

Transcriptome analyses reveal the toxicity of graphene oxide with different diameters on buckwheat root growth

CHANGYING LIU^{1,2}, HANLIN WANG^{1,2}, HAN LI³, QINGCHENG QIU^{1,2},
DABING XIANG^{1,2}, YANXIA LIU³

Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Table S1. Primers used in this study

Gene ID	Primers	
	Forward sequence	Reverse sequence
<i>FtPinG0008383600.01</i>	AAGACTTCCTAGATGCTCACAACGC	CTGAGTGTACCAGGGTGCAGTTTC
<i>FtPinG0007366400.01</i>	TTGTCAATCTCGTCATGGCTGGTG	GACGGAGGCGAGTAATAAGAAGGTG
<i>FtPinG0003438100.01</i>	CGTCAACCAACTCCCTCAACCTTAG	AGTGAATACGTCGCTTCGCCAATAG
<i>FtPinG0000777000.01</i>	CGGGTTCGGGTTTGCTAGAAAGG	CACTTCCATCTTCCATCCCACTCAC
<i>FtPinG0002120600.01</i>	AAATCAGGTGGCTATGAAGGTGGTG	TCCGTACTCCTCAGTTGCTTCTCC
<i>FtPinG0002476600.01</i>	CCGAGCTGCTGGAATCTTGGATAAC	TCGATGGCATGATTTTCAGGTGACC
<i>FtPinG0005871400.01</i>	GTCGGATTTCGTCACCTCAAACCTC	AAAGGCTAGGGCGGGAGTCTTG
<i>FtPinG0003992800.01</i>	TGCCGCCATCACTTTCGTTGTC	GCTCTCCTCCCACTTTTGTCTTG
<i>FtPinG0001089200.01</i>	TCCTTGATTCTTTGGAGGGTTTGC	CTGTACTTGCGAGGCTTGTAGATGG
<i>FtPinG0000683200.01</i>	GAAATACAAAGGCGTCCGCAAGC	AACCAGATTCTTCCCGACTGTGTG
<i>FtPinG0007163900.01</i>	GGCGACCTCGTAGTATCCAATGC	ACCTGTGGCTTCAATTCGACTCTTC
<i>FtPinG0004014300.01</i>	CTTCATCAACGGAAACATCGGCAAG	TCGGTGTAATCCTCCTCGTAGAGC
<i>FtPinG0002124000.01</i> (<i>FtACTIN7</i>)	CCGCCACTCAACACAATGTTATTAT	GAGTTATGAGCTTCCTGATGGACAA

Table S2. Details of various samples taken for study and read sequence information

Q20 and Q30 stand for the percent of the Phred number more than 20 and 30 bases within total bases, respectively; CK represents the root treated with 0 mg/L graphene oxide (GO); GO-0, GO-10 and GO-50 represent the GO with diameters of 0.5–3, 8–15 and > 50 μm , respectively

Group Name	Sample Name	Raw Reads	Clean Reads	Clean Bases (bp)	Q20 (%)	Q30 (%)	Total Mapped (%)
CK	CK_1	44 483 234	40 565 656	6 084 848 400	97.77	93.61	91.19
	CK_2	47 558 036	43 416 108	6 512 416 200	97.59	93.15	91.29
	CK_3	43 242 110	39 504 870	5 925 730 500	97.9	93.89	91.35
GO-0	GO-0_1	52 501 668	47 595 572	7 139 335 800	97.82	93.72	90.65
	GO-0_2	50 269 478	45 942 886	6 891 432 900	97.84	93.8	91.39
	GO-0_3	43 024 022	39 606 166	5 940 924 900	97.83	93.75	92.05
GO-10	GO-10_1	43 093 964	39 826 810	5 974 021 500	97.25	92.54	92.41
	GO-10_2	43 460 774	40 365 644	6 054 846 600	97.8	93.7	92.87
	GO-10_3	42 032 434	38 418 174	5 762 726 100	97.79	93.72	91.4
GO-50	GO-50_1	42 219 110	38 831 662	5 824 749 300	97.7	93.46	91.97
	GO-50_2	39 831 922	36 567 114	5 485 067 100	97.59	93.5	91.8
	GO-50_3	47 979 946	44 063 420	6 609 513 000	97.85	94.2	91.83

Table S3. The differentially expressed genes (DEGs) involved in reactive oxygen species (ROS) detoxification

CK represents the root treated with 0 mg/L graphene oxide (GO); GO-0, GO-10 and GO-50 represent the GO with diameters of 0.5–3, 8–15 and > 50 µm, respectively

Gene ID	Family	Gene Name	CK	GO-0	GO-10	GO-50	NR Description
<i>FtPinG0003250500.01</i>	PER	<i>FtPER10</i>	155.72	689.18	550.49	607.93	gi 698455889 ref XP_009780492.1 PREDICTED: peroxidase 10-like [Nicotiana glauca] >gi 1025416474 ref XP_016441219.1 PREDICTED: peroxidase 10-like [Nicotiana glauca]
<i>FtPinG0004087700.01</i>	PER	<i>FtPER12</i>	386.46	1031.60	705.14	1091.17	gi 720015983 ref XP_010261009.1 PREDICTED: peroxidase 12-like [Nelumbo nucifera]
<i>FtPinG0002320700.01</i>	PER	<i>FtPER19</i>	29.11	15.61	11.19	12.16	gi 747096911 ref XP_011096394.1 PREDICTED: peroxidase 19 [Sesamum indicum]
<i>FtPinG0006649300.01</i>	PER	<i>FtPER24</i>	273.45	130.61	126.50	185.89	gi 1028963278 ref XP_016725141.1 PREDICTED: peroxidase 3-like [Gossypium hirsutum]
<i>FtPinG0004164200.01</i>	PER	<i>FtPER26</i>	1.90	0.19	0.26	0.39	gi 720082863 ref XP_010242724.1 PREDICTED: probable peroxidase 61 [Nelumbo nucifera]
<i>FtPinG0006671400.01</i>	PER	<i>FtPER28</i>	23.57	5.39	2.78	8.67	gi 470110651 ref XP_004291587.1 PREDICTED: peroxidase 60 [Fragaria vesca subsp. vesca]
<i>FtPinG0000523600.01</i>	PER	<i>FtPER3-1</i>	75.63	23.19	22.63	57.59	gi 225447326 ref XP_002280274.1 PREDICTED: peroxidase 3 [Vitis vinifera]
<i>FtPinG0006163100.01</i>	PER	<i>FtPER3-2</i>	261.58	50.75	49.11	124.25	gi 225447326 ref XP_002280274.1 PREDICTED: peroxidase 3 [Vitis vinifera]
<i>FtPinG0008472800.01</i>	PER	<i>FtPER3-3</i>	21.49	10.16	8.40	11.11	gi 734393553 gb KHN28247.1 Peroxidase 3 [Glycine soja]
<i>FtPinG0007030800.01</i>	PER	<i>FtPER31</i>	46.96	25.27	22.86	29.07	gi 225452562 ref XP_002280547.1 PREDICTED: peroxidase 31-like [Vitis vinifera]
<i>FtPinG0002970300.01</i>	PER	<i>FtPER39</i>	55.10	144.98	104.58	91.55	gi 643729144 gb KDP37024.1 hypothetical protein JCGZ_06080 [Jatropha curcas]
<i>FtPinG0002448300.01</i>	PER	<i>FtPER4-1</i>	142.81	351.58	365.71	376.21	gi 970027511 ref XP_015075055.1 PREDICTED: peroxidase P7-like [Solanum pennellii]
<i>FtPinG0007796800.01</i>	PER	<i>FtPER4-2</i>	17.49	23.88	43.63	37.89	gi 1035916774 gb OAY46366.1 hypothetical protein MANES_07G138800 [Manihot esculenta]
<i>FtPinG0009599700.01</i>	PER	<i>FtPER40</i>	0.07	0.34	1.04	0.83	gi 731347408 ref XP_010684973.1 PREDICTED: peroxidase 57-like [Beta vulgaris subsp. vulgaris]

