

**Table S1. Sources of coding sequence annotations**

Group	Order	Species	Abbreviation	Version	Source
lamiids	Gentianales	<i>Coffea canephora</i>	Cocan	Ccanephora	solgenomics.net
lamiids	Lamiales	<i>Mimulus guttatus</i>	Migut	Mimgu1_0	ncbi.nlm.nih.gov/assembly
lamiids	Lamiales	<i>Mimulus guttatus</i>	Migut	v2.0	phytozome.jgi.doe.gov
lamiids	Lamiales	<i>Olea europaea</i>	Oleur	O_europaea_v1	ncbi.nlm.nih.gov/assembly
lamiids	Lamiales	<i>Olea europaea</i>	Oleur	v1.0	phytozome.jgi.doe.gov
lamiids	Lamiales	<i>Sesamum indicum</i>	Seind	S_indicum_v1.0	ncbi.nlm.nih.gov/assembly
lamiids	Lamiales	<i>Sesamum indicum</i>	Seind	v1.0	ocri-genomics.org/Sinbase
lamiids	Solanales	<i>Capsicum annuum</i>	Caann	Zunla_1_Ref_v1.0	ncbi.nlm.nih.gov/assembly
lamiids	Solanales	<i>Capsicum annuum</i>	Caann	CM334 v.1.55	solgenomics.net
lamiids	Solanales	<i>Ipomoea nil</i>	Ipnil	Asagao_1.1	ncbi.nlm.nih.gov/assembly
lamiids	Solanales	<i>Ipomoea nil</i>	Ipnil	Asagao_1.2	viewer.shigen.info/asagao
lamiids	Solanales	<i>Nicotiana glauca</i>	Nisyl	Nsyl	ncbi.nlm.nih.gov/assembly
lamiids	Solanales	<i>Nicotiana glauca</i>	Nisyl	Nsyl_ASAF01	solgenomics.net
lamiids	Solanales	<i>Nicotiana tabacum</i>	Nitab	Ntab-TN90	ncbi.nlm.nih.gov/assembly
lamiids	Solanales	<i>Nicotiana tabacum</i>	Nitab	v4.5	solgenomics.net
lamiids	Solanales	<i>Nicotiana tomentosiformis</i>	Nitom	Ntom_v01	ncbi.nlm.nih.gov/assembly
lamiids	Solanales	<i>Nicotiana tomentosiformis</i>	Nitom	Ntom_ASAG01	solgenomics.net
lamiids	Solanales	<i>Petunia axillaris</i>	Peaxi	v1.6.2	solgenomics.net
lamiids	Solanales	<i>Solanum lycopersicum</i>	Solyc	SL3.0	ncbi.nlm.nih.gov/assembly
lamiids	Solanales	<i>Solanum lycopersicum</i>	Solyc	ITAG3.2	solgenomics.net
lamiids	Solanales	<i>Solanum pennellii</i>	Sopen	SPENNV200	ncbi.nlm.nih.gov/assembly
lamiids	Solanales	<i>Solanum pennellii</i>	Sopen	v2	solgenomics.net
lamiids	Solanales	<i>Solanum tuberosum</i>	Sotub	SolTub_3.0	ncbi.nlm.nih.gov/assembly
lamiids	Solanales	<i>Solanum tuberosum</i>	Sotub	v4.03	phytozome.jgi.doe.gov
campanulids	Apiales	<i>Daucus carota</i>	Dacar	ASM162521v1	ncbi.nlm.nih.gov/assembly
campanulids	Apiales	<i>Daucus carota</i>	Dacar	v2.0	phytozome.jgi.doe.gov
campanulids	Asterales	<i>Cynara cardunculus</i>	Cycar	CcrdV1	ncbi.nlm.nih.gov/assembly
campanulids	Asterales	<i>Helianthus annuus</i>	Heann	HanXRQr1.0	ncbi.nlm.nih.gov/assembly
campanulids	Asterales	<i>Helianthus annuus</i>	Heann	r1.2	phytozome.jgi.doe.gov
campanulids	Asterales	<i>Lactuca sativa</i>	Lasat	Lsat_Salinas_v7	ncbi.nlm.nih.gov/assembly
campanulids	Asterales	<i>Lactuca sativa</i>	Lasat	v5	phytozome.jgi.doe.gov
rosids	Brassicales	<i>Arabidopsis thaliana</i>	Artha	TAIR10	ncbi.nlm.nih.gov/assembly
rosids	Brassicales	<i>Arabidopsis thaliana</i>	Artha	TAIR10	phytozome.jgi.doe.gov
rosids	Fabales	<i>Medicago truncatula</i>	Metru	MedtrA17_4.0	ncbi.nlm.nih.gov/assembly
rosids	Fabales	<i>Medicago truncatula</i>	Metru	Mt4.0v1	phytozome.jgi.doe.gov
rosids	Malpighiales	<i>Populus trichocarpa</i>	Potri	Pop_tri_v3	ncbi.nlm.nih.gov/assembly
rosids	Malpighiales	<i>Populus trichocarpa</i>	Potri	v3.0	phytozome.jgi.doe.gov
rosids	Vitales	<i>Vitis vinifera</i>	Vivin	12X	ncbi.nlm.nih.gov/assembly
rosids	Vitales	<i>Vitis vinifera</i>	Vivin	12X	phytozome.jgi.doe.gov

**Table S2. Comparison of anthocyanin biosynthesis genes from NCBI and genome-specific annotations**

Gene	Species	NCBI Annotation		Genome-specific Annotation		Perc ID	Classification
		Gene	Length	Gene	Length		
ANS	Artha	AT4G22870.1	339	<b>AT4G22870.2</b>	462	100.0	Imperfect RBH
ANS	Artha	<b>AT4G22880.1</b>	1071	AT4G22880.1	1071	100.0	Perfect RBH
CHI	Artha	<b>AT3G55120.1</b>	741	AT3G55120.1	741	100.0	Perfect RBH
CHI	Artha	<b>AT5G66220.1</b>	525	AT5G66220.1	525	100.0	Perfect RBH
CHS	Artha	<b>AT5G13930.1</b>	1188	AT5G13930.1	1188	100.0	Perfect RBH
DFR	Artha	<b>AT5G42800.1</b>	1149	AT5G42800.1	1149	100.0	Perfect RBH
F3'H	Artha	<b>AT5G07990.1</b>	1542	AT5G07990.1	1542	100.0	Perfect RBH
F3H	Artha	<b>AT3G51240.1</b>	1077	AT3G51240.1	1077	100.0	Perfect RBH
ANS	Caann	<b>Caann_XM_016712446.1</b>	1287	Cannu_CA01g03670	1287	99.5	Imperfect RBH
CHI	Caann	<b>Caann_XM_016697793.1</b>	699	Cannu_CA11g02280	612	99.7	Imperfect RBH
