

Table S1†. Experimental design under various treatments.

Time	Treatment	Four different modified graphene level (three replications)			
40d	Water (W, water)	W_CK	W_L (0.5%)	W_M (1%)	W_H (2%)
46d	Control (C, water)	C_CK	C_L (0.5%)	C_M (1%)	C_H (2%)
	Salt (S, 120 mmol/L)	S_CK	S_L (0.5%)	S_M (1%)	S_H (2%)
	Alkali (A, 120 mmol/L)	A_CK	A_L (0.5%)	A_M (1%)	A_H (2%)

Table S2†. Salt composition and its molar ratio within treatments

Treatments	Composition and ratios of salts			
	NaCl	Na <sub>2</sub> SO <sub>4</sub>	NaHCO <sub>3</sub>	Na <sub>2</sub> CO <sub>3</sub>
A	2	1	0	0
B	1	1	1	0
C	12	9	8	1
D	8	9	12	1
E	12	1	8	9
F	0	0	2	1

Table S3<sup>†</sup>. Main stress factors for different treatments

Treatments	pH	Salinity (mmol L <sup>-1</sup> )	Na <sup>+</sup> (mmol L <sup>-1</sup> )	Cl <sup>-</sup> (mmol L <sup>-1</sup> )	SO <sub>4</sub> <sup>2-</sup> (mmol L <sup>-1</sup> )	HCO <sub>3</sub> <sup>-</sup> (mmol L <sup>-1</sup> )	CO <sub>3</sub> <sup>2-</sup> (mmol L <sup>-1</sup> )
A1	7.03	24.0	32.0	16.0	8.0	0.0	0.0
A2	7.12	48.0	64.0	32.0	16.0	0.0	0.0
A3	7.18	72.0	96.0	48.0	24.0	0.0	0.0
A4	7.22	96.0	128.0	64.0	32.0	0.0	0.0
A5	7.26	120.0	160.0	80.0	40.0	0.0	0.0
B1	7.34	24.0	32.0	8.0	8.0	8.0	0.0
B2	7.45	48.0	64.0	16.0	16.0	16.0	0.0
B3	8.04	72.0	96.0	24.0	24.0	24.0	0.0
B4	8.22	96.0	128.0	32.0	32.0	32.0	0.0
B5	8.3	120.0	160.0	40.0	40.0	40.0	0.0
C1	8.8	24.0	32.0	9.6	7.2	6.4	0.8
C2	8.92	48.0	64.0	19.2	14.4	12.8	1.6
C3	8.95	72.0	96.0	28.8	21.6	19.2	2.4
C4	8.99	96.0	128.0	38.4	28.8	25.6	3.2
C5	9.02	120.0	160.0	48.0	36.0	32.0	4.0
D1	9.03	24.0	32.0	6.4	7.2	9.6	0.8
D2	9.05	48.0	64.0	12.8	14.4	19.2	1.6
D3	9.1	72.0	96.0	19.2	21.6	28.8	2.4
D4	9.15	96.0	128.0	25.6	28.8	38.4	3.2
D5	9.22	120.0	160.0	32.0	36.0	48.0	4.0
E1	9.45	24.0	32.0	9.6	0.8	6.4	7.2
E2	9.56	48.0	64.0	19.2	1.6	12.8	14.4
E3	9.64	72.0	96.0	28.8	2.4	19.2	21.6
E4	9.69	96.0	128.0	38.4	3.2	25.6	28.8
E5	9.79	120.0	160.0	48.0	4.0	32.0	36.0
F1	9.84	24	32	0.0	0.0	16.0	8.0
F2	9.91	48	64	0.0	0.0	32.0	16.0
F3	9.96	72	96	0.0	0.0	48.0	24.0
F4	10.11	96	128	0.0	0.0	64.0	32.0
F5	10.32	120	160	0.0	0.0	80.0	40.0

Table S4†. List of primers used in this paper.