<i>FtPinG0002970500.01</i>	PER	<i>FtPER5</i>	6.16	26.24	15.86	14.73	gi 802620959 ref XP_012075782.1 PREDICTED: peroxidase 5-like [<i>Jatropha curcas</i>] >gi 643725986 gb KDP34818.1 hypothetical protein JCGZ_11180 [<i>Jatropha curcas</i>]
<i>FtPinG0002663500.01</i>	PER	<i>FtPER51</i>	73.10	191.99	152.61	250.03	gi 1028953284 ref XP_016720060.1 PREDICTED: peroxidase 73-like [<i>Gossypium hirsutum</i>]
<i>FtPinG0004712400.01</i>	PER	<i>FtPER55</i>	3.99	9.67	10.91	7.88	gi 1025073413 ref XP_016452635.1 PREDICTED: peroxidase 55-like [<i>Nicotiana tabacum</i>]
<i>FtPinG0005295100.01</i>	PER	<i>FtPER56</i>	255.57	37.99	44.43	167.20	gi 225444399 ref XP_002268360.1 PREDICTED: peroxidase 27 [<i>Vitis vinifera</i>]
<i>FtPinG0000403400.01</i>	PER	<i>FtPER57-1</i>	80.78	18.54	11.71	52.03	gi 731349431 ref XP_010685988.1 PREDICTED: peroxidase 57-like [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>] >gi 870853580 gb KMT05461.1 hypothetical protein BVRB_7g175870 [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]
<i>FtPinG0001102900.01</i>	PER	<i>FtPER57-2</i>	47.37	29.39	16.82	54.78	gi 658039331 ref XP_008355237.1 PREDICTED: peroxidase 60-like [<i>Malus domestica</i>]
<i>FtPinG0002468000.01</i>	PER	<i>FtPER57-3</i>	72.26	12.77	9.87	38.74	gi 985462544 ref XP_006487931.2 PREDICTED: peroxidase 60 [<i>Citrus sinensis</i>]
<i>FtPinG0003444500.01</i>	PER	<i>FtPER57-4</i>	50.71	26.61	17.30	30.88	gi 731349431 ref XP_010685988.1 PREDICTED: peroxidase 57-like [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>] >gi 870853580 gb KMT05461.1 hypothetical protein BVRB_7g175870 [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]
<i>FtPinG0005294500.01</i>	PER	<i>FtPER57-5</i>	4.09	1.79	1.31	2.11	gi 702319464 ref XP_010052439.1 PREDICTED: peroxidase 57-like [<i>Eucalyptus grandis</i>]
<i>FtPinG0006523000.01</i>	PER	<i>FtPER57-6</i>	9.62	0.95	0.54	3.89	gi 731349815 ref XP_010686191.1 PREDICTED: peroxidase 60-like [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]
<i>FtPinG0006523200.01</i>	PER	<i>FtPER57-7</i>	3.97	0.11	0.31	0.45	gi 731366278 ref XP_010694983.1 PREDICTED: peroxidase 60-like [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>] >gi 870845213 gb KMS97989.1 hypothetical protein BVRB_4g096710 [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]
<i>FtPinG0006523300.01</i>	PER	<i>FtPER57-8</i>	3.63	0.14	0.31	0.21	gi 645218228 ref XP_008229576.1 PREDICTED: peroxidase 60 [<i>Prunus mume</i>]
<i>FtPinG0006523500.01</i>	PER	<i>FtPER57-9</i>	11.68	0.81	1.37	1.80	gi 645218228 ref XP_008229576.1 PREDICTED: peroxidase 60 [<i>Prunus mume</i>]
<i>FtPinG0006523700.01</i>	PER	<i>FtPER57-10</i>	21.33	2.09	1.87	8.36	gi 645218228 ref XP_008229576.1 PREDICTED: peroxidase 60 [<i>Prunus mume</i>]
<i>FtPinG0000403100.01</i>	PER	<i>FtPER60-1</i>	53.93	12.92	6.90	27.27	gi 902131189 gb KNA04246.1 hypothetical protein SOVF_201440 [<i>Spinacia oleracea</i>]
<i>FtPinG0001216400.01</i>	PER	<i>FtPER60-2</i>	7.65	2.16	0.94	5.76	gi 604313391 gb EYU26722.1 hypothetical protein MIMGU_mgv1a024318mg [<i>Erythranthe guttata</i>]

<i>FtPinG0003444900.01</i>	PER	<i>FtPER60-3</i>	17.80	6.71	6.82	16.71	gi 731349431 ref XP_010685988.1 PREDICTED: peroxidase 57-like [Beta vulgaris subsp. vulgaris] >gi 870853580 gb KMT05461.1 hypothetical protein BVRB_7g175870 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0005774000.01</i>	PER	<i>FtPER64-1</i>	33.22	9.50	8.73	10.60	gi 902180430 gb KNA09548.1 hypothetical protein SOVF_152660 [Spinacia oleracea]
<i>FtPinG0009459200.01</i>	PER	<i>FtPER64-2</i>	22.13	7.60	6.73	8.82	gi 902180430 gb KNA09548.1 hypothetical protein SOVF_152660 [Spinacia oleracea]
<i>FtPinG0005676300.01</i>	PER	<i>FtPER7</i>	23.79	7.42	5.00	17.49	gi 731346141 ref XP_010684298.1 PREDICTED: peroxidase 7 [Beta vulgaris subsp. vulgaris] >gi 870854377 gb KMT06162.1 hypothetical protein BVRB_7g163310 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0005642000.01</i>	PER	<i>FtPER71-1</i>	101.71	392.12	422.20	302.90	gi 1781324 emb CAA71489.1 peroxidase [Spinacia oleracea]
<i>FtPinG0009599500.01</i>	PER	<i>FtPER71-2</i>	6.08	22.40	43.15	28.41	gi 1781324 emb CAA71489.1 peroxidase [Spinacia oleracea]
<i>FtPinG0007739700.01</i>	PER	<i>FtPER72-1</i>	174.42	364.03	342.17	193.27	gi 719988591 ref XP_010252386.1 PREDICTED: peroxidase 72-like [Nelumbo nucifera]
<i>FtPinG0007740100.01</i>	PER	<i>FtPER72-2</i>	1.04	1.72	2.44	4.73	gi 731337447 ref XP_010679794.1 PREDICTED: peroxidase 72-like [Beta vulgaris subsp. vulgaris] >gi 870857945 gb KMT09471.1 hypothetical protein BVRB_6g129430 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0000228200.01</i>	PER	<i>FtPNC1-1</i>	45.56	90.69	90.03	164.15	gi 720003323 ref XP_010256954.1 PREDICTED: cationic peroxidase 1-like [Nelumbo nucifera]
<i>FtPinG0000230000.01</i>	PER	<i>FtPNC1-2</i>	16.90	2.15	2.51	9.52	gi 743782272 ref XP_010921098.1 PREDICTED: cationic peroxidase 1-like [Elaeis guineensis]
<i>FtPinG0001659600.01</i>	PER	<i>FtPNC1-3</i>	6.20	1.33	1.36	1.38	gi 743819966 ref XP_011021015.1 PREDICTED: cationic peroxidase 1-like [Populus euphratica]
<i>FtPinG0006420900.01</i>	PER	<i>FtPNC1-4</i>	98.78	286.91	315.84	334.59	gi 720003323 ref XP_010256954.1 PREDICTED: cationic peroxidase 1-like [Nelumbo nucifera]
<i>FtPinG0001375100.01</i>	GST	<i>FtDHAR2</i>	11.06	5.87	4.22	6.45	gi 694351834 ref XP_009357653.1 PREDICTED: glutathione S-transferase DHAR2-like [Pyrus x bretschneideri]
<i>FtPinG0003132100.01</i>	GST	<i>FtGST3</i>	46.28	121.91	85.94	110.19	gi 333690873 gb AEF79856.1 glutathione-S-transferase tau 1 [Hevea brasiliensis]
<i>FtPinG0001404500.01</i>	GST	<i>FtGSTF-1</i>	14.15	6.50	5.34	4.79	gi 1009108988 ref XP_015887675.1 PREDICTED: glutathione S-transferase-like [Ziziphus jujuba]

