

Table S1. List of 207 identified NGATHA genes and related IDs used for phylogeny analysis.

S.No.	Organism	Gene ID	Gene name
1.	<i>Arabidopsis thaliana</i>	AT2G46870	AtNGA1
2.	<i>Arabidopsis thaliana</i>	AT3G61970	AtNGA2
3.	<i>Arabidopsis thaliana</i>	AT1G01030	AtNGA3
4.	<i>Arabidopsis thaliana</i>	AT4G01500	AtNGA4
5.	<i>Arabidopsis thaliana</i>	AT2G36080	AtNGA-Like1
6.	<i>Arabidopsis thaliana</i>	AT3G11580	AtNGA-Like2
7.	<i>Arabidopsis thaliana</i>	AT5G06250	AtNGA-Like3
8.	<i>Brachypodium distachyon</i>	BRADI_1g77150v3	BdNGA1
9.	<i>Brachypodium distachyon</i>	BRADI_3g51840v3	BdNGA2
10.	<i>Brachypodium distachyon</i>	BRADI_5g19260v3	BdNGA3
11.	<i>Brachypodium distachyon</i>	BRADI_3g16500v3	BdNGA4
12.	<i>Brachypodium distachyon</i>	BRADI_3g32140v3	BdNGA5
13.	<i>Brachypodium distachyon</i>	BRADI_4g25170v3	BdNGA-Like1-1
14.	<i>Brachypodium distachyon</i>	BRADI_4g42167v3	BdNGA-Like1-2
15.	<i>Brassica rapa</i>	Bra000434	BrNGA1-1
16.	<i>Brassica rapa</i>	Bra040478	BrNGA1-2
17.	<i>Brassica rapa</i>	Bra004501	BrNGA1-3
18.	<i>Brassica rapa</i>	Bra003482	BrNGA2-1
19.	<i>Brassica rapa</i>	Bra014415	BrNGA2-2
20.	<i>Brassica rapa</i>	Bra007646	BrNGA2-3
21.	<i>Brassica rapa</i>	Bra033294	BrNGA3-1
22.	<i>Brassica rapa</i>	Bra030497	BrNGA3-2
23.	<i>Brassica rapa</i>	Bra008552	BrNGA4-1
24.	<i>Brassica rapa</i>	Bra037417	BrNGA4-2
25.	<i>Brassica rapa</i>	Bra005301	BrNGA-Like1-1
26.	<i>Brassica rapa</i>	Bra041023	BrNGA-Like2-1
27.	<i>Brassica rapa</i>	Bra034828	BrNGA-Like2-2
28.	<i>Brassica rapa</i>	Bra001411	BrNGA-Like2-3
29.	<i>Brassica rapa</i>	Bra005886	BrNGA-Like3-1
30.	<i>Brassica rapa</i>	Bra009171	BrNGA-Like3-2
31.	<i>Beta vulgaris</i>	BVRB_5g104330	BvNGA1
32.	<i>Beta vulgaris</i>	BVRB_7g158660	BvNGA-Like1

