.3*	*AET5Gv20068500*	*Chromosome 5D: 26,757,085-26,760,088 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Aegilops tauschii	*Ata*	*753*	*1,10E-95*	*AET5Gv20828700.1*	*AET5Gv20828700*	*Chromosome 5D: 450,481,493-450,484,002 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Ananas comosus	*Aco*	*581.3*	*0.0*	*Aco013002.1 (primary)*	*Aco013002.1*	*LG25:1393795..1396471 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Ananas comosus	*Aco*	*575.5*	*0.0*	*Aco009217.1 (primary)*	*Aco009217.1*	*LG22:8546722..8558411 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Ananas comosus	*Aco*	*541.6*	*0.0*	*Aco005022.1 (primary)*	*Aco005022.1*	*LG07:1487658..1490439 forward*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Brachypodium distachyon	*Bdi*	*549.7*	*0.0*	*Bradi1g29590.2 (primary)*	*Bradi1g29590.2*	*Bd1:25177642..25181644 forward*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Brachypodium distachyon	*Bdi*	*510.0*	*3.8E-179*	*Bradi4g01100.1 (primary)*	*Bradi4g01100.1*	*Bd4:683690..687242 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Brachypodium distachyon	*Bdi*	*494.2*	*4.6E-173*	*Bradi4g37520.1 (primary)*	*Bradi4g37520.1*	*Bd4:42521097..42524510 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Brachypodium stacei	*Bst*	*554.3*	*0.0*	*Brast07G241400.1 (primary)*	*Brast07G241400.1*	*Chr07:20604273..20608120 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Brachypodium stacei	*Bst*	*513.1*	*1.3E-180*	*Brast10G009800.1 (primary)*	*Brast10G009800.1*	*Chr10:577285..580570 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Brachypodium stacei	*Bst*	*488.4*	*9.2E-171*	*Brast05G209700.1 (primary)*	*Brast05G209700.1*	*Chr05:17783948..17786829 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Eragrostis tef	*Ete*	*391*	*7,70E-118*	*Et_s3092-0.38-1.mrna1*	*Et_s3092*	*SuperContig scaffold3092: 12,555-15,280 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Eragrostis tef	*Ete*	*372*	*4,00E-103*	*Et_s1813-1.34-1.mrna1*	*Et_s1813*	*SuperContig scaffold1813: 173,520-176,190 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Eragrostis tef	*Ete*	*371*	*8,10E-125*	*Et_s7091-0.40-1.mrna1*	*Et_s7091*	*SuperContig scaffold7091: 10,905-13,395 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Eragrostis tef	*Ete*	*351*	*7,00E-128*	*Et_s517-0.16-1.mrna1*	*Et_s517*	*SuperContig scaffold517: 41,323-45,588 forward strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Eragrostis tef	*Ete*	*349*	*1,20E-129*	*Et_s4159-0.20-1.mrna1*	*Et_s4159*	*SuperContig scaffold4159: 66,805-70,707 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Hordeum vulgare	*Hvu*	*1269*	*2,80E-167*	*HORVU7Hr1G120660.3*	*HORVU7Hr1G120660*	*Chromosome chr7H: 652,117,486-652,121,143 forward strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Hordeum vulgare	*Hvu*	*1258*	*9,30E-166*	*HORVU5Hr1G005740.2*	*HORVU5Hr1G005740*	*Chromosome chr5H: 9,252,064-9,255,073 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Hordeum vulgare	*Hvu*	*750*	*2,90E-95*	*HORVU5Hr1G088130.4*	*HORVU5Hr1G088130*	*Chromosome chr5H: 580,830,866-580,832,556 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Leersia perrieri	*Lpe*	*1309*	*1,70E-173*	*LPERR06G23640.1*	*LPERR06G23640*	*Chromosome 6: 20,892,913-20,895,557 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Leersia perrieri	*Lpe*	*1259*	*1,50E-166*	*LPERR12G16110.1*	*LPERR12G16110*	*Chromosome 12: 16,999,952-17,002,773 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Leersia perrieri	*Lpe*	*794*	*4,90E-102*	*LPERR09G15010.1*	*LPERR09G15010*	*Chromosome 9: 14,625,116-14,627,798 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Leersia perrieri	*Lpe*	*763*	*9,90E-98*	*LPERR09G15000.1*	*LPERR09G15000*	*Chromosome 9: 14,619,828-14,622,601 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Musa acuminata	*Mac*	*599*	*0.0*	*GSMUA_AchrUn_randomT09240_001 (primary)*	*GSMUA_AchrUn_randomT09240_001*	*chrUn_random:42933000..42935315 reverse*	*Monocots (commelinids)*	*Zingiberales*	*Solyc03g031860.2.1*

Species	Acronymon	Score	Evalue	Transcript Name	CDS Acession Number	Location	Classification group	Order	Query
Musa acuminata	*Mac*	*560.1*	*0.0*	*GSMUA_Achr9T10050_001 (primary)*	*GSMUA_Achr9T10050_001*	*chr9:6467097..6469206 forward*	*Monocots (commelinids)*	*Zingiberales*	*Solyc03g031860.2.1*
Musa acuminata	*Mac*	*537.3*	*0.0*	*GSMUA_Achr6T31560_001 (primary)*	*GSMUA_Achr6T31560_001*	*chr6:31294343..31298625 reverse*	*Monocots (commelinids)*	*Zingiberales*	*Solyc03g031860.2.1*
Musa acuminata	*Mac*	*527.3*	*0.0*	*GSMUA_Achr11T07450_001 (primary)*	*GSMUA_Achr11T07450_001*	*chr11:5827293..5829074 reverse*	*Monocots (commelinids)*	*Zingiberales*	*Solyc03g031860.2.1*
Oropetium thomaeum	*Oth*	*566.2*	*0.0*	*Oropetium_20150105_16450A (primary)*	*Oropetium_20150105_16450A*	*Oropetium_genomic_20141112_058:1394996..1399216 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oropetium thomaeum	*Oth*	*501.1*	*9,00E-176*	*Oropetium_20150105_06439A (primary)*	*Oropetium_20150105_06439A*	*Oropetium_genomic_20141112_007:2298318..2301541 forward*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oropetium thomaeum	*Oth*	*435.3*	*3.2E-2*	*Oropetium_20150105_26131A (primary)*	*Oropetium_20150105_26131A*	*Oropetium_genomic_20141112_128:102591..105980 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza barthii	*Oba*	*1304*	*7,90E-173*	*OBART06G28180.1*	*OBART06G28180*	*Chromosome 6: 25,547,527-25,550,534 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza barthii	*Oba*	*1250*	*2,50E-165*	