CHS	Caann	-	-	<b>Cannu_CA00g90780</b>	390	-	No RBH
CHS	Caann	-	-	<b>Cannu_CA05g17040</b>	741	-	No RBH
CHS	Caann	<b>Caann_XM_016694194.1</b>	1212	Cannu_CA12g20070	1011	99.6	Imperfect RBH
CHS	Caann	<b>Caann_XM_016695870.1</b>	1173	Cannu_CA00g90800	1173	100.0	Perfect RBH
CHS	Caann	<b>Caann_XM_016695871.1</b>	1170	Cannu_CA00g90790	984	99.8	Imperfect RBH
				Cannu_CA12g20050 +			
CHS	Caann	<b>Caann_XM_016696552.1</b>	1158	Cannu_CA12g20060	1053	88.4	cluster BH
CHS	Caann	<b>Caann_XM_016710598.1</b>	1170	Cannu_CA03g02050	1170	99.9	Imperfect RBH
CHS	Caann	<b>Caann_XM_016718115.1</b>	1179	-	-	-	No RBH
CHS	Caann	<b>Caann_XM_016718139.1</b>	1209	Cannu_CA05g17060	1209	99.8	Imperfect RBH
CHS	Caann	<b>Caann_XM_016726963.1</b>	798	Cannu_CA08g19650	798	100.0	Perfect RBH
DFR	Caann	<b>Caann_XM_016705224.1</b>	1236	Cannu_CA02g22270	1101	100.0	Imperfect RBH
F3'5'H	Caann	<b>Caann_XM_016691378.1</b>	1536	-	-	-	No RBH
F3'5'H	Caann	<b>Caann_XM_016693437.1</b>	1542	Cannu_CA11g18550	1374	99.9	Imperfect RBH
F3'H	Caann	<b>Caann_XM_016707872.1</b>	1542	Cannu_CA03g29350	1257	98.9	Imperfect RBH
F3H	Caann	-	-	<b>Cannu_CA02g21520</b>	546	-	No RBH
F3H	Caann	<b>Caann_XM_016705025.1</b>	1098	Cannu_CA02g21550	1101	99.7	Imperfect RBH
ANS	Cocan	-	-	<b>Ccan_Cc08_g13720</b>	-	-	No RBH
CHI	Cocan	-	-	<b>Ccan_Cc02_g08570</b>	-	-	No RBH
CHS	Cocan	-	-	<b>Ccan_Cc00_g19010</b>	-	-	No RBH
CHS	Cocan	-	-	<b>Ccan_Cc00_g32030</b>	-	-	No RBH
DFR	Cocan	-	-	<b>Ccan_Cc07_g09810</b>	-	-	No RBH
F3'H	Cocan	-	-	<b>Ccan_Cc00_g07110</b>	-	-	No RBH
F3'H	Cocan	-	-	<b>Ccan_Cc00_g07120</b>	-	-	No RBH
F3'H	Cocan	-	-	<b>Ccan_Cc02_g28860</b>	-	-	No RBH
F3'H	Cocan	-	-	<b>Ccan_Cc02_g28870</b>	-	-	No RBH
F3'H	Cocan	-	-	<b>Ccan_Cc04_g13260</b>	-	-	No RBH
F3H	Cocan	-	-	<b>Ccan_Cc07_g10740</b>	-	-	No RBH
ANS	Cycar	<b>Cycar_XM_025103808.1</b>	-	-	-	-	No RBH
CHI	Cycar	<b>Cycar_XM_025113756.1</b>	-	-	-	-	No RBH
CHI	Cycar	<b>Cycar_XM_025114537.1</b>	-	-	-	-	No RBH
CHS	Cycar	<b>Cycar_XM_025115139.1</b>	-	-	-	-	No RBH
CHS	Cycar	<b>Cycar_XM_025115340.1</b>	-	-	-	-	No RBH
CHS	Cycar	<b>Cycar_XM_025117980.1</b>	-	-	-	-	No RBH
CHS	Cycar	<b>Cycar_XM_025124791.1</b>	-	-	-	-	No RBH
CHS	Cycar	<b>Cycar_XM_025126676.1</b>	-	-	-	-	No RBH
CHS	Cycar	<b>Cycar_XM_025126677.1</b>	-	-	-	-	No RBH
DFR	Cycar	<b>Cycar_XM_025113289.1</b>	-	-	-	-	No RBH
F3'H	Cycar	<b>Cycar_XM_025120904.1</b>	-	-	-	-	No RBH
F3H	Cycar	<b>Cycar_XM_025118318.1</b>	-	-	-	-	No RBH
ANS	Dacar	<b>Dacar_XM_017380613.1</b>	1209	DCAR_006772	1209	100.0	Perfect RBH
CHI	Dacar	<b>Dacar_XM_017365109.1</b>	879	DCAR_027694	663	100.0	Imperfect RBH
CHS	Dacar	<b>Dacar_XM_017360477.1</b>	1176	DCAR_026111	1176	100.0	Perfect RBH
CHS	Dacar	<b>Dacar_XM_017364131.1</b>	1176	DCAR_026110	921	99.4	cluster BH
CHS	Dacar	<b>Dacar_XM_017368840.1</b>	1170	DCAR_030786	1170	100.0	Perfect RBH
CHS	Dacar	<b>Dacar_XM_017371435.1</b>	1173	DCAR_030785	762	100.0	Imperfect RBH
CHS	Dacar	<b>Dacar_XM_017372560.1</b>	453	DCAR_000081	465	100.0	Imperfect RBH
CHS	Dacar	<b>Dacar_XM_017384350.1</b>	753	-	-	-	No RBH

CHS	Dacar	Dacar_XM_017388617.1	1176	DCAR_014462	774	100.0	Imperfect RBH
CHS	Dacar	Dacar_XM_017394258.1	1179	DCAR_018997	1179	100.0	Perfect RBH
CHS	Dacar	Dacar_XM_017395620.1	495	-	-	-	No RBH
CHS	Dacar	Dacar_XM_017396858.1	1233	DCAR_018999	1197	100.0	cluster BH
CHS	Dacar	Dacar_XM_017396859.1	1233	DCAR_019001	1197	100.0	Imperfect RBH
CHS	Dacar	Dacar_XM_017396860.1	1179	DCAR_019002	1179	100.0	Imperfect RBH
CHS	Dacar	Dacar_XM_017397154.1	1194	DCAR_018992	1128	100.0	cluster BH
DFR	Dacar	Dacar_XM_017389661.1	1014	DCAR_013832	1014	100.0	Perfect RBH
DFR	Dacar	Dacar_XM_017394438.1	1008	DCAR_017533	813	97.7	cluster BH
		Dacar_XM_017395352.1					
DFR	Dacar	split1	1005	DCAR_017529	1005	100.0	Imperfect RBH
		Dacar_XM_017395352.1					
DFR	Dacar	split2	1005	DCAR_017530	1005	98.3	Imperfect RBH
DFR	Dacar	Dacar_XM_017396019.1	1014	DCAR_017528	1008	100.0	Imperfect RBH
DFR	Dacar	Dacar_XM_017396664.1	1044	-	-	-	No RBH
DFR	Dacar	Dacar_XM_017396665.1	1002	DCAR_017531	1014	97.5	Imperfect RBH
DFR	Dacar	Dacar_XM_017398898.1	1056	DCAR_022969	1056	100.0	Perfect RBH
DFR	Dacar	Dacar_XM_017399501.1	1143	DCAR_021485	1140	99.7	Imperfect RBH
F3'H	Dacar	Dacar_XM_017388905.1	1551	DCAR_014032	1356	100.0	Imperfect RBH
