Supplementary Table S8
Genes cited in the text that do not meet the 2-fold criterion for biological significance.

| Gene | ACE MS vs ACE PEG | DH MS vs DH PEG | DH PEG vs ACE PEG |
|---|---|---|---|
| UDP-galactose/UDP-glucose transporter, putative (At1g14360) | 2.324 | 0.812 | 4.000 |
| glycosyl hydrolase family 1 protein (At5g26000) | 1.828 | 0.907 | 1.499 |
| hexokinase 2 (HXK2) (At2g19860) | 1.732 | 0.909 | 1.915 |
| glycosyl transferase family 48 protein similar to glucan synthase (At3g07160) | 1.679 | 1.173 | 0.878 |
| endo-1,4-beta-glucanase, putative / cellulase, putative (At1g64390) | 1.619 | 1.121 | 1.353 |
| xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase (At5g57560) | 1.335 | 0.961 | 1.375 |
| glycosyl hydrolase family 32 protein similar to fructan 1-exohydrolase (At5g11920) | 1.597 | 0.984 | 3.462 |
| acyl-CoA:1-acylglycerol-3-phosphate acyltransferase, [LPAT2] putative (At3g57650) | 1.439 | 1.01 | 1.529 |
| long-chain-fatty-acid--CoA ligase (At4g23850) | 1.403 | 0.984 | 1.333 |
| omega-3 fatty acid desaturase, endoplasmic reticulum [FAD3] (At2g29980) | 1.440 | 1.008 | 1.349 |
| isoflavone reductase (At1g19540) | 1.807 | 1.045 | 1.06 |
| sinapoylglucose:malate sinapoyltransferase [SNG1] (At2g22990) | 1.388 | 1.049 | 1.066 |
| cinnamoyl-CoA reductase-related (At4g30470) | 1.820 | 1.099 | 1.637 |

Note: These genes are more highly expressed in ACE than DH, but do not meet either the 2-fold criterion of biological significance or (in one case) the statistical criterion. The results displayed are expression ratios for comparisons PEG treated vs. mature seed in each cultivar (columns 2 and 3) and direct comparison of expression between PEG treated seed of DH and ACE (column 4).