

**Additional file 5: Accession numbers and genome coordinates of ammonium transporter/ammonia permease genes included in the phylogenetic tree**

<b>Organism, gene abbreviation</b>	<b>GI number or GenBank accession number for DNA</b>	<b>Genome Region</b>	<b>GI number for mRNA</b>	<b>Clade</b>
<b>EUKARYOTES</b>				
<b>Green plants (Viridiplantae; green algae and land plants)</b>				
<i>Arabidopsis thaliana</i> , AtAMT2	GI:240254678	(16039475..16042383)	GI:42569729	MEP $\alpha$
<i>Cryptomeria japonica</i>	N/A	N/A	GI:114841288	MEP $\alpha$
<i>Lotus japonicus</i> , LiAMT2	N/A	N/A	GI:15799271	MEP $\alpha$
<i>Medicago truncatula</i> , MtAMT2	N/A	N/A	GI:22900885	MEP $\alpha$
<i>Micromonas</i> sp. RCC299, 2	GI:255081797	579223..580970	GI:255079969	MEP $\beta$
<i>Oryza sativa</i> , OsAMT2;1	GI:28875520	N/A	GI:19909967	MEP $\alpha$
↳ <i>Oryza sativa</i> , OsAMT2;2	GI:115442598	(35590381..35592277)	GI:28875522	MEP $\alpha$
<i>Oryza sativa</i> , OsAMT2;3	GI:20160632	109596..111823	GI:20160632	MEP $\alpha$
<i>Oryza sativa</i> , OsAMT3;1	GI:115442598	37720693..37731081	N/A	MEP $\alpha$
<i>Oryza sativa</i> , OsAMT3;2	GI:28269486	77711..81059	GI:32985620	MEP $\alpha$
<i>Oryza sativa</i> , OsAMT3;3	GI:46390229	104575..107816	N/A	MEP $\alpha$
<i>Ostreococcus lucimarinus</i> CCE9901, 3	GI:145327766	(334523..336339)	GI:145348948	MEP $\beta$
<i>Ostreococcus lucimarinus</i> CCE9901, 4	GI:145335532	34720..37072	GI:145356297	MEP $\beta$
<i>Physcomitrella patens</i> subsp. patens, 2.1	GI:168004612	1799359..1802286	GI:168004232	MEP $\alpha$
<i>Physcomitrella patens</i> subsp. patens, 2.2	GI:168058452	(46510..48246)	GI:168058414	MEP $\alpha$
<i>Physcomitrella patens</i> subsp. patens, 2.3	GI:168035123	(956773..959548)	GI:168052163	MEP $\alpha$
<i>Physcomitrella patens</i> subsp. patens, 2.4	GI:168052203	(228592..232717)	GI:168035109	MEP $\alpha$
<i>Physcomitrella patens</i> subsp. patens, 2.5	GI:167999745	(1405866..1407695)	GI:167999617	MEP $\alpha$
<i>Physcomitrella patens</i> subsp. patens, 2.6	GI:168020770	823947..825718	GI:168020544	MEP $\alpha$

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<i>Physcomitrella patens</i> subsp. <i>patens</i> , 2.7	GI:168003095	(2804682..2807626)	GI:168003073	MEP $\alpha$
<i>Picea sitchensis</i>	N/A	N/A	GI:148909475	MEP $\alpha$
<i>Populus trichocarpa</i> , <i>PtrAMT2</i> ;1	GI:116256301	(7169018..7171902)	GI:224091027	MEP $\alpha$
<i>Populus trichocarpa</i> , <i>PtrAMT2</i> ;2	GI:116256311	(11521306..11523746)	GI:224140458	MEP $\alpha$
<i>Populus trichocarpa</i> , <i>PtrAMT3</i> ;1	GI:116256298	(26343416..26346328)	GI:224060484	MEP $\alpha$
<i>Populus trichocarpa</i> , <i>PtrAMT4</i> ;1	GI:116256317	(3007991..3009863)	GI:224066328	MEP $\alpha$
<i>Populus trichocarpa</i> , <i>PtrAMT4</i> ;2	GI:116256313	5044547..5046163	GI:224141842	MEP $\alpha$
<i>Populus trichocarpa</i> , <i>PtrAMT4</i> ;3	GI:116256320	14994950..14996903	GI:224082701	MEP $\alpha$
<i>Populus trichocarpa</i> , <i>PtrAMT4</i> ;4	GI:116256308	2765333..2767047	GI:224123403	MEP $\alpha$
<i>Populus trichocarpa</i> , <i>PtrAMT4</i> ;5	GI:116265052	(87989..89560)	GI:224133945	MEP $\alpha$
<i>Selaginella moellendorffii</i> , 2.1 <sup>1</sup>	scaffold 37	(1469550-1470973)	N/A	MEP $\alpha$
<i>Selaginella moellendorffii</i> , 2.2 <sup>1</sup>	scaffold 62	(1059095-1060581)	N/A	MEP $\alpha$
<i>Selaginella moellendorffii</i> , 2.3 <sup>1</sup>	scaffold_28	1038805-1040650	N/A	MEP $\alpha$
<i>Vitis vinifera</i> , 2.1	gi157357314	580580..583260	N/A	MEP $\alpha$
<i>Vitis vinifera</i> , 2.2	gi157351961	1965726..1969581	N/A	MEP $\alpha$
<i>Vitis vinifera</i> , 2.3	GI:157339171	4545828..4548058	N/A	MEP $\alpha$
<i>Vitis vinifera</i> , 2.4	gi157347782	2402288..2404788	N/A	MEP $\alpha$
<i>Vitis vinifera</i> , 2.5	gi157351961	1965726..1969581	N/A	MEP $\alpha$
<i>Vitis vinifera</i> , 2.6	gi157329134	88960..90484	N/A	MEP $\alpha$
<i>Vitis vinifera</i> , 2.7	gi157344876	468779..471094	N/A	MEP $\alpha$
<i>Vitis vinifera</i> , 2.8	gi157344876	487711..495387	N/A	MEP $\alpha$
<b>Fungi</b>				
<i>Aspergillus fumigatus</i> , <i>meaA</i>	GI:71025129	1654974..1656856	GI:70989734	MEP $\gamma$
<i>Aspergillus fumigatus</i> , <i>mep2</i>	GI:71025128	(2853321..2854904)	GI:70995403	MEP $\gamma$

