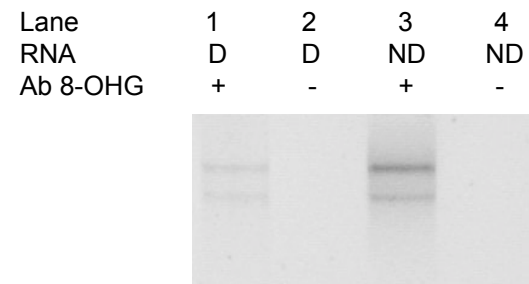


Supplemental Figure 1. Random effect of mRNA oxidation on cDNA-AFLP efficiency.

Portions of silver-stained cDNA-AFLP gels obtained with the same primer combination amplification of cDNA from 2 independently *in vitro*-oxidized mRNA. Lane 1 : Control mRNA (0 μM H_2O_2), lane 2,3,4 : mRNA oxidized in the presence of 0.1; 1 and 10 μM H_2O_2 . Primers used were Eco1 and Mse5 (see Supplemental Table 2). Arrowheads indicate polymorphisms.

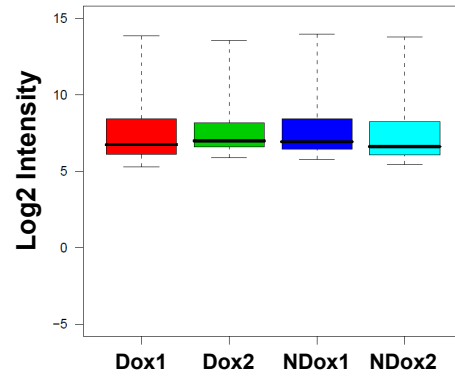


Supplemental Figure 2. RNA gel electrophoresis showing anti 8-OHG immuno-precipitation selectivity.

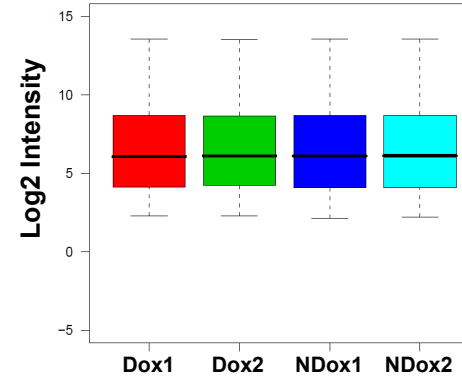
8-OHG containing RNA were immuno-precipitated from mRNA enriched fraction of dormant and non-dormant embryos and analyzed on 1.5% agarose gel. No RNA was detected on gel when antibody was omitted (lane 2 and 4) arguing for selectivity of the antibody.

A

Boxplot of raw probe values by array

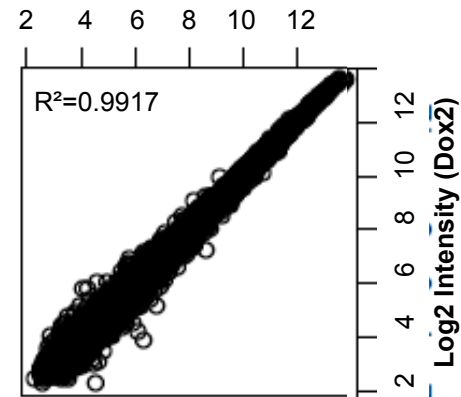


Boxplot normalized data

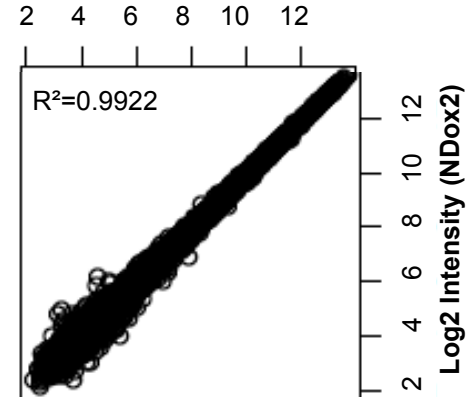


B

Log2 Intensity (Dox1)