<i>FtPinG0006077100.01</i>	<i>GST</i>	<i>FtGSTF-2</i>	150.42	54.80	55.89	74.85	gi 590718601 ref XP_007050849.1 Glutathione S-transferase phi 8 [Theobroma cacao] >gi 508703110 gb EOX95006.1 Glutathione S-transferase phi 8 [Theobroma cacao]
<i>FtPinG0008530800.01</i>	<i>GST</i>	<i>FtGSTF13</i>	93.07	170.84	252.99	124.54	gi 974031783 gb ALY05892.1 GST3 [Litchi chinensis]
<i>FtPinG0003200600.01</i>	<i>GST</i>	<i>FtGSTL1-1</i>	103.48	255.92	179.27	178.37	gi 197312863 gb ACH63212.1 glutathione-S-transferase [Rheum australe]
<i>FtPinG0001180500.01</i>	<i>GST</i>	<i>FtGSTT1-2</i>	5.42	11.87	12.17	10.42	gi 848911691 ref XP_012854239.1 PREDICTED: glutathione S-transferase T1-like [Erythranthe guttata] >gi 604304139 gb EYU23489.1 hypothetical protein MIMGU_mgv1a012760mg [Erythranthe guttata]
<i>FtPinG0008834500.01</i>	<i>GST</i>	<i>FtGSTT1-3</i>	189.30	114.61	82.26	144.78	gi 502139351 ref XP_004503735.1 PREDICTED: glutathione S-transferase T1-like [Cicer arietinum]
<i>FtPinG0008836700.01</i>	<i>GST</i>	<i>FtGSTT1-4</i>	22.52	9.07	6.17	15.38	gi 502139351 ref XP_004503735.1 PREDICTED: glutathione S-transferase T1-like [Cicer arietinum]
<i>FtPinG0000533200.01</i>	<i>GST</i>	<i>FtGSTU8-1</i>	71.51	168.79	120.86	110.66	gi 694408386 ref XP_009378879.1 PREDICTED: probable glutathione S-transferase [Pyrus x bretschneideri]
<i>FtPinG0000533500.01</i>	<i>GST</i>	<i>FtGSTU8-2</i>	214.17	479.66	429.97	357.96	gi 283135872 gb ADB11327.1 tau class glutathione transferase GSTU45 [Populus trichocarpa]
<i>FtPinG0000533700.01</i>	<i>GST</i>	<i>FtGSTU8-3</i>	15.99	53.13	131.20	74.23	gi 283135872 gb ADB11327.1 tau class glutathione transferase GSTU45 [Populus trichocarpa]
<i>FtPinG0000533900.01</i>	<i>GST</i>	<i>FtGSTU8-4</i>	62.69	278.64	133.93	148.20	gi 902186448 gb KNA10681.1 hypothetical protein SOVF_142050 [Spinacia oleracea]
<i>FtPinG0005396100.01</i>	<i>GST</i>	<i>FtGSTU8-5</i>	3.10	1.09	0.49	2.97	gi 731368443 ref XP_010696150.1 PREDICTED: glutathione S-transferase U8-like [Beta vulgaris subsp. vulgaris] >gi 870844097 gb KMS97148.1 hypothetical protein BVRB_7g178130 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0006416700.01</i>	<i>GST</i>	<i>FtGSTU9</i>	40.63	94.98	83.24	75.39	gi 186688078 gb ACC86120.1 glutathione S-transferase [Knorringia sibirica]
<i>FtPinG0003428200.01</i>	<i>GST</i>	<i>FtHSP26-A</i>	284.66	706.09	502.52	602.46	gi 1021029130 gb KZM86915.1 hypothetical protein DCAR_024049 [Daucus carota subsp. sativus]
<i>FtPinG0006850500.01</i>	<i>GST</i>	<i>FtPARC</i>	0.91	3.13	1.64	1.35	gi 802708516 ref XP_012084509.1 PREDICTED: probable glutathione S-transferase parC [Jatropha curcas]
<i>FtPinG0003306300.01</i>	<i>GRX</i>	<i>FtGRXC9-1</i>	51.37	86.69	105.10	114.25	gi 590691177 ref XP_007043710.1 Glutaredoxin, putative [Theobroma cacao] >gi 508707645 gb EOX99541.1 Glutaredoxin, putative [Theobroma cacao]
<i>FtPinG0004049700.01</i>	<i>GRX</i>	<i>FtGRXC9-2</i>	8.15	23.99	39.20	36.32	gi 702245073 ref XP_010052341.1 PREDICTED: glutaredoxin-C9-like [Eucalyptus grandis] >gi 629125159 gb KCW89584.1 hypothetical protein EUGRSUZ_A01868 [Eucalyptus grandis]

<i>FtPinG0004183200.01</i>	<i>GRX</i>	<i>FtGRXS10</i>	2.43	0.84	0.39	0.51	gi 213990447 gb ACJ60637.1 glutaredoxin S12 [<i>Populus tremula</i> x <i>Populus tremuloides</i>]
<i>FtPinG0005701100.01</i>	<i>GRX</i>	<i>FtGRXC11</i>	2.78	10.06	7.76	6.40	gi 902227801 gb KNA20839.1 hypothetical protein SOVF_048650 [<i>Spinacia oleracea</i>]
<i>FtPinG0005875300.01</i>	<i>GRX</i>	<i>FtGRXC4</i>	62.82	26.24	25.67	39.83	gi 590581982 ref XP_007014498.1 Glutaredoxin C4 [<i>Theobroma cacao</i>] >gi 508784861 gb EOY32117.1 Glutaredoxin C4 [<i>Theobroma cacao</i>]
<i>FtPinG0006374200.01</i>	<i>GRX</i>	<i>FtGRXS6</i>	16.43	9.80	4.38	8.57	gi 731346503 ref XP_010684490.1 PREDICTED: monothiol glutaredoxin-S6-like [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>] >gi 870854148 gb KMT05953.1 hypothetical protein BVRB_7g164430 [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]
<i>FtPinG0006412900.01</i>	<i>GRX</i>	<i>FtGRXC1</i>	2.40	5.59	6.50	3.98	gi 1009130905 ref XP_015882550.1 PREDICTED: glutaredoxin [<i>Ziziphus jujuba</i>]
<i>FtPinG0000976700.01</i>	<i>ASO</i>	<i>FtASO1</i>	24.70	5.43	6.03	13.98	gi 359496059 ref XP_002268020.2 PREDICTED: L-ascorbate oxidase homolog [<i>Vitis vinifera</i>]
<i>FtPinG0001404800.01</i>	<i>ASO</i>	<i>FtASO2</i>	77.29	29.65	30.14	54.22	gi 729330348 ref XP_010536445.1 PREDICTED: L-ascorbate oxidase homolog [<i>Tarenaya hassleriana</i>]
<i>FtPinG0006204200.01</i>	<i>ASO</i>	<i>FtASO3</i>	55.47	10.18	8.94	16.66	gi 255554849 ref XP_002518462.1 PREDICTED: L-ascorbate oxidase homolog [<i>Ricinus communis</i>] >gi 223542307 gb EEF43849.1 multicopper oxidase, putative [<i>Ricinus communis</i>]
<i>FtPinG0009355200.01</i>	<i>ASO</i>	<i>FtASO4</i>	8.38	3.40	2.52	5.00	gi 731338693 ref XP_010680450.1 PREDICTED: L-ascorbate oxidase homolog [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>] >gi 731338695 ref XP_010680451.1 PREDICTED: L-ascorbate oxidase homolog [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>] >gi 870857824 gb KMT09372.1 hypothetical protein BVRB_6g134640 [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]
<i>FtPinG0000941000.01</i>	<i>LEA</i>	<i>FtLEA5</i>	984.71	1693.48	2073.82	1621.17	gi 310780836 gb ADP23916.1 late embryogenesis abundant protein [<i>Sesuvium portulacastrum</i>]
<i>FtPinG0001205000.01</i>	<i>LEA</i>	<i>FtLEA14-A</i>	29.63	14.21	11.53	17.86	gi 571032303 gb AHF21584.1 late embryogenesis abundant protein [<i>Tamarix hispida</i>]
<i>FtPinG0003401000.01</i>	<i>LEA</i>	<i>FtLEA34</i>	1.45	14.10	10.05	19.77	gi 731336075 ref XP_010679062.1 PREDICTED: late embryogenesis abundant protein D-34-like [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>] >gi 870858693 gb KMT10181.1 hypothetical protein BVRB_5g119420 [<i>Beta vulgaris</i> subsp. <i>vulgaris</i>]
<i>FtPinG0007884600.01</i>	<i>LEA</i>	<i>FtLEA65</i>	10.56	4.51	3.61	6.37	gi 747075164 ref XP_011084606.1 PREDICTED: uncharacterized protein LOC105166815 [<i>Sesamum indicum</i>]

<i>FtPinG0009229300.01</i>	<i>RBOH</i>	<i>FtRBOHH</i>	14.06	3.62	2.75	8.32	gi 731349189 ref XP_010685870.1 PREDICTED: putative respiratory burst oxidase homolog protein H [Beta vulgaris subsp. vulgaris] >gi 870853472 gb KMT05353.1 hypothetical protein BVRB_7g174850 [Beta vulgaris subsp. vulgaris]
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Table S4. The differentially expressed genes (DEGs) encoding transporters

CK represents the root treated with 0 mg/L graphene oxide (GO); GO-0, GO-10 and GO-50 represent the GO with diameters of 0.5–3, 8–15 and > 50 µm, respectively

Gene ID	Family	Gene Name	CK	GO-0	GO-10	GO-50	NR Description
<i>FtPinG0000485900.01</i>	ABC	<i>FtABCC3-1</i>	3.47	1.76	1.65	1.61	gi 731343398 ref XP_010682872.1 PREDICTED: putative ABC transporter C family member 15 [Beta vulgaris subsp. vulgaris] >gi 731343400 ref XP_010682873.1 PREDICTED: putative ABC transporter C family member 15 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0005570600.01</i>	ABC	<i>FtABCB11-1</i>	51.70	19.06	17.03	13.42	gi 731354080 ref XP_010688391.1 PREDICTED: ABC transporter B family member 11-like [Beta vulgaris subsp. vulgaris] >gi 731354082 ref XP_010688392.1 PREDICTED: ABC transporter B family member 11-like [Beta vulgaris subsp. vulgaris] >gi 870851184 gb KMT03250.1 hypothetical protein BVRB_8g197930 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0007467300.01</i>	ABC	<i>FtABCB11-2</i>	6.65	25.14	25.03	25.04	gi 731354080 ref XP_010688391.1 PREDICTED: ABC transporter B family member 11-like [Beta vulgaris subsp. vulgaris] >gi 731354082 ref XP_010688392.1 PREDICTED: ABC transporter B family member 11-like [Beta vulgaris subsp. vulgaris] >gi 870851184 gb KMT03250.1 hypothetical protein BVRB_8g197930 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0002436900.01</i>	ABC	<i>FtABCB15-1</i>	17.30	31.53	36.39	31.31	gi 567876881 ref XP_006431030.1 hypothetical protein CICLE_v10010936mg [Citrus clementina] >gi 557533087 gb ESR44270.1 hypothetical protein CICLE_v10010936mg [Citrus clementina]
<i>FtPinG0005659600.01</i>	ABC	<i>FtABCB15-2</i>	71.75	189.87	207.61	248.44	gi 359488881 ref XP_003633838.1 PREDICTED: ABC transporter B family member 15-like isoform X1 [Vitis vinifera]
<i>FtPinG0007853300.01</i>	ABC	<i>FtABCB15-3</i>	6.15	13.13	10.13	10.02	gi 694415201 ref XP_009335785.1 PREDICTED: ABC transporter B family member 15-like [Pyrus x bretschneideri]
<i>FtPinG0005525800.01</i>	ABC	<i>FtABCB27</i>	8.72	3.99	3.34	4.00	gi 802715984 ref XP_012084841.1 PREDICTED: ABC transporter B family member 27 [Jatropha curcas] >gi 643714910 gb KDP27265.1 hypothetical protein JCGZ_19964 [Jatropha curcas]
<i>FtPinG0009743300.01</i>	ABC	<i>FtABCB8</i>	38.67	64.52	103.86	108.83	gi 802627848 ref XP_012076854.1 PREDICTED: putative ABC transporter B family member 8 [Jatropha curcas]

