Note:

Fig. S1†. TEM image of graphene at CK (A), 5 (B) and 20 (C) g kg^{-1} treatments of alfalfa leaves.

Fig. S2†. Effects of graphene on fresh weight (A), dry weight (B), electrolyte leakage (C), MDA (D), H$_2$O$_2$ (E), O$_2$$^{.-}$ (F), CAT (G), POD (H), SOD (I), Chl a (J) and Chl b (K) of alfalfa leaves. Every data was presented by the mean of three replications. The means followed with same letter are not significantly different according to L.S.D. test at p < 0.05. Bars indicate S.D. of means.

Fig. S3†. Effects of graphene on fresh weight (A), dry weight (B), Chl a (C), Chl b (D), electrolyte leakage (E), MDA (F), H$_2$O$_2$ (G), O$_2$$^{.-}$ (H), CAT (I), POD (G) and SOD (K) of alfalfa leaves under salt and alkali stresses, respectively. And biomass changes (L) of alfalfa in response to low-graphene treatment under salt stress. Every data was presented by the mean of three replications. The means followed with same letter are not significantly different according to L.S.D. test at p < 0.05. Bars indicate S.D. of means.

Fig. S4†. A, Boxplot showing the distribution of the FPKM values of each sample. The X-axis in the boxplot shows the ID of each sample. The Y-axis represents the log 10 (FPKM). B, Heat map of the Pearson correlation coefficient of each sample. C, number and length distribution of consensus isoforms in 1-6K. D, number and length distribution of FLNC sequences from 1-6K. E, number and length distribution of consensus isoforms in 1-6K.

Fig. S5†. Prediction of top 20 transcription factors families of all data (A), C1_vs_C2 (B), S1_vs_S2_vs_S4 (C) and A1_vs_A2_vs_A4 (D), respectively.

Fig. S6†. The volcano spots of DEGs variance analysis between control and modified graphene treatment of C1 (A) and C2 (B). The volcano spots of DEGs variance analysis of salt stress-responsive genes under graphene enviroment of S1 (C), S2 (D) and S4 (E). Red spots represent upregulated DEGs and green spots indicate downregulated DEGs. Those shown in black are transcripts that did not show differential expression. The screening condition for the differentially expressed genes was padj <0.05.

Fig. S7†. RT-PCR analysis of the expression of 17 photosynthetic-related candidate transcripts in alfalfa leaves at graphene, graphene-salt and graphene-alkali treatment.

Table S1†. Experimental design under various treatments.

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

Table S3†. Main stress factors for different treatments.

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

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.

Table S6†. Statistical results of the SMRT sequencing data.

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

Table S8†. The DEGs of photosynthesis pathway in response to graphene treatment.

Table S9†. The DEGs of antioxidant activities in response to graphene treatment.