

Supplementary Table 1. Major gene ontology functions and associated DEGs in group 2 of Clusste II

Category	GO ID	GO Term	Pop total	Pop hits	Total	Gene Count	Genes
BP	GO:0005975	carbohydrate metabolic process	44631	2738	331	36	Keumgang1SL044138t004, Keumgang1SL010658t013, Keumgang1SL001988t009, Keumgang1SL002630t002, Keumgang1SL015865t006, Keumgang1SL014234t009, Keumgang1SL024055t007, Keumgang1SL002795t013, Keumgang1SL011639t008, Keumgang1SL023642t018, Keumgang1SL100559t001, Keumgang1SL092479t001, Keumgang1SL002568t001, Keumgang1SL007595t003, Keumgang1SL003578t009, Keumgang1SL002990t005, Keumgang1SL001367t010, Keumgang1SL004459t010, Keumgang1SL061096t001, Keumgang1SL061541t001, Keumgang1SL005125t005, Keumgang1SL008483t009, Keumgang1SL044354t005, Keumgang1SL012990t001, Keumgang1SL004214t005, Keumgang1SL024542t003, Keumgang1SL022719t014, Keumgang1SL090237t002, Keumgang1SL003426t010, Keumgang1SL002448t001, Keumgang1SL032675t003, Keumgang1SL009621t001, Keumgang1SL005875t001, Keumgang1SL003362t001, Keumgang1SL059805t020, Keumgang1SL001643t003
	GO:0009725	response to hormone	44631	3421	331	33	Keumgang1SL032806t008, Keumgang1SL020189t009, Keumgang1SL060887t001, Keumgang1SL001988t009, Keumgang1SL042658t007, Keumgang1SL029417t001, Keumgang1SL100559t001, Keumgang1SL111547t001, Keumgang1SL016309t005, Keumgang1SL024544t017, Keumgang1SL010189t001, Keumgang1SL060952t008, Keumgang1SL020819t007, Keumgang1SL020617t003, Keumgang1SL003361t004, Keumgang1SL097998t001, Keumgang1SL007804t008, Keumgang1SL091194t019, Keumgang1SL061592t010, Keumgang1SL008483t009, Keumgang1SL001228t016, Keumgang1SL002056t010, Keumgang1SL004459t010, Keumgang1SL005476t008, Keumgang1SL023855t004, Keumgang1SL004317t001, Keumgang1SL060888t003, Keumgang1SL007047t006, Keumgang1SL005009t022, Keumgang1SL023471t001, Keumgang1SL017380t002, Keumgang1SL009621t001, Keumgang1SL011421t033
	GO:0044262	cellular carbohydrate metabolic process	44631	1128	331	20	Keumgang1SL011639t008, Keumgang1SL023642t018, Keumgang1SL100559t001, Keumgang1SL092479t001, Keumgang1SL022719t014, Keumgang1SL002568t001, Keumgang1SL003578t009, Keumgang1SL008483t009, Keumgang1SL002448t001, Keumgang1SL002990t005, Keumgang1SL061541t001, Keumgang1SL044354t005, Keumgang1SL014234t009, Keumgang1SL005875t001, Keumgang1SL024542t003, Keumgang1SL005125t005, Keumgang1SL001988t009, Keumgang1SL003362t001, Keumgang1SL002630t002, Keumgang1SL061096t001
	GO:0006970	response to osmotic stress	44631	1204	331	19	Keumgang1SL001228t016, Keumgang1SL002795t013, Keumgang1SL060888t003, Keumgang1SL014041t028, Keumgang1SL016309t005, Keumgang1SL024544t017, Keumgang1SL008483t009, Keumgang1SL060952t008, Keumgang1SL024055t007, Keumgang1SL004214t005, Keumgang1SL004733t003, Keumgang1SL009621t001, Keumgang1SL011421t033, Keumgang1SL014954t005, Keumgang1SL091194t019, Keumgang1SL002169t012, Keumgang1SL006295t003, Keumgang1SL004459t010, Keumgang1SL055309t001