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<i>Aspergillus fumigatus, mepA</i>	GI:71025132	(2822229..2823889)	GI:70997608	MEP $\gamma$
<i>Aspergillus nidulans, meaA</i>	GI:18693012	1478..>3330	N/A	MEP $\gamma$
<i>Aspergillus nidulans, mepA</i>	GI:18693014	1815..3504	N/A	MEP $\gamma$
<i>Batrachochytrium dendrobatidis</i> <sup>B</sup>	Supercontig 1	359666-361321	N/A	MEP $\gamma$
<i>Candida albicans, MEP1</i>	GI:68468731	(19689..21293)	GI:68468505	MEP $\gamma$
<i>Candida albicans, MEP2</i>	GI:68485553	54760..56202	GI:68485539	MEP $\gamma$
<i>Candida albicans, 3*</i>	GI:68484429	66692..68434	GI:68484407	N/A
<i>Cladonia grayi, mep1a</i>	JF833071	N/A	N/A	MEP $\alpha$
<i>Cladonia grayi, mep1b</i>	JF833070	N/A	N/A	MEP $\alpha$
<i>Cladonia grayi, mep 2</i>	JF833072	N/A	N/A	MEP $\gamma$
<i>Cladonia grayi, mep3</i>	JF833073	N/A	N/A	MEP $\gamma$
<i>Coccidioides immitis, 1</i>	GI:119185453	(3257148..3258822)	GI:119184212	MEP $\gamma$
<i>Coccidioides immitis, 2</i>	GI:119197146	2610936..2613096	GI:119193249	MEP $\gamma$
<i>Coprinopsis cinerea okayama7#130, 1</i>	GI:169866184	17197..18998	GI:169866180	MEP $\gamma$
<i>Coprinopsis cinerea okayama7#130, 2</i>	GI:169866153	6758..8559	GI:169866149	MEP $\gamma$
<i>Coprinopsis cinerea okayama7#130, 3</i>	GI:169844956	27679..29664	GI:169844550	MEP $\gamma$
<i>Coprinopsis cinerea okayama7#130, 4</i>	GI:169850323	(130995..133174)	GI:169850235	MEP $\gamma$
<i>Cryptococcus neoformans var. neoformans JEC21, AMT1</i>	GI:58271746	(585837..588247)	GI:58258402	MEP $\gamma$
<i>Cryptococcus neoformans var. neoformans JEC21, AMT2</i>	GI:58271747	(549599..551680)	GI:58259901	MEP $\gamma$
<i>Fusarium graminearum PH-1, 1</i>	GI:46562332	1934463..1936246	GI:46107473	MEP $\gamma$
<i>Fusarium graminearum PH-1, 2</i>	GI:46562332	(6866192..6867738)	GI:46110424	MEP $\gamma$
<i>Fusarium graminearum PH-1, 3</i>	GI:46562332	1609324..1611001	GI:46107291	MEP $\gamma$
<i>Fusarium graminearum PH-1, 4</i>	GI:46562343	(765169..766784)	GI:46114441	MEP $\gamma$

