

	G α		G β		G γ		RGS ⁽¹⁾		Data source
<i>Arabidopsis thaliana</i>	GPA1	AT2G26300.1	AGB1	AT4G34460.1	AGG1 AGG2 AGG3	AT3G63420.1 AT3G22942.1 AT5G20635.1	RGS1	AT3G26090.1	TAIR release 10 acquired from TAIR
<i>Arabidopsis lyrata</i>		481489		491213		873820 907928 862485		484372	JGI release v1.0
<i>Glycine max</i>	GmG α 1 GmG α 2 GmG α 3 GmG α 4	Glyma04g05960.1 Glyma14g11140.1 Glyma17g34450.1 Glyma06g05960.1	GmG β 1 GmG β 2 GmG β 3 GmG β 4	Glyma04g01460.1 Glyma06g01510.1 Glyma11g12600.1 Glyma12g04810.1		Glyma02g16190.1 Glyma07g04510.1 Glyma10g03610.1 Glyma14g17060.1 Glyma15g19630.1 Glyma17g05640.1 Glyma17g29590.1 Glyma11g18050.1	RGS1 RGS2	Glyma11g37540.1 Glyma18g01490.1	The soybean genome assembly(www.plantgdb.org/GmGDB/). See footnote ⁽²⁾ for more information.
<i>Populus trichocarpa</i>		POPTR_0018s08460.1 POPTR_0006s23610.1		POPTR_0004s16110.1 POPTR_0009s1820.1		POPTR_0005s20180.1 POPTR_0005s23760.1 POPTR_0006s14330.1 POPTR_0018s07510.1 POPTR_0015s13280.1 POPTR_0002s08200.1 POPTR_0002s04770.1		POPTR_0008s18180.1	JGI assembly release v2.0, annotation v2.2
<i>Vitis vinifera</i>		GSVIVT01035483001		GSVIVT01031958001		GSVIVT01015067001 GSVIVT01018076001 GSVIVT01035600		GSVIVT01010292001	March 2010 12X assembly and annotation from Genoscope

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<i>Cucumis sativus</i>		Cucsa.271110.1		Cucsa.240500.1	Cucsa.016430.1 Cucsa.117350.1 Cucsa.141810.1 Cucsa.310840.1 Cucsa.386730.1		Cucsa.075330.1	Roche 454-XLR assembly and JGI v1.0 annotation
<i>Medicago truncatula</i>		Medtr1g019860.1		Medtr3g159480.1	Medtr1g083530.1 Medtr2g049340.1 Medtr7g034920.1 Medtr8g132500.1		Medtr3g102890.1	Release Mt3.0 from the Medicago Genome Sequence Consortium
<i>Manihot esculenta</i>		cassava4.1_009289m cassava4.1_033716m		cassava4.1_009775m cassava4.1_009786m	cassava4.1_024861m cassava4.1_028296m cassava4.1_023456m		cassava4.1_006961m	Assembly version 4, JGI annotation v4.1
<i>Ricinus communis</i>		29739.m003634		30190.m010890	29648.m002019 29739.m003749 29844.m003197 29883.m001977		29929.m004761	TIGR release 0.1
<i>Mimulus guttatus</i>		mgv1a007908m		mgv1a008244m	mgv1a017061m mgv1a013695m mgv1a016439m		mgv1a005744m	JGI 7x assembly release v1.0 of strain IM62, annotation v1.0
<i>Eucalyptus grandis</i>		Egrandis_v1_0.043077m		Eucgr.I01264.1	Eucgr.G01916.1 Eucgr.B01476.1 Eucgr.C03259.1 Eucgr.H03396.1		Eucgr.H04699.1	JGI v1.0 assembly and annotation
<i>Citrus sinensis</i>		orange1.1g016288m		orange1.1g016458m	orange1.1g033950m orange1.1g034008m orange1.1g037836m orange1.1g0386		orange1.1g018201m	JGI v1.1 annotation on v1 assembly