*OBART12G19460.1*	*OBART12G19460*	*Chromosome 12: 19,871,917-19,874,707 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza barthii	*Oba*	*785*	*8,40E-101*	*OBART09G19150.1*	*OBART09G19150*	*Chromosome 9: 18,232,450-18,235,912 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza brachyantha	*Obr*	*1291*	*3,30E-171*	*OB06G35940.1*	*OB06G35940*	*Chromosome 6: 21,655,842-21,658,741 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza brachyantha	*Obr*	*1131*	*5,40E-149*	*OB12G26220.1*	*OB12G26220*	*Chromosome 12: 14,756,519-14,759,775 forward strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza brachyantha	*Obr*	*1076*	*2,30E-141*	*OB09G25760.1*	*OB09G25760*	*Chromosome 9: 13,346,492-13,348,554 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza glaberrima	*Ogl*	*1304*	*5,60E-173*	*ORGLA06G0287600.1*	*ORGLA06G0287600*	*Scaffold Oglab06_unplaced183: 46,183-49,189 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Oryza glaberrima	*Ogl*	*1256*	*2,60E-166*	*ORGLA12G0167800.1*	*ORGLA12G0167800*	*Chromosome 12: 18,361,617-18,364,404 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza glaberrima	*Ogl*	*1200*	*1,50E-158*	*ORGLA09G0153600.1*	*ORGLA09G0153600*	*Chromosome 9: 16,481,944-16,484,415 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza glumipatula	*Ogu*	*1304*	*9,10E-173*	*OGLUM06G29570.1*	*OGLUM06G29570*	*Chromosome 6: 31,354,021-31,357,030 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza glumipatula	*Ogu*	*1250*	*2,80E-165*	*OGLUM12G21130.1*	*OGLUM12G21130*	*Chromosome 12: 25,999,396-26,003,333 forward strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza glumipatula	*Ogu*	*694*	*4,10E-88*	*OGLUM09G19690.1*	*OGLUM09G19690*	*Chromosome 9: 22,265,018-22,267,694 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza longistaminata	*Olo*	*1311*	*5,80E-174*	*KN538785.1_FGT003*	*KN538785*	*Scaffold KN538785.1: 152,026-154,808 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza longistaminata	*Olo*	*1088*	*5,10E-143*	*KN538757.1_FGT004*	*KN538757*	*Scaffold KN538757.1: 172,790-184,307 forward strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza longistaminata	*Olo*	*764*	*4,70E-98*	*KN540821.1_FGT003*	*KN540821*	*Scaffold KN540821.1: 12,579-18,354 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza meridionalis	*Ome*	*1304*	*8,70E-173*	*OMERI06G28090.5*	*OMERI06G28090*	*Chromosome 6: 31,628,915-31,633,028 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza meridionalis	*Ome*	*1195*	*1,20E-157*	*OMERI09G14390.1*	*OMERI09G14390*	*Chromosome 9: 17,923,693-17,929,959 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza meridionalis	*Ome*	*1180*	*1,40E-155*	*OMERI12G14330.1*	*OMERI12G14330*	*Chromosome 12: 19,269,363-19,282,654 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza punctata	*Opu*	*1306*	*4,50E-173*	*OPUNC06G25700.2*	*OPUNC06G25700*	*Chromosome 6: 34,382,050-34,384,709 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza punctata	*Opu*	*1206*	*1,10E-166*	*OPUNC12G17610.1*	*OPUNC12G17610*	*Chromosome 12: 27,114,787-27,119,055 forward strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza punctata	*Opu*	*1201*	*1,70E-158*	*OPUNC09G17510.1*	*OPUNC09G17510*	*Chromosome 9: 25,407,635-25,409,731 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Oryza rufipogon	*Oru*	*1304*	*9,30E-173*	*ORUFI06G30110.1*	*ORUFI06G30110*	*Chromosome 6: 27,682,342-27,686,178 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*

Species	Acronymon	Score	Evalue	Transcript Name	CDS Acession Number	Location	Classification group	Order	Query
Oryza rufipogon	Oru	1205	2,90E-165	ORUFI12G21740.1	ORUFI12G21740	Chromosome 12: 22,831,897-22,834,687 reverse strand.	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Oryza rufipogon	Oru	793	7,60E-102	ORUFI09G20730.1	ORUFI09G20730	Chromosome 9: 19,611,150-19,617,449 reverse strand	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Oryza sativa	Osa	563.1	0.0	LOC_Os06g51290.1 (primary)	LOC_Os06g51290.1	Chr6:31051971..31055926 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Oryza sativa	Osa	514.6	0.0	LOC_Os12g43130.1 (primary)	LOC_Os12g43130.1	Chr12:26780487..26783598 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Oryza sativa	Osa	491.5	3.3E-171	LOC_Os09g38320.1 (primary)	LOC_Os09g38320.1	Chr9:22041967..22045393 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Panicum hallii	Pha	572.0	0.0	Pahal.D00247.1 (primary)	Pahal.D00247.1	Chr04:226949..230520 forward	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Panicum hallii	Pha	517.3	0.0	Pahal.C04830.1 (primary)	Pahal.C04830.1	Chr03:63469691..63473041 forward	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Panicum hallii	Pha	507.7	1,00E-177	Pahal.B03778.1 (primary)	Pahal.B03778.1	Chr02:52670089..52674217 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Panicum virgatum	Pvi	575.1	0.0	Pavir.J02631.1 (primary)	Pavir.J02631.1	contig03129:15958..19364 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Panicum virgatum	Pvi	569.3	0.0	Pavir.Db00050.1 (primary)	Pavir.Db00050.1	Chr04b:736370..740005 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Panicum virgatum	Pvi	518.5	0.0	Pavir.Db01083.1 (primary)	Pavir.Db01083.1	Chr04b:19360788..19363716 forward	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Panicum virgatum	Pvi	501.5	2.4E-176	Pavir.Ba01490.1 (primary)	Pavir.Ba01490.1	Chr02a:19032833..19035996 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Panicum virgatum	Pvi	490.3	1.1E-172	Pavir.Bb02573.1 (primary)	Pavir.Bb02573.1	Chr02b:59338774..59341023 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Panicum virgatum	Pvi	455.7	1.4E-159	Pavir.Cb00105.1 (primary)	Pavir.Cb00105.1	Chr03b:1647112..1649439 forward	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Saccharum spontaneum	Ssp	384	2,50E-125	Sspon.08G0000480-1A-mRNA-1	Sspon_08G0000480	Chromosome 8A: 1,745,103-1,748,728 forward strand	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Setaria italica	Sit	570.5	0.0	Seita.4G288600.1 (primary)	Seita.4G288600.1	scaffold_4:40043909..40046902 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Setaria italica	Sit	519.2	0.0	Seita.3G397800.1 (primary)	Seita.3G397800.1	scaffold_3:49831722..49834779 forward	Monocots (commelinids)	Poales	Solyc03g031860.2.1
