Table S3. Amino acid sequences of ALMTs in pumpkin

Gene ID and Name	Amino acid sequences
CmaCh02G014150 (CmaALMT1)	MNGKTGNTVIDIDFSTKPEPIGAKAENLAASCKAPIGSVLGFCKEDSN RVLFSLKVGLAVVLVSLLILFRAPYDVFGTNIIWAIITVAIMFEYTVGAT FNRGFNRALGSLLAGILAIAVAQLALRTGPIAEPIIIGISIFLVGSVTSFMK LWPSLVPYEYGFRVLLFTYCLIVVSGYRMGNPLRTAMDRLYSIAIGGF VAVLVNVLVFPIWAGEQLHKDLVATFNSLADSLQECVDKYLEDEGSVH NIGQQLPKAVMDEFPEEPAYKKCKATLNSSAKFEALATSAKWEPPHGR FRHFFYPWTEYVKVGAVLRYCAYEIMALHGVLHSRIQAPYKLRITFKS EIQETANQAAELLRSLGKDINNMQQSLKIYLLKNVHTAADKLQQALH THSYPLTPTCASLHLSSKLQSKLSTASSNSLYDLPSLLAELNGNGPERS LNQQNSHGVAAGTQAEAYVEFVRKQSRRQNSWPLREMDVFDDDGG VPVEFLQRMRKLESTAATSLANFTSLLIEFVARLDYLVETVDELSKMA KFKDIIIS
CmaCh04G015300 (CmaALMT2)	MTGKYGSIRQSFLDQNREQLLSRKGHSDFGLHGNDDAGADDDAKCR CFCTVSDAITNFWKGLHDTTVKLCDMSRSDPRKFYFAAKMGLSLALT SLLIFIREPLKEVAQYSIWAILTVVVVFEFSVGATLNKGFNRALGTLSA GGLALGIAEISVSAGEFEEVAIVISIFLAGFFASYCKLYPPMKTYEYGFR VFLLTFCIVLVSGSSSSFFHTAFYRLLHIAVGAGMCLVVNICIYPIWAGE DLHKLVVKNFKNVSSSLEGVVSEYLQCVEYERVSSKILTYQASDNPIY NAYRSAVQSSSQEDTLLDFARWEPPHGPYKTFKYPWHNYVKVSGALR HCAFMVMAMHGCILSEIQAPPEKRKVFAKELQRVGTEGAKFLRALGS KVEKMEKLSSGDMLFDVHDAAEALQIKIDERSNMLVNSDRWRTGKQ HREQEEPQHFIDVKDDHNKQLVIDSLNETMYAQHSSIGVHPPMTEWV STDNVFNKHLVSWPRLSFLMDTVPNERESKVHESASSLSLATFASLLIE FVARLQNLRNAFEELNRVFLFLWSLSLSFFLSDDRFLKLSQPGH
CmaCh06G005250 (CmaALMT3)	ISCKVLAMEILKNKAMEVAMKVKKLGQDDPRRIIHSIKVGVALTLVSL FYYWRPLYDGFGASGIWAVITVVVIFEFTVGATLSKGFNRGLGTLLAG GLGVGVDYLANLSGQKGEPFVLGVFVFLIAASATFSRFFPGIKARYDY GVLIFILTFSMVSVSAYRFDEFLMMAYQRLSTIVAGGAICIIICIVVCPV WAGETLHNLVTSNLDKLGDYLEGFGGEYFYCCDDEEQANFARWEPK HGNFSFRHPWKHYLKIGSYARQCAYHIQVLNTHLNFQPPNLSQFRTIIQ VQCNTLSSESGKALKALATAMKTMSDPSPTSQVHLNAAKSAINDLKN CLKSATTQTPDECSNLLAIIPDATVASILIEIVKSVEDLCEAVGELSVKA HFKSVEGSVAVEKPQLLHRGAIKPFVEAEDEGENGHVVITVREIDNED SPQKKGSSDTNGLVNKK
CmaCh07G008230	MLAMAADQPKLGAMSVMERIVKLGRDDPRRIIHSLKVGLALTFVSLL

(CmaALMT4)