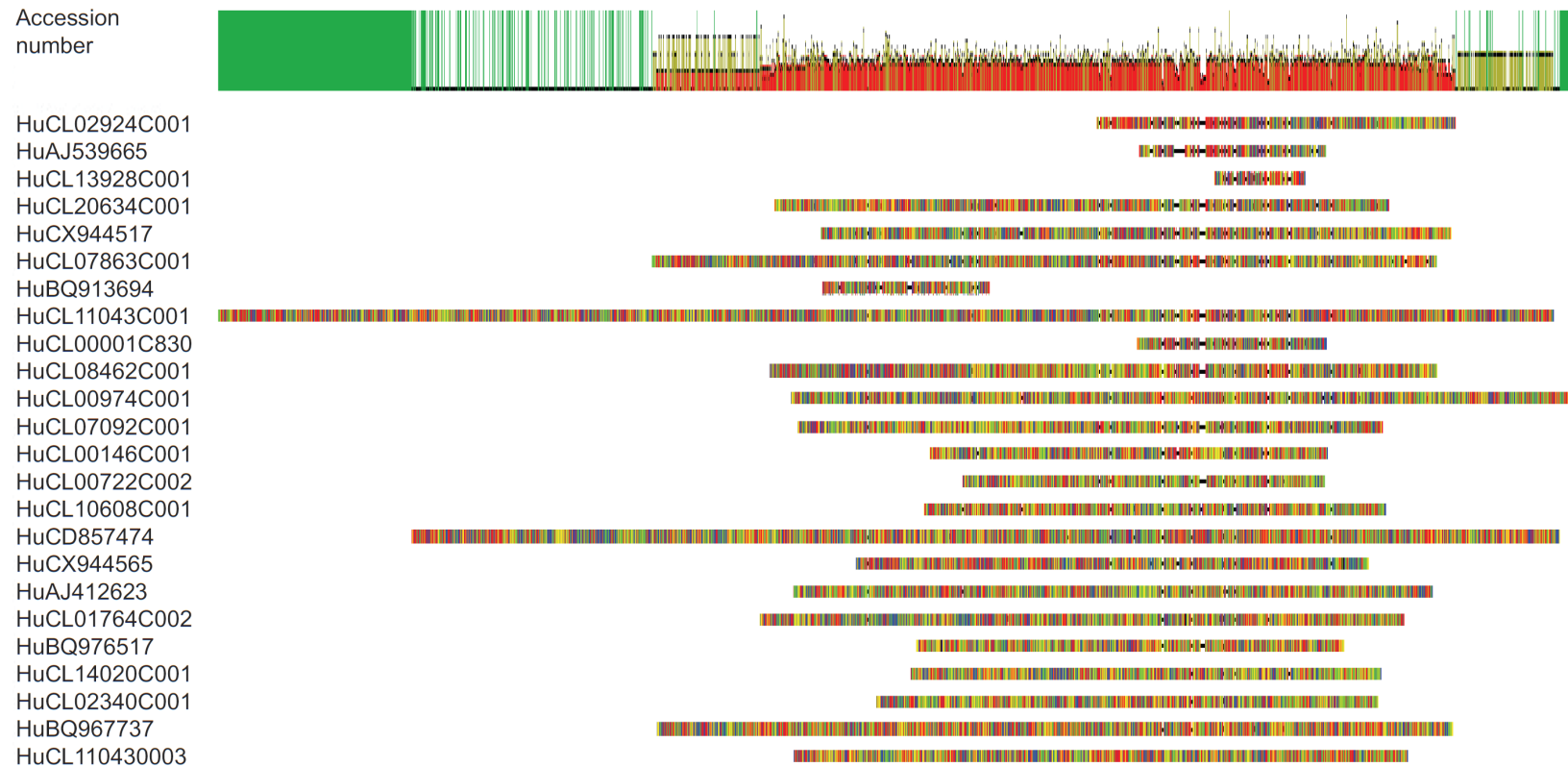
Log2 Intensity (NDox1)



Supplemental Figure 3. Reproducibility of microarray data from 8-OHG fraction of dormant and non-dormant embryonic axes.