Setaria italica	Sit	503.8	3.4E-176	Seita.2G303000.1 (primary)	Seita.2G303000.1	scaffold_2:39561335..39564733 reverse	Monocots (commelinids)	Poales	Solyc03g031860.2.1

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Setaria viridis	*Svi*	*568.2*	*0.0*	*Sevir.4G300900.1 (primary)*	*Sevir.4G300900.1*	*Chr_04:39324444..39327897 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Setaria viridis	*Svi*	*518.5*	*0.0*	*Sevir.3G415800.1 (primary)*	*Sevir.3G415800.1*	*Chr_03:48966579..48969560 forward*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Setaria viridis	*Svi*	*504.6*	*2.1E-176*	*Sevir.2G314000.1 (primary)*	*Sevir.2G314000.1*	*Chr_02:38422397..38427143 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Sorghum bicolor	*Sbi*	*526.2*	*0.0*	*Sobic.008G180800.1 (primary)*	*Sobic.008G180800.1*	*Chr08:61419851..61422820 forward*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Sorghum bicolor	*Sbi*	*508.8*	*4.9E-178*	*Sobic.002G292600.1 (primary)*	*Sobic.002G292600.1*	*Chr02:67031565..67034288 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum aestivum	*Tae*	*1276*	*2,10E-168*	*TraesCS7D02G553300.1*	*TraesCS7D02G553300*	*Chromosome 7D: 636,765,931-636,771,068 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum aestivum	*Tae*	*1273*	*5,60E-168*	*TraesCS7A02G557300.2*	*TraesCS7A02G557300*	*Chromosome 7A: 729,397,165-729,401,834 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum aestivum	*Tae*	*1270*	*1,50E-167*	*TraesCS7B02G482000.1*	*TraesCS7B02G482000*	*Chromosome 7B: 739,442,097-739,446,001 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum aestivum	*Tae*	*1254*	*2,40E-165*	*TraesCS5D02G026000.1*	*TraesCS5D02G026000*	*Chromosome 5D: 23,296,528-23,299,514 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum aestivum	*Tae*	*1254*	*2,40E-165*	*TraesCS5B02G017900.1*	*TraesCS5B02G017900*	*Chromosome 5B: 17,544,779-17,547,737 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum aestivum	*Tae*	*1251*	*6,30E-165*	*TraesCS5A02G020900.1*	*TraesCS5A02G020900*	*Chromosome 5A: 17,221,404-17,224,338 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum aestivum	*Tae*	*763*	*3,30E-97*	*TraesCS5A02G356300.2*	*TraesCS5A02G356300*	*Chromosome 5A: 558,682,954-558,688,761 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum aestivum	*Tae*	*758*	*1,60E-96*	*TraesCS5B02G358800.1*	*TraesCS5B02G358800*	*Chromosome 5B: 538,717,321-538,719,110 forward strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum aestivum	*Tae*	*753*	*8,10E-96*	*TraesCS5D02G365100.1*	*TraesCS5D02G365100*	*Chromosome 5D: 442,496,502-442,498,524 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Triticum dicoccoides	*Tdi*	*1273*	*9,10E-168*	*TRIDC7AG077320.6*	*TRIDC7AG077320*	*Chromosome 7A: 721,057,396-721,061,077 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum dicoccoides	*Tdi*	*1259*	*7,90E-166*	*TRIDC7BG073780.3*	*TRIDC7BG073780*	*Chromosome 7B: 739,010,245-739,013,465 forward strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum dicoccoides	*Tdi*	*1251*	*1,00E-164*	*TRIDC5AG002900.4*	*TRIDC5AG002900*	*Chromosome 5A: 16,297,965-16,300,537 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum dicoccoides	*Tdi*	*758*	*2,70E-96*	*TRIDC5BG056420.1*	*TRIDC5BG056420*	*Chromosome 5B: 544,909,913-544,911,433 forward strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum dicoccoides	*Tdi*	*677*	*4,70E-85*	*TRIDC5AG052060.3*	*TRIDC5AG052060*	*Chromosome 5A: 554,272,803-554,273,524 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum turgidum	*Ttu*	*1281*	*6,60E-169*	*TRITD6Bv1G228570.1*	*TRITD6Bv1G228570*	*Chromosome 6B: 696,979,833-696,983,031 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum turgidum	*Ttu*	*1147*	*2,60E-150*	*TRITD5Bv1G006790.1*	*TRITD5Bv1G006790*	*Chromosome 5B: 17,326,775-17,328,203 forward strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum turgidum	*Ttu*	*1142*	*1,30E-149*	*TRITD5Av1G008310.1*	*TRITD5Av1G008310*	*Chromosome 5A: 17,616,395-17,617,884 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum turgidum	*Ttu*	*1126*	*2,10E-147*	*TRITD5Bv1G006680.1*	*TRITD5Bv1G006680*	*Chromosome 5B: 17,026,598-17,106,302 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum urartu	*Tur*	*1079*	*9,50E-142*	*TRIUR3_33626-T1*	*TRIUR3_33626*	*SuperContig scaffold269090: 29,367-31,794 reverse strand*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Triticum urartu	*Tur*	*731*	*1,90E-93*	*TRIUR3_13950-T1*	*TRIUR3_13950*	*SuperContig scaffold52601: 21,221-22,002 reverse strand.*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Zea mays	*Zma*	*563.5*	*0.0*	*Zm00008a024386_T01*	*Zm00008a024386_T01*	*chr06:81555811..81559359 forward*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Zea mays	*Zma*	*515.4*	*0.0*	*Zm00008a032909_T01*	*Zm00008a032909_T01*	*chr08:168204484..168208257 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Zea mays	*Zma*	*335.9*	*6.4E-112*	*Zm00008a028762_T01*	*Zm00008a028762_T01*	*chr07:146291552..146293434 forward*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Zea mays (Ensembl)	*Zma*	*518.5*	*0.0*	*GRMZM2G149317_T01*	*GRMZM2G149317_T01*	*8:167823550..167826600 reverse*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Zea mays (Ensembl)	*Zma*	*345.9*	*1.3E-117*	*GRMZM2G300348_T01*	*GRMZM2G300348_T01*	*6:82182364..82184345 forward*	*Monocots (commelinids)*	*Poales*	*Solyc03g031860.2.1*
