

Table S6. Distribution of shared genes of *M. paludicola* and RC-I_{MRE50} with other methanogenic archaeal genomes.

Order	Species	No. of CDS	<i>M. paludicola</i>		RC-I _{MRE50}	
			No. and percentage of shared genes*			
<i>Methanocellales</i>	<i>M. paludicola</i> SANA E	3004	-	-	2059	66.7%
	RC-I _{MRE50}	3085	2100	69.9%	-	-
<i>Methanosarcinales</i>	<i>M. acetivorans</i> C2A	4540	1370	45.6%	1388	45.0%
	<i>M. barkeri</i> str. Fusaro	3606	1343	44.7%	1355	43.9%
	<i>M. mazei</i> Go1	3370	1365	45.4%	1374	44.5%
	<i>M. burtonii</i> DSM 6242	2273	1224	40.7%	1198	38.8%
	<i>M. thermophila</i> PT	1696	1121	37.3%	1078	34.9%
<i>Methanomicrobiales</i>	<i>M. marisnigri</i> JR1	2489	1282	42.7%	1254	40.6%
	<i>M. palustris</i> E1-9c	2655	1267	42.2%	1264	41.0%
	<i>M. boonei</i> 6A8	2450	1225	40.8%	1231	39.9%
	<i>M. hungatei</i> JF-1	3139	1230	40.9%	1228	39.8%
	<i>M. labreanum</i> Z	1739	1052	35.0%	1037	33.6%
<i>Methanobacteriales</i>	<i>M. thermautotrophicus</i> ΔH	1873	1046	34.8%	1010	32.7%
	<i>M. smithii</i> ATCC 35061	1793	962	32.0%	927	30.0%
	<i>M. stadtmanae</i> DSM 3091	1534	924	30.8%	890	28.8%
<i>Methanococcales</i>	<i>M. jannaschii</i> DSM 2661	1729	903	30.1%	901	29.2%
	<i>M. maripaludis</i> S2	1722	1038	34.6%	1019	33.0%
<i>Methanopyrales</i>	<i>M. kandleri</i> AV19	1687	785	26.1%	775	25.1%