F3H	Dacar	Dacar_XM_017383706.1	936	DCAR_009487	699	100.0	Imperfect RBH
F3H	Dacar	Dacar_XM_017385170.1	1149	DCAR_009488	711	100.0	Imperfect RBH
F3H	Dacar	Dacar_XM_017385173.1	1101	DCAR_009483	828	100.0	Imperfect RBH
F3H	Dacar	Dacar_XM_017385175.1	1074	DCAR_009489	726	100.0	Imperfect RBH
ANS	Heann	Heann_XM_022177923.1	1083	HanXRQChr04g0095451	1134	100.0	Imperfect RBH
ANS	Heann	Heann_XM_022177924.1	1068	HanXRQChr04g0095471	1068	100.0	Perfect RBH
CHI	Heann	Heann_XM_022155533.1	684	HanXRQChr15g0496901	669	100.0	Imperfect RBH
CHI	Heann	Heann_XM_022157901.1	672	HanXRQChr15g0496871	672	100.0	Perfect RBH
CHI	Heann	Heann_XM_022157902.1	666	HanXRQChr15g0496881	666	100.0	Perfect RBH
CHS	Heann	Heann_XM_022127208.1	1227	HanXRQChr09g0260921	1227	100.0	Perfect RBH
CHS	Heann	Heann_XM_022127919.1	1365	HanXRQChr09g0267961	1386	100.0	Imperfect RBH
CHS	Heann	Heann_XM_022136927.1	1212	HanXRQChr11g0324891	1212	100.0	Perfect RBH
CHS	Heann	Heann_XM_022136928.1	1299	HanXRQChr11g0324921	1239	100.0	Imperfect RBH
CHS	Heann	Heann_XM_022136929.1	1224	HanXRQChr11g0324941	960	100.0	Imperfect RBH
CHS	Heann	Heann_XM_022136930.1	609	HanXRQChr11g0324911	579	100.0	Imperfect RBH
CHS	Heann	Heann_XM_022142672.1	1209	HanXRQChr12g0375361	1209	100.0	Perfect RBH
CHS	Heann	Heann_XM_022153962.1	1197	HanXRQChr14g0440901	1344	100.0	Imperfect RBH
CHS	Heann	Heann_XM_022153975.1	1197	HanXRQChr14g0441041	1197	100.0	Perfect RBH
CHS	Heann	Heann_XM_022161268.1	1236	HanXRQChr16g0508841	1335	100.0	Imperfect RBH
CHS	Heann	Heann_XM_022178725.1	1197	HanXRQChr04g0106111	1197	100.0	Perfect RBH
CHS	Heann	Heann_XM_022179491.1	1170	HanXRQChr04g0114951	1254	100.0	cluster BH
CHS	Heann	Heann_XM_022179492.1	1170	HanXRQChr04g0114941	1170	100.0	Perfect RBH
DFR	Heann	Heann_XM_022145746.1	1068	HanXRQChr13g0407201	1068	100.0	Perfect RBH
F3'H	Heann	Heann_XM_022119664.1	705	HanXRQChr08g0233711	543	100.0	Imperfect RBH
F3'H	Heann	Heann_XM_022122577.1	1539	HanXRQChr08g0233771	1617	100.0	Imperfect RBH
F3'H	Heann	Heann_XM_022124823.1	504	HanXRQChr09g0266651	423	100.0	Imperfect RBH
F3'H	Heann	Heann_XM_022153126.1	1518	HanXRQChr14g0430831	1518	100.0	Perfect RBH
F3'H	Heann	Heann_XM_022153244.1	1539	HanXRQChr14g0432191	1539	100.0	Perfect RBH
F3H	Heann	Heann_XM_022160179.1	1095	HanXRQChr16g0531451	1095	100.0	Perfect RBH
ANS	Ipnil	Ipnil_XM_019317185.1	1116	INIL13g40254.t1	1116	100.0	Perfect RBH
CHI	Ipnil	Ipnil_XM_019337142.1	726	INIL11g18443.t1	726	100.0	Perfect RBH
CHS	Ipnil	-	-	INIL11g18930.t1	1191	-	No RBH
CHS	Ipnil	Ipnil_XM_019310063.1	1170	INIL14g35461.t1	1170	100.0	Perfect RBH
CHS	Ipnil	Ipnil_XM_019326011.1	1167	INIL12g08537.t1	1167	100.0	Perfect RBH
CHS	Ipnil	Ipnil_XM_019339953.1	1191	INIL11g18928.t1	1191	100.0	Perfect RBH
CHS	Ipnil	Ipnil_XM_019339957.1	1182	INIL11g18931.t1	1182	100.0	Perfect RBH
CHS	Ipnil	Ipnil_XM_019339958.1	1134	INIL11g18926.t1	1134	100.0	Perfect RBH
DFR	Ipnil	Ipnil_XM_019327016.1	1074	INIL05g09558.t1	1044	100.0	Imperfect RBH
DFR	Ipnil	Ipnil_XM_019327030.1	1212	INIL05g09559.t1	1212	100.0	Perfect RBH
DFR	Ipnil	Ipnil_XM_019327031.1	1071	INIL05g09560.t1	1071	100.0	Perfect RBH
F3'H	Ipnil	Ipnil_XM_019308867.1	1560	INIL04g34064.t1	756	100.0	Imperfect RBH
F3H	Ipnil	Ipnil_XM_019316832.1	1101	INIL02g39928.t1	1077	97.8	Imperfect RBH

F3H	Ipnil	Ipnil_XM_019316833.1	1002	INIL02g39929.t1	1002	100.0	Perfect RBH
F3H	Ipnil	Ipnil_XM_019327227.1	1086	INIL05g09512.t1	1086	100.0	Perfect RBH
ANS	Lasat	-	-	Lsat_1_v5_gn_9_97280.1	681	-	No RBH
CHI	Lasat	Lasat_XM_023891334.1	708	Lsat_1_v5_gn_9_66221.1	708	100.0	Perfect RBH
CHS	Lasat	-	-	Lsat_1_v5_gn_2_42901.1	531	-	No RBH
CHS	Lasat	Lasat_XM_023878437.1	1170	Lsat_1_v5_gn_2_42860.1	1170	100.0	Perfect RBH
CHS	Lasat	Lasat_XM_023878440.1	1170	Lsat_1_v5_gn_2_43721.1	1161	100.0	Imperfect RBH
CHS	Lasat	Lasat_XM_023878441.1	1170	-	-	-	No RBH
CHS	Lasat	Lasat_XM_023878447.1	1176	Lsat_1_v5_gn_2_42881.1	1170	100.0	Imperfect RBH
CHS	Lasat	Lasat_XM_023878452.1	1200	Lsat_1_v5_gn_2_43780.1	1170	100.0	Imperfect RBH
CHS	Lasat	Lasat_XM_023878453.1	1152	Lsat_1_v5_gn_2_43681.1	1152	100.0	Perfect RBH
CHS	Lasat	Lasat_XM_023878454.1	1185	Lsat_1_v5_gn_2_42941.1	1170	100.0	Imperfect RBH
CHS	Lasat	Lasat_XM_023879789.1	1200	Lsat_1_v5_gn_2_76880.1	1197	100.0	Imperfect RBH