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<i>Fusarium oxysporum</i> f. sp. lycopersici 4286, 1	GI:144922572	(54000-55395)	N/A	MEP $\gamma$
<i>Fusarium oxysporum</i> f. sp. lycopersici 4286, 2	GI:144922350	57760-59300	N/A	MEP $\gamma$
<i>Fusarium oxysporum</i> f. sp. lycopersici 4286, 3	GI:144921882	33840-35337	N/A	MEP $\gamma$
<i>Fusarium oxysporum</i> f. sp. lycopersici 4286, 4	GI:144922346	(65941-67381)	N/A	MEP $\alpha$
<i>Fusarium oxysporum</i> f. sp. lycopersici 4286, 5	GI:144922346	66000-67170	N/A	N/A
<i>Gibberella moniliformis</i> 7600, 1	GI:116139414	155125-156539	N/A	MEP $\gamma$
<i>Gibberella moniliformis</i> 7600, 2	GI:116139519	(424078-425576)	N/A	MEP $\gamma$
<i>Gibberella moniliformis</i> 7600, 3*	GI:116139519	~97480~99000	N/A	N/A
<i>Gibberella moniliformis</i> 7600, 4	GI:116139410	132661-134281	N/A	MEP $\alpha$
<i>Gibberella moniliformis</i> 7600 *	GI:116139361	59055-60699	N/A	N/A
<i>Glomus intraradices</i> , <i>Gintamt1</i>	N/A	N/A	GI:124516978	MEP $\gamma$
<i>Hebeloma cylindrosporium</i> , <i>AMT1</i>	N/A	N/A	GI:20501862	MEP $\gamma$
<i>Hebeloma cylindrosporium</i> , <i>AMT2</i>	N/A	N/A	GI:15042692	MEP $\gamma$
<i>Hebeloma cylindrosporium</i> , <i>AMT3</i>	N/A	N/A	GI:15042694	MEP $\gamma$
<i>Laccaria bicolor</i> , <i>AMT1.1a</i>	GI:170092085	(1141763..1143937	GI:170091535	MEP $\gamma$
<i>Laccaria bicolor</i> , <i>AMT1.1b</i>	GI:170115426	153134..155099	GI:17011531	MEP $\gamma$
<i>Laccaria bicolor</i> , <i>AMT1.2</i>	GI:170103048	(848838..851040)	GI:170103012	MEP $\gamma$
<i>Laccaria bicolor</i> , <i>AMT2.1</i>	GI:170086374	(798076..800048	GI:170085394	MEP $\gamma$
<i>Laccaria bicolor</i> , <i>AMT2.2</i>	GI:170110243	25357..26969	GI:170109925	MEP $\gamma$
<i>Laccaria bicolor</i> , <i>AMT2.3a</i>	GI:170112646	(379312..382864)	GI:170112632	MEP $\gamma$

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<i>Laccaria bicolor</i> , AMT2.3b	GI:170112646	(368498..370363)	GI:170112630	MEP $\gamma$
<i>Laccaria bicolor</i> , AMT2.3c	GI:170115279	60031..61896	GI:170115107	MEP $\gamma$
<i>Laurera megasperma</i> , A	JF833075	N/A	N/A	MEP $\alpha$
<i>Laurera megasperma</i> , B	JF833074	N/A	N/A	MEP $\alpha$
<i>Magnaporthe grisea</i> 70-15, 1	GI:38104209	14334..16198	N/A	MEP $\gamma$
<i>Magnaporthe grisea</i> 70-15, 2	GI:38108755	(22223..23821)	N/A	MEP $\gamma$
<i>Magnaporthe grisea</i> 70-15, 3	GI:38101984	(9146..10992)	N/A	MEP $\gamma$
<i>Microbotryum violaceum</i> , mepA	N/A	N/A	GI:5230671	MEP $\gamma$
<i>Neurospora crassa</i> , 1	GI:164426245	631321..633365	GI:164426202	MEP $\gamma$
<i>Neurospora crassa</i> , 2	GI:157070728	349091..350779	GI:85107332	MEP $\gamma$
<i>Neurospora crassa</i> , 3	GI:164427336	(221738..223494)	GI:85112787	MEP $\gamma$
<i>Neurospora crassa</i> , 4	GI:164426245	631321..633365	GI:164426202	MEP $\gamma$
<sup>5</sup> <i>Parmotrema submarginale</i> (formerly <i>Parmotrema michauxianum</i> )	JF833076	N/A	N/A	MEP $\alpha$
<i>Penicillium chrysogenum</i> , 1	GI:256353024	(8082430..8084162)	GI:255937472	MEP $\gamma$
<i>Penicillium chrysogenum</i> , 2	GI:256353024	(26853194..26855042)	GI:255948191	MEP $\gamma$
<i>Penicillium chrysogenum</i> , 3	GI:211588786	(2625848..2627524)	GI:255954772	MEP $\gamma$
<i>Penicillium chrysogenum</i> *	GI:256353024	(21836862..21838538)	GI:255954772	N/A
<i>Penicillium marneffei</i> , 1	GI:212544102	(1035187..1037338)	GI:212542532	MEP $\gamma$
<i>Penicillium marneffei</i> , 2	GI:212536833	(165518..167568)	GI:212534103	MEP $\gamma$
<i>Penicillium marneffei</i> , 3	GI:212530903	3680024..3682106	GI:212528861	MEP $\gamma$
<i>Penicillium marneffei</i> , 4	GI:212530903	(4869932..4871615)	GI:212529771	MEP $\alpha$
<i>Penicillium marneffei</i> , 5	GI:212534004	212731..214581	GI:212531034	MEP $\gamma$
<i>Pyrenophora tritici-repentis</i> , 1	GI:189192591	2218689..2220719	GI:189189627	MEP $\gamma$
<i>Pyrenophora tritici-repentis</i> , 2	GI:189206496	(1468324..1469966)	GI:189206414	MEP $\gamma$

