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WP_002887028.1	SSAL	-QSASTVGEVQIILSKGLLMGARGNSGVITSQLFRGFGQSIKD----	111
AAP56845.2	MGA_0183	-LEFNSLQSLGKVFATGLFMNACGNSGVIFSQIIRGFTKSLPD----	113
WP_010874904.1	MPN547	ISHIKSFDLKGKSFTRDLLLFSRGNISGVIFSQIMKGFSDMI	118
WP_011077239.1	MYPE4130	LPELGSIEYEVGKFCRQLLNMARGNSGVIFSQIIRGFFPEIEE----	114
WP_004025236.1	GUU_03959	ISDNSTFVETSILSRQLLNMARGNSGVIFSQIFRGGFDSIKE----	114
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WP_002887028.1	SSAL	FQTGVEVAYKAVMKPVEGTILTIVSRGAASAAIKKAESTND	171
AAP56845.2	MGA_0183	FKEAKEVAVSVIQSPVEGTILTIVVRLTADQLVQKQDEISSVEQLFELATEFAKDALKQTP	173
WP_010874904.1	MPN547	FIKAEVAVKNNVSKPVEGTMLTVIRLISTDFKNQKNRAKT	178
WP_011077239.1	MYPE4130	FISAKEKAYKISINPVEGTILTIIRIIEISEQLPK--ENIN	172
WP_004025236.1	GUU_03959	LISAKERAYSITNPIEGTILTIIRVISEEMQT--KEIDDI	172
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WP_002887028.1	SSAL	EMLPVLKEVGVVDSGGQGLVFIYEGFLSALTGEYIASEDFQATPATM----	224
AAP56845.2	MGA_0183	KMLPALKSANVVDSGGFGLVFLLEGMLTELTKDFSRLNND-----	218
WP_010874904.1	MPN547	QMLPVLKASGVVDSGAYGFAFLEGLMSFYGEKATLNDGK----	223
WP_011077239.1	MYPE4130	EILPSLKEAKVVDSGGYGLCKFLEGMYNQLVNSDDDNVQNKDIEIEK	232
WP_004025236.1	GUU_03959	EMLISLKEAKVVDSGGYGLCKFFEGMYLCVSGSLVTDKSN--	230
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WP_002887028.1	SSAL	EHHKSVAGHVATEDITFGYCTEIMIGLK----QGPTYVKDFDYEEFRNYLSNLGDSLLVV	280
AAP56845.2	MGA_0183	KKALSSKAEQELVEEGHYCTEFLKLGKAKDD--QTKIKFNEEKFKKEISKDVESLVL	277
WP_010874904.1	MPN547	LSQMTISGEKHVTEEEFGYCTEYVRLKLGMSVQSQ--VEKQKFNQKFKESKVKIATS	282
WP_011077239.1	MYPE4130	NTFIQSKVRNDISEEGFYCCEFI IQKDFITHEKQPLKIKFDLNKFEKEMLLAGESL	292
WP_004025236.1	GUU_03959	NTFINNQSRSEISEEGFYCCEFI IQQNFITYDGGQKEKEKFNKNSFEKELLAFGDSL	290
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WP_002887028.1	SSAL	ND--DEIVKVHVHTEDPGLVMQEGLYGALVKVKVDNMRNQHDAQVQKEEAIQAAPSAPK	338
AAP56845.2	MGA_0183	NDKEGIVKLAHTLTPDLVLKHAQPYGEFLKVKIENMNKQVTERKQDSDNLGQLANKPI	337
WP_010874904.1	MPN547	SDKDNQFVKVHAHTKPNLLELGLNYGEFELVKIENMNLQVAKQKPAVVK-----	333
WP_011077239.1	MYPE4130	DD--SDIVKVHIHSTITPSLVFEIGQKYGEFLKLVENMTLQYIESHPGVS-----	342
WP_004025236.1	GUU_03959	TD--EDIKVKHMALEPYKVLVVGQKYGEFLKIKVENMTQYLDTHPEIN-----	340
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WP_002887028.1	SSAL	DF-----ALIAVVAGDGLADIF--KSQGVVYVISGGQTMNPSTEDIVKAI	381
AAP56845.2	MGA_0183	DLLMDIDLKIKKDFKTETAI IATVPSRVLGKMIQVNYDQVDFIDTSATGNPTIKDFVKNI	397
WP_010874904.1	MPN547	-----RNIPKAVVTVPTTEAFADRIREDYDIQAILCTDDTGAPSVFSLLEAV	380
