

Supplemental Table III. Proteins with incomplete or no RING domain due to splicing or translation stop predictions

AGI code	Comments	Our Predicted Protein Sequences (bold text indicate RING domain)
At5g01070	RING-v, missing metal ligand 7 and 8. Metal ligand 7 and 8 found after predicted stop. Premature stop due to splicing prediction.	MSSYEISHIDLENGSGERQYRPSDVSGEDSSSCDYDYDFHSAVRSFCGEFEIADDDDET DTESVASGSIRGSPEKDCRICH LGLESSRHECGDPMVLGCSCKDDLGYVHKQCADTWFKI KGNKTCEICRSIAQNFFKVDNEIGQTTVETNVDDVEAGNTPTMVATSDSDRRRLCRGNRF LNFLT
At4g03965	RING-HCa, metal ligand 1 to 6 found in intron. RING similar to At4g22250.	MSQLGVETSQAQPETPQSTTFLDLLRLQMDGLDRSRRRRTLKERLGFKRIGCCGPTWGL RLTSNTGEDDDEPFENRLVSGSDHVTGPLNQGMNLATALAAERNYRTEETEASGSLTPLK VSLMRLLLEETAERVVVEENETERVTASASSTVRGVNNDV CCVCMGRKKGAAFPCGHTF CRVCSREVWLNRGSCPLCNRPIIEILDIY
At1g19030	RING-D predicted to be in intron. Alternate splice site located after metal ligand 8.	MDEPVRTFPITWLADYVMEDEGFSSREDINDLLMKEGFLEPDLFMETAL LIGANDTEIARKGIIEVTS SRDYSPEYALFNLNLTFRDGGISFDEIVEDDDTNIYIPYYCIPFRPASELAVRSLTKNIYYK TSSIVGDK CIICLEEFKEGARIVTLPCGHEFDKCIVDWFATSHFCPLCRFEFSFKLSEA RRSLWVELVKYLIRRGFWLVKENTTCGSIWKKILKYRDTAKSFYRVEVRNGEASSFG FDRWSEMGCLYDRLGARGCIDLGGSPMTATVGEVMAGARRRKYRVAILNQVENEIVKQKLI RSNETDVALWNGKHDHYRKEFHKTETWLQIRTAKLLMENYNGIWFKHSTPKYSLITWLQV KNRVATGDKLIKWNPQVWTKLAKGILHASFTANWTE TLKLIHDNRLSKTKCFIVX
At4g00070	RING-H2, missing metal ligand 7 and 8. metal ligand 7 and 8 found after predicted stop.	MSSLSENEFLFDLNEIPEKTVYSDDGDEFLFDLNKIPPREETVNSSDEDAEVEKSAEGY TDHLHRRNQATKRKKLRKRPKGLRMDTDPYQELRMDTDHMTYEQLLQLCENNMGYENSGV KASNIDRCLRNTPSEFQSLADK ICICQDGFQKRAGVGLNCGHNFHVNCVWPWILTKK ECPVCQKTADDDEHQTQSYQVETIELSDDDEEDMNSRDHQYDPEQLLLFYEIPKGRTHG PFLTSLRKWWDQGYFDGFPNLKVVMMGESIETAVLLTILT
At4g12150	RING-H2, missing metal ligand 8. splice prediction interrupts domain. alternate splice site downstream of metal ligand 8.	MNDPIKAVVSVQVAERVSRSQSGNTNSIFLIVNTIKDEILINPGTGHRTATSTPLSY KSLPINYTLPSCSHHHIQSLLHDLRHRDDHWLCDHLVPKISSAISSGFVDTVSVAVTYK YVRVDEAALKISRMVLQGFMSVEETKSLNAES CSICLQSLVSSSKTAPTRMSCSHVFNHG CLVEWLNKNTCPMCR TFFHMLQIDSSMFSSDYTAYIVEHCKRHDFSSGSTHVRSRYINICR STHGHIRKLLHNQFLSTISNPWRSLCDFLSPKISTEFINLGFGRNGFTLTMDAKVTYRTV SVTSNDEKSLRTLIVGKIKAEELKSLKIETERCSICLESLSVSGPKIPLTRMPCFIY

Supplemental Table IV. Related proteins with incomplete RING domains

AGI code	Related to RING Protein or Family	Identity (%)	Comments
At1g66660	At1g66650 Similar to SINA family of proteins (Group 21).	49	Incomplete RING, missing a number of metal ligands.
At2g25370	At2g25360 Similar to ARI family of proteins (Group 11.1). Contains an IBR domain.	61	Incomplete RING, missing metal ligand 2
At3g04460	At2g26350 Similar to PEX family of proteins (Group 18). Contains a Pex2_Pex12 domain.	32.1	Incomplete RING, missing 3 of the 8 metal ligands.
At3g45460	At3g45560 Similar to ARI family of proteins (Group 11.1). Contains IBR domain	52.8	Incomplete RING, missing 3 of the 8 metal ligands.
At5g37220	Similar to proteins At5g37200, At5g37230, At5g37250 and At5g37270	42.3-35.6	Incomplete RING, missing metal ligand 8

Supplemental Table V. RING protein encoding genes predicted to be pseudogenes or not annotated

AGI code	Comments	Predicted Protein Sequence/ amino acid sequence of RING domain (bold text)
At3g30733	RING-H2, predicted to be a pseudogene due to absence of start codon. Start methionine found 30 a.a. upstream.	MTSMFLHFLKAVHISTQSKRDKAILIYFKVTDYNFQADSRIDTDVLIHLETAKRVPTTS EENED CAICLQTFKGRDDINNLACNHIYHHDCIVTWLYAKKNCPICRTTEV
At2g11348	RING-D, found in non-annotated region of genome. Found in BAC F3K12, in region between At2g11280 to At2g11465	CAICFQEFKTRGREATLLCGHEFDNKCIMEWFKVRYNCPLC

Supplemental Table VI. Previously characterized RING-containing proteins found to contain incomplete or no RING domain

AGI/Name	Comments	Predicted Protein Sequence of RING domain (position of putative metal ligands are underlined)
At2g39810 /HOS1	Incomplete RING, missing metal ligand 1 or 2.	LAS <u>C</u> GRFVNYVLN <u>P</u> <u>C</u> <u>G</u> <u>H</u> ASL <u>C</u> TE <u>C</u> QRC <u>D</u> V <u>C</u> <u>P</u> <u>I</u> <u>C</u>
At5g02310 / CER3	Incomplete RING, missing metal ligand1/2 or incorrect metal ligand spacing.	AEN <u>C</u> SEKNSVGGPSTLQGRFPDIRSRQTSRRPDAGSDGFHPID <u>C</u> DGVYLSS <u>C</u> G <u>H</u> AV <u>H</u> Q <u>S</u> <u>C</u> LERYLKSLKERSGRRTVFEGAHIVDLKKKEFL <u>C</u> <u>P</u> <u>V</u> <u>C</u>