Actinidia chinensis	*Ach*	*1555*	*0.0*	*PSS00264*	*PSS00264*	*Chromosome LG21: 12,933,111-12,937,550 reverse strand*	*Eudicot (asterids)*	*Ericales*	*Solyc03g031860.2.1*
Actinidia chinensis	*Ach*	*1553*	*0.0*	*PSS30087*	*PSS30087*	*Chromosome LG5: 3,897,808-3,901,724 forward strand*	*Eudicot (asterids)*	*Ericales*	*Solyc03g031860.2.1*
Actinidia chinensis	*Ach*	*894*	*5,30E-116*	*PSR86897*	*PSR86897*	*Chromosome LG28: 15,339,888-15,343,821 reverse strand*	*Eudicot (asterids)*	*Ericales*	*Solyc03g031860.2.1*
Aquilegia coerulea	*Ace*	*570.9*	*0.0*	*Aqcoe3G009300.1 (primary)*	*Aqcoe3G009300.1*	*Chr_03:602263..605497 reverse*	*Eudicots*	*Ranunculales*	*Solyc03g031860.2.1*
Aquilegia coerulea	*Ace*	*527.7*	*0.0*	*Aqcoe1G178400.1 (primary)*	*Aqcoe1G178400.1*	*Chr_01:10395407..10398959 forward*	*Eudicots*	*Ranunculales*	*Solyc03g031860.2.1*
Aquilegia coerulea	*Ace*	*442.6*	*7.1E-153*	*Aqcoe1G050500.1 (primary)*	*Aqcoe1G050500.1*	*Chr_01:2555174..2556931 reverse*	*Eudicots*	*Ranunculales*	*Solyc03g031860.2.1*
Coffea canephora	*Cca*	*1566*	*0.0*	*CDP21283*	*CDP21283*	*SuperContig scaffold_3092: 6,986-12,616 reverse strand*	*Eudicots (asterids)*	*Gentianales*	*Solyc03g031860.2.1*
Coffea canephora	*Cca*	*1195*	*6,50E-158*	*CDP08373*	*CDP08373*	*Chromosome 8: 26,570,827-26,572,985 reverse strand*	*Eudicots (asterids)*	*Gentianales*	*Solyc03g031860.2.1*
Coffea canephora	*Cca*	*1101*	*7,20E-145*	*CDP17352*	*CDP17352*	*Chromosome 1: 4,751,718-4,753,782 reverse strand*	*Eudicots (asterids)*	*Gentianales*	*Solyc03g031860.2.1*
Cynara cardunculus	*Ccr*	*1581*	*0.0*	*KVI08675*	*KVI08675*	*SuperContig scaffold_374: 148,566-152,979 reverse strand*	*Eudicots (asterids)*	*Asterales*	*Solyc03g031860.2.1*
Cynara cardunculus	*Ccr*	*1126*	*2,60E-148*	*KVH90844*	*KVH90844*	*SuperContig scaffold_62: 345,600-347,490 reverse strand*	*Eudicots (asterids)*	*Asterales*	*Solyc03g031860.2.1*
Cynara cardunculus	*Ccr*	*780*	*2,70E-100*	*KVI03037*	*KVI03037*	*SuperContig scaffold_2482: 24,347-27,848 reverse strand*	*Eudicots (asterids)*	*Asterales*	*Solyc03g031860.2.1*
Daucus carota	*Dca*	*641.3*	*0.0*	*DCAR_010057 (primary)*	*DCAR_010057*	*DCARv2_Chr3:14246823..14250604 reverse*	*Eudicots (asterids)*	*Apiales*	*Solyc03g031860.2.1*

Species	Acronymon	Score	Evalue	Transcript Name	CDS Acession Number	Location	Classification group	Order	Query
Daucus carota	*Dca*	*530.0*	*0.0*	*DCAR_023043 (primary)*	*DCAR_023043*	*DCARv2_Chr6:2377864..2379676 forward*	*Eudicots (asterids)*	*Apiales*	*Solyc03g031860.2.1*
Daucus carota	*Dca*	*447.2*	*6,00E-155*	*DCAR_024333 (primary)*	*DCAR_024333*	*DCARv2_Chr7:12326481..12328432 forward*	*Eudicots (asterids)*	*Apiales*	*Solyc03g031860.2.1*
Helianthus annuus	*Han*	*392*	*6,40E-156*	*PSY1-1 OTG04734*	*OTG04734*	*Chromosome 12: 39,201,022-39,205,788 reverse strand*	*Eudicots (asterids)*	*Asterales*	*Solyc03g031860.2.1*
Helianthus annuus	*Han*	*378*	*2,60E-137*	*PSY-1 OTG06350*	*OTG06350*	*Chromosome 12: 159,042,358-159,047,933 reverse strand*	*Eudicots (asterids)*	*Asterales*	*Solyc03g031860.2.1*
Helianthus annuus	*Han*	*353*	*1,80E-95*	*OTG35442*	*OTG35442*	*Chromosome 2: 171,868,581-171,871,894 reverse strand*	*Eudicots (asterids)*	*Asterales*	*Solyc03g031860.2.1*
Ipomoea triloba	*Itr*	*393*	*3,50E-162*	*itb03g05110.t1*	*itb03g05110*	*Chromosome 3: 3,439,071-3,443,392 forward strand*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Ipomoea triloba	*Itr*	*391*	*1,70E-136*	*itb12g01910.t1*	*itb12g01910*	*Chromosome 12: 1,291,564-1,295,742 forward strand*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Ipomoea triloba	*Itr*	*327*	*3,80E-110*	*itb14g11400.t1*	*itb14g11400*	*Chromosome 14: 13,043,653-13,045,702 forward strand*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Mimulus guttatus	*Mgu*	*646.7*	*0.0*	*Migut.K00976.1 (primary)*	*Migut.K00976.1*	*scaffold_11:14010950..14014009 forward*	*Eudicots (asterids)*	*Lamiales*	*Solyc03g031860.2.1*
Mimulus guttatus	*Mgu*	*458.8*	*2.5E-159*	*Migut.O00865.1 (primary)*	*Migut.O00865.1*	*scaffold_2956:1797..3477 forward*	*Eudicots (asterids)*	*Lamiales*	*Solyc03g031860.2.1*
Mimulus guttatus	*Mgu*	*458.0*	*5.4E-159*	*Migut.D02541.1 (primary)*	*Migut.D02541.1*	*scaffold_4:20917941..20919586 reverse*	*Eudicots (asterids)*	*Lamiales*	*Solyc03g031860.2.1*
Nicotiana attenuata	*Nat*	*1627*	*0.0*	*OIT35874*	*OIT35874*	*SuperContig scaffold00503: 205,508-208,871 reverse strand*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Nicotiana attenuata	*Nat*	*1591*	*0.0*	*OIT34597*	*OIT34597*	*SuperContig scaffold00685: 31,867-35,812 reverse strand.*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Nicotiana attenuata	*Nat*	*1132*	*4,30E-149*	*OIT32024*	*OIT32024*	*SuperContig scaffold01147: 16,867-20,125 reverse strand.*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Solanum lycopersicum	*Sly*	*852.4*	*0.0*	*Solyc03g031860.2.1 (primary)*	*Solyc03g031860.2.1*	*SL2.50ch03:4326134..4330127 forward*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*