Gene IDs	Forward primer (5'-3')	Reverse primer (5'-3')
F01_transcript_333	GCCATTCTAACACTTCTCG	ATACTGTGCCCAATACCG
F01_transcript_17953	AAGGCAAACGCAAGCAAA	GCAGTGGCAACAACAGCA
F01_transcript_15420	AAAGAACATCACCGACTA	TTGTAATACTGTTTCCCAC
F01_transcript_16115	GGAAGTGGACCTTTGGAG	ATTGATTTGAGGGAGATG
F01_transcript_15580	CCAGGAGGACAAGCAACC	GCACCACCAGGGTATTTTC
F01_transcript_19553	GCTCCATCTTTGACCTTA	AACACCAGAAATTCCTCC
F01_transcript_18132	AAAGGGATTGGCTAAGGA	GCAGGAGGAGTAGGGAAG
F01_transcript_1971	TTGAAGAGGGTACTGTAGG	ACCCTCACTTACTGGTATCT
F01_transcript_8045	TCCGCTGTGGGTATCAA	ATCGGTCAAATCGTCTGC
F01_transcript_16432	GCAGCACAAACCAGGAA	GGTGTTAGGCCGGAGAT
F01_transcript_18286	AAAATGGCAACAACAACC	AACCCAAATCCAATCACA
F01_transcript_16196	CTCTAAGGAACACCGAATA	GAACCTGGACCAACCATC
F01_transcript_21099	ACATATCAGTTTTGACAAGG	GTTCTTAATTTAGGCAACAC
F01_transcript_12300	AGGCTTGACTTTGCTGTG	TTCCCTTCTCCATTCTTTC
F01_transcript_17186	TGATTGGATTTGGGTGA	GCAGGAGGAGTAGGGAAG
F01_transcript_13755	CTTCAGGCTTGACTTTGC	CATTATGTCATCAATTCCCT
F01_transcript_17401	ACCGCACCTGCTTTGTAT	GATCACCACGCTTTCCTG
F01_transcript_21686	ATACAATGACCAAGGAAG	AAGAAGTCTAAGACCACC
<i>β-actin</i>	TTTGAGACTTTCAATGTGCCCGC	TAGCATGTGGGAGTGCATAACCC
	C	T

Table S5†. Sequencing statistics of RNA-Seq data analysis. Q20, The percentage of bases with a Phred value > 20; Q30, The percentage of bases with a Phred value > 30.

Sample_ID	Treatment	ReadSum	BaseSum	GC(%)	Q20(%)	Q30(%)
T01	W_CK	22385039	6696959632	44.08	98.17	94.61
T02	W_CK	22942724	6860430558	43.24	98.79	96.13
T03	W_CK	23038754	6886517616	43.53	98.6	95.59
T04	W_L	27064363	8088756762	43.17	98.71	95.86
T05	W_L	22786481	6820753320	42.92	98.44	95.16
T06	W_L	22625941	6769610896	43.13	98.71	95.82
T07	A_L	23761695	7099101886	42.95	98.4	95.09
T08	A_L	23288096	6960002134	42.9	98.27	94.78
T09	A_L	20900351	6249320334	42.93	98.5	95.34
T10	A_CK	25151561	7518281274	42.84	97.99	94.05
T11	A_CK	27488499	8226678910	42.88	98.15	94.49
T12	A_CK	24665884	7370545000	43.03	98.08	94.27
T13	C_CK	22911205	6844949054	43.14	98.5	95.3
T14	C_CK	20690858	6179328042	43.18	98.33	94.89
T15	C_CK	21450830	6405870458	42.98	98.46	95.18
T16	C_L	24279308	7262579690	42.8	98.52	95.25
T17	C_L	25581643	7646291924	42.74	98.69	95.78
T18	C_L	22980543	6874432510	42.69	98.53	95.34
T19	S_CK	26306065	7852760210	43.33	98.69	95.77
T20	S_CK	23842439	7116224672	44.1	98.71	95.78
T21	S_CK	23718867	7083391414	43.57	98.66	95.64
T22	S_L	20923767	6256936400	43.14	98.25	94.74
T23	S_L	21455846	6419300682	43.13	98.29	94.81
T24	S_L	22176884	6631682012	43.14	98.33	94.97

Table S6†. Statistical results of the SMRT sequencing data

Samples	F01
cDNA size	1-6K
CCS Number	265,811
Read Bases of CCS	520,402,849
Mean Read Length of CCS	1,957
Mean Number of Passes	51
Number of undesired primer reads	30,754
Number of filtered short reads	66
Number of full-length non-chimeric reads	219,162
Full-length non-chimeric percentage (FLNC%)	82.45%
Number of consensus isoforms	22,608
Average consensus isoforms read length	1,786
Number of polished high-quality isoforms	22,499
Number of polished low-quality isoforms	98
Percent of polished high-quality isoforms(%)	99.52%

Table S7†. Annotation of the transcript datasets to public databases

Annotated databases	Annotated number	Percentage (%)
COG	5,943	45.86
GO	10,726	82.76
KEGG	5,748	44.35
KOG	7,511	57.96
Pfam	10,572	81.57
Swiss-Prot	9,536	73.58
eggNOG	11,716	90.40
NR	12,364	95.40
All annotated	12,389	95.59
All analysed	12,960	100.00