

		321	507	558	580	745	
qnorB	A	Geobacillus stearothermophilus	MFGALLAHYYTEPD---SFFG	IHLWVEG	GHHYYY	LEVIP	PDT
		Staphylococcus aureus	LLGELLAHYYVENK----FFG	VHLWVEG	GHHYYW	LEVVP	WDI
	B	Herminiimonas arsenicoxydans	FLGGLTAHYTIEGQ---HFYG	VHLWVEG	FHHMYF	LEVVP	GDV
		Hahella chejuensis	LLGGFTAHTYTVEGH---HFYG	VHLWVEG	FHHLYF	LEVVP	GDV
		Cellvibrio japonicus	LLGGFTAHYTIEGQ---QFYG	VHLWVEG	FHHLYF	LEVVP	GDV
		Polaromonas naphthalenivorans	GMGVITAHYAVEGQ---SFFG	VHLWVEG	LHHLYF	LEVVP	GDV
		Parvibaculum lavamentivorans	LLGAMTAHYQIEGQ---LVYG	VHLWVEG	LHHLYF	LEVVP	GDT
		Xanthobacter autotrophicus	LLGIVTAHYAVEGQ---GLYG	VHLWVEG	FHHLYF	LEVVP	GDV
nod	Methylomirabilis oxyfera p2434	LAGILSAEDFVGGGPGSAIAT	IHMWVEV	SHNFWY	MQVLP	GGA	
	Methylomirabilis oxyfera p2437	LAGILGAEDFVGGGPGEAILG	IHMWVEV	SHNFWY	MQVLP	GGV	
I	ETNP 160m PROKKA 33601	IAGLLTVADFTHFF---AKYD	VHMWVEA	SHNFWY	LQVAP	GVV	
	ETNP 120m free PROKKA 265821	IAGLLTVADFTHFF---AKYD	VHMWVEA	SHNFWY	LQVAP	GVV	
II	ETNP 120m PROKKA 89302	LAGII IATDFVRPF-----G	VHMWVEV	SHNFWY	LQVLP	GGL	
	ETNP 120m Part PROKKA 50886	LGGVIAATDFVRPG-----G	VHMWVEV	SHNFWY	LQVLP	GGA	
III	ETNP 300m PROKKA 194139	LAGI I SATDFIRPF-----G	VHMWVEV	SHNFWY	LQVLP	GGG	
	ETNP 300m Part PROKKA 193327	LAGI I GASDFIRPF-----G	VHMWVEV	SHNFWY	LQVLP	GGG	
	ETNP 2013 Stn6 300m	LAGI I GASDFIRPF	VHMWVEV	SHNFWY	LQVLP	GGG	
IV	ETNP 120m PROKKA 15008	FAGIACSIDFVRPW-----G	VHMWVEV	GHNFWY	TQVLP	GGH	
qnorB-like	Algoriphagus mannitolivorans	LAGVLTVDHDFVGFT---SFFG	VHMWVEA	SHNFWY	LQVVP	GGG	
	Mariniradius saccharolyticus	LAGVLTVDHDFVGFT---NFFG	VHMWVEA	SHNFWY	LQVVP	GGG	
	Indibacter alkaliphilus	LAGVLTVDHDFVGFT---KFFG	VHMWVEA	SHNFWY	LQVVP	GGA	
	Cecembia lonarensis	LAGVLTVDHDFVGFT---KFFG	VHMWVEA	SHNFWY	LQVVP	GGA	
	Muricauda ruestringensis	SSGFVTINEFVDYL---GFFG	VHMWVEA	SHNFWY	LQFVP	GAC	
	Arenibacter algicola	SSGFITINEFIDYL---GYFG	VHMWVEA	SHNFWY	LQFVP	GAC	
	Chlorobi bacterium OLB7	LAGILTVHDFVGVFV---NFFG	VHMWVEA	SHNFWY	LQVIP	GGA	
	Bacteroidetes bacterium OLB12	LAGVLTVDHDFVGVFV---NFFG	VHMWVEA	SHNFWY	LQVVP	GGG	
	Flavohumibacter sp ZG627	LAGILTVHDFVGVFV---NFFG	VHMWVEA	SHNFWY	LQVIP	GGG	
	Sediminibacterium sp OR53	LAGILTVHDFVGVFV---HFFG	VHMWVEA	SHNFWY	LQVIP	GGA	

Figure S10. Alignment showing the active site (red) and quinol binding site (blue) for qnorB, putative nod, qnorB-like, and assembled ETNP sequences. Residues comprising the active site were determined by modeling in Ettwig et al (2012). Colored boxes indicate key residues indicated in Ettwig et al (2012). Numbers delineate the residue number in *G. stearothermophilus*. Accession numbers are found on the phylogenetic tree in Figure 7. The active and binding sites for ETNP 2013 Stn6 300m is found in Padilla et al. (2016).