Species	Acronymon	Score	Evalue	Transcript Name	CDS Acession Number	Location	Classification group	Order	Query
Solanum lycopersicum	*Sly*	*682.6*	*0.0*	*Solyc02g081330.2.1 (primary)*	*Solyc02g081330.2.1*	*SL2.50ch02:45335358..45339157 forward*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Solanum lycopersicum	*Sly*	*449.5*	*8.7E-156*	*Solyc01g005940.2.1 (primary)*	*Solyc01g005940.2.1*	*SL2.50ch01:613955..617183 forward*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Solanum tuberosum	*Stu*	*826.2*	*0.0*	*PGSC0003DMT400061846 (primary)*	*PGSC0003DMT400061846*	*ST4.03ch03:2742065..2744858 forward*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Solanum tuberosum	*Stu*	*778.5*	*0.0*	*PGSC0003DMT400061845*	*GSC0003DMT400061845*	*ST4.03ch03:2742065..2744858 forward*	*Eudicots (asterids)*	*Solanales*	*Solyc03g031860.2.1*
Linum usitatissimum	*Lus*	*525.8*	*0.0*	*Lus10001416 (primary)*	*Lus10001416*	*scaffold85:30097..32075 reverse*	*Eudicots (rosid)*	*Malpighiales*	*Solyc03g031860.2.1*
Linum usitatissimum	*Lus*	*509.2*	*7.6E-179*	*Lus10001050 (primary)*	*Lus10001050*	*scaffold964:24886..26882 reverse*	*Eudicots (rosid)*	*Malpighiales*	*Solyc03g031860.2.1*
Linum usitatissimum	*Lus*	*476.9*	*1.8E-166*	*Lus10020729 (primary)*	*Lus10020729*	*scaffold303:421222..428724 reverse*	*Eudicots (rosid)*	*Malpighiales*	*Solyc03g031860.2.1*
Linum usitatissimum	*Lus*	*478.8*	*1.2E-165*	*Lus10029809 (primary)*	*Lus10029809*	*scaffold416:121008..122994 reverse*	*Eudicots (rosid)*	*Malpighiales*	*Solyc03g031860.2.1*
Linum usitatissimum	*Lus*	*445.7*	*4.5E-154*	*Lus10013753 (primary)*	*Lus10013753*	*scaffold1168:335239..337750 forward*	*Eudicots (rosid)*	*Malpighiales*	*Solyc03g031860.2.1*
Linum usitatissimum	*Lus*	*438.7*	*3,00E-151*	*Lus10039186 (primary)*	*Lus10039186*	*scaffold34:2009013..2011210 reverse*	*Eudicots (rosid)*	*Malpighiales*	*Solyc03g031860.2.1*
Lupinus angustifolius	*Lan*	*471*	*4,10E-147*	*OIW22018*	*OIW22018*	*SuperContig Scaffold_702: 7,016-9,463 reverse strand.*	*Eudicots (rosid)*	*Fabales*	*Solyc03g031860.2.1*
Lupinus angustifolius	*Lan*	*385*	*1,00E-121*	*OIW02629*	*OIW02629*	*Chromosome LG11: 2,451,597-2,454,165 forward strand*	*Eudicots (rosid)*	*Fabales*	*Solyc03g031860.2.1*
Lupinus angustifolius	*Lan*	*377*	*1,00E-120*	*OIW16120*	*OIW16120*	*Chromosome LG02: 21,937,526-21,941,060 reverse strand*	*Eudicots (rosid)*	*Fabales*	*Solyc03g031860.2.1*
Malus domestica	*Mdo*	*536.6*	*0.0*	*MDP0000237124 (primary)*	*MDP0000237124*	*MDC004033.136:2450..5320 reverse*	*Eudicots (rosid)*	*Rosales*	*Solyc03g031860.2.1*
Malus domestica	*Mdo*	*484.6*	*4.7E-169*	*MDP0000177623 (primary)*	*MDP0000177623*	*MDC008336.467:13749..16522 reverse*	*Eudicots (rosid)*	*Rosales*	*Solyc03g031860.2.1*
Malus domestica	*Mdo*	*446.0*	*5.5E-154*	*MDP0000151924 (primary)*	*MDP0000151924*	*MDC016098.147:8268..10540 forward*	*Eudicots (rosid)*	*Rosales*	*Solyc03g031860.2.1*
Malus domestica	*Mdo*	*360.5*	*6,00E-119*	*MDP0000261447 (primary)*	*MDP0000261447*	*MDC019810.234:891..3831 forward*	*Eudicots (rosid)*	*Rosales*	*Solyc03g031860.2.1*

Species	Acronymon	Score	Evalue	Transcript Name	CDS Acession Number	Location	Classification group	Order	Query
Malus domestica	*Mdo*	*360.5*	*6.5E-119*	*MDP0000321586 (primary)*	*MDP0000321586*	*MDC019810.242:8443..11383 forward*	*Eudicots (rosid)*	*Rosales*	*Solyc03g031860.2.1*
Manihot esculenta	*Mes*	*634.4*	*0.0*	*Manes.01G124200.1 (primary)*	*Manes.01G124200.1*	*Chromosome01:24153420..24156720 forward*	*Eudicots (rosid)*	*Malpighiales*	*Solyc03g031860.2.1*
Manihot esculenta	*Mes*	*612.8*	*0.0*	*Manes.02G081700.1 (primary)*	*Manes.02G081700.1*	*Chromosome02:6091016..6093529 forward*	*Eudicots (rosid)*	*Malpighiales*	*Solyc03g031860.2.1*
Manihot esculenta	*Mes*	*452.6*	*9.8E-157*	*Manes.03G084700.1 (primary)*	*Manes.03G084700.1*	*Chromosome03:13755566..13757622 forward*	*Eudicots (rosid)*	*Malpighiales*	*Solyc03g031860.2.1*
Medicago truncatula	*Mtr*	*607.1*	*0.0*	*Medtr5g076620.1 (primary)*	*Medtr5g076620.1*	*chr5:32685852..32690189 reverse*	*Eudicots (rosid)*	*Fabales*	*Solyc03g031860.2.1*
Medicago truncatula	*Mtr*	*546.2*	*0.0*	*Medtr3g450510.1 (primary)*	*Medtr3g450510.1*	*chr3:17379804..17382838 reverse*	*Eudicots (rosid)*	*Fabales*	*Solyc03g031860.2.1*
Medicago truncatula	*Mtr*	*535.8*	*0.0*	*Medtr5g090780.1 (primary)*	*Medtr5g090780.1*	*chr5:39516910..39526617 reverse*	*Eudicots (rosid)*	*Fabales*	*Solyc03g031860.2.1*
Medicago truncatula	*Mtr*	*448.7*	*3.6E-155*	*Medtr3g083630.1 (primary)*	*Medtr3g083630.1*	*chr3:37749162..37751789 forward*	*Eudicots (rosid)*	*Fabales*	*Solyc03g031860.2.1*
Arabidopsis halleri	*Aha*	*602.8*	*0.0*	*Araha.10007s0012.1 (primary)*	*Araha.10007s0012.1*	*Scaffold10007:28956..32226 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Arabidopsis lyrata	*Aly*	*599.4*	*0.0*	*AL6G28280.t1 (primary)*	*AL6G28280.t1*	*scaffold_6:7059473..7062737 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Arabidopsis thaliana	*Ath*	*604.4*	*0.0*	*AT5G17230.1*	*AT5G17230.1*	*Chr5:5659574..5662865 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Boechera stricta	*Bsr*	*606.7*	*0.0*	*Bostr.2618s0058.1 (primary)*	*Bostr.2618s0058.1*	*Scaffold2618:293687..296867 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Brassica napus	*Brn*	*630*	*4,00E-179*	*NM_001315554*	*NM_001315554*	*Chr9 NC_027775.2 (44447856..44450852)*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Brassica oleracea	*Bol*	*589.3*	*0.0*	*Bol019820 (primary)*	*Bol019820*	*C09:32393730..32395844 