	GO:0048367	shoot system development	44631	1110	331	12	Keumgang1SL007047t006, Keumgang1SL007727t004, Keumgang1SL060824t004, Keumgang1SL003953t015, Keumgang1SL011421t033, Keumgang1SL097998t001, Keumgang1SL009676t004, Keumgang1SL023323t019, Keumgang1SL013875t001, Keumgang1SL002061t005, Keumgang1SL009312t002, Keumgang1SL020617t003
	GO:0009793	embryo development ending in seed dormancy	44631	133	331	2	Keumgang1SL007047t006, Keumgang1SL011421t033
	GO:0009845	seed germination	44631	89	331	1	Keumgang1SL002056t010
CC	GO:0043231	intracellular membrane-bounded organelle	44631	17810	331	153	Keumgang1SL014699t006, Keumgang1SL014041t028, Keumgang1SL000378t086, Keumgang1SL012206t018, Keumgang1SL003127t016, Keumgang1SL010170t003, Keumgang1SL018924t001, Keumgang1SL020189t009, Keumgang1SL002630t002, Keumgang1SL015865t006, Keumgang1SL004733t003, Keumgang1SL092042t010, Keumgang1SL013875t001, Keumgang1SL010306t014, Keumgang1SL023801t007, Keumgang1SL009194t012, Keumgang1SL007804t008, Keumgang1SL002519t001, Keumgang1SL024470t007, Keumgang1SL003578t009, Keumgang1SL003043t011, Keumgang1SL068160t001, Keumgang1SL002061t005, Keumgang1SL025189t023, Keumgang1SL023855t004, Keumgang1SL001507t014, Keumgang1SL022719t014, Keumgang1SL005427t009, Keumgang1SL023471t001, Keumgang1SL009106t004, Keumgang1SL106126t001, Keumgang1SL001268t009, Keumgang1SL007200t011, Keumgang1SL038894t003, Keumgang1SL009621t001, Keumgang1SL005918t002, Keumgang1SL014954t005, Keumgang1SL033776t002, Keumgang1SL037588t005, Keumgang1SL041487t004, Keumgang1SL001995t007, Keumgang1SL018970t004, Keumgang1SL010658t013, Keumgang1SL005476t008, Keumgang1SL098820t001, Keumgang1SL015745t004, Keumgang1SL002795t013, Keumgang1SL010733t028, Keumgang1SL007066t010, Keumgang1SL006295t003, Keumgang1SL016309t005, Keumgang1SL010709t010, Keumgang1SL006400t017, Keumgang1SL014234t009, Keumgang1SL024055t007, Keumgang1SL101769t002, Keumgang1SL002619t004, Keumgang1SL008483t009, Keumgang1SL092391t001, Keumgang1SL024025t003, Keumgang1SL003953t015, Keumgang1SL024542t003, Keumgang1SL003750t001, Keumgang1SL003437t009, Keumgang1SL003397t006, Keumgang1SL004220t003, Keumgang1SL012341t011, Keumgang1SL002062t009, Keumgang1SL004674t008,

Supplementary Table 1. Continued

Category	GO ID	GO Term	Pop total	Pop hits	Total	Gene Count	Genes
	GO:0043231	intracellular membrane-bounded organelle	44631	17810	331	153	Keumgang1SL003790t013, Keumgang1SL002448t001, Keumgang1SL059805t020, Keumgang1SL022980t012, Keumgang1SL006918t019, Keumgang1SL095837t001, Keumgang1SL024544t017, Keumgang1SL002470t003, Keumgang1SL009659t006, Keumgang1SL093705t002, Keumgang1SL003157t003, Keumgang1SL032276t004, Keumgang1SL020617t003, Keumgang1SL051430t001, Keumgang1SL002626t004, Keumgang1SL029417t001, Keumgang1SL006631t007, Keumgang1SL060952t008, Keumgang1SL003285t014, Keumgang1SL091762t008, Keumgang1SL024071t002, Keumgang1SL004459t010, Keumgang1SL006299t005, Keumgang1SL097998t001, Keumgang1SL002533t001, Keumgang1SL001228t016, Keumgang1SL097