



Contact SiREM to learn more about how Gene-Trac[®] can enhance your monitoring and remediation program

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The quantification of key microorganisms and functional genes is critical to understanding and optimizing bioremediation of contaminants including chlorinated solvents, 1,4-dioxane, PCBs and petroleum hydrocarbon compounds. Gene-Trac[®] testing uses quantitative polymerase chain reaction (qPCR) combined with rigorous quality control to provide accurate enumeration of critical targets in soil, sediment and groundwater using our growing selection of available tests.

Gene-Trac[®] NGS (next generation sequencing) provides comprehensive microbial community characterization for microbiological systems including bioreactors, landfills, wastewater treatment and in bioremediation.

Quantify and characterize microorganisms
essential to success of enhanced
bioremediation and MNA remedies

Gene-Trac[®] testing is used by remediation professionals to:

- Assess the suitability of microbial populations to degrade target contaminants
- Provide evidence for monitored natural attenuation (MNA)
- Assess the need for bioaugmentation
- Determine the impact of electron donors, pH buffers, nutrients & bioaugmentation
- Identify inhibitory conditions for specific microorganisms for improved site management
- Provide early evidence of remediation progress, often before VOCs or other parameters

Gene-Trac[®] Features

- Comprehensive reports provide detailed testing and quality control parameters
- Electronic data deliverables, Level IV data validation and database uploads available
- USA or Canada sample reception options
- Unparalleled technical support for data interpretation and planning
- Competitive pricing



Available Gene-Trac® Tests

Contaminant Class	Redox	Gene-Trac® Test Name	Target	Relevance
Chlorinated Ethenes	Anaerobic	Dhc	<i>Dehalococcoides</i>	Dechlorinates PCE, TCE, all DCE isomers, VC
		Dhb	<i>Dehalobacter</i>	Dechlorination of PCE & TCE to cDCE
		Dsm	<i>Desulfuromonas</i>	Dechlorination of PCE & TCE to cDCE
		Dsb	<i>Desulfitobacterium</i>	Partial dechlorination of PCE and TCE to cDCE
		Geo	<i>Geobacter</i>	Dechlorinates PCE to cDCE/biogeochemical degradation
		Dhg	<i>Dehalogenimonas</i>	Dechlorination of tDCE to VC and VC to ethene
	Chloroethene FGA	Vinyl Chloride Reductase (<i>vcrA</i>)	Dechlorination of cDCE & VC to ethene	
		BAV1 Reductase (<i>bvcA</i>)	Dechlorination of cDCE and VC to ethene	
		Trichloroethene Reductase (<i>tceA</i>)	Dechlorination of PCE and TCE to cDCE and VC	
		Polaromonas	<i>Polaromonas</i>	Aerobic dechlorination of cDCE
Aerobic	etn	<i>etnE</i>	Aerobic degradation of VC	
	Chlorinated Ethanes	Anaerobic	Dhb	<i>Dehalobacter</i>
Dhg			<i>Dehalogenimonas</i>	Dechlorinates 1,2- DCA, 1,1,2,2-TeCA , 1,1,2-TCA
Dhc			<i>Dehalococcoides</i>	Dechlorinates 1,2-DCA to ethene
Dsb			<i>Desulfitobacterium</i>	Dechlorinates 1,1,2-TCA & 1,2-DCA
cfrA/dcrA		Dichloroethane Dehalogenase (<i>dcrA</i>)	Dechlorinates 1,1,1-TCA & 1,1-DCA	
Aerobic		sMMO	Soluble Methane Monooxygenase	Co-metabolism of 1,1,1-TCA & 1,1-DCA by methanotrophs
		PMO	Propane Monooxygenase	Co-metabolism of chlorinated ethanes by propanotrophs
	dhIA	Haloalkane Dehalogenase (<i>dhIA</i>)	Aerobic dechlorination of 1,2-DCA	
Chlorinated Methanes	Anaerobic	Dhb	<i>Dehalobacter</i>	Dechlorination of chloroform to DCM; DCM to acetate
		cfrA/dcrA	Chloroform Reductase (<i>cfrA</i>)	Converts chloroform to dichloromethane
	Aerobic	sMMO	Soluble Methane Monooxygenase	Co-metabolism of chloroform & dichloromethane
Chlorinated Propanes	Anaerobic	Dhg	<i>Dehalogenimonas</i>	Converts TCP to allyl chloride; DCP to propene
		Dhc	<i>Dehalococcoides</i>	Converts DCP to propene
		Dhb	<i>Dehalobacter</i>	Converts DCP to propene
		Dsb	<i>Desulfitobacterium</i>	Dechlorination of TCP & DCP
Chlorinated Benzenes	Anaerobic	Dhc	<i>Dehalococcoides</i>	Partial dechlorination of HCB/PCB
		Dhb	<i>Dehalobacter</i>	Reductive dechlorination of DCB, MCB
Chlorinated Phenols	Anaerobic	Dhc	<i>Dehalococcoides</i>	Dechlorination of 2,3-dichlorophenol, TCP and PCP
PCBs	Anaerobic	Dhc	<i>Dehalococcoides</i>	Dechlorinates select Arochlor 1260 congeners
		Dhb	<i>Dehalobacter</i>	Dechlorinates 2,3,4-trichlorobiphenyl; 2,3,4,5-tetrachlorobiphenyl
		Dhg	<i>Dehalogenimonas</i>	Dechlorinates select Arochlor 1260 congeners
BTEX	Anaerobic	SRB	Sulfate reducing bacteria (<i>dsrA</i>)	Partners to ORM-2 in anaerobic benzene degradation
		ORM-2	<i>Deltaproteobacterium ORM-2</i>	Anaerobic benzene degrader (SO ₄ /CH ₄ reducing conditions)
		Pepto-ben	Benzene degrading <i>Peptococcaceae</i>	Anaerobic benzene degrader under NO ₃ reducing conditions
		abcA	Benzene Carboxylase (<i>abcA</i>)	Involved in benzene ring cleavage
Fuel Oxygenates	Aerobic	MTBE/TBA	<i>Methylibium petroleiphilum</i> PM1	MTBE/TBE degrading microorganism
			tert-butyl alcohol hydroxylase (<i>mdpJ</i>)	Active on TBA in aerobic MTBE degradation pathway
			HIBA mutase (<i>hcmA</i>)	Active on 2-HIBA in aerobic MTBE degradation pathway
1,4-Dioxane	Aerobic metabolism	1,4-dioxane	Dioxane monooxygenase (<i>dxmb</i>)	Energy yielding 1,4-dioxane degradation
		1,4-dioxane	Aldehyde Dehydrogenase	Energy yielding 1,4-dioxane degradation
	Aerobic Cometabolism	pMMO	Particulate Methane Monooxygenase	Co-oxidation of 1,4-dioxane in presence of methane
		sMMO	Soluble Methane Monooxygenase	Co-oxidation of 1,4-dioxane
		PMO	Propane Monooxygenase	Co-oxidation of 1,4-dioxane in presence of propane
Nitrogen	Anaerobic	Anammox	Major anammox genera	Anaerobic co-removal of ammonium and nitrite
Prokaryotic Groups	Variable	Universal	Bacteria	Quantifies <i>Bacteria</i> -measure of total biomass
		Arch	Archaea	Quantifies <i>Archaea</i> biomass
		SRB	Sulfate reducing bacteria (<i>dsrA</i>)	Anaerobic hydrocarbon oxidation/biogeochemical reduction/MIC
		NGS	<i>Bacteria/Archaea</i>	Comprehensive characterization of microbial communities