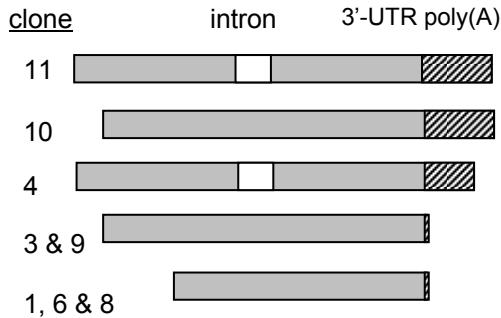


**Figure S2**

**A**



**B**

|        |     |  |   |
|--------|-----|--|---|
| At3ox1 | 1   | ---  | MPAMLTDVFRGHIPLPHSHIPDFTSLRELPPDSYKWTPKDLLFSAAPSP-PATGENIPIDEIDLD-----HPDATNQ |
| At3ox2 | 1   | ---  | MSSTLSDFRSHPIHILPSNPDPFK---SLPDSYTWPKDPLLFSAS---ASDEFLPBDIDS-----DTHVATL      |
| Ls3h1  | 1   | ---  | MHTRVADAFKAHPMVNQKEELDLKSMKELPESHAWSQ-DGSPSYG----SSSECVPVINLK-----DPNAMKL     |
| Ls3h2  | 1   | ---  | MSLQLDAFREKEELPSYAVSSIDNCP-S---SSNSEVPVINK-----DGNAMKH                        |
| Le3ox1 | 1   | ---  | MPSRISDSCRPHHSQKEFDLNSIXELPESHAWSNDHYTQEEN---SCNFESIPVIDLNDNNNNNNNNNILDH      |
| St3ox1 | 1   | ---  | MPTRISDSCRPHHSQKEFDLNSIXELPESHAWSNDHYTQEEN---SCNFESIPVIDLNDNNNNNNNNNILDH      |
| Nty    | 1   | ---  | MPSRISDSFR-AHSKEELDLNSIXELPESHAWSNDYPS-EN---SCNFESIPVIDLNDYINNNNNINVLEH       |
| Le3ox2 | 1   | ---  | MPSIISOLDLNSIXELPESHAWSNDDDGSRN----INAESIPVIDLN---RDHKFVMDT                   |
| St3ox2 | 1   | ---  | MPSIISOLDLNSIXELPESHAWSNDDDGSRN----INAESIPVIDLN---RDHKFVMDT                   |
| Ps3ox1 | 1   | ---  | MPSLSEAYRAHNVNHEKPDNFSLQHEDHTLDSNNIMESTTTVPVIDLN----DPNASKL                   |
| Os3ox1 | 1   | MTSSSTPSLPLAAAHNGVTAAXENFGAERVPEHVWKGMEHKDTAPAVADGGDAVPVWDM-----GGDDAAVA               |   |
| Os3ox2 | 1   | -----MPTPSHLKNPLCDFRAARRVPETPHAWGLDDHP--VVVDGGGGGEDAVPVVWDM-----AGD-----AAAR           |   |
| At3ox1 | 71  | TIGHACRTWGAFQISNHGVPLGLLODIEPLTGTSLFGLPWPORKLKSGARSE-TGVSGYGVARTIASFPNKQMWSSEGFTIIG-GP |   |
| At3ox2 | 64  | VGHACTTWGAFQIITNGCVPSELPDIEPLTGTSLFGLPWPORKLKSGARSE-NGVSGYGVARTIASFPNKQMWSSEGFTIIG-GP  |   |
| Ls3h1  | 65  | VGHACKTWGQFQVTPNEQGPVNLLBEMEAGCRKLFAPQOKLKAARSD-DGVSGYGVARTISSFPKLMWSSEGFTIIG-GP       |   |
| Ls3h2  | 57  | VGHACKTWGQFQVTPNEQGPVNLLBEMEAGCRKLFAPQOKLKAARSD-DGVSGYGVARTISSFPKLMWSSEGFTIIG-GP       |   |
| Le3ox1 | 70  | IGHACKTWGAFQIINNSSEKLLQDIEVAGKTLFSLPMQOKLKAARSD-DGVSGYGVARTISSFPKLMWSSEGFTIIG-GP       |   |
| St3ox1 | 70  | IGHACKTWGAFQIINNSSEKLLQDIEVAGKTLFSLPMQOKLKAARSD-DGVSGYGVARTISSFPKLMWSSEGFTIIG-GP       |   |
| Nty    | 68  | IGHACKTWGAFQIINNSSEKLLQDIEVAGKTLFSLPMQOKLKAARSD-DGVSGYGVARTISSFPKLMWSSEGFTIIG-GP       |   |
| Le3ox2 | 56  | IGHACKTWGAFQIVVNENIISHLRNHMETHGTRLFLSPMOKLKAARSD-DGAGYGVARISSFPDKLMWSSEGFTIIG-GP       |   |
| St3ox2 | 56  | IGHACKTWGAFQIVVNENIISHLRNHMETHGTRLFLSPMOKLKAARSD-DGAGYGVARISSFPDKLMWSSEGFTIIG-GP       |   |
| Ps3ox1 | 70  | IGHACKTWGQFQIVVNENIISHLRNHMETHGTRLFLSPMOKLKAARSD-DGAGYGVARISSFPDKLMWSSEGFTIIG-GP       |   |
| Os3ox1 | 77  | VARNAEEGGFLVVGTVTAEARLVEQAARFLPALDADKCARREPGCNGTGYGVPPYLRYPKQWMAEGYTFFPPAI             |   |