YYWRPLYDGFGIAAIWAVLTVVVIFEFTVGATLSKGLNRGLGTLLAGA
LGVGAQHFASLFGQIGEPIVLGFFVFLLAAASTFSRFFPRIKARYDYGV
LIFILTFSLVSVSGYRVEKILELAHQRLSTILIGGATCIFISLFICPVWAGE
SLHNIIVSNIEKLANYLEGFGGEYFRYEDRENVDEDSTHNKSSSLQAY
KTVLTSQSSEESLANFASWEPRHGKFSFRHPWKQYLKIGSLARQCAYQ
IESLNGYINVPTDIQVAIQFRRRIEESCNAISSESGKALRILASSIKTMTN
PSLSSKTHIENATAAIDELKNTLKTGYMESSDLLGIIPDATVCCILIDIVK
SVEKILEAIEELGVLASFKSVEPTVSPEKSTQLLHRGIVNPLFDGECGD
HVVIMVDNEVEVGKSQGLEGKPSNGEMVCK

CmaCh08G001080

(CmaALMT5)

MASGGSLEWRVNVGDGATEVLRPEGSFVSRMVMGVKGFVWGLFMK
GWMFLEKAWGIANSEPKKAVHGLKVGLALSIVSVFYYMRPLYEGIGG
NAMWAIMTVVVTFESSVGATFYKCVNRVIGTSLAGGLGIGVHWVAA
ESGDRFEPIILGISLFLLASATTFSRFIPSIKTKFDYGAMIFILTFCLVSISS
YRVDKLFELAHTRLTTIAIGTSLCIIISMLFCPMWAGSQLHSLVFRNLD
KLADGLDGCVSEYFKNVDDPEMENEDQECHDSKAQSYKCVLNSKAS
EESMANFARWEPAHGRFGFRHPWKQYLEVGVAMRKCAYCIEALHDC
LNSEIKAPNSLKLLLVEPCKALSTSSSKVLKELSIVIKTMKKSTKIDLEV
SDMNIAVQELQAAIASFPSTQTANEEHEAATIPPLMELLPLATLVSLLIE
TASRIEHVVNAVETLANVANFDSEEEKKRSCLDNNDHVAMRVFPEA

CmaCh10G002420
(CmaALMT6)

MAAKYGSFKQSFAEKRERLLSAKEFPDLIYGTLQDNPSFCSSFRSVPY
RISNLWNSVQDVLCKSWQMGVSDPRKIVFSAKMALALTLISLLIFFKQ
PVEELSRYSVWAILTVVVVFEFSIGATLSKGLNRGLGTLSAAGLALGM
AGLSVLAGEWEELVVAISIFITGFFATYAKLYPTMKPYEYGFRVFLLTY
CFIMVSGYRTRDFIHTAITRFLLIALGAGVCLVVNICIYPIWAGEDLHNL
VVKNFAGVAASLEGCVDSYLNCVEYERIPSKILTYQASDDPLYKGYRS
AMESMSQEESLMGFAIWEPPHGRYKMLKYPWKSYVEVAGALRHCAF
AIMGLHGSILSEIQAPAERRHVFRNELRRVSYEGAKVLHELGNKLKK
METLDCAAILSEVHDAAEELQKKIDAKSYLLVNSESWEIGNHHDDNV
GRSQELLNMDDEETRFHEYRSLSEAVLDLRAFPVPKTWNDPRPSDINS
VQAAAFPPTNKMFKKLGSWPAQVSNKPNGVIHAEESKTYENASALSL
ATFTSLLIEFVARLQNVVDSFEELSKKAKFKDPMERETSKAPEC

CmaCh10G008660
(CmaALMT7)

MEMGSDEKVGLMSGRFVWVKGLFAKLVEVANKTRALGKDDPRRVIH
SLKLGLTLTIVSMLYYYKPLFANFGVSAMWAVITVVVVFEFSVGATLG
KGLNRAFATLFAGALGAGAHHLAALSGHVGQPIITSIFVFLLACILTFM
RFFPSIKAKYDYGMMIGILTFSFVSISGVGDDEILLLLQKRVSTIFLGVC
VCVVISIFISPFWAGQDLHNRIALNIENLALFFEGYGSVEYFKTLQDRE
AKDDKSIQAYKSILKSSGIEDTLYNFARWEPGHGCFQFRHPWKQYLKI
GALTYQCAFRIDALHRNLSSSSFQVSQEIQTQIQEPCMEMSMETGKAL