515t001, Keumgang1SL038258t008, Keumgang1SL005875t001, Keumgang1SL008268t007, Keumgang1SL001981t003, Keumgang1SL019151t017, Keumgang1SL005723t005, Keumgang1SL002958t015, Keumgang1SL026807t002, Keumgang1SL060888t003, Keumgang1SL010076t006, Keumgang1SL032675t003, Keumgang1SL000132t017, Keumgang1SL005191t007, Keumgang1SL004615t012, Keumgang1SL002305t002, Keumgang1SL011333t006, Keumgang1SL007736t010, Keumgang1SL012208t001, Keumgang1SL002076t009, Keumgang1SL011639t008, Keumgang1SL092702t001, Keumgang1SL024741t001, Keumgang1SL000151t001, Keumgang1SL001264t011, Keumgang1SL096327t006, Keumgang1SL002990t005, Keumgang1SL006694t001, Keumgang1SL019564t002, Keumgang1SL004317t001, Keumgang1SL004022t004, Keumgang1SL003079t009, Keumgang1SL026278t019, Keumgang1SL004920t002, Keumgang1SL003426t010, Keumgang1SL005125t005, Keumgang1SL038209t005, Keumgang1SL002056t010, Keumgang1SL012029t004, Keumgang1SL001971t019, Keumgang1SL004214t005, Keumgang1SL018848t001, Keumgang1SL039511t001, Keumgang1SL009312t002, Keumgang1SL00559t001, Keumgang1SL001617t008, Keumgang1SL007047t006, Keumgang1SL007727t004, Keumgang1SL003362t001, Keumgang1SL008212t001, Keumgang1SL009676t004, Keumgang1SL003568t003, Keumgang1SL012204t001, Keumgang1SL090237t002, Keumgang1SL023323t019, Keumgang1SL023226t005, Keumgang1SL096195t001, Keumgang1SL002129t001
CC	GO:0005737	cytoplasm	44631	13556	331	124	Keumgang1SL001228t016, Keumgang1SL000378t086, Keumgang1SL012206t018, Keumgang1SL060887t001, Keumgang1SL018924t001, Keumgang1SL028168t012, Keumgang1SL020189t009, Keumgang1SL002630t002, Keumgang1SL015865t006, Keumgang1SL004733t003, Keumgang1SL092042t010, Keumgang1SL013875t001, Keumgang1SL010306t014, Keumgang1SL023801t007, Keumgang1SL009194t012, Keumgang1SL007804t008, Keumgang1SL002519t001, Keumgang1SL024470t007, Keumgang1SL007736t010, Keumgang1SL003578t009, Keumgang1SL068160t001, Keumgang1SL004317t001, Keumgang1SL071267t001, Keumgang1SL022719t014, Keumgang1SL090237t002, Keumgang1SL023471t001, Keumgang1SL009106t004, Keumgang1SL0106126t001, Keumgang1SL092702t001, Keumgang1SL001268t009, Keumgang1SL009621t001, Keumgang1SL002619t004, Keumgang1SL014954t005, Keumgang1SL002169t012, Keumgang1SL011639t008, Keumgang1SL033776t002, Keumgang1SL037588t005, Keumgang1SL099322t001, Keumgang1SL041487t004, Keumgang1SL018970t004, Keumgang1SL010658t013, Keumgang1SL098820t001, Keumgang1SL010733t028, Keumgang1SL100559t001, Keumgang1SL006295t003, Keumgang1SL089447t019, Keumgang1SL006400t017, Keumgang1SL014234t009, Keumgang1SL024055t007, Keumgang1SL101769t002, Keumgang1SL002061t005, Keumgang1SL092391t001, Keumgang1SL024025t003, Keumgang1SL024542t003, Keumgang1SL003397t006, Keumgang1SL012341t011, Keumgang1SL004674t008, Keumgang1SL003426t010, Keumgang1SL008483t009, Keumgang1SL003790t013, Keumgang1SL002448t001, Keumgang1SL059805t020, Keumgang1SL022980t012, Keumgang1SL006918t019, Keumgang1SL009659t006, Keumgang1SL011650t007, Keumgang1SL093705t002, Keumgang1SL003157t