CHS	Lasat	Lasat_XM_023897706.1	1215	Lsat_1_v5_gn_4_147220.1	1215	100.0	Perfect RBH
DFR	Lasat	Lasat_XM_023893302.1	1062	Lsat_1_v5_gn_2_77261.1	1062	100.0	Perfect RBH
F3'H	Lasat	Lasat_XM_023887166.1	1539	Lsat_1_v5_gn_5_23101.1	1539	100.0	Perfect RBH
F3'H	Lasat	Lasat_XM_023904089.1	1557	Lsat_1_v5_gn_5_22780.1	1551	100.0	Imperfect RBH
F3H	Lasat	Lasat_XM_023893557.1	1095	Lsat_1_v5_gn_3_74560.1	1095	100.0	Perfect RBH
ANS	Metru	Metru_XM_003611141.2	1071	Medtr5g011250.1	1071	100.0	Perfect RBH
CHI	Metru	Metru_XM_003592713.2	669	Medtr1g115820.1	669	100.0	Perfect RBH
CHI	Metru	Metru_XM_003592715.2	678	Medtr1g115840.1	678	100.0	Perfect RBH
CHI	Metru	Metru_XM_003592718.2	675	Medtr1g115870.1	675	100.0	Perfect RBH
CHI	Metru	Metru_XM_003592720.2	681	Medtr1g115890.1	681	100.0	Perfect RBH
CHI	Metru	Metru_XM_013592455.1	465	Medtr7g027135.1	465	100.0	Perfect RBH
CHI	Metru	Metru_XM_013615033.1	693	Medtr1g115850.2	693	100.0	Perfect RBH
CHS	Metru	Metru_XM_003591974.2	1269	Medtr1g097910.1	1170	100.0	Imperfect RBH
CHS	Metru	Metru_XM_003591996.2	1170	Medtr1g098140.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003595597.2	1170	Medtr2g058470.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003601599.2	1170	Medtr3g083910.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003601600.2	1170	Medtr3g083920.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003601819.2	1170	Medtr3g086260.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003610804.2	1170	Medtr5g007730.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003610805.2	981	Medtr5g007740.1	981	100.0	Perfect RBH
CHS	Metru	Metru_XM_003610807.2	1170	Medtr5g007760.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003610808.1	810	Medtr5g007770.1	810	100.0	Perfect RBH
CHS	Metru	Metru_XM_003621482.2	1170	Medtr7g016700.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003621484.2	1170	Medtr7g016720.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003621486.1	1170	Medtr7g016780.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003621488.1	1170	Medtr7g016800.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003621490.2	1170	Medtr7g016820.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_003624476.2	1176	Medtr7g084300.1	1176	100.0	Perfect RBH
CHS	Metru	Metru_XM_013595036.1	912	Medtr7g113405.1	912	100.0	Perfect RBH
CHS	Metru	Metru_XM_013597892.1	1242	Medtr5g007713.1	1170	100.0	Imperfect RBH
CHS	Metru	Metru_XM_013597893.1	1170	Medtr5g007717.1	1170	100.0	Perfect RBH
CHS	Metru	Metru_XM_013597894.1	1197	Medtr5g007723.1	1197	100.0	Perfect RBH
CHS	Metru	Metru_XM_013605871.1	1230	Medtr3g088670.1	1179	100.0	Imperfect RBH
CHS	Metru	Metru_XM_013605872.1	1182	Medtr3g088675.1	1182	100.0	Perfect RBH
CHS	Metru	Metru_XM_013614150.1	1272	Medtr1g097935.1	1170	100.0	Imperfect RBH
DFR	Metru	Metru_XM_013610679.1	1020	Medtr1g022440.1	1020	100.0	Perfect RBH
DFR	Metru	Metru_XM_013610680.1	1005	Medtr1g022445.1	1005	100.0	Perfect RBH
F3'5'H	Metru	Metru_XM_013603872.1	1548	Medtr3g436390.1	1521	100.0	Imperfect RBH
F3'5'H	Metru	Metru_XM_013603876.1	1548	Medtr3g436540.1	1548	100.0	Perfect RBH
F3'H	Metru	Metru_XM_003598897.2	1551	Medtr3g025230.1	1551	100.0	Perfect RBH
F3'H	Metru	Metru_XM_003598899.1	861	Medtr3g025250.1	861	100.0	Perfect RBH
F3'H	Metru	Metru_XM_003598900.2	1551	Medtr3g025260.1	1551	100.0	Perfect RBH
F3'H	Metru	Metru_XM_013602525.1	1533	Medtr4g109470.1	1533	100.0	Perfect RBH
F3'H	Metru	Metru_XM_013603646.1	1551	Medtr3g024520.1	1551	100.0	Perfect RBH
F3H	Metru	Metru_XM_003612118.2	1074	Medtr5g022020.1	1074	100.0	Perfect RBH
F3H	Metru	Metru_XM_003629272.2	1098	Medtr8g075830.1	1098	100.0	Perfect RBH
F3H	Metru	Metru_XM_003629275.2	1098	Medtr8g075890.1	1098	100.0	Perfect RBH
F3H	Metru	Metru_XM_013604559.1	1065	Medtr3g058610.1	1065	100.0	Perfect RBH

ANS	Migut	Migut_XM_012991981.1	1161	Migut.E01023.1	1182	100.0	Imperfect RBH
CHI	Migut	Migut_XM_012978000.1	756	Migut.D00159.1	720	100.0	Imperfect RBH
CHI	Migut	Migut_XM_012982352.1	531	-	-	-	No RBH
CHS	Migut	Migut_XM_012973820.1	1179	Migut.G00627.1	1179	100.0	Perfect RBH
CHS	Migut	Migut_XM_012973831.1	1173	Migut.G00628.1	1173	100.0	Perfect RBH
CHS	Migut	Migut_XM_012982223.1	501	Migut.B01017.1	504	100.0	Imperfect RBH
CHS	Migut	Migut_XM_012988049.1	501	Migut.H00487.1	579	100.0	cluster BH