<i>FtPinG0006219700.01</i>	<i>ABC</i>	<i>FtABCC3-2</i>	25.20	50.94	48.28	20.65	gi 148524780 dbj BAF63397.1 multidrug resistance-associated protein [Fagopyrum esculentum]
<i>FtPinG0000543900.01</i>	<i>ABC</i>	<i>FtABCG11-1</i>	19.22	7.68	12.28	13.07	gi 255569405 ref XP_002525670.1 PREDICTED: ABC transporter G family member 11 [Ricinus communis] >gi 1000952721 ref XP_015578765.1 PREDICTED: ABC transporter G family member 11 [Ricinus communis] >gi 223535106 gb EEF36788.1 ATP-binding cassette transporter, putative [Ricinus communis]
<i>FtPinG0005480600.01</i>	<i>ABC</i>	<i>FtABCG11-2</i>	0.94	7.70	5.09	9.98	gi 147856246 emb CAN81792.1 hypothetical protein VITISV_020570 [Vitis vinifera]
<i>FtPinG0005480800.01</i>	<i>ABC</i>	<i>FtABCG11-3</i>	0.21	4.45	2.71	4.12	gi 641841804 gb KDO60715.1 hypothetical protein CISIN_1g038004mg, partial [Citrus sinensis]
<i>FtPinG0003821400.01</i>	<i>ABC</i>	<i>FtABCG20</i>	146.39	66.70	52.34	83.54	gi 731345918 ref XP_010684173.1 PREDICTED: ABC transporter G family member 20 [Beta vulgaris subsp. vulgaris] >gi 870854399 gb KMT06177.1 hypothetical protein BVRB_7g162500 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0008924300.01</i>	<i>ABC</i>	<i>FtABCG22</i>	4.37	9.11	10.99	6.61	gi 224138238 ref XP_002322764.1 ABC transporter family protein [Populus trichocarpa] >gi 222867394 gb EEF04525.1 ABC transporter family protein [Populus trichocarpa]
<i>FtPinG0002261900.01</i>	<i>ABC</i>	<i>FtABCG24</i>	2.34	0.78	0.71	1.16	gi 902160551 gb KNA06455.1 hypothetical protein SOVF_180860, partial [Spinacia oleracea]
<i>FtPinG0006920200.01</i>	<i>ABC</i>	<i>FtABCG25</i>	19.72	36.34	43.57	45.81	gi 225460745 ref XP_002268373.1 PREDICTED: ABC transporter G family member 25 [Vitis vinifera]
<i>FtPinG0002261500.01</i>	<i>ABC</i>	<i>FtABCG28</i>	1.46	0.63	0.22	0.62	gi 743895528 ref XP_011041034.1 PREDICTED: ABC transporter G family member 24-like isoform X1 [Populus euphratica]
<i>FtPinG0000608300.01</i>	<i>ABC</i>	<i>FtABCG3</i>	6.52	3.21	2.90	3.32	gi 590590792 ref XP_007016835.1 ABC-2 type transporter family protein isoform 1 [Theobroma cacao] >gi 508787198 gb EOY34454.1 ABC-2 type transporter family protein isoform 1 [Theobroma cacao]
<i>FtPinG0005458900.01</i>	<i>ABC</i>	<i>FtABCG36-1</i>	5.00	1.44	1.41	1.49	gi 731385715 ref XP_010648604.1 PREDICTED: pleiotropic drug resistance protein 1-like isoform X2 [Vitis vinifera] >gi 296081973 emb CBI20978.3 unnamed protein product [Vitis vinifera]
<i>FtPinG0006978500.01</i>	<i>ABC</i>	<i>FtABCG36-2</i>	10.74	25.40	30.38	25.32	gi 902211394 gb KNA16701.1 hypothetical protein SOVF_086630 [Spinacia oleracea]
<i>FtPinG0002696700.01</i>	<i>ABC</i>	<i>FtABCG5</i>	11.09	2.32	1.81	1.58	gi 702458917 ref XP_010027638.1 PREDICTED: ABC transporter G family member 5 isoform X1 [Eucalyptus grandis] >gi 629087951 gb KCW54204.1 hypothetical protein EUGRSUZ_I00190 [Eucalyptus grandis]

<i>FtPinG0006751000.01</i>	<i>ABC</i>	<i>FtABCG53</i>	5.24	1.62	1.78	2.86	gi 719994712 ref XP_010254261.1 PREDICTED: pleiotropic drug resistance protein 1-like isoform X1 [Nelumbo nucifera]
<i>FtPinG0002489300.01</i>	<i>ABC</i>	<i>FtABCG6</i>	4.91	2.77	2.15	2.60	gi 1035916376 gb OAY45968.1 hypothetical protein MANES_07G106700 [Manihot esculenta]
<i>FtPinG0006322800.01</i>	<i>ABC</i>	<i>FtABCG8</i>	12.65	2.22	1.75	2.07	gi 764525020 ref XP_004289783.2 PREDICTED: ABC transporter G family member 4-like [Fragaria vesca subsp. vesca]
<i>FtPinG0001965300.01</i>	<i>ABC</i>	<i>FtABCI17-1</i>	20.55	75.99	91.73	59.34	gi 255562070 ref XP_002522043.1 PREDICTED: ABC transporter I family member 17 isoform X1 [Ricinus communis] >gi 223538642 gb EEF40243.1 phosphate abc transporter, putative [Ricinus communis]
<i>FtPinG0006216500.01</i>	<i>ABC</i>	<i>FtABCI17-2</i>	196.97	451.57	578.90	653.90	gi 703153608 ref XP_010110724.1 ABC transporter I family member 17 [Morus notabilis] >gi 587941313 gb EXC27889.1 ABC transporter I family member 17 [Morus notabilis]
<i>FtPinG0002020300.01</i>	<i>SULTR</i>	<i>FtSULTR3</i>	53.34	24.55	20.49	29.29	gi 731428315 ref XP_002284234.2 PREDICTED: low affinity sulfate transporter 3 [Vitis vinifera] >gi 731428317 ref XP_010664300.1 PREDICTED: low affinity sulfate transporter 3 [Vitis vinifera] >gi 731428319 ref XP_010664301.1 PREDICTED: low affinity sulfate transporter 3 [Vitis vinifera] >gi 302141918 emb CBI19121.3 unnamed protein product [Vitis vinifera]
<i>FtPinG0007572400.01</i>	<i>SULTR</i>	<i>FtSULTR31</i>	68.73	156.40	170.34	110.68	gi 1035926119 gb OAY55707.1 hypothetical protein MANES_03G174000 [Manihot esculenta]
<i>FtPinG0007884200.01</i>	<i>SULTR</i>	<i>FtSULTR35</i>	14.03	38.36	31.46	33.94	gi 902231178 gb KNA22166.1 hypothetical protein SOVF_036330 [Spinacia oleracea]
<i>FtPinG0001701300.01</i>	<i>IRT</i>	<i>FtIRT3</i>	3.54	1.11	1.12	2.13	gi 225429546 ref XP_002279424.1 PREDICTED: zinc transporter 4, chloroplastic isoform X1 [Vitis vinifera] >gi 731385016 ref XP_010648355.1 PREDICTED: zinc transporter 4, chloroplastic isoform X1 [Vitis vinifera]
<i>FtPinG0003990300.01</i>	<i>ZIP</i>	<i>FtZIP6</i>	48.04	90.86	96.50	67.94	gi 694387699 ref XP_009369589.1 PREDICTED: zinc transporter 6, chloroplastic-like [Pyrus x bretschneideri] >gi 694387702 ref XP_009369590.1 PREDICTED: zinc transporter 6, chloroplastic-like [Pyrus x bretschneideri] >gi 694422262 ref XP_009338959.1 PREDICTED: zinc transporter 6, chloroplastic-like [Pyrus x bretschneideri] >gi 694422265 ref XP_009338960.1 PREDICTED: zinc transporter 6, chloroplastic-like [Pyrus x bretschneideri]
<i>FtPinG0004012100.01</i>	<i>ZIP</i>	<i>FtZIP1-1</i>	7.42	16.76	8.18	9.79	gi 225464748 ref XP_002264621.1 PREDICTED: zinc transporter 8 [Vitis vinifera]