33.	<i>Capsicum annum</i>	CA01g34800	CaNGA1
34.	<i>Capsicum annum</i>	CA01g00060	CaNGA3
35.	<i>Capsicum annum</i>	CA10g17390	CaNGA-Like1-1
36.	<i>Capsicum annum</i>	CA09g00050	CaNGA-Like1-2
37.	<i>Camelina sativa</i>	Csa04g066000	CsNGA1-1
38.	<i>Camelina sativa</i>	Csa05g002280	CsNGA1-2
39.	<i>Camelina sativa</i>	Csa06g053390	CsNGA1-3
40.	<i>Camelina sativa</i>	Csa05g094180	CsNGA2-1
41.	<i>Camelina sativa</i>	Csa07g002630	CsNGA2-2
42.	<i>Camelina sativa</i>	Csa16g002690	CsNGA2-3
43.	<i>Camelina sativa</i>	Csa03g002200	CsNGA3-1
44.	<i>Camelina sativa</i>	Csa11g027850	CsNGA3-2
45.	<i>Camelina sativa</i>	Csa12g042130	CsNGA3-3
46.	<i>Camelina sativa</i>	Csa14g002160	CsNGA3-4
47.	<i>Camelina sativa</i>	Csa17g001510	CsNGA3-5
48.	<i>Camelina sativa</i>	Csa02g004620	CsNGA4-1
49.	<i>Camelina sativa</i>	Csa08g053000	CsNGA4-2
50.	<i>Camelina sativa</i>	Csa13g055780	CsNGA4-3
51.	<i>Camelina sativa</i>	Csa01g012670	CsNGA-Like2-1
52.	<i>Camelina sativa</i>	Csa15g015410	CsNGA-Like2-2
53.	<i>Camelina sativa</i>	Csa19g015730	CsNGA-Like2-3
54.	<i>Camelina sativa</i>	Csa08g058280	CsNGA-Like3-1
55.	<i>Camelina sativa</i>	Csa13g008230	CsNGA-Like3-2
56.	<i>Camelina sativa</i>	Csa20g008460	CsNGA-Like3-3
57.	<i>Daucus carota</i>	DCAR_006572	DcNGA1
58.	<i>Daucus carota</i>	DCAR_020732	DcNGA-Like1-1
59.	<i>Daucus carota</i>	DCAR_013418	DcNGA-Like1-2
60.	<i>Eucalyptus grandis</i>	EUGRSUZ_L00348	EgNGA1
61.	<i>Eucalyptus grandis</i>	EUGRSUZ_E01093	EgNGA2
62.	<i>Eucalyptus grandis</i>	EUGRSUZ_A02625	EgNGA-Like
63.	<i>Glycine max</i>	GLYMA_19G261300	GmNGA1-1
64.	<i>Glycine max</i>	GLYMA_03G262200	GmNGA1-2
65.	<i>Glycine max</i>	GLYMA_16G017100	GmNGA1-3
66.	<i>Glycine max</i>	GLYMA_07G048200	GmNGA1-4

67.	<i>Glycine max</i>	GLYMA_03G199000	GmNGA-Like1-1
68.	<i>Glycine max</i>	GLYMA_19G196600	GmNGA-Like1-2
69.	<i>Glycine max</i>	GLYMA_02G200500	GmNGA-Like1-3
70.	<i>Glycine max</i>	GLYMA_10G076100	GmNGA-Like1-4
71.	<i>Gossypium raimondii</i>	B456_008G132400	GrNGA1-1
72.	<i>Gossypium raimondii</i>	B456_001G150200	GrNGA1-2
73.	<i>Gossypium raimondii</i>	B456_007G114200	GrNGA1-3
74.	<i>Gossypium raimondii</i>	B456_004G128200	GrNGA1-4
75.	<i>Gossypium raimondii</i>	B456_003G073600	GrNGA1-5
76.	<i>Gossypium raimondii</i>	B456_008G261100	GrNGA1-6
77.	<i>Gossypium raimondii</i>	B456_002G237900	GrNGA-Like1-1
78.	<i>Gossypium raimondii</i>	B456_009G399000	GrNGA-Like1-2
79.	<i>Gossypium raimondii</i>	B456_006G152400	GrNGA-Like1-3
80.	<i>Helianthus annuus</i>	HannXRQ Chr03g0083171	HaNGA1-1
81.	<i>Helianthus annuus</i>	HannXRQ Chr17g0534081	HaNGA1-2
82.	<i>Helianthus annuus</i>	HannXRQ Chr06g0167091	HaNGA1-3
83.	<i>Helianthus annuus</i>	HannXRQ Chr09g0238331	HaNGA-Like
84.	<i>Hordeum vulgare</i>	HORVU4Hr1G084950	HvNGA1-1
85.	<i>Hordeum vulgare</i>	HORVU7Hr1G046950	HvNGA1-2
86.	<i>Hordeum vulgare</i>	HORVU6Hr1G066190	HvNGA2
87.	<i>Hordeum vulgare</i>	HORVU7Hr1G002230	HvNGA4-1
88.	<i>Hordeum vulgare</i>	HORVU0Hr1G022200	HvNGA4-2
89.	<i>Hordeum vulgare</i>	HORVU5Hr1G040620	HvNGA-Like
90.	<i>Musa acuminata</i>	GSMUA_Achr4G26430_001	MaNGA1-1
91.	<i>Musa acuminata</i>	GSMUA_Achr4G30170_001	MaNGA1-2
92.	<i>Musa acuminata</i>	GSMUA_Achr5G12850_001	MaNGA3-1
93.	<i>Musa acuminata</i>	GSMUA_Achr2G00400_001	MaNGA3-2
94.	<i>Musa acuminata</i>	GSMUA_Achr1G03600_001	MaNGA3-3
95.	<i>Musa acuminata</i>	GSMUA_Achr5G20340_001	MaNGA3-4
96.	<i>Musa acuminata</i>	GSMUA_Achr5G10220_001	MaNGA3-5