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<i>Pyrenophora tritici-repentis</i> , 3	GI:189192591	5135420..5137396	GI:189191563	MEP $\gamma$
<i>Pyrenophora tritici-repentis</i> , 4	GI:189196879	1673492..1675071	GI:189196725	MEP $\gamma$
<i>Pyrenophora tritici-repentis</i> , 5	GI:189198580	1673492..1675071	GI:189197910	MEP $\gamma$
<i>Pyrenula cruenta</i>	JF833077	N/A	N/A	MEP $\alpha$
<i>Ramalina</i> sp., A	JF833078	N/A	N/A	MEP $\alpha$
<i>Ramalina</i> sp., B	JF833079	N/A	N/A	MEP $\alpha$
<i>Rhizopus oryzae</i> , 1 <sup>B</sup>	Supercontig 3	(407915-410079)	N/A	MEP $\gamma$
<i>Rhizopus oryzae</i> , 2 <sup>B</sup>	Supercontig 9	(212386-214521)	N/A	MEP $\gamma$
<i>Rhizopus oryzae</i> , 3 <sup>B</sup>	Supercontig 10	1263026-1264373	N/A	MEP $\gamma$
<i>Rhizopus oryzae</i> , 4 <sup>B</sup>	Supercontig 10	1726208-1727707	N/A	MEP $\gamma$
<i>Rhizopus oryzae</i> , 5 <sup>B</sup>	Supercontig 4	(668186-669408)	N/A	MEP $\gamma$
<i>Saccharomyces cerevisiae</i> , MEP1	GI:162949218	(731454..732932)	N/A	MEP $\gamma$
<i>Saccharomyces cerevisiae</i> , MEP2	GI:117937805	357455..358954	N/A	MEP $\gamma$
<i>Saccharomyces cerevisiae</i> , MEP3	GI:50593503	(810980..812449)	N/A	MEP $\gamma$
<i>Schizosaccharomyces pombe</i> , amt1	GI:63054406	2069806..2071299	GI:68037248	MEP $\gamma$
<i>Schizosaccharomyces pombe</i> , amt2	GI:162312575	1731627..1733165	GI:67999505	MEP $\gamma$
<i>Schizosaccharomyces pombe</i> , amt3	GI:162312575	(2924893..2926446)	GI:68000034	MEP $\gamma$
<i>Sclerotinia sclerotiorum</i> , 1	GI:156053526	(748453..750262)	GI:156052866	MEP $\gamma$
<i>Sclerotinia sclerotiorum</i> , 2	GI:156058194	(1380869..1382769)	GI:156057540	MEP $\gamma$
<i>Sclerotinia sclerotiorum</i> , 3	GI:156056511	145159..146698	GI:156055065	MEP $\gamma$
<i>Stereocaulon tennesseense</i>	JF833080	N/A	N/A	MEP $\alpha$
<i>Talaromyces stipitatus</i> , 1	GI:242771011	(4296843..4298562)	GI:242768291	MEP $\gamma$
<i>Talaromyces stipitatus</i> , 2	GI:242797504	(198426..200031)	GI:218717854	MEP $\gamma$
<i>Talaromyces stipitatus</i> , 3	GI:242771011	(2855574..2857925)	GI:242765292	MEP $\gamma$
<i>Talaromyces stipitatus</i> , 4	GI:242771011	1387342..1389023	GI:242762291	MEP $\alpha$

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<i>Talaromyces stipitatus</i> , 5	GI:218721414	259064..260882	GI:242771613	MEP $\gamma$
<i>Trypethelium virens</i>	JF833081	N/A	N/A	MEP $\alpha$
<i>Tuber borchii</i> , AMT1	N/A	N/A	GI:17221149	MEP $\gamma$
<i>Usnea mutabilis</i> , A	JF833082	N/A	N/A	MEP $\alpha$
<i>Usnea mutabilis</i> , B	JF833083	N/A	N/A	MEP $\alpha$
<i>Ustilago maydis</i> 521, <i>mep1</i>	GI:49083521	(110635..112196)	GI:71023612	MEP $\gamma$
<i>Ustilago maydis</i> 521, <i>ump2</i>	GI:49083411	45715..47301	GI:71020878	MEP $\gamma$
<b>Slime molds (Amoebozoa)</b>				
<i>Dictyostelium discoideum</i> AX4, <i>amtC</i>	GI:269316041	1034624-1036114	GI:31323876	grade
<b>Chromalveolates</b>				
<b>Stramenopiles (Heterokonts)</b>				
<i>Phytophthora infestans</i> T30-4, 1 <sup>†</sup>	>gnl WGS:AATU c ont1.466	35000-39000	N/A	MEP $\beta$
<i>Phytophthora infestans</i> T30-4, 2 <sup>†</sup>	>gnl WGS:AATU c ont1.2760	2830-4800	N/A	MEP $\beta$
<i>Phytophthora infestans</i> T30-4, 3 <sup>†</sup>	>gnl WGS:AATU c ont1.8908	1-700	N/A	MEP $\beta$
<b>Excavates</b>				
<b>Euglenozoa</b>				
<i>Trypanosoma cruzi</i> strain CL Brener	GI:70876681	73022-74566	GI:71421943	grade
<b>Heterolobosea</b>				
<i>Naegleria gruberi</i> , <i>amtA</i> <sup>†</sup>	scaffold_4	165684-167083	N/A	grade