<i>FtPinG0009199900.01</i>	<i>ZIP</i>	<i>FtZIP1-2</i>	72.03	26.65	37.17	40.07	gi 695043618 ref XP_009409509.1 PREDICTED: zinc transporter 1 [Musa acuminata subsp. malaccensis]
<i>FtPinG0002391500.01</i>	<i>COPT</i>	<i>FtCOPT6</i>	0.85	3.28	3.03	2.60	gi 567864620 ref XP_006424959.1 hypothetical protein CICLE_v10029475mg [Citrus clementina] >gi 568870462 ref XP_006488421.1 PREDICTED: copper transporter 1-like [Citrus sinensis] >gi 557526893 gb ESR38199.1 hypothetical protein CICLE_v10029475mg [Citrus clementina]
<i>FtPinG0001509300.01</i>	<i>MRS</i>	<i>FtMRS2-1.1</i>	13.26	30.39	30.25	20.26	gi 356556780 ref XP_003546700.1 PREDICTED: magnesium transporter MRS2-1 [Glycine max] >gi 947060375 gb KRH09636.1 hypothetical protein GLYMA_15G002700 [Glycine max] >gi 947060376 gb KRH09637.1 hypothetical protein GLYMA_15G002700 [Glycine max] >gi 947060377 gb KRH09638.1 hypothetical protein GLYMA_15G002700 [Glycine max]
<i>FtPinG0006143600.01</i>	<i>MRS</i>	<i>FtMRS2-1.2</i>	23.65	12.71	9.25	14.40	gi 1012339197 gb KYP50434.1 hypothetical protein KK1_027799 [Cajanus cajan]
<i>FtPinG0006104000.01</i>	<i>LSI</i>	<i>FtLSI2</i>	8.02	18.63	18.24	13.90	gi 697098669 ref XP_009627874.1 PREDICTED: putative transporter arsB [Nicotiana tomentosiformis] >gi 697098672 ref XP_009627884.1 PREDICTED: putative transporter arsB [Nicotiana tomentosiformis] >gi 697098674 ref XP_009627892.1 PREDICTED: putative transporter arsB [Nicotiana tomentosiformis]

Table S5. The graphene oxide (GO)-responsive transcription factors (TFs) genes

CK represents the root treated with 0 mg/L GO; GO-0, GO-10 and GO-50 represent the GO with diameters of 0.5–3, 8–15 and > 50 µm, respectively

Gene ID	Family	Gene Name	CK	GO-0	GO-10	GO-50	NR Description
<i>FtPinG0002691400.01</i>	ERF	<i>FtABR1</i>	2.63	7.37	7.49	22.52	gi 566180010 ref XP_002310625.2 hypothetical protein POPTR_0007s07090g [Populus trichocarpa] >gi 550334305 gb EEE91075.2 hypothetical protein POPTR_0007s07090g [Populus trichocarpa]
<i>FtPinG0002177000.01</i>	ERF	<i>FtBBM</i>	31.66	14.75	12.66	17.24	gi 731387338 ref XP_010649213.1 PREDICTED: AP2-like ethylene-responsive transcription factor BBM [Vitis vinifera]
<i>FtPinG0007425700.01</i>	ERF	<i>FtCRF3</i>	4.73	2.31	1.37	1.69	gi 1035930040 gb OAY59626.1 hypothetical protein MANES_01G046200 [Manihot esculenta]
<i>FtPinG0003023300.01</i>	ERF	<i>FtERF061</i>	6.54	6.07	12.92	6.17	gi 731330755 ref XP_010676304.1 PREDICTED: ethylene-responsive transcription factor ERF061 [Beta vulgaris subsp. vulgaris] >gi 870860621 gb KMT11929.1 hypothetical protein BVRB_5g098930 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0002019600.01</i>	ERF	<i>FtERF110-1</i>	0.61	14.67	25.53	38.71	gi 565395634 ref XP_006363442.1 PREDICTED: ethylene-responsive transcription factor ABR1-like [Solanum tuberosum]
<i>FtPinG0007401700.01</i>	ERF	<i>FtERF110-2</i>	14.80	74.62	100.11	84.50	gi 359493145 ref XP_002264797.2 PREDICTED: ethylene-responsive transcription factor ABR1 [Vitis vinifera] >gi 147834261 emb CAN66025.1 hypothetical protein VITISV_028773 [Vitis vinifera]
<i>FtPinG0001787700.01</i>	ERF	<i>FtERF114</i>	4.06	9.62	7.24	6.60	gi 1029004741 ref XP_016666270.1 PREDICTED: ethylene-responsive transcription factor ERF113-like [Gossypium hirsutum]
<i>FtPinG0000683200.01</i>	ERF	<i>FtERF18</i>	221.27	157.54	445.84	373.63	gi 470102440 ref XP_004287662.1 PREDICTED: ethylene-responsive transcription factor ERF017 [Fragaria vesca subsp. vesca]
<i>FtPinG0000634000.01</i>	ERF	<i>FtERF1A</i>	103.03	233.63	290.40	214.59	gi 7528276 gb AAF63205.1 AF245119_1 AP2-related transcription factor [Mesembryanthemum crystallinum] >gi 32401273 gb AAP80810.1 ethylene responsive protein [Mesembryanthemum crystallinum]
<i>FtPinG0001645100.01</i>	ERF	<i>FtERF1B-1</i>	17.56	78.49	105.97	75.14	gi 720060144 ref XP_010274787.1 PREDICTED: ethylene-responsive transcription factor 1B-like [Nelumbo nucifera]
<i>FtPinG0009372500.01</i>	ERF	<i>FtERF1B-2</i>	10.64	46.79	35.67	31.78	gi 1021037453 gb KZM95236.1 hypothetical protein DCAR_018478 [Daucus carota subsp. sativus]
<i>FtPinG0000080400.01</i>	ERF	<i>FtERF25</i>	12.91	14.53	36.89	13.33	gi 643712085 gb KDP25513.1 hypothetical protein JCGZ_20669 [Jatropha curcas]

<i>FtPinG0003345600.01</i>	<i>ERF</i>	<i>FtERF4-1</i>	2.40	3.11	8.09	7.41	gi 947072493 gb KRH21384.1 hypothetical protein GLYMA_13G236500 [Glycine max]
<i>FtPinG0005339700.01</i>	<i>ERF</i>	<i>FtERF4-2</i>	40.91	78.09	87.21	86.63	gi 356517102 ref XP_003527229.1 PREDICTED: ethylene-responsive transcription factor 4-like [Glycine max] >gi 947106812 gb KRH55195.1 hypothetical protein GLYMA_06G236400 [Glycine max]
<i>FtPinG0000634300.01</i>	<i>ERF</i>	<i>FtERF5</i>	528.12	884.75	1357.69	1140.38	gi 763784738 gb KJB51809.1 hypothetical protein B456_008G232600 [Gossypium raimondii]
<i>FtPinG0004060200.01</i>	<i>ERF</i>	<i>FtERF53</i>	1.04	3.52	4.71	3.79	gi 702490571 ref XP_010035718.1 PREDICTED: ethylene-responsive transcription factor ERF054 [Eucalyptus grandis] >gi 629080711 gb KCW47156.1 hypothetical protein EUGRSUZ_K00961 [Eucalyptus grandis]
<i>FtPinG0000415700.01</i>	<i>ERF</i>	<i>FtERF98-1</i>	2.23	13.84	8.07	7.27	gi 590715937 ref XP_007050315.1 Integrase-type DNA-binding superfamily protein, putative [Theobroma cacao] >gi 508702576 gb EOX94472.1 Integrase-type DNA-binding superfamily protein, putative [Theobroma cacao]
<i>FtPinG0009372200.01</i>	<i>ERF</i>	<i>FtERF98-2</i>	3.22	13.88	10.67	11.40	gi 731336421 ref XP_010679244.1 PREDICTED: ethylene-responsive transcription factor ERF098-like [Beta vulgaris subsp. vulgaris] >gi 870858868 gb KMT10356.1 hypothetical protein BVRB_5g121050 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0009380600.01</i>	<i>ERF</i>	<i>FtPLT2</i>	29.00	8.07	7.08	10.46	gi 566147378 ref XP_002299238.2 ovule development family protein [Populus trichocarpa] >gi 550346582 gb EEE84043.2 ovule development family protein [Populus trichocarpa]
<i>FtPinG0003194700.01</i>	<i>ERF</i>	<i>FtRAP2-1</i>	47.44	67.89	95.02	62.61	gi 763752000 gb KJB19388.1 hypothetical protein B456_003G0997002, partial [Gossypium raimondii]
<i>FtPinG0001757700.01</i>	<i>ERF</i>	<i>FtRAP2-4</i>	69.86	192.08	289.32	184.08	gi 802537176 ref XP_012093083.1 PREDICTED: ethylene-responsive transcription factor RAP2-4-like [Jatropha curcas] >gi 643741386 gb KDP46862.1 hypothetical protein JCGZ_24071 [Jatropha curcas]
<i>FtPinG0001439000.01</i>	<i>ERF</i>	<i>FtRAP2-7</i>	67.25	93.16	123.68	127.35	gi 902139754 gb KNA04594.1 hypothetical protein SOVF_198230 isoform A [Spinacia oleracea]
<i>FtPinG0008861700.01</i>	<i>ERF</i>	<i>FtWIN1</i>	2.75	5.84	7.02	5.40	gi 1002352518 gb AMN10043.1 ethylene-responsive transcription factor WIN1 [Hordeum vulgare]
<i>FtPinG0002688700.01</i>	<i>WRKY</i>	<i>FtWRKY13</i>	5.66	9.03	12.57	10.10	gi 568819976 ref XP_006464513.1 PREDICTED: probable WRKY transcription factor 13 isoform X1 [Citrus sinensis]
<i>FtPinG0007226700.01</i>	<i>WRKY</i>	<i>FtWRKY18</i>	1.74	22.47	82.45	30.62	gi 1029050421 ref XP_016688892.1 PREDICTED: probable WRKY transcription factor 40 [Gossypium hirsutum]