forward*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Brassica oleracea	*Bol*	*586.3*	*0.0*	*Bol021326 (primary)*	*Bol021326*	*C02:4117261..4119269 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Brassica oleracea	*Bol*	*582.4*	*0.0*	*Bol034439 (primary)*	*Bol034439*	*C03:3362597..3364641 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Brassica rapa	*Bra*	*589.0*	*0.0*	*Brara.J01825.1 (primary)*	*Brara.J01825.1*	*A10:14948644..14951545 forward*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Brassica rapa	*Bra*	*584.7*	*0.0*	*Brara.B00699.1 (primary)*	*Brara.B00699.1*	*A02:3229295..3232410 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Brassica rapa	*Bra*	*575.5*	*0.0*	*Brara.C00758.1 (primary)*	*Brara.C00758.1*	*A03:3462822..3465336 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Capsella grandiflora	*Cgr*	*600.9*	*0.0*	*Cagra.4849s0011.1 (primary)*	*Cagra.4849s0011.1*	*Scaffold4849:47602..50896 forward*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Capsella rubella	*Cru*	*601.7*	*0.0*	*Carubv10001034m (primary)*	*Carubv10001034m*	*scaffold_6:5698892..5702297 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Carica papaya	*Cpa*	*274.2*	*2.9E-90*	*evm.model.supercontig_119.76 (primary)*	*evm.model.supercontig_119.76*	*supercontig_119:492097..492902 forward*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Citrus clementina	*Ccl*	*620.9*	*0.0*	*Ciclev10011751m*	*Ciclev10011751m*	*scaffold_6:21390477..21396087 reverse*	*Eudicots (rosids)*	*Sapindales*	*Solyc03g031860.2.1*
Citrus clementina	*Ccl*	*531.9*	*0.0*	*Ciclev10011841m (primary)*	*Ciclev10011841m*	*scaffold_6:21390477..21396087 reverse*	*Eudicots (rosids)*	*Sapindales*	*Solyc03g031860.2.1*
Citrus clementina	*Ccl*	*443.0*	*4.1E-153*	*Ciclev10018150m (primary)*	*Ciclev10018150m*	*scaffold_2:587065..588778 forward*	*Eudicots (rosids)*	*Sapindales*	*Solyc03g031860.2.1*
Citrus clementina	*Ccl*	*421.0*	*1.6E-144*	*Ciclev10015582m (primary)*	*Ciclev10015582m*	*scaffold_2:4441285..4443386 forward*	*Eudicots (rosids)*	*Sapindales*	*Solyc03g031860.2.1*
Citrus clementina	*Ccl*	*313.5*	*5,00E-105*	*Ciclev10018272m (primary)*	*Ciclev10018272m*	*scaffold_2:593780..594691 forward*	*Eudicots (rosids)*	*Sapindales*	*Solyc03g031860.2.1*
Citrus sinensis	*Csi*	*623.6*	*0.0*	*orange1.1g044623m (primary)*	*orange1.1g044623m*	*scaffold00091:64686..69575 reverse*	*Eudicots (rosids)*	*Sapindales*	*Solyc03g031860.2.1*
Citrus sinensis	*Csi*	*443.0*	*3.8E-153*	*orange1.1g036368m (primary)*	*orange1.1g036368m*	*scaffold00043:537648..539344 reverse*	*Eudicots (rosids)*	*Sapindales*	*Solyc03g031860.2.1*
Citrus sinensis	*Csi*	*421.0*	*1.8E-144*	*orange1.1g016696m (primary)*	*orange1.1g016696m*	*scaffold00043:507836..509918 reverse*	*Eudicots (rosids)*	*Sapindales*	*Solyc03g031860.2.1*
Citrus sinensis	*Csi*	*318.9*	*1.4E-106*	*orange1.1g036976m (primary)*	*orange1.1g036976m*	*scaffold00043:531582..532841 reverse*	*Eudicots (rosids)*	*Sapindales*	*Solyc03g031860.2.1*
Corchorus capsularis	*Ccp*	*1523*	*0.0*	*OMO59822*	*OMO59822*	*SuperContig contig13869: 10,338-13,426 reverse strand*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Corchorus capsularis	*Ccp*	*1305*	*3,40E-173*	*OMP12065*	*OMP12065*	*SuperContig contig00482: 2,804-5,324 reverse strand*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Corchorus capsularis	*Ccp*	*1134*	*1,80E-149*	*OMO80986*	*OMO80986*	*SuperContig contig10253: 32,456-34,004 forward strand.*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Cucumis sativus	*Csa*	*612.1*	*0.0*	*Cucsa.173570.1 (primary)*	*Cucsa.173570.1*	*scaffold01209:280607..283995 forward*	*Eudicots (rosids)*	*Cucurbitales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Cucumis sativus	*Csa*	*538.5*	*0.0*	*Cucsa.179860.1 (primary)*	*Cucsa.179860.1*	*scaffold01233:223487..227034 forward*	*Eudicots (rosids)*	*Cucurbitales*	*Solyc03g031860.2.1*
Cucumis sativus	*Csa*	*459.5*	*4.8E-161*	*Cucsa.153210.1 (primary)*	*Cucsa.153210.1*	*scaffold01124:412600..414885 forward*	*Eudicots (rosids)*	*Cucurbitales*	*Solyc03g031860.2.1*
Eucalyptus grandis	*Egr*	*597.4*	*0.0*	*Eucgr.F02913.1 (primary)*	*Eucgr.F02913.1*	*Chr06:41294911..41299376 forward*	*Eudicots (rosids)*	*Myrtales*	*Solyc03g031860.2.1*
Eucalyptus grandis	*Egr*	*532.3*	*0.0*	*Eucgr.A02030.1 (primary)*	*Eucgr.A02030.1*	*Chr01:35731243..35734193 forward*	*Eudicots (rosids)*	*Myrtales*	*Solyc03g031860.2.1*
Eucalyptus grandis	*Egr*	*527.3*	*0.0*	*Eucgr.F02914.1 (primary)*	*Eucgr.F02914.1*	*hr06:41301565..41304622 forward*	*Eudicots (rosids)*	*Myrtales*	*Solyc03g031860.2.1*
Eucalyptus grandis	*Egr*	*455.3*	*1.7E-158*	*Eucgr.B03619.1 (primary)*	*Eucgr.B03619.1*	*Chr02:55924946..55927040 forward*	*Eudicots (rosids)*	*Myrtales*	*Solyc03g031860.2.1*
Eutrema salsugineum	*Esa*	*593.2*	*0.0*	*Thhalv10013646m*	*Thhalv10013646m*	*scaffold_2:5787369..5790424 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Eutrema salsugineum	*Esa*	*585.9*	*0.0*	*Thhalv10013608m (primary)*	*Thhalv10013608m*	*scaffold_2:5787369..5790790 reverse*	*Eudicots (rosids)*	*Brassicales*	*Solyc03g031860.2.1*
Fragaria vesca	*Fve*	*583.2*	*0.0*	*mrna31674.1-v1.0-hybrid (primary)*	*mrna31674.1-v1.0-hybrid*	*LG1:10143441..10147256 reverse*	*Eudicots (rosids)*	*Rosales*	*Solyc03g031860.2.1*
Fragaria vesca	*Fve*	*548.9*	*0.0*	*mrna28765.1-v1.0-hybrid (primary)*	*mrna28765.1-v1.0-hybrid*	*LG6:30207289..30209752 forward*	*Eudicots (rosids)*	*Rosales*	*Solyc03g031860.2.1*