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<b>PROKARYOTES</b>				
<b>Archaea</b>				
<i>Archaeoglobus fulgidus, amt-1</i>	GI:11497621	879899..881074	N/A	MEP $\alpha$
<i>Archaeoglobus fulgidus, amt-3</i>	GI:11497621	1570632..1571798	N/A	MEP $\alpha$
<i>Caldivirga maquilingensis IC-167</i>	GI:159040592	715687..717117	N/A	MEP $\alpha$
<i>Ferroplasma acidarmanus</i>	GI:126008996	221620..222921	N/A	MEP $\alpha$
<i>Methanosarcina acetivorans C2A, amtB (1)</i>	GI:20088899	4815556..4816764	N/A	grade
<i>Methanosarcina barkeri Meth_1922, 2</i>	GI:23052039	(985..2202)	N/A	grade
<i>Methanosarcina barkeri Meth_1922, 1</i>	GI:23052039	(2418..3617)	N/A	MEP $\beta$
<i>Methanosarcina mazei Go1 1</i>	GI:21226102	881714..882913	N/A	MEP $\beta$
<i>Methanosphaera stadtmanae DSM 3091</i>	GI:84488831	774206-775429	N/A	MEP $\alpha$
$\infty$ <i>Methanothermobacter thermautotrophicus</i> str. Delta H, 1	GI:15678031	588943-590166	N/A	MEP $\alpha$
<i>Methanothermobacter thermautotrophicus</i> str. Delta H, 2	GI:15678031	590781-592019	N/A	MEP $\alpha$
<i>Picrophilus torridus DSM 9790</i>	GI:48477072	1460613-1461911	N/A	MEP $\alpha$
<i>Sulfolobus tokodaii str. 7</i>	GI:24473558	643486-645042	N/A	MEP $\alpha$
<i>Sulfolobus solfataricus</i>	GI:15896971	914084..915613	N/A	MEP $\alpha$
<b>Bacteria</b>				
<i>Acidimicrobium ferrooxidans DSM 10331</i>	GI:256370824	2108845-2110290	N/A	MEP $\alpha$
<i>Acidithiobacillus caldus ATCC 51756, amt-1</i>	ACVD01000125.1	109..834	N/A	MEP $\alpha$
<i>Acidithiobacillus caldus ATCC 51756, amt-</i>	ACVD01000080.1	19056..20363	N/A	N/A



**Additional file 5 (continued):** Accession numbers and genome coordinates of ammonium transporter/ammonia permease genes included in the phylogenetic tree

Organism, gene abbreviation	GI number or GenBank accession number for DNA	Genome Region	GI number for mRNA	Clade
2*				
<i>Acidithiobacillus ferrooxidans</i> ATCC 53993 <i>amt-2</i>	GI:198282148	2491440..2492756	N/A	MEP $\beta$
<i>Acidithiobacillus ferrooxidans</i> ATCC 53993, <i>amt-1</i>	GI:198282148	2497431-2498735	N/A	MEP $\alpha$
<i>Acidithiobacillus ferrooxidans</i> ATCC 23270 <i>amt-2</i>	GI:218665024	2589616-2590932	N/A	MEP $\beta$
<i>Acidithiobacillus ferrooxidans</i> ATCC 23270 <i>amt-1</i>	GI:218665024	2595607-2596911	N/A	MEP $\alpha$
<i>Agrobacterium tumefaciens</i> str. C58 (Cereon), <i>amtB</i>	GI:159184118	2757775..2758980	N/A	MEP $\beta$
<i>Aquifex aeolicus</i> VF5	GI:15282445	69169-70440	N/A	MEP $\alpha$
6 <i>Azoarcus</i> sp. BH72, <i>amtB</i> %	GI:19851906	N/A	N/A	MEP $\beta$
<i>Azorhizobium caulinodans</i> , <i>amtB</i>	GI:2980822	N/A	N/A	MEP $\beta$
<i>Azospirillum brasilense</i> , <i>amtB</i>	GI:3136067	N/A	N/A	MEP $\beta$
<i>Azotobacter vinelandii</i> DJ, <i>amtB</i>	GI:226942170	4846081-4847397	N/A	MEP $\beta$
<i>Azotobacter vinelandii</i> , <i>amtB</i>	GI:29359385	165528..166787	N/A	MEP $\beta$
<i>Bacillus cereus</i> ATCC 14579	GI:30018278	(1135908..1137140)	N/A	MEP $\beta$
<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168 <i>amtB</i>	GI:255767013	3756790..3758004	N/A	MEP $\beta$
<i>Bifidobacterium longum</i> DJO10A, <i>amtB</i>	GI:29251702	(91351..92583)	N/A	MEP $\beta$
<i>Bifidobacterium longum</i> NCC2705, <i>amtP</i>	GI:58036264	(1382167..1383462)	N/A	MEP $\beta$
<i>Bordetella bronchiseptica</i> RB50, <i>amtB</i>	GI:33575370	(93085..94323)	N/A	MEP $\beta$
<i>Bordetella parapertussis</i>	GI:33573592	(10300..11538)	N/A	MEP $\beta$
<i>Bradyrhizobium japonicum</i> USDA 110	GI:27375111	652211..653227	N/A	N/A

**Additional file 5 (continued):** Accession numbers and genome coordinates of ammonium transporter/ammonia permease genes included in the phylogenetic tree