<i>FtPinG0000403800.01</i>	<i>WRKY</i>	<i>FtWRKY23</i>	54.03	96.76	90.04	106.82	gi 1012336287 gb KYP47592.1 putative WRKY transcription factor 23 [Cajanus cajan]
<i>FtPinG0001577500.01</i>	<i>WRKY</i>	<i>FtWRKY24</i>	204.95	390.46	416.85	418.33	gi 702280972 ref XP_010045395.1 PREDICTED: probable WRKY transcription factor 26 [Eucalyptus grandis] >gi 702280977 ref XP_010045396.1 PREDICTED: probable WRKY transcription factor 26 [Eucalyptus grandis] >gi 629123073 gb KCW87563.1 hypothetical protein EUGRSUZ_B04010 [Eucalyptus grandis]
<i>FtPinG0002374400.01</i>	<i>WRKY</i>	<i>FtWRKY29</i>	4.32	9.68	16.14	23.47	gi 902239180 gb KNA25486.1 hypothetical protein SOVF_006240 [Spinacia oleracea]
<i>FtPinG0009186100.01</i>	<i>WRKY</i>	<i>FtWRKY33</i>	244.46	411.91	491.41	461.34	gi 197312905 gb ACH63233.1 WRKY protein [Rheum australe]
<i>FtPinG0000354800.01</i>	<i>WRKY</i>	<i>FtWRKY41</i>	60.83	17.05	26.07	30.24	gi 225454483 ref XP_002281031.1 PREDICTED: probable WRKY transcription factor 46 [Vitis vinifera]
<i>FtPinG0002524500.01</i>	<i>WRKY</i>	<i>FtWRKY53</i>	60.24	123.69	131.57	85.63	gi 409923413 gb AEO31476.2 WRKY transcription factor 6-1 [Dimocarpus longan]
<i>FtPinG0005364100.01</i>	<i>WRKY</i>	<i>FtWRKY6</i>	51.05	99.96	93.61	104.56	gi 225444291 ref XP_002263115.1 PREDICTED: probable WRKY transcription factor 31 [Vitis vinifera]
<i>FtPinG0004237400.01</i>	<i>WRKY</i>	<i>FtWRKY60</i>	0.17	5.68	11.49	8.12	gi 731384780 ref XP_010648274.1 PREDICTED: uncharacterized protein LOC100264507 isoform X1 [Vitis vinifera]
<i>FtPinG0003193100.01</i>	<i>WRKY</i>	<i>FtWRKY7</i>	50.72	94.03	94.36	101.32	gi 1035904133 gb OAY33732.1 hypothetical protein MANES_13G119700 [Manihot esculenta]
<i>FtPinG0004829100.01</i>	<i>WRKY</i>	<i>FtWRKY70</i>	54.89	72.87	140.59	110.22	gi 1023043332 gb ANA95961.1 WRKY transcription factor [Citrus maxima]
<i>FtPinG0000497200.01</i>	<i>WRKY</i>	<i>FtWRKY75-1</i>	36.16	151.92	129.06	134.47	gi 719983109 ref XP_010250654.1 PREDICTED: probable WRKY transcription factor 75 [Nelumbo nucifera]
<i>FtPinG0005486000.01</i>	<i>WRKY</i>	<i>FtWRKY75-2</i>	1.84	20.39	6.61	7.11	gi 731367023 ref XP_010695387.1 PREDICTED: probable WRKY transcription factor 75 [Beta vulgaris subsp. vulgaris] >gi 870844853 gb KMS97724.1 hypothetical protein BVRB_5g124680 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0003184500.01</i>	<i>bZIP</i>	<i>FtbZIP1</i>	0.72	6.23	9.70	7.15	gi 747056640 ref XP_011074583.1 PREDICTED: basic leucine zipper 43-like [Sesamum indicum]
<i>FtPinG0008657100.01</i>	<i>bZIP</i>	<i>FtbZIP18</i>	692.45	456.00	340.58	499.46	gi 657955792 ref XP_008369370.1 PREDICTED: transcription factor RF2b [Malus domestica]
<i>FtPinG0005336400.01</i>	<i>bZIP</i>	<i>FtbZIP34-1</i>	35.21	9.30	7.33	15.27	gi 359493805 ref XP_002285311.2 PREDICTED: basic leucine zipper 34-like [Vitis vinifera]
<i>FtPinG0009278900.01</i>	<i>bZIP</i>	<i>FtbZIP34-2</i>	59.00	16.42	19.34	29.77	gi 359493805 ref XP_002285311.2 PREDICTED: basic leucine zipper 34-like [Vitis vinifera]

<i>FtPinG0002136200.01</i>	<i>bZIP</i>	<i>FtbZIP53-1</i>	27.40	131.73	126.89	110.87	gi 763796639 gb KJB63594.1 hypothetical protein B456_010G008000 [Gossypium raimondii]
<i>FtPinG0009423600.01</i>	<i>bZIP</i>	<i>FtbZIP53-2</i>	27.61	103.65	98.94	91.29	gi 763765288 gb KJB32542.1 hypothetical protein B456_005G245700 [Gossypium raimondii]
<i>FtPinG0000966800.01</i>	<i>bZIP</i>	<i>FtbZIP6</i>	40.69	11.01	11.75	20.14	gi 695037514 ref XP_009406251.1 PREDICTED: transcription factor RF2a-like isoform X1 [Musa acuminata subsp. malaccensis]
<i>FtPinG0001861000.01</i>	<i>bZIP</i>	<i>FtRF2b</i>	27.49	12.44	12.94	16.40	gi 902153604 gb KNA05724.1 hypothetical protein SOVF_187760 isoform A [Spinacia oleracea]
<i>FtPinG0007266400.01</i>	<i>bZIP</i>	<i>FtTGA10</i>	4.09	8.49	6.77	8.09	gi 1000940818 ref XP_002532393.2 PREDICTED: transcription factor HBP-1b(c38) [Ricinus communis]
<i>FtPinG0008123200.01</i>	<i>bZIP</i>	<i>FtTGA21</i>	18.14	9.46	7.31	9.23	gi 359482245 ref XP_003632741.1 PREDICTED: transcription factor HBP-1b(c38) [Vitis vinifera] >gi 297739945 emb CBI30127.3 unnamed protein product [Vitis vinifera]
<i>FtPinG0002093800.01</i>	<i>bZIP</i>	<i>FtTGA3</i>	6.91	14.41	14.61	10.96	gi 225459415 ref XP_002285820.1 PREDICTED: transcription factor TGA4 [Vitis vinifera] >gi 731428244 ref XP_010664271.1 PREDICTED: transcription factor TGA4 [Vitis vinifera] >gi 731428247 ref XP_010664272.1 PREDICTED: transcription factor TGA4 [Vitis vinifera] >gi 731428249 ref XP_010664273.1 PREDICTED: transcription factor TGA4 [Vitis vinifera] >gi 731428251 ref XP_010664274.1 PREDICTED: transcription factor TGA4 [Vitis vinifera] >gi 302141896 emb CBI19099.3 unnamed protein product [Vitis vinifera]
<i>FtPinG0007275100.01</i>	<i>GATA</i>	<i>FtGATA12-1</i>	114.88	17.78	19.31	40.42	gi 719979656 ref XP_010249552.1 PREDICTED: GATA transcription factor 12 [Nelumbo nucifera]
<i>FtPinG0007668800.01</i>	<i>GATA</i>	<i>FtGATA12-2</i>	10.07	4.40	4.43	4.36	gi 1035897187 gb OAY26789.1 hypothetical protein MANES_16G074900 [Manihot esculenta]
<i>FtPinG0002716100.01</i>	<i>GATA</i>	<i>FtGATA19</i>	13.30	7.66	6.22	12.43	gi 720024481 ref XP_010263645.1 PREDICTED: GATA transcription factor 19 [Nelumbo nucifera] >gi 720024484 ref XP_010263646.1 PREDICTED: GATA transcription factor 19 [Nelumbo nucifera] >gi 720024487 ref XP_010263647.1 PREDICTED: GATA transcription factor 19 [Nelumbo nucifera]
<i>FtPinG0001937100.01</i>	<i>GATA</i>	<i>FtGATA20</i>	7.47	1.17	0.24	2.70	gi 743919421 ref XP_011003734.1 PREDICTED: GATA transcription factor 18 [Populus euphratica]