WP_011077239.1	MYPE4130	DL-----FNKFSLDDVQIVATCPSRKIADYLKNEFGINNVIIVTEETGNPSTNEIMNQI	396
WP_004025236.1	GUU_03959	DM-----FKTTQLVDDVVLVVTLPQKISEYYLEELNIENSIITEDTGNPSTNDILNSI	394
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WP_002887028.1	SSAL	EQVNAKNVILPNNKNI FMAAQSAAEVVD---VNAAVVETRTVPQGFTSLLAFDPSQSIE	438
AAP56845.2	MGA_0183	YSVKSKNVIVVDDTNLLLSAKEAIALK--HINCELISCQNFIEALS AISGYMRSDSLK	456
WP_010874904.1	MPN547	KLTHSSNIIIFLLHDKNYFLSANEALKQLKHQKISADCVMTNP IESLAALTVFNSDLNIH	440
WP_011077239.1	MYPE4130	INCKSRNIVLTDSDSNI ILSAEQAATFMKE--RYDVVVLKSKNIEVINACLVSSEKSI	455
WP_004025236.1	GUU_03959	KDTSKKNVIVVTDSDSNI ILSAEQTVELLKN--KVVNSIVRGNLMESMLACLNFNSLSIY	453
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WP_002887028.1	SSAL	ANVEAMTASLSDVTSGSVTLAVRDTTIDGLEIHENDILGMVDGKILVSTPDMQALD	498
AAP56845.2	MGA_0183	SNVKVLHKKIKSTGSFAFISTSVKNIKYPHLQVHKGDYIGVMKKKIIVSDSDIYKCLL	516
WP_010874904.1	MPN547	TNVKTMRRFVKGFASATITQASKKYENR IEVNKGFDFIAVANNSICVSEKELVQCV	500
WP_011077239.1	MYPE4130	ENARVMNRAIRKQDSAMLSVSVKTSKFNQVHVEKNDFIGIYDKKIVLAEKNSEIAIT	515
WP_004025236.1	GUU_03959	ENQKEMKNVVKKSI TGLISKSVKTAKFNDVMVQKGNIGILDKRIIVLSEKSTESA	513
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WP_002887028.1	SSAL	DKMIDEDES--EIVMIYVGEENQEQALAEKLEEAHEGIEVEIFQGDQPVYYPYLSV	555
AAP56845.2	MGA_0183	AQLIDEVKKPELVLI IYGKNTSSSEVRTIV--KLISEKFGIYCEAINGSQKLYQYYIGV	574
WP_010874904.1	MPN547	DHLLKVKVKKPEFLLAYGKIDITAEAEAMK--EKIEKKYKLFCEFPGEQKVFYSYILGI	558
WP_011077239.1	MYPE4130	KKLDRNKKQAQLLYIVYGGQVTLREIRNIE--KFANENYGIKCKLIDGGQKTYRYF	573
WP_004025236.1	GUU_03959	KKMKAKIRKPEMYYLIYGGQISLREVRNIE--KFNENYGIKIKAVSGNQKLYQYYIG	571
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SSAL, *Streptococcus salivarius*; MYPE4130, *M. penetrans*; GUU, *M. iowae*

Figure S2. Multiple sequence alignments of proteins (referred to in Table S3) that were assigned new enzyme annotations in this study for *M. gallisepticum*. Multiple sequence alignments were constructed for the assigned proteins in *M. gallisepticum* with homologous proteins identified in other mycoplasma and bacterial species using Clustal Omega at <http://www.ebi.ac.uk/Tools/msa/clustalo/>. Numbers on right indicate the position of the adjacent amino acid residue. An asterisk (*) indicates an amino acid that is conserved in all aligned sequences, a colon (:) indicates one substitution with a very similar amino acid, and a full stop (.) indicates at least one substitution with a similar amino acid. Dashed lines (-) indicate gaps in the amino acid sequence alignment.