	RQLVSSIREMTQPTLAEIHTNNSKAAAKKLKASLKSSRLWENCDLLTL IPAANVGTLLVDVVDITEKIAEAVQELASLAHFKAAKPADSAIQSEKEK LEPNIGALVGLSFQVGVNGNFGSYAALAVEMSDEKNEGVLARWGEG LKAKSSSLKAKVVELLRKTKKLAKDDPRRIVHSFKVGLAITLVSLFYY FEPLYDGLGASAMWAVLTVVVVFEFSVGATLGRGLNRVLATSLAASL GFGAHFLADLAGDKAQPVILSLSVFIFAAITTFIRFFPRIKARYDYGFLIF ILTFCLVSVSGYRDDEILQVAYRRALTILLGTFIAILICLFICPVWAGDDL HSLVSNNIQLLANFLQGFGVQYSNESKEDELLEGCKSVLTSRQTEESL VNFARWEPRHGAFKFRHPWKQYRKIGSLTRQSAYRLESLNSYLVTET QTPLHIRDRLMKSCSKMSIESSNALEDIASDLRTMTQPTFPNPHIEKSK AAMKDLKAALKIGPGDGDIDLLEIVPIATVASLLIDTISCIEKIAESVGE LGSLANFKCVEAGKSSGLELEQEHQKLPNSAIVNDHCHVVIVD
CmaCh10G008670 (CmaALMT8)	MATEKSSNEYEGLLPFCLRWVKPIFTKLPAMAVELATMTKKLAKDDT RRVVHALKVGLAITLVSLFYYFKPLYDGFGTSTIWAVVTVVVVFEFSV GGTLGRGLNRVMATLLAGALGFGAHYLASLGGDTGRPIMLGLFVFVL AAISTFIRFFPKMKARYDYGLLIFILTFCMVSLSGYRDDEIAKLAYSRM LTILIGCCFTVFVCVFVCPVWAGTDLHHLVASNIDSLATFFHGFGAEYF GLLQEQGEVGKVDMQKYRTVLNSKSNEESLTNLARWEPRHGKFRYR HPWKVYLEIGSLNRECACRLEVLNGYLQTKRTQVRFDASFAR
CmaCh11G002660 (CmaALMT9)	MVAKYGSFKHSFAERRERLLSAKEFPDLAFGAFQTIQENPSSCSPFLGI SRLWKSAKDVVYEAWQMGVSDPRKIVFSAKMGLALMLISLLIFFKQP VEELSRYSVWAILTVVVVFEFSIGATLSKGFNRGLGTLSAGGLALGMA ELSVLAGDWEEVVVVISIFITGFFATYAKLYPTMKPYEYGFRVFLLTYC FIMVSGYRTREFIHTAVTRFLLIALGAGVCLVVNICIYPIWAGEDLHNLV VKNFAGVAASLEGCVDNYLNCVEYERIPSKILTYQASDDPLYKGYRSA VESMSQEESLMGFAIWEPPHGRYKILKYPWKNYVQVAGALRHCAFAV MALHGCILSEIQAPAERRQVFGNELRRVGYEGAKVLRELGNKLKRME TLDSASILSEVHDAAEELQKKIDAKSYLLVNSESWEIGNRSEDVGQPQ ELLNLDDEETRFREYRSLSEAVLDLRAFPVPKSSDYTVSSDMNSIHSAA VPPTKMFKKLGSWPAQISVKPNGVIQEESKTYENASALSLATFTSLLIE FVARLQNLVDSFDELSAKATFNDPVEWENLKSPGFWRRFCNCFKV
CmaCh11G009010 (CmaALMT10)	MVEGSKETLTNDHHGWLKAKAWKLHKKMVELLNNATKVGKDDPR RIVHSLKLGLAITTVSLFFYFEPLYDGLGASSIWAIITVVVVFEFSVGAT LGKGMNRAIATLIAGAIGFGAHYITSFTGNIWHPILLGILIYTISATASYC RFFPKLKAKYDYGLLIFILTFNMVALSGFRDDEILKLAWHRLANILVG AFIAVAICIFVRPVWAGADLHQFVATNIENLGTFLEGFGIEYFGACQGE MVGGGNVMKYRSVLCSKQNEEALKIGTLSRDCAYCFEILNLYLNTDQ IQLPLEIQRQYQEQCVQVCIESSKALKAMAKALRDIVPPALAKSHIEIA