<i>FtPinG0005993400.01</i>	<i>GATA</i>	<i>FtGATA26</i>	1.10	0.63	0.34	0.71	gi 567895390 ref XP_006440183.1 hypothetical protein CICLE_v10019614mg [Citrus clementina] >gi 567895392 ref XP_006440184.1 hypothetical protein CICLE_v10019614mg [Citrus clementina] >gi 557542445 gb ESR53423.1 hypothetical protein CICLE_v10019614mg [Citrus clementina] >gi 557542446 gb ESR53424.1 hypothetical protein CICLE_v10019614mg [Citrus clementina]
<i>FtPinG0002724100.01</i>	<i>GATA</i>	<i>FtGATA5-1</i>	9.71	5.43	6.24	3.67	gi 731337522 ref XP_010679831.1 PREDICTED: GATA transcription factor 7 [Beta vulgaris subsp. vulgaris] >gi 870857984 gb KMT09510.1 hypothetical protein BVRB_6g129760 isoform B [Beta vulgaris subsp. vulgaris]
<i>FtPinG0005561100.01</i>	<i>GATA</i>	<i>FtGATA5-2</i>	18.19	50.15	48.16	31.81	gi 731358477 ref XP_010690771.1 PREDICTED: GATA transcription factor 7-like [Beta vulgaris subsp. vulgaris] >gi 870848056 gb KMT00345.1 hypothetical protein BVRB_9g216560 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0007959700.01</i>	<i>GATA</i>	<i>FtGATA5-3</i>	27.37	59.07	63.96	60.52	gi 731358477 ref XP_010690771.1 PREDICTED: GATA transcription factor 7-like [Beta vulgaris subsp. vulgaris] >gi 870848056 gb KMT00345.1 hypothetical protein BVRB_9g216560 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0009088500.01</i>	<i>HD-ZIP</i>	<i>FtATHB-16</i>	152.27	270.19	369.08	324.38	gi 747098991 ref XP_011097532.1 PREDICTED: homeobox-leucine zipper protein ATHB-6 [Sesamum indicum]
<i>FtPinG0001531600.01</i>	<i>HD-ZIP</i>	<i>FtATHB-20</i>	8.61	2.48	5.84	5.69	gi 731376357 ref XP_010667539.1 PREDICTED: homeobox-leucine zipper protein HAT7-like [Beta vulgaris subsp. vulgaris]
<i>FtPinG0000179600.01</i>	<i>HD-ZIP</i>	<i>FtATHB-6</i>	71.11	149.86	183.21	145.14	gi 697113469 ref XP_009610614.1 PREDICTED: homeobox-leucine zipper protein HAT5-like [Nicotiana tomentosiformis] >gi 1025023674 ref XP_016442143.1 PREDICTED: homeobox-leucine zipper protein HAT5-like [Nicotiana tabacum]
<i>FtPinG0003181200.01</i>	<i>HD-ZIP</i>	<i>FtHAT22</i>	1.57	6.34	7.16	4.92	gi 224067146 ref XP_002302378.1 hypothetical protein POPTR_0002s11410g [Populus trichocarpa] >gi 222844104 gb EEE81651.1 hypothetical protein POPTR_0002s11410g [Populus trichocarpa]
<i>FtPinG0000638300.01</i>	<i>HD-ZIP</i>	<i>FtHAT4</i>	68.55	142.35	204.37	148.42	gi 1009157211 ref XP_015896650.1 PREDICTED: homeobox-leucine zipper protein HAT4-like [Ziziphus jujuba]
<i>FtPinG0000332400.01</i>	<i>HD-ZIP</i>	<i>FtHOX22-1</i>	166.58	389.83	527.59	396.71	gi 743790427 ref XP_011038888.1 PREDICTED: homeobox-leucine zipper protein ATHB-7 [Populus euphratica]
<i>FtPinG0007473900.01</i>	<i>HD-ZIP</i>	<i>FtHOX22-2</i>	40.21	17.99	21.43	27.44	gi 902228268 gb KNA21035.1 hypothetical protein SOVF_046880 [Spinacia oleracea]
<i>FtPinG0004666000.01</i>	<i>HD-ZIP</i>	<i>FtHOX16</i>	23.71	44.11	53.46	47.81	gi 590667344 ref XP_007037211.1 Homeobox protein, putative isoform 1 [Theobroma cacao] >gi 508774456 gb EOY21712.1 Homeobox protein, putative isoform 1 [Theobroma cacao]

<i>FtPinG0001727900.01</i>	<i>HSF</i>	<i>FtHSFA2C-1</i>	42.71	8.75	5.71	15.24	gi 698475490 ref XP_009785117.1 PREDICTED: heat stress transcription factor A-7a isoform X3 [Nicotiana glauca] >gi 1025181240 ref XP_016472864.1 PREDICTED: heat stress transcription factor A-7a-like isoform X3 [Nicotiana glauca]
<i>FtPinG0001924400.01</i>	<i>HSF</i>	<i>FtHSFA2C-2</i>	83.26	55.81	30.14	33.46	gi 731336196 ref XP_010679125.1 PREDICTED: heat stress transcription factor A-2c-like [Beta vulgaris subsp. vulgaris] >gi 870858751 gb KMT10239.1 hypothetical protein BVRB_5g119970 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0003045600.01</i>	<i>HSF</i>	<i>FtHSFA2C-3</i>	1.30	3.44	8.24	4.06	gi 731369361 ref XP_010696526.1 PREDICTED: heat stress transcription factor A-7a-like [Beta vulgaris subsp. vulgaris] >gi 731369365 ref XP_010696527.1 PREDICTED: heat stress transcription factor A-7a-like [Beta vulgaris subsp. vulgaris] >gi 111184724 gb ABH08433.1 putative heat shock factor [Beta vulgaris] >gi 121501694 gb ABM55235.1 heat stress transcription factor HSF [Beta vulgaris] >gi 870843707 gb KMS96841.1 hypothetical protein BVRB_8g1199170 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0003351900.01</i>	<i>HSF</i>	<i>FtHSFA4A</i>	2.27	7.75	9.67	5.40	gi 902086116 gb KNA03209.1 hypothetical protein SOVF_211390 [Spinacia oleracea]
<i>FtPinG0005895400.01</i>	<i>HSF</i>	<i>FtHSFB3</i>	138.75	646.80	552.62	458.50	gi 702247598 ref XP_010056944.1 PREDICTED: heat stress transcription factor B-3 [Eucalyptus grandis] >gi 702247604 ref XP_010056951.1 PREDICTED: heat stress transcription factor B-3 [Eucalyptus grandis] >gi 629125721 gb KCW90146.1 hypothetical protein EUGRSUZ_A02338 [Eucalyptus grandis]
<i>FtPinG0004354800.01</i>	<i>HSF</i>	<i>FtHSFB4-1</i>	17.09	5.89	4.12	8.23	gi 870863456 gb KMT14620.1 hypothetical protein BVRB_4g073880 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0007112900.01</i>	<i>HSF</i>	<i>FtHSFB4-2</i>	22.16	8.01	5.75	10.21	gi 720093848 ref XP_010246178.1 PREDICTED: heat stress transcription factor B-4b-like [Nelumbo nucifera]
<i>FtPinG0007888700.01</i>	<i>HSF</i>	<i>FtHSFC1</i>	14.03	27.41	25.18	17.50	gi 1009160399 ref XP_015898330.1 PREDICTED: heat stress transcription factor C-1 [Ziziphus jujuba]
<i>FtPinG0006260600.01</i>	<i>MADS</i>	<i>FtAGL19</i>	18.13	8.61	9.36	10.24	gi 902234911 gb KNA23649.1 hypothetical protein SOVF_023090 isoform B [Spinacia oleracea]
<i>FtPinG0001341800.01</i>	<i>MADS</i>	<i>FtAGL8-1</i>	1.82	0.52	0.75	0.43	gi 702466257 ref XP_010029407.1 PREDICTED: truncated transcription factor CAULIFLOWER A isoform X1 [Eucalyptus grandis] >gi 629090065 gb KCW56318.1 hypothetical protein EUGRSUZ_I02059 [Eucalyptus grandis]
<i>FtPinG0004498000.01</i>	<i>MADS</i>	<i>FtAGL8-2</i>	2.44	1.07	0.88	0.59	gi 1483232 emb CAA67969.1 MADS5 protein [Betula pendula]