97.	<i>Musa acuminata</i>	GSMUA_Achr5G10230_001	MaNGA3-6
98.	<i>Musa acuminata</i>	GSMUA_Achr4G24970_001	MaNGA3-7
99.	<i>Musa acuminata</i>	GSMUA_Achr7G04630_001	MaNGA4-1
100.	<i>Musa acuminata</i>	GSMUA_Achr4G12210_001	MaNGA4-2
101.	<i>Musa acuminata</i>	GSMUA_Achr6G35600_001	MaNGA-Like1-1
102.	<i>Musa acuminata</i>	GSMUA_Achr6G18320_001	MaNGA-Like1-2
103.	<i>Musa acuminata</i>	GSMUA_Achr3G19210_001	MaNGA-Like1-3
104.	<i>Musa acuminata</i>	GSMUA_Achr6G13140_001	MaNGA-Like1-4
105.	<i>Musa acuminata</i>	GSMUA_Achr9G08980_001	MaNGA-Like1-5
106.	<i>Musa acuminata</i>	GSMUA_Achr9G02600_001	MaNGA-Like1-6
107.	<i>Manihot esculenta</i>	MANES_05G015100	MeNGA1-1
108.	<i>Manihot esculenta</i>	MANES_01G238800	MeNGA1-2
109.	<i>Manihot esculenta</i>	MANES_01G001000	MeNGA3
110.	<i>Manihot esculenta</i>	MANES_08G029200	MeNGA-Like1-1
111.	<i>Manihot esculenta</i>	MANES_09G051400	MeNGA-Like1-2
112.	<i>Medicago truncatula</i>	MTR_7g117455	MtNGA1-1
113.	<i>Medicago truncatula</i>	MTR_8g023990	MtNGA1-2
114.	<i>Medicago truncatula</i>	MTR_1g058350	MtNGA-Like1-1
115.	<i>Medicago truncatula</i>	MTR_7g105370	MtNGA-Like1-2
116.	<i>Nicotiana tabacum</i>	Nitab4.5_0000799g0050.1	NtNGA1-1
117.	<i>Nicotiana tabacum</i>	Nitab4.5_0005519g0040.1	NtNGA1-2
118.	<i>Nicotiana tabacum</i>	Nitab4.5_0015619g0010.1	NtNGA3-1
119.	<i>Nicotiana tabacum</i>	Nitab4.5_0012411g0010.1	NtNGA3-2
120.	<i>Nicotiana tabacum</i>	Nitab4.5_0000573g0030.1	NtNGA-Like
121.	<i>Oryza sativa Japonica group</i>	LOC_Os03g02900.1	OsNGA1
122.	<i>Oryza sativa Japonica group</i>	LOC_Os02g45850.1	OsNGA2
123.	<i>Oryza sativa Japonica group</i>	LOC_Os04g49230.1	OsNGA3
124.	<i>Oryza sativa Japonica group</i>	LOC_Os08g06120.1	OsNGA4
125.	<i>Oryza sativa Japonica group</i>	LOC_Os10g39190.1	OsNGA5
126.	<i>Oryza sativa Japonica group</i>	LOC_Os11g05740.1	OsNGA-Like1-1
127.	<i>Oryza sativa Japonica group</i>	LOC_Os12g06080.1	OsNGA-Like1-2

