

Available Gene-Trac® Tests

Contaminant Class	Gene-Trac® Test Name	Target	Relevance	
Reductive Dechlorination	Dhc	<i>Dehalococcoides</i>	Dechlorinates PCE, TCE, DCE, VC, 1,2-DCA, chlorobenzenes	
	Dhb	<i>Dehalobacter</i>	Dechlorinates 1,1,1-TCA, chloroform, DCM, PCE & TCE	
	Dsm	<i>Desulfuromonas</i>	Dechlorinates PCE & TCE to cDCE	
	Dsb	<i>Desulfitobacterium</i>	Partial dechlorination of PCE & TCE to cDCE	
	Geo	<i>Geobacter</i>	Dechlorinates PCE to cDCE/important in biogeochemical degradation	
	Dhgm	<i>Dehalogenimonas</i>	Dechlorinates tDCE, VC, chloropropanes, 1,2-DCA	
	SSP	<i>Sulfurospirillum</i>	<i>Sulfurospirillum multivorans</i> dechlorinates PCE to cDCE	
	Dehalobium	<i>Dehalobium chlorocoercia</i>	Hexachlorobenzene, PCBs	
	Chloroethene FGA	Vinyl Chloride Reductase (<i>vcrA</i>)		Dechlorination of cDCE & VC to ethene
		BAV1 Reductase (<i>bvcA</i>)		Dechlorination of cDCE & VC to ethene
		Trichloroethene Reductase (<i>tceA</i>)		Dechlorination of PCE & TCE to cDCE & VC
		<i>cerA</i>	<i>Dehalogenimonas</i> VC-Reductase (<i>cerA</i>)	Dechlorinates VC to ethene
	<i>ctrA/dcrA</i>	Chloroform/DCA dehalogenase (<i>dcrA</i>)	<i>Dehalobacter</i> , chloroform, 1,1,1-TCA & 1,1-DCA reductase	
Aerobic chlorinated compounds degradation	Polaromonas	<i>Polaromonas JS666</i>	Aerobic degradation of cDCE	
	etn	<i>etnE</i>	Aerobic degradation of VC	
	<i>dhIA</i>	Haloalkane dehalogenase	Aerobic dechlorination of 1,2-DCA by <i>Xanthobacter</i>	
	pMMO	Particulate Methane Monooxygenase (<i>pMMO</i>)	Co-oxidation of 1,4-dioxane and TCE in presence of methane	
	sMMO	Soluble Methane Monooxygenase	Co-metabolism of chlorinated compounds by methanotrophs	
	PMO	Propane Monooxygenase	Co-metabolism of chlorinated compounds by propanotrophs	
Anaerobic BTEX	<i>dhIA</i>	Haloalkane Dehalogenase (<i>dhIA</i>)	Aerobic dechlorination of 1,2-DCA	
	ORM-2	<i>Deltaproteobacterium</i> ORM-2	Anaerobic benzene degrader (SO ₄ /CH ₄ reducing conditions)	
	Pepto-ben	Benzene degrading <i>Peptococcaceae</i>	Anaerobic benzene degrader under NO ₃ ⁻ reducing conditions	
	<i>abcA</i>	Benzene Carboxylase (<i>abcA</i>)	Involved in benzene ring cleavage under anaerobic conditions	
	<i>bssA</i>	Benzyl Succinate Synthase (<i>bssA</i>)	Functional gene for anaerobic toluene biodegradation	
Aerobic hydrocarbon degradation	TMO	Toluene Monooxygenase	Aerobic oxidation of toluene	
	TDO	Toluene Dioxygenase	Degrades toluene and benzene by incorporating two oxygen molecules into the aromatic ring	
	PhMO	Phenol Monooxygenase	Hydroxylates phenol to catechol which is subject to further degradation under aerobic and anaerobic conditions	
	XMO	Xylene Monooxygenase	Degrades xylene and toluene by oxidizing methyl groups	
	NDO	Naphthalene Dioxygenase (<i>nahAc</i>)	Catalyzes the first step in aerobic degradation of naphthalene, reported activity for other polycyclic compounds with less than 3 rings	
	MTBE/TBA	<i>Methylibium petroleiphilum</i> PM1		MTBE/TBA degrading microorganism
		tert-butyl alcohol hydroxylase (<i>mdpJ</i>)		Active on 2-HIBA in aerobic MTBE degradation pathway
HIBA mutase (<i>hcmA</i>)			Active on 2-HIBA in aerobic MTBE degradation pathway	
1,4 -Dioxane	1,4 -Dioxane	Dioxane monooxygenase (<i>dxmb</i>)	Energy yielding 1,4-dioxane degradation	
		Aldehyde Dehydrogenase	Energy yielding 1,4-dioxane degradation	
Nitrogen Metabolism	Denitrification	Three target test: nitrous oxide reductase (<i>nosZ</i>) & nitrite reductases (<i>nirS</i> & <i>nirK</i>)	Functional genes in anaerobic pathway that converts nitrate to dinitrogen gas	
	Nitrification	Three target test: Bacteria and Archaea ammonia monooxygenases (<i>amoA</i>) and 16S rRNA gene for <i>Nitrobacter</i>	Functional genes in aerobic pathway that converts ammonium to nitrate	
	Anammox	Major anammox genera via 16S rRNA	Anammox = anaerobic metabolism of ammonium and nitrite	
Perchlorate	Perchlorate	Two target test: Perchlorate reductases (<i>pcrA</i>) of <i>Dechloromonas agitata</i> & <i>aromatica</i>	Reduces perchlorate to chlorate and chlorite-diagnostic for perchlorate degrading bacteria	

Available Gene-Trac® Tests Continued...

Metals and Metalloids	Selenium	Identifies selenium-reducing bacteria via selenate reductase (<i>serA</i>) of <i>Thauera selenatis</i>	The presence of selenate reductases signals increased likelihood of selenium precipitation in aqueous systems
	Selenium	Identifies selenium-reducing bacteria via selenate reductase (<i>srdA</i>) of <i>Bacillus selenatarsenatis</i>	
	Mercury	Two target test: mercuric ion reductase (<i>merA</i>) and organomercurial lyase (<i>merB</i>)	<i>merA</i> converts Hg^{2+} to Hg^0 reducing toxicity, <i>merB</i> converts methylmercury to less toxic elemental mercury -these genes are important in bacterial mercury resistance
Microbial Groups	Universal	<i>Bacteria</i>	Quantifies Bacteria-measure of total biomass
	Arch	<i>Archaea</i>	Quantifies Archaea biomass
	SRB	Sulfate Reducing bacteria (<i>dsrA</i>)	Partners to ORM-2 in anaerobic benzene degradation
	Methanogens	quantifies methyl coenzyme reductase (<i>mcrA</i>)	<i>mcrA</i> catalyzes the final step in methanogenesis and is highly conserved among methanogens
	SOX-B	Sulfur-oxidizing bacteria (SOB) via Sox enzyme system (<i>soxB</i>) of non-filamentous chemolithotrophic SOB	Sulfur oxidizing bacteria produce sulfuric acid and are important in acid mine drainage and in microbially induced corrosion (MIC) of concrete and metal
	Gene-Trac NGS	Next generation sequencing of 16S rRNA gene of Bacteria and Archaea	Characterize entire microbial communities to determine metabolic functions and response to changing conditions