

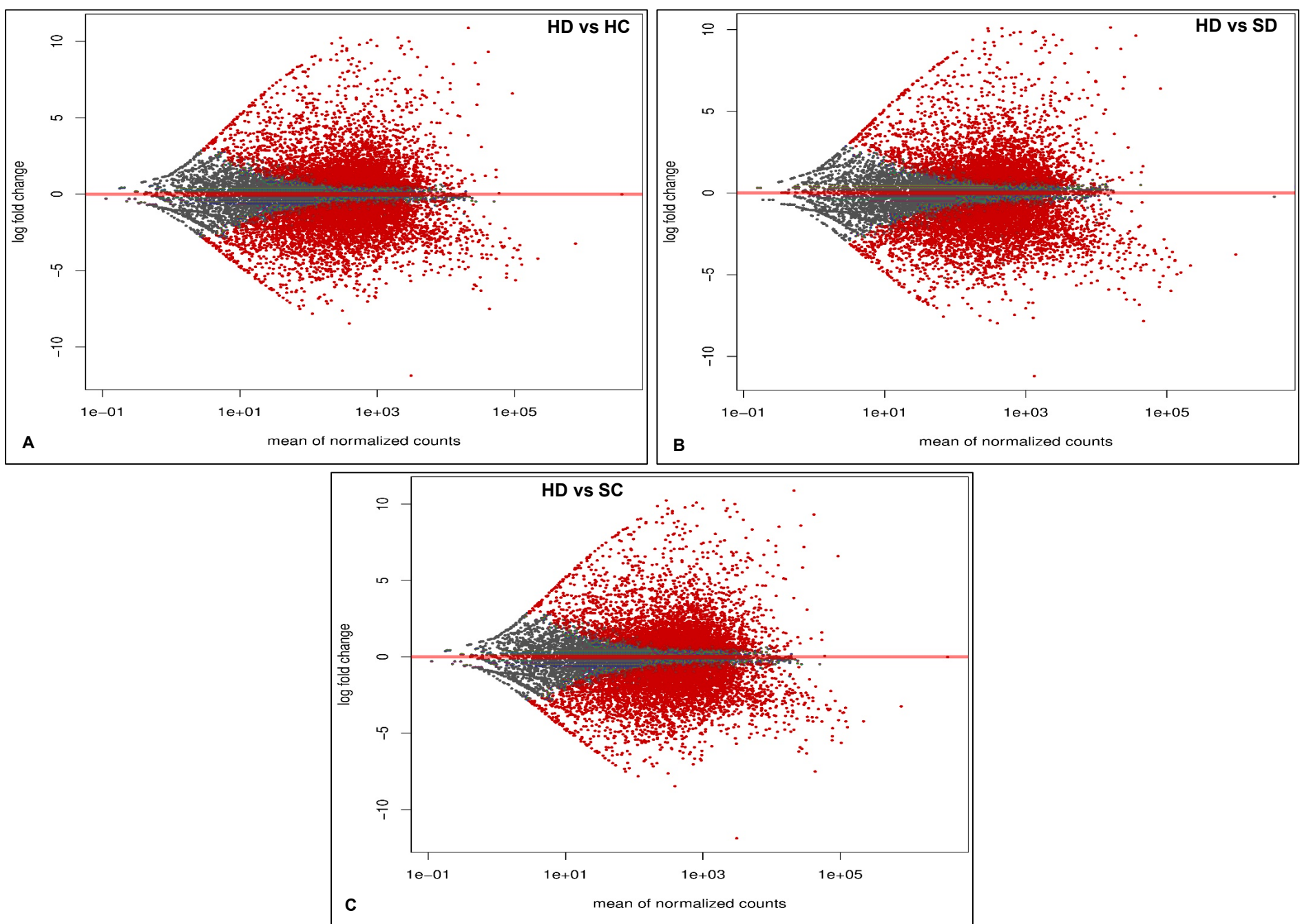
n = 4 (SR1); n = 8 (H6)