CHS	Migut	Migut_XM_012988726.1	1164	Migut.G00629.1	1080	100.0	Imperfect RBH
CHS	Migut	Migut_XM_012988738.1	843	Migut.G00630.1	597	100.0	Imperfect RBH
DFR	Migut	Migut_XM_012989820.1	1230	Migut.H02531.1	1296	99.6	Imperfect RBH
F3'H	Migut	Migut_XM_012982675.1	1107	Migut.O00721.1	1032	100.0	Imperfect RBH
F3'H	Migut	Migut_XM_012998441.1	1617	Migut.D01697.1	1617	100.0	Perfect RBH
F3H	Migut	Migut_XM_012980274.1	1128	Migut.C00836.1	1128	100.0	Perfect RBH
F3H	Migut	Migut_XM_012983725.1	1071	Migut.N03161.1	1071	100.0	Perfect RBH
ANS	Nisyl	Nisyl_XM_009777817.1	1260	Nsyl_mRNA_82018_cds	1260	100.0	Perfect RBH
CHI	Nisyl	Nisyl_XM_009805808.1	735	Nsyl_mRNA_10796_cds	735	100.0	Perfect RBH
CHS	Nisyl	Nisyl_XM_009766636.1	1170	Nsyl_mRNA_65311_cds	1170	100.0	Perfect RBH
CHS	Nisyl	Nisyl_XM_009768850.1	1296	Nsyl_mRNA_68684_cds	1296	100.0	Perfect RBH
CHS	Nisyl	Nisyl_XM_009776625.1	1170	Nsyl_mRNA_80210_cds	1170	100.0	Perfect RBH
CHS	Nisyl	Nisyl_XM_009789215.1	1173	Nsyl_mRNA_25875_cds	1173	100.0	Perfect RBH
DFR	Nisyl	-	-	Nsyl_mRNA_14898_cds	468	-	No RBH
DFR	Nisyl	Nisyl_XM_009761654.1	1146	Nsyl_mRNA_57456_cds	1146	100.0	Perfect RBH
F3'5'H	Nisyl	Nisyl_XM_009790406.1	993	Nsyl_mRNA_27603_cds	639	100.0	Imperfect RBH
F3'H	Nisyl	Nisyl_XM_009773108.1	1548	Nsyl_mRNA_74969_cds	1056	99.9	cluster BH
F3'H	Nisyl	Nisyl_XM_009790192.1	1545	Nsyl_mRNA_27286_cds	1641	100.0	Imperfect RBH
F3H	Nisyl	Nisyl_XM_009767241.1	1110	Nsyl_mRNA_66230_cds	1110	100.0	Perfect RBH
ANS	Nitab	Nitab_XM_016598316.1	1260	Nitab4.5_0010547g0010.1	1125	100.0	Imperfect RBH
ANS	Nitab	Nitab_XM_016645479.1	1260	Nitab4.5_0003274g0110.1	1098	100.0	Imperfect RBH
CHI	Nitab	Nitab_XM_016600175.1	735	Nitab4.5_0005313g0010.1	645	100.0	cluster BH
CHI	Nitab	Nitab_XM_016652447.1	735	Nitab4.5_0000027g0470.1	735	100.0	Perfect RBH
CHS	Nitab	-	-	Nitab4.5_0001998g0020.1	1023	-	No RBH
				Nitab4.5_0003185g0100.1			
CHS	Nitab	-	-	split2	1066	-	No RBH
CHS	Nitab	Nitab_XM_016624553.1	1296	Nitab4.5_0010357g0030.1	1233	97.9	Imperfect RBH
CHS	Nitab	Nitab_XM_016625162.1	1170	Nitab4.5_0003904g0060.1	1107	100.0	Imperfect RBH
CHS	Nitab	Nitab_XM_016634418.1	1170	Nitab4.5_0001066g0070.1	1170	99.9	Imperfect RBH
				Nitab4.5_0003185g0100.1			
CHS	Nitab	Nitab_XM_016638700.1	1173	split1	1101	93.2	Imperfect RBH
CHS	Nitab	Nitab_XM_016638898.1	1170	Nitab4.5_0002920g0060.1	762	100.0	Imperfect RBH
CHS	Nitab	Nitab_XM_016653399.1	1170	Nitab4.5_0014110g0010.1	1326	100.0	Imperfect RBH
CHS	Nitab	Nitab_XM_016660053.1	1173	Nitab4.5_0006945g0020.1	1107	100.0	Imperfect RBH
DFR	Nitab	Nitab_XM_016620104.1	1146	Nitab4.5_0007490g0080.1	1014	100.0	Imperfect RBH
DFR	Nitab	Nitab_XM_016622310.1	399	Nitab4.5_0007770g0040.1	816	100.0	cluster BH
DFR	Nitab	Nitab_XM_016626713.1	1149	Nitab4.5_0000178g0360.1	1053	100.0	Imperfect RBH
F3'5'H	Nitab	Nitab_XM_016597113.1	1590	Nitab4.5_0000173g0310.1	1524	100.0	Imperfect RBH
F3'H	Nitab	Nitab_XM_016592903.1	1548	Nitab4.5_0001410g0070.1	1641	99.2	Imperfect RBH
F3'H	Nitab	Nitab_XM_016618350.1	1548	Nitab4.5_0001485g0210.1	1587	99.9	cluster BH
F3'H	Nitab	Nitab_XM_016656982.1	591	Nitab4.5_0001410g0020.1	1419	100.0	cluster BH
F3H	Nitab	Nitab_XM_016590223.1	1110	Nitab4.5_0000864g0050.1	1110	100.0	Perfect RBH
F3H	Nitab	Nitab_XM_016630614.1	1110	Nitab4.5_0026775g0010.1	1110	100.0	Perfect RBH
ANS	Nitom	Nitom_XM_009605813.2	1260	Ntom_mRNA_13259_cds	1260	100.0	Perfect RBH
CHI	Nitom	Nitom_XM_009588739.2	735	Ntom_mRNA_7985_cds	735	100.0	Perfect RBH
CHS	Nitom	Nitom_NM_001319862.1	1170	Ntom_mRNA_18483_cds	1170	100.0	Perfect RBH
CHS	Nitom	Nitom_XM_009610476.2	1173	Ntom_mRNA_27571_cds	1173	100.0	Perfect RBH
CHS	Nitom	Nitom_XM_009610477.2	1170	Ntom_mRNA_27574_cds	1170	100.0	Perfect RBH
CHS	Nitom	Nitom_XM_009618342.2	1170	Ntom_mRNA_38569_cds	1170	100.0	Perfect RBH
DFR	Nitom	Nitom_NM_001302522.1	1149	Ntom_mRNA_5184_cds	1149	99.8	Imperfect RBH
F3'5'H	Nitom	Nitom_XM_009621551.2	1524	Ntom_mRNA_18488_cds	1524	100.0	Perfect RBH
F3'H	Nitom	Nitom_XM_009598972.2	1548	Ntom_mRNA_74743_cds	1548	100.0	Perfect RBH
F3H	Nitom	Nitom_XM_009605261.2	1110	Ntom_mRNA_83308_cds	1110	100.0	Perfect RBH
ANS	Oleur	Oleur_XM_022990294.1	1062	Oeu059047.1	1014	100.0	Imperfect RBH
CHI	Oleur	Oleur_KF886191.1	750	Oeu057578.1	381	100.0	Imperfect RBH