128.	<i>Populus trichocarpa</i>	POPTR_014G107200v3	PtNGA1
129.	<i>Populus trichocarpa</i>	POPTR_002G181600v3	PtNGA2
130.	<i>Populus trichocarpa</i>	POPTR_001G452200v3	PtNGA3
131.	<i>Populus trichocarpa</i>	POPTR_011G149700v3	ptNGA4
132.	<i>Populus trichocarpa</i>	POPTR_006G208100v3	PtNGA-Like1-1
133.	<i>Populus trichocarpa</i>	POPTR_016G074500v3	PtNGA-Like1-2
134.	<i>Phaseolus vulgaris</i>	PHAVU_010G120900g	PvNGA1-1
135.	<i>Phaseolus vulgaris</i>	PHAVU_009G260100g	PvNGA1-2
136.	<i>Phaseolus vulgaris</i>	PHAVU_007G230700g	PvNGA-Like1-1
137.	<i>Phaseolus vulgaris</i>	PHAVU_001G193100g	PvNGA-Like1-2
138.	<i>Sorghum bicolor</i>	SORBI_3001G528200	SbNGA1
139.	<i>Sorghum bicolor</i>	SORBI_3004G280500	SbNGA2
140.	<i>Sorghum bicolor</i>	SORBI_3006G190400	SbNGA3
141.	<i>Sorghum bicolor</i>	SORBI_3007G047500	SbNGA4
142.	<i>Sorghum bicolor</i>	SORBI_3001G313800	SbNGA5
143.	<i>Sorghum bicolor</i>	SORBI_3005G041400	SbNGA-Like1-1
144.	<i>Sorghum bicolor</i>	SORBI_3008G041100	SbNGA-Like1-2
145.	<i>Setaria italica</i>	SETIT 036864mg	SiNGA1
146.	<i>Setaria italica</i>	SETIT 020241mg	SiNGA2
147.	<i>Setaria italica</i>	SETIT 011823mg	SiNGA3
148.	<i>Setaria italica</i>	SETIT 014362mg	SiNGA4-1
149.	<i>Setaria italica</i>	SETIT 008509mg	SiNGA4-2
150.	<i>Setaria italica</i>	SETIT 039972mg	SiNGA5
151.	<i>Setaria italica</i>	SETIT 027632mg	SiNGA-Like1-1
152.	<i>Setaria italica</i>	SETIT 010849mg	SiNGA-Like1-2
153.	<i>Solanum lycopersicum</i>	Solyc08g013700.1.1	SINGA1
154.	<i>Solanum lycopersicum</i>	Solyc08g013690.1.1	SINGA2
155.	<i>Solanum lycopersicum</i>	Solyc05g004000.1.1	SINGA3
156.	<i>Solanum lycopersicum</i>	Solyc10g083210.2.1	SINGA-Like1-1

157.	<i>Solanum lycopersicum</i>	Solyc09g010230.2.1	SINGA-Like1-3
158.	<i>Solanum tuberosum</i>	PGSC0003DMP400010383	StNGA1
159.	<i>Solanum tuberosum</i>	PGSC0003DMP400010384	StNGA2
160.	<i>Solanum tuberosum</i>	PGSC0003DMP400021619	StNGA3
161.	<i>Solanum tuberosum</i>	PGSC0003DMP400048918	StNGA-Like1-1
162.	<i>Solanum tuberosum</i>	PGSC0003DMP400048917	StNGA-Like1-2
163.	<i>Solanum tuberosum</i>	PGSC0003DMP400015721	StNGA-Like1-3
164.	<i>Solanum tuberosum</i>	PGSC0003DMP400015722	StNGA-Like1-4
165.	<i>Triticum aestivum</i>	TraesCS4B02G348500	TaNGA1-1
166.	<i>Triticum aestivum</i>	TraesCS5A02G516600	TaNGA1-2
167.	<i>Triticum aestivum</i>	TraesCS6B02G286900	TaNGA2-1
168.	<i>Triticum aestivum</i>	TraesCS6A02G259600	TaNGA2-2
169.	<i>Triticum aestivum</i>	TraesCS6D02G240600	TaNGA2-3
170.	<i>Triticum aestivum</i>	TraesCS2A02G394700	TaNGA3-1
171.	<i>Triticum aestivum</i>	TraesCS2D02G392400	TaNGA3-2
172.	<i>Triticum aestivum</i>	TraesCS2B02G412700	TaNGA3-3
173.	<i>Triticum aestivum</i>	TraesCS7D02G448900	TaNGA4-1
174.	<i>Triticum aestivum</i>	TraesCS7A02G461000	TaNGA4-2
175.	<i>Triticum aestivum</i>	TraesCS7B02G362500	TaNGA4-3
176.	<i>Triticum aestivum</i>	TraesCS7A02G020800	TaNGA4-4
177.	<i>Triticum aestivum</i>	TraesCS7A02G020700	TaNGA4-5
178.	<i>Triticum aestivum</i>	TraesCS7D02G017000	TaNGA4-6
179.	<i>Triticum aestivum</i>	TraesCS4A02G472700	TaNGA4-7
180.	<i>Triticum aestivum</i>	TraesCS1A02G200500	TaNGA5-1
181.	<i>Triticum aestivum</i>	TraesCS1B02G215000	TaNGA5-2
182.	<i>Triticum aestivum</i>	TraesCS1D02G203900	TaNGA5-3
183.	<i>Triticum aestivum</i>	TraesCS4D02G114900	TaNGA-Like1-1
184.	<i>Triticum aestivum</i>	TraesCS4B02G117100	TaNGA-Like1-2
185.	<i>Triticum aestivum</i>	TraesCS4A02G198300	TaNGA-Like1-3