003, Keumgang1SL001995t007, Keumgang1SL049065t001, Keumgang1SL020617t003, Keumgang1SL051430t001, Keumgang1SL061592t010, Keumgang1SL029417t001, Keumgang1SL023226t005, Keumgang1SL006631t007, Keumgang1SL060952t008, Keumgang1SL014699t006, Keumgang1SL003285t014, Keumgang1SL024071t002, Keumgang1SL004459t010, Keumgang1SL097998t001, Keumgang1SL002533t001, Keumgang1SL005009t022, Keumgang1SL097515t001, Keumgang1SL007047t006, Keumgang1SL001981t003, Keumgang1SL019151t017, Keumgang1SL005723t005, Keumgang1SL060888t003, Keumgang1SL032675t003, Keumgang1SL005191t007, Keumgang1SL004615t012, Keumgang1SL011333t006, Keumgang1SL001264t011, Keumgang1SL002076t009, Keumgang1SL004143t003, Keumgang1SL007727t004, Keumgang1SL002990t005, Keumgang1SL001367t010, Keumgang1SL012208t001, Keumgang1SL003079t009, Keumgang1SL026278t019, Keumgang1SL004920t002, Keumgang1SL010709t010, Keumgang1SL005125t005, Keumgang1SL038209t005, Keumgang1SL001971t019, Keumgang1SL004214t005, Keumgang1SL023855t004, Keumgang1SL060829t005, Keumgang1SL018848t001, Keumgang1SL039511t001, Keumgang1SL001617t008, Keumgang1SL002795t013, Keumgang1SL003362t001, Keumgang1SL003043t011, Keumgang1SL005875t001, Keumgang1SL003568t003, Keumgang1SL096195t001, Keumgang1SL011094t010, Keumgang1SL025189t023, Keumgang1SL012204t001, Keumgang1SL111547t001

Supplementary Table 1. Continued

Category	GO ID	GO Term	Pop total	Pop hits	Total	Gene Count	Genes
MF	GO:0043169	cation binding	44631	4536	331	59	Keumgang1SL040543t004, Keumgang1SL003424t003, Keumgang1SL002470t003, Keumgang1SL113091t001, Keumgang1SL040006t004, Keumgang1SL032675t003, Keumgang1SL115839t003, Keumgang1SL002121t032, Keumgang1SL003157t003, Keumgang1SL088982t001, Keumgang1SL009194t012, Keumgang1SL098820t001, Keumgang1SL003155t011, Keumgang1SL045808t004, Keumgang1SL023226t005, Keumgang1SL096327t006, Keumgang1SL032219t001, Keumgang1SL002626t004, Keumgang1SL112932t001, Keumgang1SL012208t001, Keumgang1SL024071t002, Keumgang1SL003285t014, Keumgang1SL097701t004, Keumgang1SL009312t002, Keumgang1SL061096t001, Keumgang1SL061541t001, Keumgang1SL012206t018, Keumgang1SL097515t001, Keumgang1SL004920t002, Keumgang1SL019564t002, Keumgang1SL092391t001, Keumgang1SL002125t008, Keumgang1SL065935t001, Keumgang1SL038209t005, Keumgang1SL060831t002, Keumgang1SL060824t004, Keumgang1SL003953t015, Keumgang1SL001981t003, Keumgang1SL023855t004, Keumgang1SL003750t001, Keumgang1SL001367t010, Keumgang1SL117215t001, Keumgang1SL003741t005, Keumgang1SL005723t005, Keumgang1SL066096t009, Keumgang1SL012341t011, Keumgang1SL005427t009, Keumgang1SL007047t006, Keumgang1SL023642t018, Keumgang1SL055311t015, Keumgang1SL061030t003, Keumgang1SL006918t019, Keumgang1SL009621t001, Keumgang1SL005125t005, Keumgang1SL007139t008, Keumgang1SL002122t007, Keumgang1SL055309t001, Keumgang1SL002129t001, Keumgang1SL012204t001
