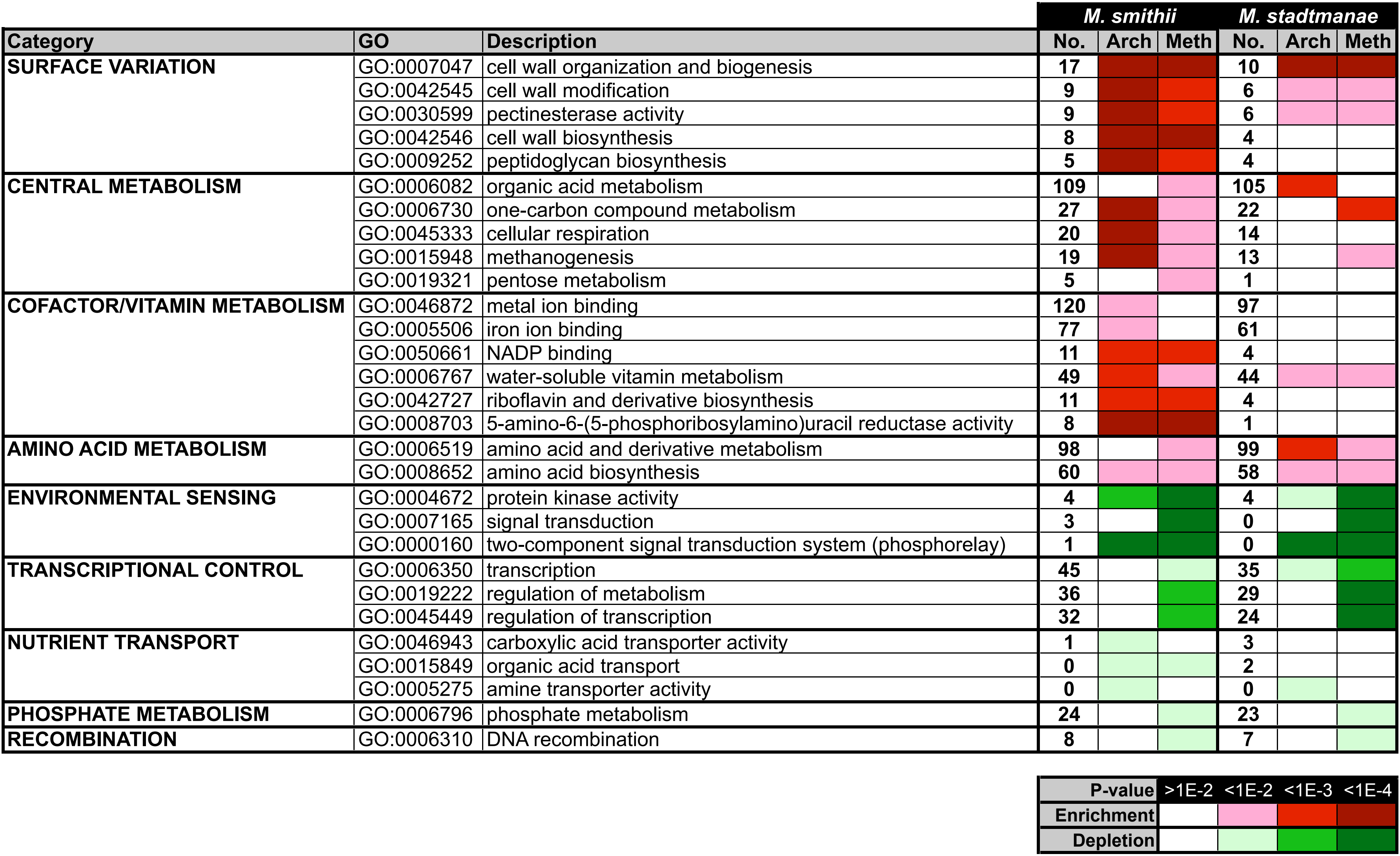
Table 6. Representation of enriched gene ontology (GO) categories in the *M. smithii* and *M. stadtmanae* proteomes compared to the proteomes of all sequenced methanogenic archaea and all archaea



			M. smithii			*M. stadtmanae*		
Category	**GO**	**Description**	**No.**	**Arch**	**Meth**	**No.**	**Arch**	**Meth**
SURFACE VARIATION	GO:0007047	cell wall organization and biogenesis	**17**	🟫	🟫	**10**	🟫	🟫
	GO:0042545	cell wall modification	**9**	🟫	🟥	**6**	🟪	🟪
	GO:0030599	pectinesterase activity	**9**	🟫	🟥	**6**	🟪	🟪
	GO:0042546	cell wall biosynthesis	**8**	🟫	🟫	**4**		
	GO:0009252	peptidoglycan biosynthesis	**5**	🟫	🟥	**4**		
CENTRAL METABOLISM	GO:0006082	organic acid metabolism	**109**		🟪	**105**	🟥	
	GO:0006730	one-carbon compound metabolism	**27**	🟫	🟪	**22**		🟥
	GO:0045333	cellular respiration	**20**	🟫	🟪	**14**		
	GO:0015948	methanogenesis	**19**	🟫	🟪	**13**		🟪
	GO:0019321	pentose metabolism	**5**		🟪	**1**		
COFACTOR/VITAMIN METABOLISM	GO:0046872	metal ion binding	**120**	🟪		**97**		
	GO:0005506	iron ion binding	**77**	🟪		**61**		
	GO:0050661	NADP binding	**11**	🟥	🟥	**4**		
	GO:0006767	water-soluble vitamin metabolism	**49**	🟥	🟪	**44**	🟪	🟪
	GO:0042727	riboflavin and derivative biosynthesis	**11**	🟥	🟥	**4**		
	GO:0008703	5-amino-6-(5-phosphoribosylamino)uracil reductase activity	**8**	🟫	🟫	**1**		
AMINO ACID METABOLISM	GO:0006519	amino acid and derivative metabolism	**98**		🟪	**99**	🟥	🟪
	GO:0008652	amino acid biosynthesis	**60**	🟪	🟪	**58**	🟪	🟪
ENVIRONMENTAL SENSING	GO:0004672	protein kinase activity	**4**	🟩	▓	**4**	░	▓
	GO:0007165	signal transduction	**3**		▓	**0**		▓
	GO:0000160	two-component signal transduction system (phosphorelay)	**1**	▓	▓	**0**	▓	▓
TRANSCRIPTIONAL CONTROL	GO:0006350	transcription	**45**		░	**35**	░	🟩
	GO:0019222	regulation of metabolism	**36**		🟩	**29**		▓
	GO:0045449	regulation of transcription	**32**		🟩	**24**		▓
NUTRIENT TRANSPORT	GO:0046943	carboxylic acid transporter activity	**1**	░		**3**		
	GO:0015849	organic acid transport	**0**	░	░	**2**		
	GO:0005275	amine transporter activity	**0**	░		**0**	░	
PHOSPHATE METABOLISM	GO:0006796	phosphate metabolism	**24**		░	**23**		░
RECOMBINATION	GO:0006310	DNA recombination	**8**		░	**7**		░

P-value	>1E-2	<1E-2	<1E-3	<1E-4
Enrichment		🟪	🟥	🟫
Depletion		░	🟩	▓

Abbreviations: 'non-gut-associated methanogens' (Meth) or 'all Archaea' (Arch) [see SI **Table 5**]; No., number of genes associated with gene ontology (GO) term.