186.	<i>Triticum aestivum</i>	TraesCS5B02G126200	TaNGA-Like1-4
187.	<i>Triticum aestivum</i>	TraesCS5A02G127100	TaNGA-Like1-5
188.	<i>Triticum aestivum</i>	TraesCS2A02G460700	TaNGA-Like1-6
189.	<i>Triticum aestivum</i>	TraesCS2D02G460900	TaNGA-Like1-7
190.	<i>Triticum aestivum</i>	TraesCS2B02G482400	TaNGA-Like1-8
191.	<i>Vitis vinifera</i>	GSVIVT01027463001	VvNGA1
192.	<i>Vitis vinifera</i>	GSVIVT01019699001	VvNGA3
193.	<i>Vitis vinifera</i>	GSVIVT01033902001	VvNGA-Like
194.	<i>Zea mays</i>	Zm00001d027409	ZmNGA1-1
195.	<i>Zea mays</i>	Zm00001d010077	ZmNGA1-2
196.	<i>Zea mays</i>	Zm00001d048815	ZmNGA1-3
197.	<i>Zea mays</i>	Zm00001d017618	ZmNGA2-1
198.	<i>Zea mays</i>	Zm00001d051471	ZmNGA2-2
199.	<i>Zea mays</i>	Zm00001d026005	ZmNGA3-1
200.	<i>Zea mays</i>	Zm00001d002562	ZmNGA3-2
201.	<i>Zea mays</i>	Zm00001d024545	ZmNGA4-1
202.	<i>Zea mays</i>	Zm00001d024103	ZmNGA4-2
203.	<i>Zea mays</i>	Zm00001d035903	ZmNGA4-3
204.	<i>Zea mays</i>	Zm00001d047359	ZmNGA5-1
205.	<i>Zea mays</i>	Zm00001d029749	ZmNGA5-2
206.	<i>Zea mays</i>	Zm00001d052591	ZmNGA-Like1-1
207.	<i>Zea mays</i>	Zm00001d023446	ZmNGA-Like1-2

Table S2. The similarity matrix of NGA proteins of *A. thaliana*, *S. lycopersicum* and *O.sativa* L. Japonica