<b>Organism, gene abbreviation</b>	<b>GI number or GenBank accession number for DNA</b>	<b>Genome Region</b>	<b>GI number for mRNA</b>	<b>Clade</b>
chromosome*				
<i>Bradyrhizobium japonicum</i> USDA 110	GI:27375111	652842..653513	N/A	N/A
chromosome*				
<i>Bradyrhizobium japonicum</i> USDA 110	GI:27375111	655678..657210	N/A	MEP $\beta$
chromosome, amtB				
<i>Brevibacterium linens</i> BL2	GI:62422953	(16634..17854)	N/A	MEP $\beta$
<i>Brevibacterium linens</i> = <i>Burkholderia vietnamensis</i> G4 (1)	GI:134137285	(3282231..3283730)	N/A	MEP $\beta$
<i>Brucella melitensis</i>	GI:17986284	161196..162497	N/A	MEP $\beta$
<i>Brucella suis</i> 1330, amt	GI:56968325	(1831408..1832709)	N/A	MEP $\beta$
<i>Brucella suis</i> ATCC 23445 chromosome I	GI:163673000	1647375-1648676	N/A	MEP $\beta$
<i>Burkholderia fungorum</i> Bcep_273, 1	GI:28873745	45938..47218	N/A	MEP $\beta$
<i>Burkholderia</i> sp. 383 (= <i>Burkholderia cepacia</i> R-18194) (1)	GI:77965403	(3341542..3343056)	N/A	MEP $\beta$
<i>Carboxydotherrmus hydrogenoformans</i> Z-2901	GI:77994731	62220-63536	N/A	MEP $\beta$
<i>Caulobacter crescentus</i> CB15	GI:16124256	(1492580..1494112)	N/A	MEP $\beta$
<i>Chlorobium chlorochromatii</i> CaD3 (= <i>Chlorochromatium aggregatum</i> )	GI:78170183	2533520..2534854	N/A	MEP $\beta$
<i>Chlorobium tepidum</i> TLS, amt-3	GI:21672841	128241..12957	N/A	MEP $\beta$
<i>Chromobacterium violaceum</i> ATCC 12472, amtB	GI:34495455	4329876..4331186	N/A	MEP $\beta$
<i>Clostridium acetobutylicum</i> , nrgA	GI:15893970	(787791..789008)	N/A	MEP $\beta$
<i>Corynebacterium efficiens</i> YS-314, 2	GI:25028257	(1790505..1791824)	N/A	MEP $\beta$
<i>Corynebacterium efficiens</i> YS-314, amtP	GI:25028524	(2073802..2075127)	N/A	MEP $\beta$

**Additional file 5 (continued):** Accession numbers and genome coordinates of ammonium transporter/ammonia permease genes included in the phylogenetic tree

<b>Organism, gene abbreviation</b>	<b>GI number or GenBank accession number for DNA</b>	<b>Genome Region</b>	<b>GI number for mRNA</b>	<b>Clade</b>
<i>Corynebacterium glutamicum</i> ATCC 13032, 2	GI:58036263	1675265-1676623	N/A	MEP $\beta$
<i>Corynebacterium glutamicum</i> ATCC 13032, 1	GI:58036263	(2172151..2173467)	N/A	MEP $\beta$
<i>Cyanothece</i> sp. PCC 7822	GI:196258658	210450..211856	N/A	MEP $\beta$
<i>Cytophaga hutchinsonii</i> , amtB, 1	GI:110636427	(3786660..3787988)	N/A	N/A
<i>Dechloromonas aromatica</i> RCB, 1	GI:71845263	62898..64397	N/A	MEP $\beta$
<i>Deinococcus radiodurans</i>	GI:15805720	708354..709673	N/A	MEP $\beta$
<i>Desulfitobacterium hafniense</i>	GI:30471518	19330..20676	N/A	MEP $\beta$
<i>Desulfococcus oleovorans</i> Hxd3, 2	GI:158520017	(633089-634375)	N/A	MEP $\alpha$
<i>Desulfococcus oleovorans</i> Hxd3, 1	GI:158520017	(634397-635680)	N/A	MEP $\beta$
<i>Desulfovibrio desulfuricans</i> G20, 1	GI:28877455	62208..63413	N/A	MEP $\beta$
$\Pi$ <i>Desulfovibrio desulfuricans</i> , 2	GI:78217452	(2328899..2330104)	N/A	MEP $\beta$
<i>Desulfuromonas acetoxidans</i> , DSM 684 ctg55, 1	GI:95133343	70185..71510	N/A	MEP $\beta$
<i>Enterococcus faecium</i>	GI:22992526	3209..4423	N/A	grade
<i>Escherichia coli</i> B str. REL606*	GI:253972022	445033-446319	N/A	N/A
<i>Escherichia coli</i> str. K-12 substr. MG1655	GI:49175990	472256..473473	N/A	MEP $\beta$
<i>Geobacter metallireducens</i> GS-15, 1	GI:23054753	7603..9069	N/A	MEP $\beta$
<i>Geobacter sulfurreducens</i> PCA, 1	GI:39995111	1009771..1011240	N/A	MEP $\beta$
<i>Geobacter sulfurreducens</i> PCA, 2	GI:39995111	(1324618..1325838)	N/A	grade
<i>Gloeobacter violaceus</i> *	GI:37519569	(2798589..2799443)	N/A	N/A
<i>Gloeobacter violaceus</i>	GI:37519569	3253283..3254719	N/A	MEP $\beta$
<i>Gluconacetobacter diazotrophicus</i> , amtB2*	GI:209542188	1454476..1455855	N/A	N/A
<i>Gluconacetobacter diazotrophicus</i> , amtB1	GI:209542188	669752..671143	N/A	MEP $\beta$

**Additional file 5 (continued):** Accession numbers and genome coordinates of ammonium transporter/ammonia permease genes included in the phylogenetic tree