CHS	Oleur	Oleur_XM_022997057.1	1173	Oeu006719.1	1173	100.0	Perfect RBH
CHS	Oleur	Oleur_XM_022997058.1	1173	Oeu006720.1	1173	100.0	Perfect RBH
CHS	Oleur	Oleur_XM_023002817.1	1173	Oeu022348.1	1173	100.0	Perfect RBH
CHS	Oleur	Oleur_XM_023018865.1	1170	Oeu016712.1	1170	100.0	Perfect RBH
DFR	Oleur	Oleur_XM_022999201.1	351	Oeu012314.1	351	100.0	Perfect RBH
DFR	Oleur	Oleur_XM_023039626.1	759	Oeu057948.1	561	100.0	Imperfect RBH
F3'H	Oleur	Oleur_XM_023029392.1	1644	-	-	-	No RBH
F3H	Oleur	Oleur_XM_023003872.1	387	-	-	-	No RBH
F3H	Oleur	Oleur_XM_023028959.1	1110	Oeu046264.1	1110	100.0	Perfect RBH
ANS	Peaxi	-	-	Peaxi162Scf00620g00533.1	-	-	No RBH
CHI	Peaxi	-	-	Peaxi162Scf00006g00088.1	-	-	No RBH
CHI	Peaxi	-	-	Peaxi162Scf00038g01957.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00047g01225.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00126g01326.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00164g00313.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00536g00092.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00817g00216.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00830g00016.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00830g00048.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00830g00067.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00938g00001.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf00938g00118.1	-	-	No RBH
CHS	Peaxi	-	-	Peaxi162Scf08277g00001.1	-	-	No RBH
DFR	Peaxi	-	-	Peaxi162Scf00366g00630.1	-	-	No RBH
F3'5'H	Peaxi	-	-	Peaxi162Scf00108g00417.1	-	-	No RBH
F3'5'H	Peaxi	-	-	Peaxi162Scf00150g00218.1	-	-	No RBH
F3'H	Peaxi	-	-	Peaxi162Scf00201g00243.1	-	-	No RBH
F3H	Peaxi	-	-	Peaxi162Scf00328g01214.1	-	-	No RBH
ANS	Potri	Potri_XM_002298045.2	1083	Potri.001G113100.1	1083	100.0	Perfect RBH
ANS	Potri	Potri_XM_002304416.3	1197	Potri.003G119100.1	1086	100.0	Imperfect RBH
CHI	Potri	Potri_XM_002315222.3	672	Potri.010G213000.1	675	99.6	Imperfect RBH
CHS	Potri	Potri_XM_002299161.3	1131	Potri.001G028600.1	1131	100.0	Perfect RBH
CHS	Potri	Potri_XM_002299245.3	1176	Potri.001G051500.1	1176	100.0	Perfect RBH
CHS	Potri	Potri_XM_002299246.3	1173	Potri.001G051600.1	1173	100.0	Perfect RBH
CHS	Potri	Potri_XM_002303783.3	1176	Potri.003G176700.1	1176	100.0	Perfect RBH
CHS	Potri	Potri_XM_002303784.3	1176	Potri.003G176800.1	1176	100.0	Perfect RBH
CHS	Potri	Potri_XM_002303785.3	1176	Potri.003G176900.1	1176	100.0	Perfect RBH
CHS	Potri	Potri_XM_002321045.3	1191	Potri.014G145100.1	1206	98.8	Imperfect RBH
CHS	Potri	Potri_XM_006377012.2	1188	Potri.012G138800.1	1188	100.0	Perfect RBH
CHS	Potri	Potri_XM_006383408.2	1182	Potri.005G175200.1	1014	100.0	Imperfect RBH
DFR	Potri	Potri_XM_002300723.3	1041	Potri.002G033600.1	1041	100.0	Perfect RBH
DFR	Potri	Potri_XM_006383649.2	1131	Potri.005G229500.1	1164	100.0	Imperfect RBH
F3'5'H	Potri	Potri_XM_002298428.2	1527	Potri.001G274600.1	1527	100.0	Perfect RBH
F3'5'H	Potri	Potri_XM_002313968.3	1530	Potri.009G069100.1	1530	100.0	Perfect RBH
F3'H	Potri	Potri_XM_002319725.3	1566	Potri.013G073300.1	1566	100.0	Perfect RBH
F3H	Potri	-	-	Potri.005G114000.1	1158	-	No RBH
F3H	Potri	Potri_XM_006383041.2	1092	Potri.005G113700.1	1092	100.0	Perfect RBH
F3H	Potri	Potri_XM_006383044.2	1092	Potri.005G113900.1	1092	100.0	Perfect RBH
ANS	Seind	Seind_XM_011073005.2	1092	SIN_1026305	1092	100.0	Perfect RBH
CHI	Seind	Seind_XM_011081420.2	669	-	-	-	No RBH
CHS	Seind	Seind_XM_011073310.2	1161	-	-	-	No RBH
CHS	Seind	Seind_XM_011093097.2	1176	SIN_1018959	1176	100.0	Perfect RBH
CHS	Seind	Seind_XM_011093098.2	1176	SIN_1018960	1176	100.0	Perfect RBH
CHS	Seind	Seind_XM_011093100.2	1173	SIN_1018961	1173	100.0	Perfect RBH
DFR	Seind	Seind_XM_011084901.2	1146	SIN_1022200	1047	99.9	Imperfect RBH
F3'H	Seind	Seind_XM_011074564.2	1593	SIN_1017435	1536	100.0	Imperfect RBH
F3H	Seind	Seind_XM_011085253.2	1101	SIN_1002345	1101	100.0	Perfect RBH
ANS	Solyc	Solyc_XM_010327136.3	1326	Solyc08g080040.3.1	1311	100.0	Imperfect RBH
CHI	Solyc	Solyc_NM_001320711.1	681	Solyc05g010320.3.1	615	100.0	Imperfect RBH
CHI	Solyc	Solyc_XM_004239382.4	669	Solyc05g010310.3.1	669	100.0	Perfect RBH
CHS	Solyc	Solyc_NM_001247104.2	1170	Solyc09g091510.3.1	1170	100.0	Perfect RBH

