

**Table S1. The ATO family**

Gene <sup>1</sup>	Orf19	<i>ach1</i> Δ <sup>2</sup>	WT+Glu <sup>2</sup>	BLAST score vs. Ato1p <sup>3</sup>	Sequence at consensus site <sup>4</sup>
<i>ATO1</i>	19.6169	<b>79.0</b>	<b>176.9</b>	(1325)	51-FGG <b><u>T</u></b> TLN
<i>ATO2</i>	19.2496	0.37	0.74	1066	51-FGGTLN
<i>ATO3</i>	19.1224	<b>36.6</b>	<b>7.6</b>	648	70-FGGTLN
<i>ATO4</i>	19.3441	<b>16.6</b>	<b>3.6</b>	620	53-FLGTFN
<i>ATO5</i>	19.6997	2.6	<b>6.4</b>	604	55-FGGTFN
<i>ATO6</i>	19.6995	2.1	1.4	597	56-FGGTFN
<i>ATO7</i>	19.1571	0.81	1.6	596	51-LAHNAQ
<i>ATO8</i>	19.3440	<b>10.1</b>	<b>9.2</b>	562	61-FLGTMN
<i>ATO9</i>	19.3261	0.39	0.74	305	None <sup>5</sup>
<i>ATO10</i>	19.3263	0.71	2.1	304	58-FGGTFD <sup>5</sup>

1. Gene name assigned by this work
2. Fold-induction in the array comparisons described here
3. BLASTp scores vs. the Ato1p protein
4. Sequence in the region defined by Augstein. The mutated residue in Ato1 is indicated in bold and underlined
5. *ATO9* and *ATO10* appear to be a single ancestral gene interrupted by a Tca9 retrotransposon, thus, *ATO9* does not have a sequence similar to the consensus.