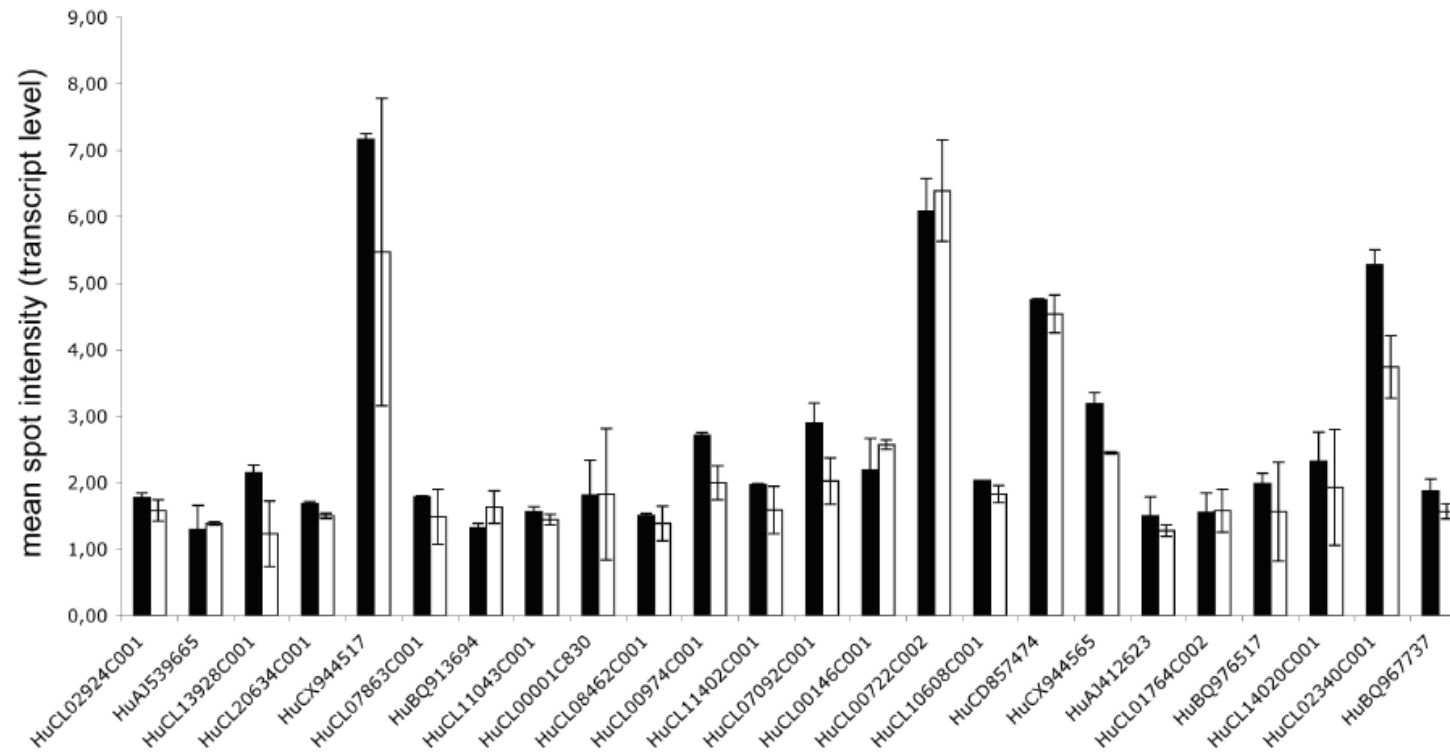
(A) Boxplot analysis of raw probe value per array and after normalization using the RMAgc method (Irizarry *et al.*, 2003).

(B) Reproducibility between replicates was high, as shown by the values of correlation coefficients (R^2) for each set of replicates. Dox1, Dox2; replicates of oxidized transcripts from dormant embryonic axes; NDox1, NDox2; replicates of oxidized transcripts from dormant embryonic axes.



Supplemental Figure 4. Geneious® software sequences alignment of the 24 oxidized transcripts obtained using ClustalW algorithm.

Coloured bars represent DNA bases (Blue, Guanine; Green, thymine; Red, Adenine; Blue, cytosine). The top row represents calculated identity of sequences with a colour range system from red (no identity) to green (full identity) highlighting the lack of similarities between those 24 sequences.



Supplemental Figure 5. Mean Log₂ (intensity) values of the 24 oxidized transcripts in dormant (black bars) and non-dormant (white bars) total transcriptome.

GenBank accession number	TDF number	Size (bp)	Annotation	Score (e value)
JG728171	3	349	Heat shock transcription factor : AtHsfA5, At4g13980 (<i>Arabidopsis thaliana</i>)	1e ⁻²
JG728172	5	239	Putative protein At3g58180.1 (<i>Arabidopsis Thaliana</i>)	1e ⁻²⁸
JG728173	6	187	UBC gene; ubiquitin conjugating enzyme type E2 AtUBC9, At4g27960.1 (<i>Arabidopsis thaliana</i>)	7e ⁻⁸⁹
JG728174	18	220		
JG728175	12	208		
JG728176	7	226	mRNA for aspartic proteinase, complete CDS (<i>Helianthus annuus</i>)	7e ⁻³⁷
JG728177	38	241		
JG728178	4	184		
JG728179	24	174	Clone pHaS211 (<i>Helianthus annuus</i>) RNase-H gene of Ty1-copia retroelements	3e ⁻⁶⁰
JG728180	48	271	Putative senescence-associated protein (<i>Pisum sativum</i>)	7e ⁻⁴⁰
JG728181	8	164	No significant blast results	
JG728182	9	238	No significant blast results	
JG728183	13	143	No significant blast results	
JG728184	20	214	No significant blast results	

Supplemental Table 1. Differentially expressed TDFs during after ripening of sunflower seeds at 60 % and 75 % RH (Group A+B).

Annotations correspond to the best sequence homologies obtained using BlastP or BlastN algorithm.

Name	Sequence
Eco 1	GAC-TGC-GTA-CCA-ATT-CAC
Eco 2	GAC-TGC-GTA-CCA-ATT-CCT
Eco 3	GAC-TGC-GTA-CCA-ATT-CGC
Eco 4	GAC-TGC-GTA-CCA-ATT-CTC
Mse 5	GAT-GAG-TCC-TGA-GTA-AAG
Mse 6	GAT-GAG-TCC-TGA-GTA-ACA
Mse 7	GAT-GAG-TCC-TGA-GTA-AGA
Mse 8	GAT-GAG-TCC-TGA-GTA-ATC

Supplemental Table 2. Primers used in this study.