AtNGA1	100%																		
AtNGA2	68.22%	100%																	
AtNGA3	54.51%	52.17%	100%																
AtNGA4	47.41%	46.15%	52.25%	100%															
SINGA1	48.97%	45.57%	51.36%	44.21%	100%														
SINGA2	49.03%	47.49%	50.3%	43.2%	80.95%	100%													
SINGA3	57.41%	53.17%	44.69%	43.24%	60.88%	58.95%	100%												
OsNGA1	45.8%	47.15%	49.19%	45.33%	47.95%	46.62%	47.9%	100%											
OsNGA2	46.12%	45.15%	42.17%	40.54%	48.63%	48.14%	43.12%	57.87%	100%										
OsNGA3	37.41%	38.12%	39.24%	34.17%	42.17%	38.92%	42.08%	45.98%	62.97%	100%									
OsNGA4	41.81%	38.67%	42.5%	38.67%	39.37%	40.76%	38.32%	46.68%	47.73%	39.02%	100%								
OsNGA5	42.9%	44.81%	44.55%	42.3%	44.55%	45.19%	44.87%	60.77%	53.2%	43.26%	42.5%	100%							
AtNGA-Like1	47.95%	43.03%	47.54%	42.21%	43.85%	47.54%	47.13%	44.67%	47.54%	40.98%	44.67%	43.85%	100%						
AtNGA-Like2	45.31%	41.57%	44.94%	39.7%	43.07%	42.69%	40.82%	45.31%	42.32%	38.95%	38.57%	44.19%	57.37%	100%					
AtNGA-Like3	40.07%	37.23%	42.9%	39.36%	39.36%	40.78%	41.13%	41.84%	42.55%	37.94%	36.17%	41.84%	59.83%	62.54%	100%				
SINGA-like1-1	36.12%	36.12%	39.87%	35.12%	38.77%	37.97%	39.24%	35.69%	39.24%	35.12%	36.58%	34.93%	61.06%	52.43%	51.41%	100%			
SINGA-like1-3	42.25%	40.8%	37.97%	36.93%	40.81%	39.19%	36.52%	40.19%	37.1%	36.7%	38.32%	39.42%	61.88%	54.68%	53.9%	67.72%	100%		
OsNGA-Like1-1	39.78%	39.42%	40.86%	37.63%	39.06%	43.36%	43.72%	46.95%	43.72%	37.63%	37.63%	43.01%	49.18%	43.82%	42.29%	43.36%	45.16%	100%	
OsNGA-Like1-2	40.79%	40.43%	41.51%	37.9%	38.98%	41.15%	42.59%	46.93%	42.59%	38.62%	36.46%	41.87%	50%	46.44%	44.76%	45.12%	47.29%	79.06%	100%
	AtNGA1	AtNGA2	AtNGA3	AtNGA4	SINGA1	SINGA2	SINGA3	OsNGA1	OsNGA2	OsNGA3	OsNGA4	OsNGA5	AtNGA-Like1	AtNGA-Like2	AtNGA-Like3	SINGA-like1-1	SINGA-like1-3	OsNGA-Like1-1	OsNGA-Like1-2

Table S3. List of primers used for qPCR.

Gene name	Forward primer (5'→3')	Reverse primer (5'→3')
<i>AtNGA1</i>	TTGATATGGAATGCGGCGAGAGC	GCAAACCTCCACCGGAAGATGATG
<i>AtNGA2</i>	TCAGCAATTCGCCGGAGCTATG	TTGTCGGCATCTGAGGATGAGG
<i>AtNGA3</i>	ACGGCAAGATGTGGAGATTCCG	CGGCTCCATCCTTTGGTCATAACG
<i>AtNGA4</i>	AGAAACTCTTCGCCGGAGACAC	TCCGGTTGTGCGTTATCGTCAG
<i>AtNGA-LIKE 1</i>	ATCCTCCTCCGTACTACATGGAC	TCTAGCTCGTCCGGTTCATATCTC
<i>AtNGA-LIKE 2</i>	GCTGTCTCCGTTGTGTCTCAAG	TAGTCAAGCCGCTCCAATACGC
<i>AtNGA-LIKE 3</i>	CGCCGTGAATACGAGTTCTATGGG	GGCTCTAGTGGCGTGGATTTGATG
<i>SINGA1</i>	AAACTTGATGCTGGTGATGTTG	AGTCAATGAAGAGACGGTGC
<i>SINGA2</i>	CGGAGAAGTATTTCCCTCTTG	CCATGGCTTCCCATTACTATC
<i>SINGA3</i>	TGTCTCATTTTCAGCGTGGAG	CTGGGTACTGAATATTAGAGCGG
<i>SINGA-LIKE1-1</i>	CTCCGAAGCAAAACAGCAATC	CAACATCACTCGGCGTTAATG
<i>SINGA-LIKE1-3</i>	AAATATTGGCGGAGGTGGAG	GACAGTCAGGTTGGTATGGAAG
<i>ACTIN</i>	TGTCCCTATTTACGAGGGTTATGC	AGTTAAATCACGACCAGCAAGAT
<i>UBIQUITIN</i>	GCCGACTACAACATCCAGAAGG	TGCAACACAGCGAGCTTAACC
<i>RNaseH</i>	ACTCTCGAAGCTCCACAAGGAAG	AAGCCACTTCAACTTCTCCTTCAG