CHS	Solyc	<b>Solyc_NM_001247107.2</b>	1170	Solyc05g053550.3.1	1170	100.0	Perfect RBH
CHS	Solyc	<b>Solyc_XM_004239850.1</b>	1179	Solyc05g053170.3.1	1179	100.0	Perfect RBH
CHS	Solyc	<b>Solyc_XM_010316555.2</b>	1227	Solyc12g098090.1.1	1317	100.0	Imperfect RBH
				Solyc06g043120.1.1 +			
CHS	Solyc	<b>Solyc_XM_026031338.1</b>	1164	Solyc06g043130.1.1	996	100.0	Imperfect RBH
DFR	Solyc	<b>Solyc_XM_010317577.3</b>	1149	Solyc02g085020.3.1	1149	100.0	Perfect RBH
F3'5'H	Solyc	<b>Solyc_NM_001247911.2</b>	1599	Solyc11g066580.2.1	1536	100.0	Imperfect RBH
F3'H	Solyc	<b>Solyc_NM_001302915.1</b>	1545	Solyc03g115220.3.1	1545	99.9	Imperfect RBH
F3H	Solyc	<b>Solyc_NM_001329483.1</b>	1089	Solyc02g083860.3.1	1089	100.0	Perfect RBH
ANS	Sopen	<b>Sopen_XM_015229000.1</b>	1368	Sopen08g028390.1	1368	100.0	Perfect RBH
CHI	Sopen	<b>Sopen_XM_015219774.1</b>	669	Sopen05g006080.1	669	100.0	Perfect RBH
CHI	Sopen	<b>Sopen_XM_015221071.1</b>	681	Sopen05g006090.1	603	100.0	Imperfect RBH
CHS	Sopen	-	-	<b>Sopen06g013590.1</b>	486	-	No RBH
CHS	Sopen	-	-	<b>Sopen12g032910.1</b>	1086	-	No RBH
CHS	Sopen	<b>Sopen_XM_015205152.1</b>	1191	Sopen12g032900.1	1173	100.0	Imperfect RBH
CHS	Sopen	<b>Sopen_XM_015221148.1</b>	1170	Sopen05g032070.1	1170	100.0	Perfect RBH
CHS	Sopen	<b>Sopen_XM_015221406.1</b>	1296	Sopen05g031680.1	981	100.0	Imperfect RBH
CHS	Sopen	<b>Sopen_XM_015232996.1</b>	1170	Sopen09g034440.1	1170	100.0	Perfect RBH
DFR	Sopen	<b>Sopen_XM_015210279.1</b>	1149	Sopen02g029720.1	1149	100.0	Perfect RBH
F3'5'H	Sopen	<b>Sopen_XM_015203537.1</b>	1536	Sopen11g026310.1	1368	100.0	Imperfect RBH
F3'H	Sopen	<b>Sopen_XM_015215550.1</b>	1560	Sopen03g034260.1	1368	100.0	Imperfect RBH
F3H	Sopen	<b>Sopen_XM_015211594.1</b>	1089	Sopen02g028650.1	1089	100.0	Perfect RBH
ANS	Sotub	<b>Sotub_XM_006358783.2</b>	1368	PGSC0003DMT400058554	1368	100.0	Perfect RBH
CHI	Sotub	<b>Sotub_XM_006348548.2</b>	669	-	-	-	No RBH
CHI	Sotub	<b>Sotub_XM_006348549.2</b>	765	-	-	-	No RBH
CHS	Sotub	-	-	<b>PGSC0003DMT400022255</b>	1002	-	No RBH
CHS	Sotub	-	-	<b>PGSC0003DMT400022261</b>	438	-	No RBH
CHS	Sotub	<b>Sotub_NM_001288367.1</b>	1170	PGSC0003DMT400049165	1170	97.9	Imperfect RBH
CHS	Sotub	<b>Sotub_NM_001288423.1</b>	1170	PGSC0003DMT400076178	1170	98.3	Imperfect RBH
CHS	Sotub	<b>Sotub_XM_006349878.2</b>	1173	PGSC0003DMT400043447	1173	100.0	Perfect RBH
CHS	Sotub	<b>Sotub_XM_006349914.1</b>	1215	PGSC0003DMT400043464	1215	100.0	Perfect RBH
CHS	Sotub	<b>Sotub_XM_006355644.2</b>	1179	PGSC0003DMT400069814	1179	100.0	Perfect RBH
CHS	Sotub	<b>Sotub_XM_006367256.2</b>	1173	PGSC0003DMT400022254	1173	100.0	Perfect RBH
CHS	Sotub	<b>Sotub_XM_006367257.2</b>	1179	PGSC0003DMT400022258	1179	100.0	Perfect RBH
CHS	Sotub	<b>Sotub_XM_015314781.1</b>	1155	PGSC0003DMT400076179	1140	100.0	Imperfect RBH
DFR	Sotub	<b>Sotub_NM_001288480.1</b>	1155	PGSC0003DMT400009287	1149	100.0	Imperfect RBH
F3'5'H	Sotub	<b>Sotub_XM_015309422.1</b>	1530	PGSC0003DMT400001124	1344	100.0	Imperfect RBH
F3'H	Sotub	<b>Sotub_XM_006345070.2</b>	1545	PGSC0003DMT400063351	1368	100.0	Imperfect RBH
F3H	Sotub	<b>Sotub_NM_001288001.1</b>	1077	PGSC0003DMT400009175	1083	98.8	Imperfect RBH
ANS	Vivin	<b>Vivin_NM_001281218.1</b>	1068	GSVIVT01019892001	720	100.0	Imperfect RBH
CHI	Vivin	<b>Vivin_NM_001281104.1</b>	714	GSVIVT01032619001	705	99.4	Imperfect RBH
CHS	Vivin	<b>Vivin_NM_001280950.1</b>	1182	-	-	-	No RBH
CHS	Vivin	<b>Vivin_NM_001281005.1</b>	1179	GSVIVT01010554001	1035	99.1	cluster BH
CHS	Vivin	<b>Vivin_NM_001281010.1</b>	1179	-	-	-	No RBH
CHS	Vivin	<b>Vivin_NM_001281117.1</b>	1179	GSVIVT01010590001	1179	94.5	cluster BH
CHS	Vivin	<b>Vivin_NM_001281135.1</b>	1365	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_002263686.4</b>	1179	GSVIVT01010556001	897	100.0	cluster BH
CHS	Vivin	<b>Vivin_XM_002263771.3</b>	1179	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_002263845.4</b>	1179	GSVIVT01010561001	771	100.0	cluster BH
CHS	Vivin	<b>Vivin_XM_002263983.3</b>	1170	GSVIVT01000521001	300	100.0	cluster BH
CHS	Vivin	<b>Vivin_XM_002264419.4</b>	1179	GSVIVT01010565001	1095	100.0	Imperfect RBH
CHS	Vivin	<b>Vivin_XM_002264953.4</b>	1179	GSVIVT01010572001	1284	100.0	Imperfect RBH