Fragaria vesca	*Fve*	*446.8*	*7.4E-155*	*mrna24795.1-v1.0-hybrid (primary)*	*mrna24795.1-v1.0-hybrid*	*LG3:28382548..28384477 reverse*	*Eudicots (rosids)*	*Rosales*	*Solyc03g031860.2.1*
Glycine max	*Gma*	*612.5*	*0.0*	*Glyma.02G240200.1 (primary)*	*Glyma.02G240200.1*	*Chr02:42872399..42878147 reverse*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Glycine max	*Gma*	*552.7*	*0.0*	*Glyma.14G209700.1 (primary)*	*Glyma.14G209700.1*	*Chr14:47496019..47500526 reverse*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Glycine max	*Gma*	*548.9*	*0.0*	*Glyma.18G111900.1 (primary)*	*Glyma.18G111900.1*	*Chr18:13308532..13312028 forward*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Glycine max	*Gma*	*547.7*	*0.0*	*Glyma.08G306200.1 (primary)*	*Glyma.08G306200.1*	*Chr08:42422270..42425862 reverse*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Glycine max	*Gma*	*547.4*	*0.0*	*Glyma.14G031200.1 (primary)*	*Glyma.14G031200.1*	*Chr14:2263622..2266628 forward*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Glycine max	*Gma*	*543.5*	*0.0*	*Glyma.02G283400.1 (primary)*	*Glyma.02G283400.1*	*Chr02:46520816..46523824 reverse*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Glycine max	*Gma*	*445.3*	*1.2E-153*	*Glyma.18G000600.1 (primary)*	*Glyma.18G000600.1*	*Chr18:99110..101506 forward*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Glycine max	*Gma*	*386.7*	*6.9E-131*	*Glyma.11G256400.1 (primary)*	*Glyma.11G256400.1*	*Chr11:34614957..34616879 reverse*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Gossypium raimondii	*Gra*	*579.3*	*0.0*	*Gorai.001G083700.1 (primary)*	*Gorai.001G083700.1*	*Chr01:8837490..8839782 reverse*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Gossypium raimondii	*Gra*	*547.0*	*0.0*	*Gorai.006G009400.1 (primary)*	*Gorai.006G009400.1*	*Chr06:2095293..2098359 forward*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Gossypium raimondii	*Gra*	*473.0*	*4.7E-165*	*Gorai.012G039100.1 (primary)*	*Gorai.012G039100.1*	*Chr12:4858435..4862016 forward*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Gossypium raimondii	*Gra*	*462.2*	*2.1E-160*	*Gorai.010G126900.1 (primary)*	*Gorai.010G126900.1*	*Chr10:26981829..26983602 forward*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Kalanchoe fedtschenko	*Kfe*	*536.6*	*0.0*	*Kaladp0038s0121.1 (primary)*	*Kaladp0038s0121.1*	*Scaffold_38:972031..974522 reverse*	*Eudicots (rosids)*	*Saxifragales*	*Solyc03g031860.2.1*
Kalanchoe fedtschenko	*Kfe*	*469.5*	*1.8E-163*	*Kaladp0037s0246.1 (primary)*	*Kaladp0037s0246.1*	*Scaffold_37:1750094..1751770 forward*	*Eudicots (rosids)*	*Saxifragales*	*Solyc03g031860.2.1*
Kalanchoe fedtschenko	*Kfe*	*330.5*	*9.2E-112*	*Kaladp0673s0002.1 (primary)*	*Kaladp0673s0002.1*	*Scaffold_673:4911..5844 reverse*	*Eudicots (rosids)*	*Saxifragales*	*Solyc03g031860.2.1*
Kalanchoe laxiflora	*Kla*	*545.4*	*0.0*	*Kalax.0456s0024.1 (primary)*	*Kalax.0456s0024.1*	*scaffold_456:221357..224086 forward*	*Eudicots (rosids)*	*Saxifragales*	*Solyc03g031860.2.1*
Kalanchoe laxiflora	*Kla*	*542.0*	*0.0*	*Kalax.0207s0024.1 (primary)*	*Kalax.0207s0024.1*	*scaffold_207:338827..341588 reverse*	*Eudicots (rosids)*	*Saxifragales*	*Solyc03g031860.2.1*
Kalanchoe laxiflora	*Kla*	*538.5*	*0.0*	*Kalax.0551s0002.1 (primary)*	*Kalax.0551s0002.1*	*scaffold_551:16039..18637 reverse*	*Eudicots (rosids)*	*Saxifragales*	*Solyc03g031860.2.1*
Kalanchoe laxiflora	*Kla*	*533.5*	*0.0*	*Kalax.0033s0007.1 (primary)*	*Kalax.0033s0007.1*	*scaffold_33:58871..61590 reverse*	*Eudicots (rosids)*	*Saxifragales*	*Solyc03g031860.2.1*
Kalanchoe laxiflora	*Kla*	*468.8*	*6,00E-163*	*Kalax.0026s0034.1 (primary)*	*Kalax.0026s0034.1*	*scaffold_26:332064..333638 forward*	*Eudicots (rosids)*	*Saxifragales*	*Solyc03g031860.2.1*
Kalanchoe laxiflora	*Kla*	*468.0*	*1.2E-162*	*Kalax.1101s0008.1 (primary)*	*Kalax.1101s0008.1*	*scaffold_1101:71236..72950 forward*	*Eudicots (rosids)*	*Saxifragales*	*Solyc03g031860.2.1*
Phaseolus vulgaris	*Pvu*	*601.3*	*0.0*	*Phvul.008G241500.1 (primary)*	*Phvul.008G241500.1*	*Chr08:59009458..59014705 forward*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Phaseolus vulgaris	*Pvu*	*553.9*	*0.0*	*Phvul.006G024100.1 (primary)*	*Phvul.006G024100.1*	*Chr06:9727535..9730509 reverse*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Phaseolus vulgaris	*Pvu*	*543.9*	*0.0*	*Phvul.008G195800.1 (primary)*	*Phvul.008G195800.1*	*Chr08:54004623..54007080 forward*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Phaseolus vulgaris	Pvu	446.0	2.7E-154	Phvul.001G268600.1 (primary)	Phvul.001G268600.1	Chr01:51323835..51325905 reverse	Eudicots (rosids)	Fabales	Solyc03g031860.2.1
Populus trichocarpa	Ptr	533.1	0.0	Potri.005G205800.1 (primary)	Potri.005G205800.1	Chr05:22042708..22046398 forward	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1
Populus trichocarpa	Ptr	531.2	0.0	Potri.002G056800.1 (primary)	Potri.002G056800.1	Chr02:3799091..3802364 reverse	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1
Populus trichocarpa	Ptr	516.5	0.0	Potri.004G081500.1 (primary)	Potri.004G081500.1	Chr04:6717614..6720756 forward	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1
Populus trichocarpa	Ptr	498.0	9.9E-176	Potri.017G138900.1 (primary)	Potri.017G138900.1	Chr17:14712482..14716973 reverse	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1
Populus trichocarpa	Ptr	452.6	1.2E-156	Potri.001G007700.1 (primary)	Potri.001G007700.1	Chr01:518243..520451 forward	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1
Populus trichocarpa	Ptr	424.1	1.7E-145	Potri.003G218000.1 (primary)	Potri.003G218000.1	Chr03:21421621..21423998 reverse	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1