<b>Organism, gene abbreviation</b>	<b>GI number or GenBank accession number for DNA</b>	<b>Genome Region</b>	<b>GI number for mRNA</b>	<b>Clade</b>
<i>Haemophilus somnus</i> 129PT, <i>amtB</i>	GI:28301892	19208..20506	N/A	MEP $\beta$
<i>Lactobacillus casei</i> , str. Zhang, <i>amtB</i>	GI:300437532	(592027-593343)	N/A	MEP $\beta$
<i>Lactobacillus plantarum</i> WCFS1, <i>amtB</i>	GI:28269805	(318549..319865)	N/A	MEP $\beta$
<i>Lactococcus lactis</i> subsp. cremoris MG1363, <i>amtB</i>	GI:124491690	876626..877867	N/A	MEP $\beta$
<i>Lactococcus lactis</i> subsp. lactis II1403, <i>amtB</i>	GI:13400022	(1635861..1637102)	N/A	MEP $\beta$
<i>Leptospira interrogans</i> serovar lai str. 56601, <i>amtB</i> *	GI:294827553	(3577147..3579492)	N/A	N/A
<i>Leptospirillum rubarum</i> LeptoII_Scaffold_8241	GI:124516098	100910-102217	N/A	MEP $\alpha$
<i>Leuconostoc mesenteroides</i> subsp. mesenteroides ATCC 8293	GI:28876869	51528..52724	N/A	MEP $\beta$
<i>Listeria innocua</i>	GI:16414035	2144..3362	N/A	MEP $\beta$
<i>Listeria monocytogenes</i> EGD-e	GI:1641081	138688..139906	N/A	MEP $\beta$
<i>Magnetococcus</i> sp. MC-1	GI:23000293	19671..20981	N/A	MEP $\beta$
<i>Mesorhizobium loti</i> , <i>amtB</i>	GI:57165207	(3387960..3389315)	N/A	MEP $\beta$
<i>Methanocaldococcus jannaschii</i> , <i>amtB</i> *	GI:15668172	(57588..58763)	N/A	N/A
<i>Methylobacillus flagellatus</i> KT, 1	GI:91774356	2693851-2695236	N/A	MEP $\beta$
<i>Methylobacillus flagellatus</i> KT, 2	GI:91774356	442257-443561	N/A	MEP $\beta$
<i>Mycobacterium tuberculosis</i> H37Rv, <i>amt</i>	GI:41352756	(112036..113469)	N/A	MEP $\beta$
<i>Nautilia profundicola</i> AmH, <i>amt</i> (1)	GI:224372070	185564-186844	N/A	MEP $\alpha$
<i>Nautilia profundicola</i> AmH (duplicate)*	GI:223588326	185564-186844	N/A	N/A
<i>Neisseria meningitidis</i> MC58, <i>amtB</i>	GI:7735869	(645072..646376)	N/A	MEP $\beta$
<i>Neisseria meningitidis</i> Z2491, <i>amtB</i>	GI:15793034	(801446..802750)	N/A	MEP $\beta$

**Additional file 5 (continued):** Accession numbers and genome coordinates of ammonium transporter/ammonia permease genes included in the phylogenetic tree

<b>Organism, gene abbreviation</b>	<b>GI number or GenBank accession number for DNA</b>	<b>Genome Region</b>	<b>GI number for mRNA</b>	<b>Clade</b>
<i>Nostoc punctiforme</i> PCC 73102 (1)	GI:186680550	4091213-4092625	N/A	MEP $\beta$
<i>Nostoc punctiforme</i> PCC 73102*	GI:30581866	99651..101111	N/A	N/A
<i>Nostoc punctiforme</i> PCC 73102*	GI:30581855	(31482..32906)	N/A	N/A
<i>Nostoc</i> sp. PCC 7120*	GI:17227497	1158426..1159982	N/A	N/A
<i>Nostoc</i> sp. PCC 7120, 2	GI:17227497	1160381..1161793	N/A	MEP $\beta$
<i>Novosphingobium aromaticivorans</i> , DSM 12444	GI:87198026	2449396..2450709	N/A	MEP $\beta$
<i>Novosphingobium aromaticivorans</i> , DSM 12444*	GI:87198026	733046..734404	N/A	N/A
<i>Oenococcus oeni</i> MC	GI:29378884	(34354..35700)	N/A	MEP $\beta$
<i>Photorhabdus luminescens</i> subsp. laumondii TTO1, <i>amtB</i>	GI:37524032	(4529787..4531106)	N/A	MEP $\beta$
<sup>1</sup> <i>Pseudomonas aeruginosa</i> PA01, <i>amtB</i>	GI:110645304	(5951115..5952443)	N/A	MEP $\beta$
<i>Pseudomonas fluorescens</i> PfO-1, 1	GI:253992019	(6170031..6171368)	N/A	MEP $\beta$
<i>Pseudomonas putida</i> KT2440, <i>amtB</i>	GI:26986745	(5966352..5967683)	N/A	MEP $\beta$
<i>Pseudomonas stutzeri</i> , <i>amtB2</i>	GI:19033132	3281..4534	N/A	grade
<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a, 1	GI:66043271	(200642..201979)	N/A	MEP $\beta$
<i>Pseudomonas syringae</i> pv. <i>syringae</i> B728a, 2	GI:66043271	2643672..2644997	N/A	MEP $\beta$
<i>Pseudomonas syringae</i> pv. tomato str. DC3000, <i>amt-1</i>	GI:28867243	240728..242065	N/A	MEP $\beta$
<i>Pseudomonas syringae</i> pv. tomato str. DC3000, <i>amt-2</i>	GI:28867243	2856588..2857913	N/A	MEP $\beta$
<i>Ralstonia eutropha</i> JMP134, 1	GI:72117119	324070..325611	N/A	MEP $\beta$