					68m			
<i>Citrus clementina</i>		clementine0.9_012405m		clementine0.9_012998m		clementine0.9_026147m clementine0.9_023217m clementine0.9_026133m		clementine0.9_009530m JGI v0.9 assembly and annotation
<i>Prunus persica</i>		ppa006908m		ppa007241m		ppa013611m ppa013749m ppa021140m		ppa005608m JGI release v1.0
<i>Oryza sativa</i>	RGA1	LOC_Os05g26890.1	RGB1	LOC_Os03g46650.1	RG2	LOC_Os02g04520.1 LOC_Os09g26999.1		Not found MSU Release 6.0 of the Rice Genome Annotation
<i>Brachypodium distachyon</i>		Bradi2g60350.1		Bradi1g12820.1		Bradi1g14140.1 Bradi3g03350.1 Bradi4g31420.1		Not found JGI 8x assembly release v1.0 of strain Bd21 with JGI/MIPS PASA annotation
<i>Sorghum bicolor</i>		Sb01g045320.1		Sb01g012370.1		Sb01g014060.1 Sb01g032830.1 Sb02g025860.1 Sb07g022330.1		Not found Sbi1.4 models from MIPS/PASA on v1.0 assembly
<i>Zea mays</i>		GRMZM2G064732_T01		GRMZM2G045314_T03		GRMZM2G172320_T01 GRMZM2G001660_T01 GRMZM2G139878_T01 GRMZM2G028726_T02 GRMZM2G015578_T03		Not found Unfiltered protein coding models from Maizesequence.org release 5a.59
<i>Setaria italica</i>		Si022288m		Si036161m		Si039839m Si019618m Si033308m		Si031119m JGI 8.3X chromosome-scale assembly release 2.0, annotation version 2.1
<i>Phoenix dactylifera</i>		PDK_30s918561g015		PDK_30s660001L033		Not analyzed		PDK_30s709111L00 New Draft Sequence Version 3

<i>Triticum aestivum</i>	TaGA1 TaGA2 TaGA3	AB090158.2 AB090159.1 HQ020506.1	TaGB1	AB090160.1		Not analyzed		Not found	Nucleotide database in NCBI
<i>Hordeum vulgare</i>		AF267485.2		AK251844		Not analyzed		Not found	Nucleotide database in NCBI
<i>Pinus taeda</i>	PtGα1	Cloned in this study		DR692385.1/CX651314.1/DR047972.1		CX650880 DT638145 R093761.1	PtRGS1	Cloned in this study	EST database in NCBI
<i>Picea glauca</i>		Cloned in this study		EX353861.1/EX406541.1		EX423497 EX374535.1 EX380234.1		BT111406	EST database in NCBI
<i>Selaginella moellendorffii</i>	GPA-1	XM_002960950.1	AGB1-1	XP_002964323.1		See footnote ⁽³⁾		XM_002984541.1	Nucleotide database in NCBI
<i>Marchantia polymorpha</i>	MpGα1	isotig19630		isotig30299		isotig30025		Not found	EST database (See footnote).
<i>Physcomitrella patens</i>		Not found ⁽⁴⁾		Pp1s7_401V6.2 Pp1s28_162V6.1		Pp1s22_182V6.1 CAYZ19681 ⁽⁵⁾		Not found	JGI assembly release v1.1 and COSMOSS annotation v1.6 or EST database in NCBI
<i>Volvox carteri</i>		Not found		Not found		Not found		Not found	GenBank annotations based on JGI v1.0
<i>Chlamydomonas reinhardtii</i>		Not found		Not found		Not found		Not found	Augustus update 10.2 (u10.2) annotation of JGI assembly v4

Table S1. G-protein components in the land plant kingdom

Homologous genes of *A. thaliana* AtGPA1, AGB1, and AtRGS1 were assembled from plant genome database through Phytozome v7.0 (released on Apr/8/2011; www.phytozome.net), nucleotide or EST database registered in NCBI (www.ncbi.nlm.nih.gov), and EST database of *M. polymorpha* (<http://Marchantia.pmb.lif.kyoto-u.ac.jp>). (1) All RGS genes were predicted to have 7- or 5-transmembrane domain, except non-transmembrane *S. italica* and *P. dactylifera* RGS. (2) Sequences of *G. max* G protein components were corrected according to previous research [13], because sequences registered in the soybean genome assembly (www.plantgdb.org/GmGDB/, Soybean Transcript (GenBank 170)) contain some deletions. (3) A Gγ homologous sequence is found highly in the *S. moellendorffii* genome (scaffold_123: 288795-289362 base) in JGI genome database, although the sequence has not assembled as Gγ gene. (4) A *P. patens* gene (XP_001772174.1) is incorrectly annotated as Gα in NCBI database. It is highly homologous to Arabidopsis extra-large GTP-binding protein (XP_002890957.1). (5) A *P. patens* Gγ gene is found in the EST and genome database, although it has not been assembled as a gene.