

**Table 2. Fold increase and database matches for top target sequences**

REF ID/ RANK	PXO99 <sup>A</sup> average *	ME2 average†	<u>PXO99<sup>A</sup></u> ME2	cDNA match‡	Similarity‡
1	31878	310	103	AK070510	MtN3
2	11435	567	20	U60097	dehydrin
3	6526	441	15	U60097	dehydrin
4	3979	456	9	AK063714	HSP20
5	3195	410	8	AK071240	Mitochondrial import
6	12252	2563	5	U57641	LEA-like protein mRNA, embryo-specific
7	5238	1104	5	AK106962	GDSL-like Lipase/Acylhydrolase
8	2109	457	5	CF311010	Protein phosphatase 2C-like
9	973	230	4	AK121202	UDP-glucuronosyl/UDP-glucosyl transferase
10	3486	879	4	AK107980	Plastocyanin-like
11	922	240	4	CF337042	Hypothetical protein
12	1983	530	4	AK102303	None
13	6581	1762	4	AU183565	putative indole-3-acetate beta-glucosyltransferase
14	5624	1523	4	AK070124	Mitochondrial import
15	6114	1679	4	AK108785	None
16	2986	823	4	AK119261	HSP20
17	5111	1414	4	AB040744	RERJ1 transcription factor
18	4400	1227	4	tigr:9637.m02954	glucose:salicylic acid glucosyltransferase
19	3545	1014	4	X89891	Ca binding EF hand protein

\* Average of three values for PXO99<sup>A</sup> in Table 1.

† Average of three values for ME2 in Table 2.

‡ cDNA and similarity matches provided at Affymetrix Netaffx Analysis Center web site [www.affymetrix.com/analysis/index.affx](http://www.affymetrix.com/analysis/index.affx).