	KKTAGELKLLLASSHFHGDMNMVSTTTLILLLIDSFSCVEKIVDSIHEL VSLARLNTALQKSDVTPTEQKGSGDKASSQPHHIVTIAQSQFADLLLC NKAMATQALVSSSSLTSSVGAARQRLGPKPSLGSSRKAASFVVRAEAT PPVKQGANRQLWFASKQSLTYLDGSLPGDYGFDPLGLSDPEGTGGFIE PKWLAYGEVINGRFAMLGAAGAIAPEIFGSLGLIPPETALPWFKTGVIP PAGTYNYWADPYTLFVLEMALMGFAEHRRFQDWYNPGSMGKQYFL GLEKFLGGSGDPAYPGGPLFNPLGFGKDEKSMKELKLKEIKNGRLAM LAILGYFIQGLVTGVGPYQNLLDHLSDPVNNNVLTSLKFH
CmaCh11G009020 (CmaALMT11)	MEMGSDEKVGLMRKGFEWVKKWVKGLVGKLVEVRSKATALGKDD PRRVIHSLKLGLALTIVSILYYYNPLYANFGVSAMWAVMTVVVVFEFS VGATLRKGLNRTFATLFAGALGAGAHYLAALSGHVGQPIITSIFVFLLA CILTFMRFVPSIKAKYDYGMMIGILTFALVSISGIQDDEVVLLFEKRISTI FLGVCVCVLISISISPVWAGQDLHNRIALNIENLAIFLEGYGSVECLKSL QDEQFTQEYKSILKSSGIEETLYNSARWEPGHGCFQFRHPWNQYLKIG ALTSQCAFRIDALCRNLSSSNIQVSQKIQTEIQETCMEMSMESGKALR QLVSSIRELTQPTRAQIYTHNSKSAAKRLKTSLRSSHLWEDCDFLTLIPA ATVGLLLVDVVECTEKISEAVQELASLAHFKSGKAEPMQSEKEKVQP NIGVAFVTIPISSV
CmaCh14G003580 (CmaALMT12)	MGIEAVKNKAMEIAMKIKKLGQDDPRRIIHSIKVGVALTLVSLFYYWK PLYDGFGASGIWAVMTVVVIFEFTVGATLSKGLNRGLGTLLAGSLGVG VNYLANLSGQKGEPFVLGIFVFLIAASATFSRFFPGIKARYDYGVLIFIL TFSLVSISGYRMDEFLTLAHQRLSTILVGGAICIMISILVFPVWAGETLH NSVTSNINKLADYLEGFGGEYFYCCEDGEHGVATEKDKSFVEGYKAV LNSKSMEDSMANFARWEPKHGKFRFRHPWKHYLKIGSLTRHCAYQIE ALNRHLCPQLQTQDPSQLRRMIEVPCKTLSSESGKALKALATGMKAM TNPSPSSQVHLNAAKSAMNDLKDSLKLTTAQTTNLLAIIPDATVASILIE IVKSVEDLSEAVVELSLKAHFKSIEATVSPEKPQLLHKGTINPFVEAED EQPHVVIRVRGTEDEDLTEKKGSSGTTSLPT
CmaCh18G010330 (CmaALMT13)	MAGKYGSIRQSFLDQNREKAFSRKGYSDFGLNSYDGAGDNVKCRCF RTLTDSITNFLKGLRDTTVKLYEMGRSDPRKIFFAAKMGLSLAFVSLVI FFREALKEVGQYTIWAILTVVVVFEFSVGATLSKGFNRALGTFSAGGL AIGIAELSVLAGPFKEVIIVISIFLAGFFASYCKLYPPMKSYEYGFRLDFA CWEPPHGPYKTFNYPWYNYVRVSGALRHCAFMVMAMHGCILSEIQA PPEKRKVFAKELQRVGTEGAKFLRELGSKVEKMEKLSSVDMLLDVH DAAEALQMKIDEKSDILVNSANWRPGKQHKEHEDLQHLIDTKDDHG RQLVIESLNDTLDAQHSSIGFNPSITEWVSTESVFNKHLVSWPRLSFLN DTVPNERESKVYESASSLSLATFTSLLIEFVARLQNLLNAFEELSEKAN FKSPAEIKIEKEKVGCDVKEVDCAVRLRCAAAAAAALRVLNILLHAQA