■ Standard

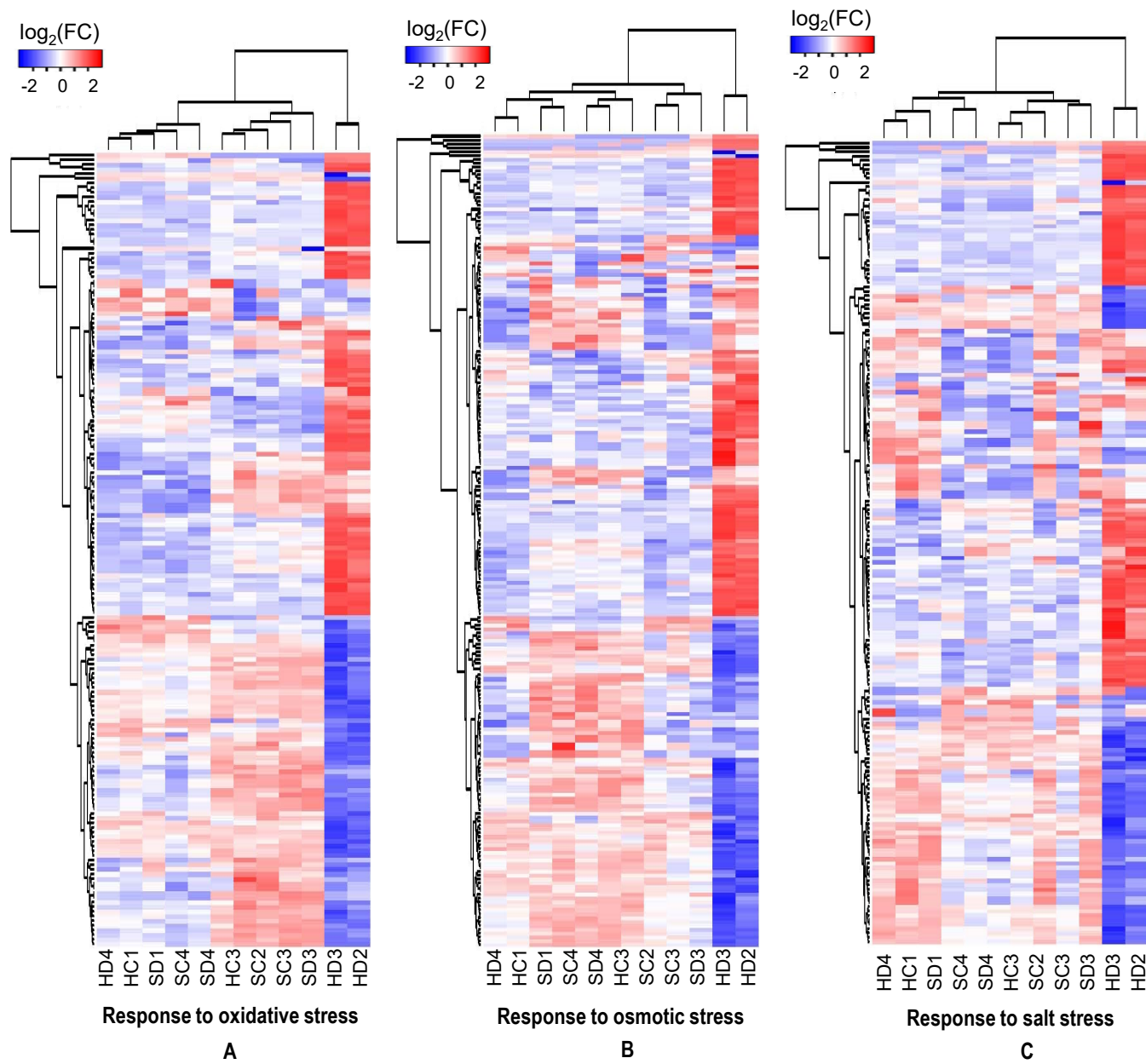
▲ Dex

● Control

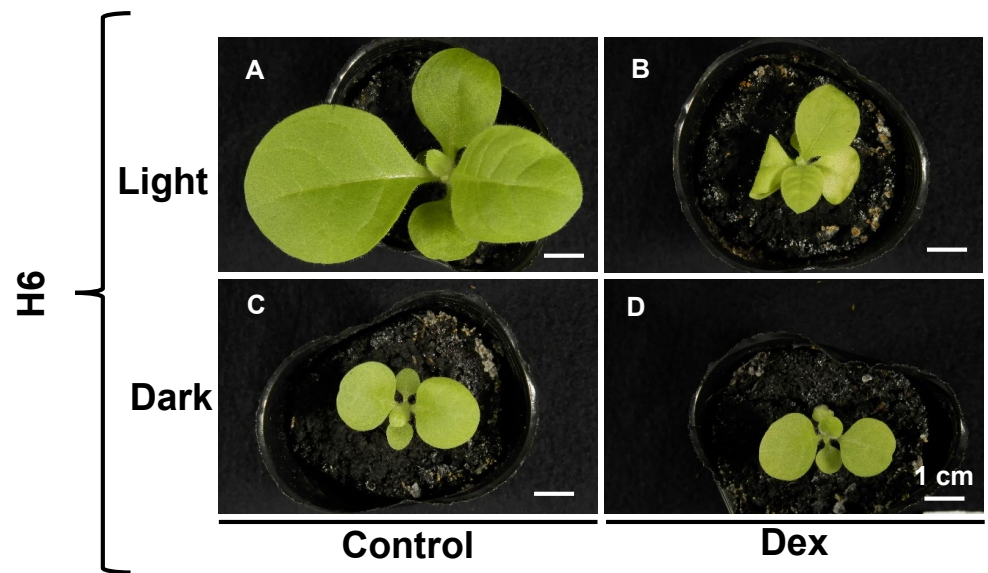
Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3



Supplementary Figure 4

Table S2 Primers used for qRT-PCR analysis in the present study

Primer name	Sequence (5'→3')
NtEF1 α -qRT-867F	TGAGATGCACCACGAAGCTC
NtEF1 α -qRT-917R	CCAACATTGTCACCAGGAAGTG
Nt-HSP90C-qRT-2111F	GGTTGAGCTCATCACCAT
Nt-HSP90C-qRT-2235R	CTTCTCCCTCTCATAAACTCC
Nt-SARD1-qRT-353F	CCACCCTCTCCAGCTCCTACT
Nt-SARD1-qRT-408R	TGGTCGGAACCAGGCAAT
NtLHCab-qRT-263F	ACCATCAAACCTTGGAGAGATAC
NtLHCab-qRT-373R	GCCCATTCTTGAGCCTTTA
NtCHLI-qRT-94F	GCTTCTACACCCTTGTCTTC
NtCHLI-qRT-224R	ATTGGGACCTCCCTTTCT

Supplementary Table S3. Summary of RNA-Seq data and results of mapping the clean reads with *N. tabacum* TN90 reference transcriptome.

Samples	Raw Reads	Clean Reads	% Clean Reads	Mapped Reads	% of Mapped Reads	%GC	Clean Bases (GB)
HC 1	20750739	20578808	99.17	17026147.92	82.74	42	4.9
HC 3	20740275	20608050	99.36	17694591.10	85.86	43	4.9
HC 4	36041966	35624591	98.84	31677521.57	88.92	43	8.5
HD 2	20455475	20329474	99.38	17600838.91	86.58	42	4.8
HD 3	19697415	19536082	99.18	15658746.50	80.15	41	4.7
HD 4	31430805	31240952	99.40	27430721.18	87.80	42	7.4
SC 2	20017103	19680889	98.32	17027290.40	86.52	43	4.7
SC 3	20290025	20171373	99.42	17639037.56	87.45	43	4.8
SC 4	22178805	22058449	99.46	19887761.05	90.16	43	5.3
SD 1	20550937	20409895	99.31	17754024.25	86.99	42	4.9
SD 3	24776662	24512461	98.93	20121025.56	82.08	42	5.8
SD 4	21715526	21547699	99.23	17654566.15	81.93	42	5.1
	278645733	276298723	99.17	237172272.10	85.60		
	(Total)	(Total)	(Average)	(Total)	(Average)		

S, SR1 (non-transformant); H, line 4 of i-hpHSP90C; D, Dex treatment; C, Control.