Prunus avium	Pav	466	1,00E-143	Pav_sc0001215.1_g280.1.mk:mrna	sc0001215	SuperContig Pav_sc0001215.1.: 135,814-138,824 reverse strand	Eudicots (rosids)	Rosales	Solyc03g031860.2.1
Prunus avium	Pav	375	2,50E-164	Pav_sc0001124.1_g480.1.mk:mrna	sc0001124	SuperContig Pav_sc0001124.1.: 341,607-346,067 reverse strand	Eudicots (rosids)	Rosales	Solyc03g031860.2.1
Prunus avium	Pav	335	1,90E-99	Pav_sc0000909.1_g650.1.mk:mrna	sc0000909	SuperContig Pav_sc0000909.1.: 406,876-408,851 reverse strand	Eudicots (rosids)	Rosales	Solyc03g031860.2.1
Prunus persica	Ppe	631.7	0.0	Prupe.3G013200.1 (primary)	Prupe.3G013200.1	Pp03:938428..942844 forward	Eudicots (rosids)	Rosales	Solyc03g031860.2.1
Prunus persica	Ppe	553.5	0.0	Prupe.3G178500.1 (primary)	Prupe.3G178500.1	Pp03:19498687..19501428 forward	Eudicots (rosids)	Rosales	Solyc03g031860.2.1
Prunus persica	Ppe	438.7	3,00E-151	Prupe.6G006800.1 (primary)	Prupe.6G006800.1	Pp06:572052..574223 forward	Eudicots (rosids)	Rosales	Solyc03g031860.2.1
Ricinus communis	Rco	617.8	0.0	28611.m000105 (primary)	28611.m000105	28611:72961..77067 reverse	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1
Ricinus communis	Rco	451.4	1.4E-156	29835.m000639 (primary)	29835.m000639	29835:165737..167782 forward	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1
Ricinus communis	Rco	398.7	3.9E-136	29835.m000640 (primary)	29835.m000640	29835:168336..171416 reverse	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1
Salix purpurea	Spu	618.6	0.0	SapurV1A.0549s0100.1 (primary)	SapurV1A.0549s0100.1	chr17:16798169..16802345 reverse	Eudicots (rosids)	Malpighiales	Solyc03g031860.2.1

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Salix purpurea	*Spu*	*538.5*	*0.0*	*SapurV1A.1979s0010.1 (primary)*	*apurV1A.1979s0010.1*	*chr05:17477652..17480791 forward*	*Eudicots (rosids)*	*Malpighiales*	*Solyc03g031860.2.1*
Salix purpurea	*Spu*	*537.0*	*0.0*	*SapurV1A.0076s0100.1 (primary)*	*SapurV1A.0076s0100.1*	*chr05:17594349..17597440 forward*	*Eudicots (rosids)*	*Malpighiales*	*Solyc03g031860.2.1*
Salix purpurea	*Spu*	*535.0*	*0.0*	*SapurV1A.4120s0010.1 (primary)*	*SapurV1A.4120s0010.1*	*Scaffold4120:6004..8854 forward*	*Eudicots (rosids)*	*Malpighiales*	*Solyc03g031860.2.1*
Salix purpurea	*Spu*	*529.6*	*0.0*	*SapurV1A.0354s0270.1 (primary)*	*SapurV1A.0354s0270.1*	*chr15:13280059..13282909 reverse*	*Eudicots (rosids)*	*Malpighiales*	*Solyc03g031860.2.1*
Salix purpurea	*Spu*	*405.2*	*4.4E-138*	*SapurV1A.0081s0270.1 (primary)*	*SapurV1A.0081s0270.1*	*chr03:16337996..16340689 reverse*	*Eudicots (rosids)*	*Malpighiales*	*Solyc03g031860.2.1*
Theobroma cacao	*Tca*	*633.3*	*0.0*	*Thecc1EG017615t1 (primary)*	*Thecc1EG017615t1*	*scaffold_4:5316486..5321472 forward*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Theobroma cacao	*Tca*	*552.7*	*0.0*	*Thecc1EG001945t1 (primary)*	*Thecc1EG001945t1*	*scaffold_1:10439470..10442560 reverse*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Theobroma cacao	*Tca*	*459.5*	*1.1E-159*	*Thecc1EG040196t1 (primary)*	*Thecc1EG040196t1*	*scaffold_9:27850549..27853174 forward*	*Eudicots (rosids)*	*Malvales*	*Solyc03g031860.2.1*
Vigna radiata	*Vra*	*476*	*9,80E-136*	*Vradi01g13040.1*	*Vradi01g13040.1*	*Chromosome 1: 29,983,650-29,986,312 forward strand*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Vigna radiata	*Vra*	*459*	*2,10E-129*	*Vradi06g02420.1*	*Vradi06g02420.1*	*Chromosome 6: 2,396,136-2,398,470 forward strand.*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Vigna radiata	*Vra*	*379*	*1,30E-146*	*Vradi06g05990.1*	*Vradi06g05990.1*	*Chromosome 6: 7,578,171-7,583,722 forward strand.*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Vigna radiata	*Vra*	*334*	*4,30E-102*	*Vradi0246s00050.1*	*Vradi0246s00050.1*	*SuperContig scaffold_246: 120,684-123,023 forward strand*	*Eudicots (rosids)*	*Fabales*	*Solyc03g031860.2.1*
Vitis vinifera	*Vvi*	*664.8*	*0.0*	*GSVIVT01035255001*	*GSVIVT01035255001*	*chr4:11494435..11499618 forward*	*Eudicots (rosids)*	*Vitales*	*Solyc03g031860.2.1*
Vitis vinifera	*Vvi*	*510.4*	*0.0*	*GSVIVT01020828001*	*GSVIVT01020828001*	*chr12:1467463..1470527 forward*	*Eudicots (rosids)*	*Vitales*	*Solyc03g031860.2.1*
Vitis vinifera	*Vvi*	*451.8*	*3,00E-157*	*GSVIVT01025421001*	*GSVIVT01025421001*	*chr6:935380..940685 forward*	*Eudicots (rosids)*	*Vitales*	*Solyc03g031860.2.1*
Beta vulgaris	*Bvu*	*392*	*7,00E-143*	*KMT13325*	*KMT13325*	*Chromosome 4: 20,504,431-20,508,295 reverse strand*	*Eudicots (superasterids)*	*Caryophyllales*	*Solyc03g031860.2.1*
Trifolium pratense	*Tpr*	*602.8*	*0.0*	*Tp57577_TGAC_v2_mRNA5500 (primary)*	*Tp57577_TGAC_v2_mRNA5500*	*Tp57577_TGAC_v2_LG2:23973554..23978020 forward*	*Eudicots(rosids)*	*Fabales*	*Solyc03g031860.2.1*

Species	**Acronymon**	**Score**	**Evalue**	**Transcript Name**	**CDS Acession Number**	**Location**	**Classification group**	**Order**	**Query**
Trifolium pratense	*Tpr*	*537.7*	*0.0*	*Tp57577_TGAC_v2_mRNA26125 (primary)*	*Tp57577_TGAC_v2_mRNA26125*	*Tp57577_TGAC_v2_LG5:14102402..14106056 forward*	*Eudicots(rosids)*	*Fabales*	*Solyc03g031860.2.1*
Trifolium pratense	*Tpr*	*460.3*	*5.8E-160*	*Tp57577_TGAC_v2_mRNA19990 (primary)*	*Tp57577_TGAC_v2_mRNA19990*	*Tp57577_TGAC_v2_scaf_333:243896..246365 forward*	*Eudicots(rosids)*	*Fabales*	*Solyc03g031860.2.1*
Trifolium pratense	*Tpr*	*443,7*	*1.6E-152*	*Tp57577_TGAC_v2_mRNA9064 (primary)*	*Tp57577_TGAC_v2_mRNA9064*	*Tp57577_TGAC_v2_scaf_512:4326..10060 forward*	*Eudicots(rosids)*	*Fabales*	*Solyc03g031860.2.1*