	GO:0003676	nucleic acid binding	44631	4161	331	26	Keumgang1SL002305t002, Keumgang1SL003127t016, Keumgang1SL018924t001, Keumgang1SL041487t004, Keumgang1SL032276t004, Keumgang1SL029417t001, Keumgang1SL023801t007, Keumgang1SL016309t005, Keumgang1SL024055t007, Keumgang1SL097998t001, Keumgang1SL004022t004, Keumgang1SL010733t028, Keumgang1SL000151t001, Keumgang1SL024025t003, Keumgang1SL095837t001, Keumgang1SL003953t015, Keumgang1SL024542t003, Keumgang1SL008268t007, Keumgang1SL003157t003, Keumgang1SL039511t001, Keumgang1SL002062t009, Keumgang1SL092702t001, Keumgang1SL000132t017, Keumgang1SL023471t001, Keumgang1SL005918t002, Keumgang1SL023323t019
	GO:0000166	nucleotide binding	44631	4031	331	19	Keumgang1SL001367t010, Keumgang1SL002533t001, Keumgang1SL002630t002, Keumgang1SL002795t013, Keumgang1SL007066t010, Keumgang1SL024544t017, Keumgang1SL020617t003, Keumgang1SL101769t002, Keumgang1SL004214t005, Keumgang1SL024542t003, Keumgang1SL003437t009, Keumgang1SL007047t006, Keumgang1SL009106t004, Keumgang1SL003790t013, Keumgang1SL032675t003, Keumgang1SL007315t056, Keumgang1SL014954t005, Keumgang1SL014091t010, Keumgang1SL096195t001
	GO:0016798	hydrolase activity, acting on glycosyl bonds	44631	763	331	16	Keumgang1SL011639t008, Keumgang1SL048725t014, Keumgang1SL001373t020, Keumgang1SL008483t009, Keumgang1SL044354t005, Keumgang1SL003354t001, Keumgang1SL022980t012, Keumgang1SL003353t001, Keumgang1SL055754t010, Keumgang1SL003355t021, Keumgang1SL003568t003, Keumgang1SL001947t016, Keumgang1SL001311t014, Keumgang1SL006295t003, Keumgang1SL061879t011, Keumgang1SL003079t009
	GO:0016757	transferase activity, transferring glycosyl groups	44631	949	331	12	Keumgang1SL010306t014, Keumgang1SL003578t009, Keumgang1SL011333t006, Keumgang1SL002448t001, Keumgang1SL002990t005, Keumgang1SL044354t005, Keumgang1SL005875t001, Keumgang1SL003362t001, Keumgang1SL008230t009, Keumgang1SL010658t013, Keumgang1SL022719t014, Keumgang1SL059805t020

Supplementary Table 2. List of seed dormancy-related amylase and UDP-glucose DEGs expression pattern in Cluster K0 vs KM0

Gene Description	Assembled transcripts	Log2FC	E-value	GO	TAIR gene ID	TAIR Symbol	TAIR Description	RICE gene ID	RICE Description
Amylase	Keumgang1SL001254019	6.91	0	GO:0016787, GO:0009607, GO:0008152, GO:0005829, GO:0005975, GO:0009987, GO:0009056, GO:0016161, GO:0000272	AT4G15210	AT-BETA-AMY, ATBETA-AMY, BAM5_BMY1, RAM1	beta-amylase 5		
	Keumgang1SL011639008	1.49	0	GO:0003824, GO:0043169, GO:0005975, GO:0004553	AT2G39930	ATISA1,ISA1	isoamylase 1	LOC_Os08g 40930.1	Alpha amylase, catalytic domain containing protein, expressed
	Keumgang1SL060896012	-0.43	0	GO:0003824, GO:0043169, GO:0005975, GO:0004556, GO:0005509	AT4G25000	AMY1, ATAMY1	alpha-amylase-like	LOC_Os09g 28400.1	alpha-amylase precursor, putative, expressed
UDP-Glucose	Keumgang1SL114606001	2.26	0	GO:0016758, GO:0008152	AT1G05675		UDP-Glycosyltransferase superfamily protein	LOC_Os04g 12970.1	UDP-glucuronosyl/UDP-glucosyl transferase, putative, expressed