**Additional file 5 (continued):** Accession numbers and genome coordinates of ammonium transporter/ammonia permease genes included in the phylogenetic tree

<b>Organism, gene abbreviation</b>	<b>GI number or GenBank accession number for DNA</b>	<b>Genome Region</b>	<b>GI number for mRNA</b>	<b>Clade</b>
<i>Ralstonia metallidurans, amtB</i> (= <i>Cupriavidus metallidurans</i> CH34)	GI:93352797	256874..258406	N/A	MEP $\beta$
<i>Ralstonia solanacearum, amtB</i>	GI:17544719	374899..376209	N/A	MEP $\beta$
<i>Rhizobium etli, amtB</i>	GI:6599354	787..2211	N/A	MEP $\beta$
<i>Rhodobacter sphaeroides, amtB</i>	GI:77461965	(2636500..2637852	N/A	MEP $\beta$
<i>Rhodospirillum baltica</i> SH1, 2	GI:32397972	137662..139158	N/A	grade
<i>Rhodopseudomonas palustris, amtB1</i>	GI:39652705	300666..301997	N/A	MEP $\beta$
<i>Rhodopseudomonas palustris, amtB2</i>	GI:39652705	302683..304125	N/A	MEP $\beta$
<i>Rhodospirillum rubrum</i> ATCC 11170, 1	GI:83574254	(1330513..1331808)	N/A	MEP $\beta$
<i>Saccharophagus degradans</i> (=Microbulbifer degradans) <i>amtB1</i>	GI:89949249	(2643236..2644531)	N/A	MEP $\beta$
<i>Salmonella enterica</i> subsp. enterica serovar Typhi, <i>amtB</i>	GI:16501496	262755..264041	N/A	MEP $\beta$
<i>Shigella flexneri</i> 2a str. 301, <i>amtB</i>	GI:24111450	408059..409345	N/A	MEP $\beta$
<i>Sinorhizobium meliloti, amtB</i>	GI:15963753	3471607..3472962	N/A	MEP $\beta$
<i>Staphylococcus aureus</i> subsp. aureus Mu50, <i>nrgA</i>	GI:57634611	(2162727..2163977)	GI:83574254	MEP $\beta$
<i>Staphylococcus aureus</i> subsp. aureus MW2, <i>nrgA</i>	GI:47118312	(2114899..2116149)	N/A	MEP $\beta$
<i>Staphylococcus epidermidis</i> ATCC 12228	GI:27466918	(1696434..1697684)	N/A	MEP $\beta$
<i>Streptococcus mutans</i> UA159, <i>nrgA</i>	GI:24378532	1575845..1577080)	N/A	MEP $\beta$
<i>Streptomyces avermitilis</i> MA-4680, <i>amtB1</i>	GI:162960844	(3248960..3250300)	N/A	MEP $\beta$
<i>Streptomyces avermitilis</i> MA-4680, <i>amtB2</i>	GI:162960844	(6766506..6767816)	N/A	MEP $\beta$
<i>Streptomyces coelicolor</i>	GI:24413886	105031..106377	N/A	MEP $\beta$
<i>Sulfurihydrogenibium</i> sp. YO3AOP1	GI:188931022	(55106..56395)	N/A	MEP $\alpha$

**Additional file 5 (continued):** Accession numbers and genome coordinates of ammonium transporter/ammonia permease genes included in the phylogenetic tree

<b>Organism, gene abbreviation</b>	<b>GI number or GenBank accession number for DNA</b>	<b>Genome Region</b>	<b>GI number for mRNA</b>	<b>Clade</b>
<i>Synechococcus elongatus</i> PCC 7942, 1	GI:81167692	2347614..2349026	N/A	MEP $\beta$
<i>Synechocystis</i> sp. PCC 6803, <i>amt2</i>	GI:16329170	(400720..402048)	N/A	grade
<i>Thermobifida fusca</i> , <i>amtB</i>	GI:72160406	764337..765656	N/A	MEP $\beta$
<i>Ureaplasma urealyticum</i> , <i>amt-1</i>	GI:13357558	260648..262180	N/A	grade
<i>Ureaplasma urealyticum</i> , <i>amt-2</i>	GI:13357558	262345..263910	N/A	grade
<i>Wolinella succinogenes</i> , <i>amtB</i>	GI:34482500	(51759..53072)	N/A	MEP $\alpha$
<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 33913, <i>amtB</i>	GI:21166373	243559..245034	N/A	MEP $\beta$
<i>Xanthomonas citri</i> , <i>amtB</i>	GI:5917780	N/A	N/A	MEP $\beta$
<i>Xylella fastidiosa</i> 9a5c	GI:57014152	1759686..1761164	N/A	MEP $\beta$
<i>Xylella fastidiosa</i> Dixon	GI:22994217	20672..22057	N/A	MEP $\beta$
<i>Xylella fastidiosa</i> Temecula1, <i>amtB</i>	GI:28197945	(1222493..1223947)	N/A	MEP $\beta$
<sup>†</sup> <i>Yersinia pestis</i> CO92, <i>amtB</i>	GI:16120353	(3501231..3502526)	N/A	MEP $\beta$

%= duplicate sequence in the analysis, \* = excluded or omitted from the analysis, <sup>†</sup> = data from <http://www.jgi.doe.gov/>;  
<sup>B</sup>=data from <http://www.broadinstitute.org/>;