

Supplemental data online

Control of compound leaf development by *FLO/LFY* ortholog *Single Leaflet1* in *Medicago truncatula*

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SGL1 MDPDAFTASLFWKWP.RTVLPTAPPLRPQLLDYAVTPSTAP.....SPYYPAR
UNI MDPDAFTASLFWKWP.RTVLSTAPSPRPQLLDYAVTPTTAP.....MTYHPAR
PFM MDPDAFTASLFWKWP.RTVLPTTGPLRPQLLDYAVAPPAPA.....AVYHPAR
FA MDPDAFSASLFWKWP.RGAMPPP...SRLLEPVAPPQPPPSLPPPPPPQLPTSSYSIR
ALF MDPEAFSASLFWKWP.RGAMPPP...NRLLEAVAPPQPPP..PPLPPPQLPP.AYSIR
NFL MDPEAFSASLFWKWP.RGAMPPP...TRLLEAAVAPPPPP..PVLPPPQLSA.AYSIR
FLO MDPDAF...LFWKWDH.RTALPQP...NRLLDVAVAPPPPP..PQAP.....SYSMR
Imp-FLO MDPEAFSASLFWKWP.RGPIAPP...TNRLLEAAAAAAPPHP.....AAMMSYSGR
LFY MDPEGFTSGLFRWNPTRALVQAPPVPPPLQQQPVTPQTAA.....FGMR

SGL1 L.PRELGGLEELFQAYGIRYYTAAKIAELGFTVSTLVDMKDEELDDMMNSLSQIFRWDL
UNI L.PRELGGLEELFQAYGIRYYTAAKIAELGFTVSTLVDMKDEELDDMMNSLSQIFRWDL
PFM A.PREIGGLEELFQAYGIRYYTAAKIAELGFTVSTLVDMKDEELDDMMNSLSQIFRWDL
FA S.TRELGGLEELFQAYGIRYYTAAKIAELGFTVNTLLDMKDEELDDMMNSLSQIFRWDL
ALF ..TRELGGLEEMFQAYGIRYYTAAKITELGFTVNTLLDMKDEELDDMMNSLSQIFRWELL
NFL ..TRELGGLEELFQAYGIRYYTAAKIAELGFTVNTLLDMKDEELDDMMNSLSQIFRWELL
FLO ..PRELGGLEELFQAYGIRYYTAAKIAELGFTVNTLLDMRDEELDEMNSLQCIFRWDL
Imp-FLO PHQRDLGGLEDLFQAYGIRYYTAAKISELGFTVSTLIDMKDEELDDMMNSLSHLFRWELL
LFYLGGLEGLFGPYGIRFYTAAKIAELGFTASTLVGMKDEELEEMNSLSHIFRWELL

SGL1 VGERYGKAAIRAERRRLDEE...EIKRRGLLSG.....DTT.NALDALSQE.....GL
UNI VGERYGKAAIRAERRRLDEE...EIKRRGLLSG.....DTT.NALDALSQE.....GL
PFM VGERYGKAAVRAERRRLDEE...DMKRRNLLST.....DTTINALDALSQEGVNKFVGL
FA VGERYGKAAIRAERWRLEEE...EARRRGHILS.....DGGTNVLDALSQE.....GL
ALF VGERYGKAAIRAERRRLEEE...EGRRR.HILS.....DGGTNVLDALSQE.....GL
NFL VGERYGKAAIRAERRRLEEE...ELRRRSHLLS.....DGGTNALDALSQE.....GL
FLO VGERYGKAAVRAERRRIDE...EVRRR.HLLL.....GDTTHALDALSQE.....GL
Imp-FLO VGERYGKAAVRAEQRRR.....HLIYASEQQQ.....QPSINALDALSQE.....GL
LFY VGERYGKAAVRAERRRLQEEEEESSRRRHLLLSAAGDSGTHHALDALSQE.....GL

SGL1 SEEPVVQR.EKEAVGSGGGST...WEVAVVEERRKRQQIRRRR.....MKMKGNG...DH
UNI SEEPVVQR.EKEAMGSGGGST...WEVAVVEERRKRQQIRRRR.....MKMKGN...DH
PFM SEEPVVQR.EKEVVGSGGGST...WEVAVVAEERRKKQRRRSR.....MKQHGD...NEE
FA SEEPVQQHEREAAGSGGGGT...WEVAAG.GGGRMKQRRRKK...AGRERRG...EED
ALF SEEPVQQQ.EREAGSGGGGTA...WEVAVP.GGGRMRQRRRKKVV.VGRERRGSS.MEED

