Table S5. Gene Ontology (GO) enrichment analysis of DEGs that were up and down expressed in the comparison of GOIAS aged-seeds vs MINAS aged-seeds.

GOIAS aged-seeds vs MINAS aged-seeds up-regulated genes				
Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway
8.03E-05	3	4	259.0125	Cellular response to UV-C
0.010182	2	8	86.3375	Transcription, RNA-templated
0.00094	3	13	79.69615	Response to UV-C
0.002755	4	60	23.02333	Negative regulation of gene expression, epigenetic
0.002755	4	62	22.28065	Detection of external stimulus
0.000895	5	86	20.07849	Regulation of gene expression, epigenetic
0.000895	6	137	15.12482	Cellular response to light stimulus
0.000895	6	144	14.38958	Cellular response to radiation
0.009287	4	97	14.24124	Phosphatidylinositol metabolic process
0.009287	5	183	9.435792	Gene silencing
0.000895	8	329	8.397568	Chromatin organization
0.002894	9	564	5.510904	Chromosome organization
0.007264	10	813	4.247847	Cellular lipid metabolic process
0.009287	12	1217	3.405259	Negative regulation of biological process
0.010182	15	1845	2.807724	Organelle organization

GOIAS aged-seeds vs MINAS aged-seeds down-regulated genes				
Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway
0.023395	9	850	5.318759	Organonitrogen compound catabolic process
0.023395	11	1422	3.885795	Cellular catabolic process
0.023395	13	1914	3.411836	Response to external stimulus