<i>FtPinG0005485500.01</i>	<i>MADS</i>	<i>FtMADS14</i>	0.00	1.49	2.77	0.35	gi 731426856 ref XP_010663758.1 PREDICTED: MADS-box transcription factor 15-like isoform X5 [Vitis vinifera]
<i>FtPinG0003196200.01</i>	<i>ABF</i>	<i>FtABF2</i>	3.48	4.51	4.68	6.74	gi 645262055 ref XP_008236589.1 PREDICTED: ABSCISIC ACID-INSENSITIVE 5-like protein 7 [Prunus mume]
<i>FtPinG0001309200.01</i>	<i>ARR</i>	<i>FtARR26</i>	4.24	1.63	1.30	1.63	gi 225425924 ref XP_002267616.1 PREDICTED: two-component response regulator ARR11 [Vitis vinifera] >gi 297738324 emb CBI27525.3 unnamed protein product [Vitis vinifera]
<i>FtPinG0006548500.01</i>	<i>DEFA</i>	<i>FtDEFA</i>	0.39	3.38	2.84	2.75	gi 398330378 gb AFO83618.1 APETALA3-like protein [Fagopyrum tataricum]
<i>FtPinG0009745000.01</i>	<i>DREB</i>	<i>FtDREB3</i>	6.82	1.96	3.60	9.30	gi 672190168 ref XP_008775170.1 PREDICTED: ethylene-responsive transcription factor TINY-like [Phoenix dactylifera]
<i>FtPinG0002473600.01</i>	<i>E2F</i>	<i>FtE2FE</i>	7.24	2.58	2.48	4.15	gi 731335346 ref XP_010678680.1 PREDICTED: E2F transcription factor-like E2FE isoform X1 [Beta vulgaris subsp. vulgaris] >gi 870859033 gb KMT10497.1 hypothetical protein BVRB_5g116210 [Beta vulgaris subsp. vulgaris]
<i>FtPinG0008174900.01</i>	<i>EIN3</i>	<i>FtEIL1</i>	70.83	174.93	197.56	197.21	gi 703136344 ref XP_010106128.1 Protein ETHYLENE INSENSITIVE 3 [Morus notabilis] >gi 587920347 gb EXC07788.1 Protein ETHYLENE INSENSITIVE 3 [Morus notabilis]
<i>FtPinG0006538300.01</i>	<i>NF-Y</i>	<i>FtNF-YA9</i>	5.71	14.02	18.34	11.00	gi 225450115 ref XP_002278849.1 PREDICTED: nuclear transcription factor Y subunit A-1-like [Vitis vinifera] >gi 731414953 ref XP_010659347.1 PREDICTED: nuclear transcription factor Y subunit A-1-like [Vitis vinifera]
<i>FtPinG0001216900.01</i>	<i>PTI</i>	<i>FtPTI5</i>	19.69	134.00	105.22	123.09	gi 1009106376 ref XP_015874196.1 PREDICTED: pathogenesis-related genes transcriptional activator PTI5-like [Ziziphus jujuba] >gi 1009106378 ref XP_015874202.1 PREDICTED: pathogenesis-related genes transcriptional activator PTI5-like [Ziziphus jujuba]

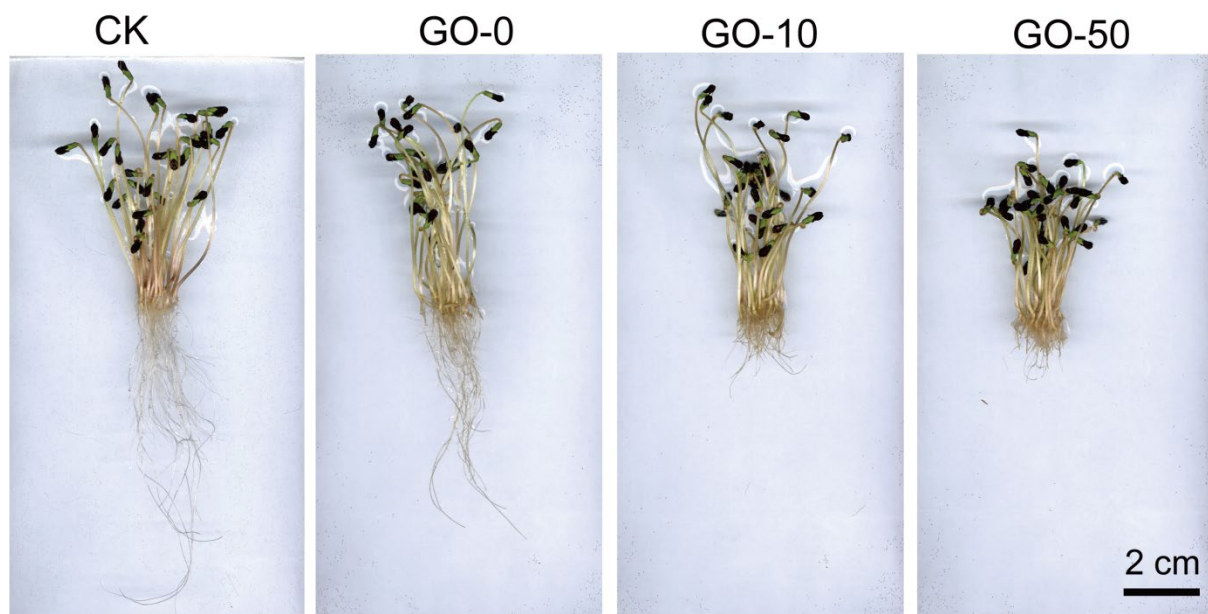


Figure S1. Architectural changes of seedlings as affected by graphene oxide (GO) stress

CK represents the root treated with 0 mg/L GO; GO-0, GO-10 and GO-50 represent the GO with diameters of 0.5–3, 8–15 and > 50 μm , respectively

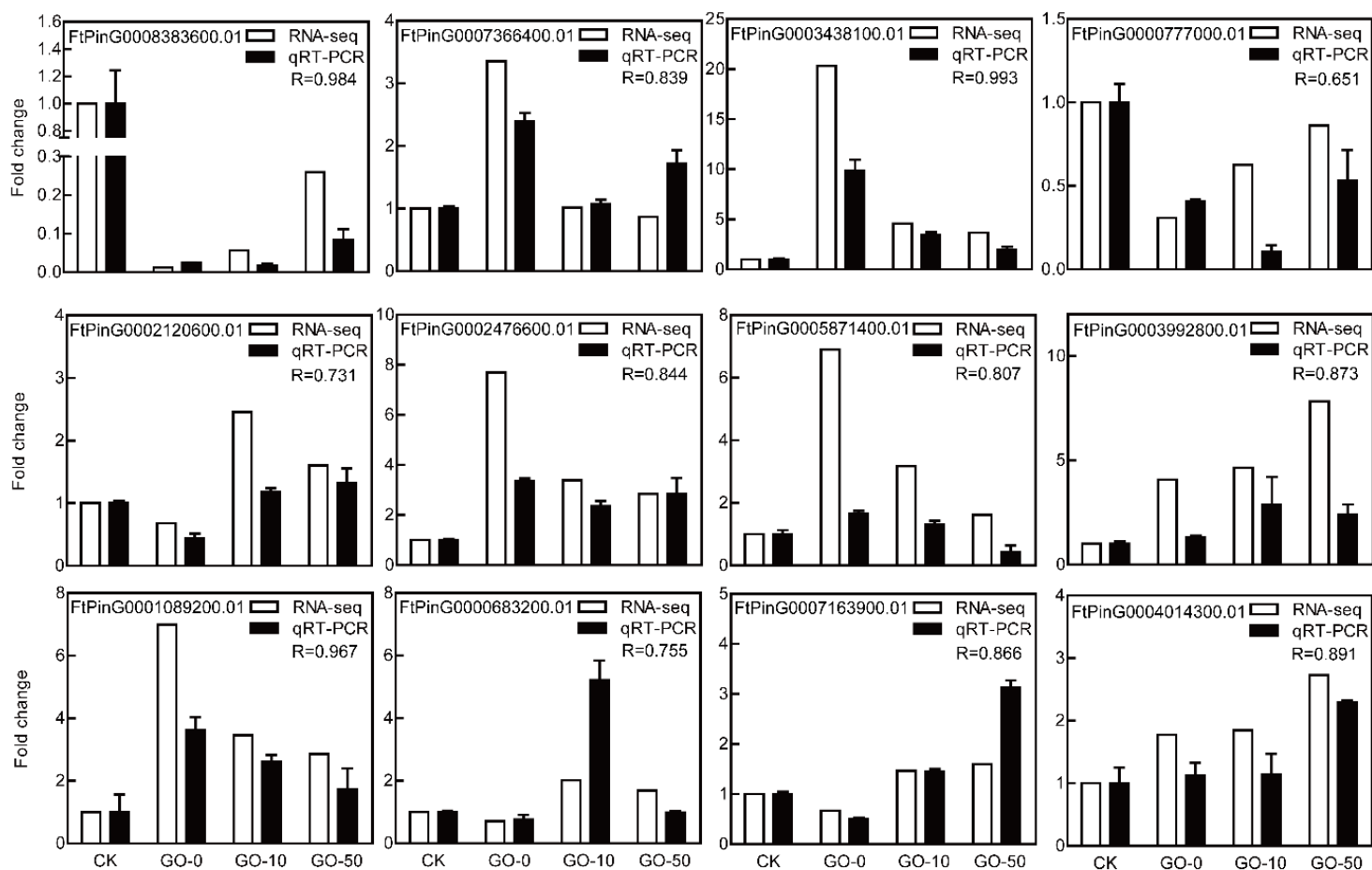


Figure S2. Validation of expression profile through quantitative real-time PCR (qRT-PCR) analysis

A total of 12 graphene oxide (GO)-responsive genes were validated using qRT-PCR against their expression profile from RNA-seq; The relative expression levels of genes were quantitated using $2^{-\Delta\Delta C_t}$; qRT-PCR data are means $\pm$ SDs, and the means were compared by Duncan's test; CK represents the root treated with 0 mg/L GO; GO-0, GO-10 and GO-50 represent the GO with diameters of 0.5–3, 8–15 and > 50 μ m, respectively; R – the correlations between RNA-seq and qRT-PCR data