	CQSDLISIAVRAAFCLIWISLLYFVVDRKGIRSYGALILSTCILHVRKAR VYRKRFYRKSLYKMSMVHEPLYPIAVLIDELKNDDIQLRLNSIHRLSTI ARALGEERTRKELIPFLSENNDDDDEVLLAMAEELGVFIPYVGGVEH AHVLLPPLETLCTVEETCVRDKAVESLCRIGSQMRESDLVDWFIPLVK RLAAGEWFTARVSACGLFHIAYPSAPEMLKTELRSMYGQLCQDDMP MVRRSAATNLGKFAATIEPAHLKTDTMTIFEDLTQDDQDSVRLLAVEG CAALGKLLEPQDCVSHILPVMVNFSQDKSWRVRYMVANQLYELCEA VGPEPTRTDLVPAYVRLLRDNEAEVRIAAAGKVTKFCRILSPELAIQHI LPCVKELSSDSSQHVRSALASVIMGMAPVLGKVIHPSTRGIDGLTSLP VLFNDATIEQLLPIFLSLLKDEFPDVRLNIISKLDQVNQVIGIDLLSQSLL PAIVELAEDRHWRVRLAIIEYIPLLASQLGVGFFDDKLGALCMQWLQD KILVLWTRIPKFYRGGYPYPSRRAMEKCLVYIWGQKANFGCFFDGDL VYSIRDAAANNLKRLAEEFGPEWAMQHIVPQVLDMINNPHYLYRMT VLRAVSLLAPVMGSEITCTKLLPVVISSSKDRVPNIKFNVAKVLQSLIPI VDQPITLAMQVVEKTIRPSLVELSEDPDVDVRFFANQALQSIDHNLKR MANSFMNHIIDQLTLSM
CmaCh19G000480 CmaALMT14	MGSAVVVSIPEEIQDQRVTDDVPVDQNKNKNKNKTAAVNKFRNLFDS TRDRIKKQDMKKIFHSIKLGIALVVVSLLYLLNPLYKQVGDNAMWAI MTVIVVFEFYAGATLSKGLNRGLGTIFGGGLGCFAGSFAQDVGGVAC ASIIGVSVFVFGGIATYLRLIPSIKKKYDYGVMISILTFNLVVVSGMREE KIMALARERLSTIAMGFAVCIFINLLIFPAWASDELHHSTVQSFHNLAN SIQGCMEDYFSSADDKKKNKSDASFSSCKAILNTKSKEESLANFAKW EPWHGKFGLNYPWNRYLQIGEVLRELAATVLSIKGCLQSPRQPTSGM REAIKEACEMGGSSIAWALKELGEGIKNMKRCQIEGVIVPKLKLVRQE MSGLITPSKLGVIENGDELAMASFVFLIMEILEKVEEVAREVEELEEAG RFRTT
CmaCh19G004590 (CmaALMT15)	MQVNKHIQVTMDKIQHFPVLCWKTSKKVGAEDPRRIIHSLKVGLSLT LVSLLYLIEPLFKRIGSNATWAVMTVVVVLEFTAGATLCKGLNRGLGT LLAGSLAFFIEGVANRSGRVFRACFIGAAVFLIGAAATYMRFFPKIKKN YDYGVVIFLLTFNLITVSSYRVDNVLKIAHDRLYTIAIGCGVCLLMSLL IFPNWSGEELHNSTVLKLEGLAKSIEGCVNEYFFDTEIDDNKESCSGD QIYKGYKAVLDSKSIDESLALQASWEPRHSSHCYRIPWQQYVKLGGV LRHFGYTVVALHGCLQTEIQTPRSVRILFKDPCTRVAREVSKALIELAN SIRNRRHCSPEILSDHLHEALQDLNKAIKSQPRLFLGSNRNKASNMLA LAAAEAGQKRCRSGGSLSSVKTDSSALMEWKTKRASVQSREAERKV LRPQLSKIAITSLEFSEALPFAAFASLLVETVAKLDNIIDEVEELGRIACF KEFINGDDQEQQHITVKCEKPNINVSQNQLSSVSGAE