	Keumgang1SL002169012	1.74	0	GO:0016779, GO:0008152	AT5G17310	AtUGP2, UGP2	UDP-glucose pyrophosphorylase 2	LOC_Os09g 38030.1	UTP—glucose-1-phosphate uridylyltransferase, putative, expressed
	Keumgang1SL062528001	1.44	0	GO:0016758, GO:0008152	AT3G16520	UGT88A1	UDP-glucosyl transferase 88A1	LOC_Os01g 50200.1	UDP-glucuronosyl and UDP-glucosyl transferase domain containing protein, expressed
	Keumgang1SL069784001	1.23	3.00E-177	GO:0016758, GO:0008152	AT1G05675		UDP-Glycosyltransferase superfamily protein	LOC_Os04g 12970.1	UDP-glucuronosyl/UDP-glucosyl transferase, putative, expressed
	Keumgang1SL044138004	1.08	0	GO:0003854, GO:0016616, GO:0006694, GO:0055114, GO:0003824, GO:0050662, GO:0044237, GO:0009058, GO:0008831, GO:0045226	AT2G28760	UXS6	UDP-XYL synthase 6	LOC_Os03g 16980.1	NAD dependent epimerase/dehydratase family domain containing protein, expressed
	Keumgang1SL091853013	0.90	3.00E-124	GO:0016758, GO:0008152	AT1G22360	AtUGT85A2, UGT85A2	UDP-glucosyl transferase 85A2	LOC_Os02g 51930.1	cytokinin-O-glucosyltransferase 2, putative, expressed
	Keumgang1SL062446001	0.64	0	GO:0016758, GO:0008152	AT1G22360	AtUGT85A2, UGT85A2	UDP-glucosyl transferase 85A2	LOC_Os02g 51930.1	cytokinin-O-glucosyltransferase 2, putative, expressed
	Keumgang1SL055415002	0.61	2.00E-153	GO:0016758, GO:0008152	AT1G05680	UGT74E2	Uridine diphosphate glycosyltransferase 74E2	LOC_Os04g 12970.1	UDP-glucuronosyl/UDP-glucosyl transferase, putative, expressed
	Keumgang1SL030320007	0.08	0	GO:0016758, GO:0008152	AT4G15490	UGT84A3	UDP-Glycosyltransferase superfamily protein	LOC_Os02g 09510.1	limonoid UDP-glucosyltransferase, putative, expressed
	Keumgang1SL022919021	-0.15	0	GO:0016758, GO:0008152	AT3G16520	UGT88A1	UDP-glucosyl transferase 88A1	LOC_Os05g 45110.1	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed
	Keumgang1SL029141022	-0.43	0	GO:0016758, GO:0008152	AT2G15480	UGT73B5	UDP-glucosyl transferase 73B5	LOC_Os01g 45110.1	anthocyanin 3-O-beta-glucosyltransferase, putative, expressed
	Keumgang1SL001924017	-0.64	0	GO:0016758, GO:0008152	AT2G36770		UDP-Glycosyltransferase superfamily protein		
	Keumgang1SL096481002	-0.94	0	GO:0016758, GO:0008152	AT3G16520	UGT88A1	UDP-glucosyl transferase 88A1	LOC_Os01g 53330.1	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed
	Keumgang1SL062836007	-0.99	0	GO:0016758, GO:0008152	AT3G16520	UGT88A1	UDP-glucosyl transferase 88A1	LOC_Os01g 53330.1	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed
	Keumgang1SL097435001	-1.01	5.00E-35	GO:0016758, GO:0008152	AT3G16520	UGT88A1	UDP-glucosyl transferase 88A1	LOC_Os01g 53330.1	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed
Keumgang1SL033435002	-1.04	0	GO:0016758, GO:0008152	AT3G16520	UGT88A1	UDP-glucosyl transferase 88A1	LOC_Os01g 53330.1	anthocyanidin 5,3-O-glucosyltransferase, putative, expressed	
Keumgang1SL030714006	-1.43	0	GO:0016758, GO:0008152	AT1G22360	AtUGT85A2, UGT85A2	UDP-glucosyl transferase 85A2	LOC_Os02g 36830.1	cytokinin-O-glucosyltransferase 2, putative, expressed	