NFL	SEEPVQQQ.EREAVGSGGGGTT..WEVVAAVGGGRMKQRRRKKVSTGRERRGRASAEED
FLO	SEEPVQQE..KEAMGSGGGVGGVWEMMGA.GGRKAPQRRRKNYK..GRSRMAS..MEED
Imp-FLO	SEE.....KEAAGSGGVGSAG.WEMTAVVAGAIIGNTRDRRR.....RSRKGNSCDEER
LFY	SEEPVQQDQTDAAAGNNGGGGGSGYWDAGQGKMKKQQQRRRKK.....PMLTS..VETD
SGL1	GENEEGDEE..EEDNISGG...GERQREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRE
UNI	GENEEGEEE..EEDNISGGGVGGGERQREHPFIVTEPAEVARGKKNGLDYLFHLYEQCRE
PFM	GEDEEGEDD..DEGNNSGGGGGCERQREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRE
FA	EETEELGEEDEENMNQGGGGGGSERQREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRD
ALF	EDTEEGQEDNEDYNINNEGGGGISERQREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRD
NFL	EETEEGQED..EWNIN.DAGGGISERQREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRD
FLO	DDDDDDDETEGAEDDEN.....IVSERQREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRD
Imp-FLO	GSDGEGGGD.....ERQREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRE
LFY	EDVNEGEDDD.GMDNGNGGSGLGTERRQREHPFIVTEPGEVARGKKNGLDYLFHLYEQCRE
SGL1	FLIQVQAIAKERGEKCPKVTNQVFRYAKKAGASYINKPKMRHYVHCYALHCLDDEEVSNE
UNI	FLIQVQAIAKERGEKCPKVTNQVFRYAKKAGASYINKPKMRHYVHCYALHCLDDEEVSNE
PFM	FLIQVQAIADRGEKCPKVTNQVFRYAKKAGASYINKPKMRHYVHCYALHCLDDEEVSNE
FA	FLIQVQTIAKERGEKCPKVTNQVFRYAKKAGASYINKPKMRHYVHCYALHCLDEDASNA
ALF	FLIQVQNIAKERGEKCPKVTNQVFRFAKKAGASYINKPKMRHYVHCYALHCLDEDASNA
NFL	FLIQVQNIAKERGEKCPKVTNQVFRYAKKAGASYINKPKMRHYVHCYALHCLDDEEASNA
FLO	FLIQVQTIAKERGEKCPKVTNQVFRYAKKAGANYINKPKMRHYVHCYALHCLDDEEASNA
Imp-FLO	FLIQVQNIAKERGEKCPKVTNQVFRYAKKAGASYINKPKMRHYVHCYALHCLDDEEASNA
LFY	FLLQVQTIADRGEKCPKVTNQVFRYAKKSGASYINKPKMRHYVHCYALHCLDDEEASNA
SGL1	LRRGFKERGENVGAWRQACYKPLVAIAARQGWIDIDAI FNAHPRLSIWYVPTKLRQLCHAE
UNI	LRRGFKERGENVGAWRQACYKPLVAIAARQGWIDIDAI FNAHPRLSIWYGPTKLRQLCHAE
PFM	LRRGFKERGENVGAWRQACYKPLVAIAARQGWIDIDAI FNAHPRLSIWYVPTKLRQLCHAE
FA	LRRAFKERGENVGAWRQACYKPLVAIAARQGWIDIDAI FNAHPRLAIWYVPTKLRQLCHSE
ALF	LRRAFKERGENVGAWRQACYKPLVAIAARQGWIDIDAI FNGHPRLSIWYVPTKLRQLCHSE
NFL	LRRAFKERGENVGAWRQACYKPLVAIAARQGWIDITIFNAHPRLAIWYVPTLRQLCHSE
FLO	LRRAFKERGENVGAWRQACYKPLVAIAARQGWIDITIFNAHPRLSIWYVPTKLRQLCHAE
Imp-FLO	LRRAFKERGENVGAWRQACYRPLVNVAARREWDIDAVFN SHPRLSVWYVPTKLRQLCHAE
LFY	LRRAFKERGENVGSWRQACYKPLVNIACRHGWDIDAVFN AHPRLSIWYVPTKLRQLCHLE
SGL1	RN..SAAASSSVS.....VGT..AHLPF.
UNI	RN..GAAASSSVS.....FGT..THLPF.
PFM	RN..SAAASSSVS.....VGT..AHLPF.
FA	RSNAAAAASSSVS.....GGV.ADHLPHF
ALF	RSNAAAAASTSVS.....GGG.VDHLPHF
NFL	RSNAAAAASSSVS.....GGV.GDHLPHF
FLO	RSSAAVAATSSIT.....GGGPADHLPF.
Imp-FLO	RSSSVSAGAASSS.....GGT..VLMPF.
LFY	RNNAVAAAAALVGGISCTGSSTSGRGGCGDDLRF.

Supplemental Figure 1 Amino acid sequence alignment of SGL1 and its orthologs.

Supplemental Table 1 Genetic segregation analysis of *sgll-1* mutant suggests that *sgll-1* segregates as a single recessive locus.

	Wild-type-like	<i>sgll-1</i>	Wild-type-like : mutant
<i>sgll-1</i> (+/-) self pollination	105	34	3:1

Supplemental Table 2 Distribution of floral organ number in homozygous *lfy* transgenic plants compared with wild-type *Col-0* plants.

Transgenic line	Floral organ	Floral organ number						
		0	1	2	3	4	5	6
<i>LFY:LFY</i> (n=56)	Sepal	0	0	0	0	56	0	0
	Petal	0	1	2	0	51	2	0
	Stamen	0	0	0	0	1	21	34
<i>LFY:SGL1</i> (n=305)	Sepal	0	0	0	1	300	4	0
	Petal	0	5	30	72	186	7	5
	Stamen	4	14	37	56	116	66	12
<i>SGL1:SGL1</i> (n=117)	Sepal	0	0	0	0	117	0	0
	Petal	1	1	9	7	93	5	1
	Stamen	0	0	3	13	22	28	51
Wild-type (<i>Col-0</i>) (n=60)	Sepal	0	0	0	0	60	0	0
	Petal	0	0	0	0	60	0	0
	Stamen	0	0	0	0	0	1	59