| Os3ox2 | 61  | BKMAAEQWGAPLVLHGIVGPAALIERSVERARVFLVPLASBKLMAEVGEPE-CGYSPPSSFPKLMWSSEGFTFSPSLSL        |   |
| At3ox1 | 149 | LNDPRKLPW---QHHNYCDIWBVEYYEEHMKKLASKLMLWALNLNSLGVSBDIEIWAS-LSSIDLNWAAQ-RALQLNHYPVCPPEP |   |
| At3ox2 | 142 | LHDPRKLPW---SHHUKYCEIIIWBVEYYEMQKLAALMWFALGSLGVEEKDIOWAG-PNSDFQGTO-RAHQLNHYCPPEP       |   |
| Ls3h1  | 143 | YEHARKLWP---NRYSEFCDVIEQYKHEMNNIAQRLMWMWLGSLGVEEKDIOWAG-PNSDFQGTO-RAHQLNHYCPPEP        |   |
| Ls3h2  | 135 | HQHAKQLWP---QGSGNFCDVIREYNEKEMMKLUSNRPWMMWLGSLGVEEKDIOWAG-PNSDFQGTO-RAHQLNHYCPPEP      |   |
| Le3ox1 | 148 | IEHARQOLWP---KDYNFKCIVBREYENEMEKLAGRMLMWLGSLGVEEKDIOWAG-PNSDFQGTO-RAHQLNHYCPPEP        |   |
| St3ox1 | 148 | IEHARQOLWP---KDYNFKCIVBREYENEMEKLAGRMLMWLGSLGVEEKDIOWAG-PNSDFQGTO-RAHQLNHYCPPEP        |   |
| Nty    | 146 | LEHARQLPW---HDYDVKFCDVIEYYEMEKLAGRMLMWLGSLGVEEKDIOWAG-PNSDFQGTO-RAHQLNHYCPPEP          |   |
| Le3ox2 | 134 | LEHARQLPW---YDYMFKCIVBREYENEMEKLAGRMLMWLGSLGVEEKDIOWAG-PNSDFQGTO-RAHQLNHYCPPEP         |   |
| St3ox2 | 134 | LEHARQLPW---YDYMFKCIVBREYENEMEKLAGRMLMWLGSLGVEEKDIOWAG-PNSDFQGTO-RAHQLNHYCPPEP         |   |
| Ps3ox1 | 148 | LDEHARQLPW---QDVTFCDVIEYYQDTEMKKLAGLQPMCLDLSLGIKEDWVKAQVGRS---GS-SALQLNHYCPDP          |   |
| Os3ox1 | 157 | RDEERRWVPPDAGDDYHRCFCSAMEEYDSSMRLAERLJLAMPFKALGAGNDLPGGETERKIRETLTSTSIIHLNMF-CPDP      |   |
| Os3ox2 | 140 | RSEDRERWPKSGDDYLLFCDVMEZFHKEMRRLADELLRPLRALGLTGEVAGVAAERRIERGRT-MTVHNLWYPRCPPEP        |   |
| At3ox1 | 224 | DRAMGLAAHTDSTLLTILQNNNTGLQVFRDDLG-WWTVPPFPGLSVLNVNGDLPFHLISNLGFKNSVLRHARVNQTRARLSV     |   |
| At3ox2 | 217 | DRAMGLAAHTDSTLLTILQNNNTGLQVFRDDVG-WWTVPPFPGLSVLNVNGDLLHILTFPVSVLHRARVNHVRSRFSM         |   |
| Ls3h1  | 214 | DRAMGLAAHTDSTLLTILQNNNTSGLQHREGAG-WWTVPPFPGLAVNVNGDLLHILTSNLGYPVSLHRAMVNRTOHRLSV       |   |
| Ls3h2  | 210 | DRAMGLAAHTDSTLLTILQNNNTSGLQHORG-WWTVPPFPGLAVNVNGDLPFHLISNLGYPVSLHRAMVNRTOHRLSV         |   |
| Le3ox1 | 224 | GRAMGLAAHTDSTLTILQNNNTSGLQYQEGNG-WWTVPPFPGLAVNVNGDLLHILTSNLGYPVSLHRAVVNRTRVRLSV        |   |
| St3ox1 | 224 | GRAMGLAAHTDSTLTILQNNNTSGLQYQEGNG-WWTVPPFPGLAVNVNGDLLHILTSNLGYPVSLHRAVVNRTRVRLSV        |   |
| Nty    | 222 | DRAMGLAAHTDSTLTILQNNNTSGLQVEKCGN-WWTVPPFPGLAVNVNGDLPFHLISNLGYPVSLHRAVVNRTRVRLSV        |   |
| Le3ox2 | 206 | DRAMGLAAHTDSTLTILQNNNTSGLQVEKCGN-WWTVPPFPGLAVNVNGDLLHILTSNLGYPVSLHRAVVNRTRVRLSV        |   |
| St3ox2 | 206 | DRAMGLAAHTDSTLTILQNNNTSGLQVEKCGN-WWTVPPFPGLAVNVNGDLPFHLISNLGYPVSLHRAVVNRTRVRLSV        |   |
| Ps3ox1 | 223 | DHAMGLAHTDSTLTILQNNNTSGLQVNRREGS-WWTVPPFPGLAVNVNGDLPFHLISNLGYPVSLHRAVVNRTRVRLSV        |   |