CHS	Vivin	<b>Vivin_XM_002265955.3</b>	1161	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_002268720.4</b>	1179	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_002269350.4</b>	1179	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_002269415.4</b>	1161	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_002271335.4</b>	1179	GSVIVT01026213001	558	95.7	cluster BH
CHS	Vivin	<b>Vivin_XM_002272093.4</b>	1179	GSVIVT01026220001	729	100.0	cluster BH
CHS	Vivin	<b>Vivin_XM_002278318.4</b>	1179	GSVIVT01010589001	1179	99.9	Imperfect RBH
CHS	Vivin	<b>Vivin_XM_002278447.4</b>	1179	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_003634009.3</b>	1155	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_003634015.3</b>	1272	-	-	-	No RBH

CHS	Vivin	<b>Vivin_XM_003634016.3</b>	1179	GSVIVT01010563001	1053	100.0	Imperfect RBH
CHS	Vivin	<b>Vivin_XM_003634017.3</b>	1269	GSVIVT01010570001	327	91.1	cluster BH
CHS	Vivin	<b>Vivin_XM_003634018.3</b>	1275	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_003634019.3</b>	1179	GSVIVT01010574001	990	100.0	Imperfect RBH
CHS	Vivin	<b>Vivin_XM_003634020.3</b>	1179	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_003634021.3</b>	1179	GSVIVT01010583001	411	96.1	cluster BH
CHS	Vivin	<b>Vivin_XM_003634022.3</b>	1179	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_003634023.3</b>	1179	GSVIVT01010579001	381	99.7	cluster BH
CHS	Vivin	<b>Vivin_XM_003634024.3</b>	1179	GSVIVT01010580001	1035	100.0	Imperfect RBH
CHS	Vivin	<b>Vivin_XM_003634025.3</b>	1179	GSVIVT01010581001	990	100.0	cluster BH
CHS	Vivin	<b>Vivin_XM_003634026.3</b>	1179	GSVIVT01010582001	1035	100.0	Imperfect RBH
CHS	Vivin	<b>Vivin_XM_003634027.3</b>	1179	GSVIVT01010584001	444	100.0	cluster BH
CHS	Vivin	<b>Vivin_XM_003634028.3</b>	1179	GSVIVT01010585001	990	100.0	cluster BH
CHS	Vivin	<b>Vivin_XM_010657617.2</b>	1101	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_010664169.1</b>	1032	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_010664197.2</b>	1263	GSVIVT01010568001	450	100.0	cluster BH
CHS	Vivin	<b>Vivin_XM_010664198.2</b>	1179	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_010664202.2</b>	1179	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_019224647.1</b>	1182	GSVIVT01032968001	1107	100.0	Imperfect RBH
CHS	Vivin	<b>Vivin_XM_019225976.1</b>	579	-	-	-	No RBH
CHS	Vivin	<b>Vivin_XM_019225977.1</b>	924	-	-	-	No RBH
DFR	Vivin	-	-	<b>GSVIVT01009742001</b>	429	-	No RBH
DFR	Vivin	<b>Vivin_XM_010666645.2</b>	1041	GSVIVT01009745001	1335	100.0	Imperfect RBH
DFR	Vivin	<b>Vivin_XM_019216415.1</b>	1020	GSVIVT01009743001	1017	100.0	Imperfect RBH
DFR	Vivin	<b>Vivin_XM_019219312.1</b>	486	GSVIVT01018927001	486	100.0	Perfect RBH
F3'5'H	Vivin	<b>Vivin_NM_001281228.1</b>	1527	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_NM_001281235.1</b>	1527	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_002271703.3</b>	1542	GSVIVT01033633001	1659	100.0	Imperfect RBH
F3'5'H	Vivin	<b>Vivin_XM_002280626.3</b>	1530	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_002280903.4</b>	1542	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_003632161.3</b>	1542	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_003632164.3</b>	1527	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_003632194.3</b>	1542	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_010653221.2</b>	1527	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_010653223.2</b>	1527	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_010653225.2</b>	1527	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_010653372.1</b>	1215	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_019220452.1</b>	1329	-	-	-	No RBH
F3'5'H	Vivin	<b>Vivin_XM_019220476.1</b>	486	-	-	-	No RBH
F3'H	Vivin	<b>Vivin_NM_001280987.1</b>	1530	GSVIVT01007878001	1356	99.4	Imperfect RBH
F3'H	Vivin	<b>Vivin_XM_002284115.4</b>	1530	GSVIVT01007877001	588	99.5	cluster BH
F3H	Vivin	<b>Vivin_NM_001281105.1</b>	1092	GSVIVT01018781001	687	100.0	Imperfect RBH
F3H	Vivin	<b>Vivin_XM_002275527.3</b>	1077	GSVIVT01009907001	765	100.0	Imperfect RBH
F3H	Vivin	<b>Vivin_XM_010650732.2</b>	1101	GSVIVT01018780001	1320	100.0	Imperfect RBH

Annotated genes listed in bold were included in phylogenetic analyses





**Fig S1.** Populations of  $T_1$  generation lines in comparison to WT.