| Os3ox1 | 237 | DRVWGLAHTDGSFFPGLSPVPGLOEHLRHPDRWVTVGTPHLLTNQREHFSVFRAVVNRTRVRLSV                      |   |
| Os3ox2 | 219 | RRALGLWAHTDGSFFPGLSPVPGLOEHLRHPDRWVAVAGFVVNVNGDLPHILTNGRFHSVFRAVVNRTRVRLSV             |   |
| At3ox1 | 303 | AFLWGPQCDIKISPWKLVSPVSPLSQSVTWKEXIRTKATHPNKALSMIRNHREE-                                |   |
| At3ox2 | 293 | AYLWGPSPDVISPLSKLVDPLQSPLYPSLTWKQYLATKATHPNQSLIIRN-                                    |   |
| Ls3h1  | 293 | AYLYGPSPGVNCISPLSKLVDHREPPLYPWTSEYLGTKAKHPNKALSVRLCPDN---                              |   |
| Ls3h2  | 283 | AYLYGPSPGVNCISPLSKLVDHREPPLYPWTSEYLGTKAKHPNKALSVRLCPDN---                              |   |
| Le3ox1 | 303 | AYLYGPSPGVRVSPLSKLVDHREPPLYAFTWSEYLGTKAKHPNKALSVRLCPDN---                              |   |
| St3ox1 | 303 | AYLYGPSPGVRVSPLSKLVDHREPPLYAFTWSEYLGTKAKHPNKALSVRLCPDN---                              |   |
| Nty    | 301 | AYLYGPSPGVKISPLSKLVDHREPPLYAFTWSEYLGTKAKHPNKALSVRLCPDN---                              |   |
| Le3ox2 | 285 | AYLYGPSPGVKISPLSKLVDHREPPLYAFTWSEYLGTKAKHPNKALSVRLCPDN---                              |   |
| St3ox2 | 285 | AYLYGPSPGVKISPLSKLVDHREPPLYAFTWSEYLGTKAKHPNKALSVRLCPDN---                              |   |
| Ps3ox1 | 302 | AYLYGPSPGVNVEICPHAKLIGPTKPPLYRSVTWNEYLGTKAHPNKALSVRLCPDN-LFDVNDSNKNSVQVG-              |   |
| Os3ox1 | 317 | PYFNGPSPADMVKTPVLAAGSPESKAVQAVTWEPEYMAVRDVKLPGTNTISALSMIRVAKER-EDKES-                  |   |
| Os3ox2 | 299 | GYFLGPPDPAEYPLPAGRSPAYBAVTPWPEYMAVRKKAATGGALKMVSTDAA-AAADHDVAAAADVHA                   |   |

**Figure S2. Structure of StGA3ox2 clones isolated from potato.** (A) Schematic representation of the different clones corresponding to StGA3ox2 mRNA. An unspliced intron is present in clones 11 and 4. Multiple poly-adenylation sites are used during transcription, with a poly-A tail added directly after the stop codon in clones 3 & 9, or clones 1, 6 & 8. (B) Comparison of potato StGA3ox1 and StGA3ox2 amino acid sequences with other GA 3-oxidases from Arabidopsis (*At3ox1* NM\_101424 and *At3ox2* NM\_106683), pea (*Ps3ox1* AF010167), lettuce (*Ls3h1* AB012205 and *Ls3h2* AB012206), tomato (*Le3ox1*~*S/3ox1* AB010991 and *Le3ox2*~*S/3ox2* AB010992), tobacco (*Nty* AB032198) and rice (*Os3ox1* AB054084 and *Os3ox2* AB056519) genes. Black boxes indicate identical residues, and gray boxes indicate conserved residues. Dashes indicate gaps in the sequences. Sequence corresponding to the B3ox fragment is shown on top of the alignment with a thick black line.