

Table S1. Strains used in this study.

Strain name	Genotype	Reference
G37	Wild-type	ATCC 33530
<i>fur</i>	Δ MG_236:: <i>tetM</i>	This work
<i>fur</i> COM	Δ MG_236:: <i>tetM</i> , MG_438::Tn <i>Cm</i> MG_236	This work
G37-Hrl _{wt} :CatCh	Tn <i>Pac</i> Hrl _{wt} : <i>cat:mcherry</i>	This work
G37-Hrl _{mut} :CatCh	Tn <i>Pac</i> Hrl _{mut} : <i>cat:mcherry</i>	This work
<i>fur</i> -Hrl _{wt} :CatCh	Tn <i>Pac</i> Hrl _{wt} : <i>cat:mcherry</i> , Δ MG_236:: <i>tetM</i>	This work
<i>fur</i> -Hrl _{mut} :CatCh	Tn <i>Pac</i> Hrl _{mut} : <i>cat:mcherry</i> , Δ MG_236:: <i>tetM</i>	This work

Table S2. Plasmids used in this manuscript.

Plasmid name	Description	Source
p Δ MG_236	Suicide vector pBE (Pich <i>et al.</i> , 2006b) derivative used to create an MG_236 defective mutant. Selectable marker: tetracycline.	This work
pMTnCatMG_236	Minitransposon miniTn4001 (Calisto <i>et al.</i> , 2012) derivative bearing an ectopic copy of MG_236 to complement the defective mutant. Selectable marker: chloramphenicol.	This work
pMTnWT149CatCh	Minitransposon miniTn4001 derivative carrying a chloramphenicol acetyl transferase resistance marker fused to an mCherry tag. Used to create the G37-Hrl _{wt} :CatCh strain. Selectable marker: puromycin.	This work
pMTnMUT149CatCh	Minitransposon miniTn4001 derivative carrying a chloramphenicol acetyl transferase resistance marker fused to an mCherry tag. Selectable marker: puromycin.	This work
pC1wtCatCh	Suicide vector pBE derivative used to create the <i>fur</i> -Hrl _{wt} :CatCh strain. Selectable marker: puromycin.	This work
pC1mutCatCh	Suicide vector pBE derivative used to create the G37-Hrl _{mut} :CatCh and <i>fur</i> -Hrl _{mut} :CatCh strains. Selectable marker: puromycin.	This work

Table S3. Primers used in this study.

	Primer Name	Sequence (5'-3')
Mutants	mg236 Up-F	CTTTGCAGGACAAAATGTTGC
	mg236 Up-R	TAATTCTAAATACTAGAAATTCACATAACTAGTTAGCATCTGG
	mg236 Down-F	CAATAAAATAAECTTAGGGATCCCCTTACCTTTAACAGATGGC
	mg236 Down-R	CATCTTTTGTATCTACTAGTGC
	TER305-F	GCGGGATCCCACAAGCAAATAACCTGTTC
	TER305-R	GCGGGATCCCCTCGAGCTAAAAATCTGTTTTTTGGT
	COMmg236-F (XbaI)	AGTTCTAGAGTTTGTCTATCTAACTATTAAGCAGTTAGAATTTG TTAGAATTACTTGTTTTAAACTATGCTAACTAGTTATGTGAAGG
	COMmg236-R (NotI)	AAAGCGGCCGCTTAATCATTGTTTATCTCACCCC
	wtMG149furbox-F	ATTGGGCCCGCTTATTTAGAAAAATTCAAATAAGCAAATTATAAT TAGGTGTCTTTCTTTACTAAAAATATGGAGAAAAAAATCACTGG
	mutMG149furbox-F	ATTGGGCCCGCTACTATAGTAAAATACAAATCTAGCAAATTATAAT TAGGTGTCTTTCTTTACTAAAAATATGGAGAAAAAAATCACTGG
	Clwt149CatCh-F	GATTGCTGCTCAATCAATTG
	Clwt149CatCh-R	GACAACGCTTCAAATTCACC
	Cherry-R	AGTCTCGAGTTACTTGTACAGCTCGTCC
	Tc-F	GAATTCTAGTATTTAGAATTAATAAAG
	Tc-R	GGATCCCTAAGTTATTTTATTGAAC
Screening	mg236SCR-F	GTTGGTCAGATTATCTATAG
	mg236SCR-R	CTCAACTTCCAAACAAAGAC
	mg293SCR-F	GAAAAC TAGCTAGTCAACAAG
	mg293SCR-R	CGTCTTAAAAGTCTTCTTAC
qRT-PCR	RTPCRmg177-F	TGAGTGTCCAGCTGGTTTTG
	RTPCRmg177-R	AACCGGGGAAAAGTTAGCAT
	RTPCRmg418-F	TGTTGACGCTAGTGGTTTTGG
	RTPCRmg418-R	TTCCACCCATGTATTGAGAGTG
	RTPCRmg430-F	GGAAGCAGTTGGATTGCCTA
	RTPCRmg430-R	ATGCACCTCCTCATTGGAAA
	RTPCRmg236-F	AATTGAACACCAAGATTGGC
	RTPCRmg236-R	AGATAGATATGGTTATGCTC
	RTPCRmg149-F	ACCAGGGATATGCACTAGCA
	RTPCRmg149-R	TGCAACACTTTGGGTAGCTG
	RTPCRmg304-F	GCTGATACACTCCACCAGGAA
	RTPCRmg304-R	CAAGCAAAAACAGCACGTTG
	RTPCRmCherry-F	GCCCCTAATGCAGAAGAAG
	RTPCRmCherry-R	GTGTAGTCCTCGTTGTGGGA
	RTPCRmg239-F	ATGCGAGAAAGCGCTAATGT
	RTPCRmg239-R	TGCAGTTACCAAAGCAGCAC
	RTPCRmg305-F	ATTTTGCTTGTGGACCTTGT
	RTPCRmg305-R	GATATTAGCAAGTCCTGATG
RTPCRmg355-F	CACACCTGCTGGTGAAAATC	

RTPCRmg355-R

CCAACTCCAGGTTACCAAT

	Primer Name	Sequence (5'-3')
Sequencing	Fup-24	CGCCAGGGTTTTCCCAGTCACGAC
	Rup-24	TCACACAGGAAACAGCTATGACCA
	TetUp	TTCTGCATCAACATGAG
	TetDown	GTCGTCCAAATAGTCGGA
	CmUp	CAACGGTGGTATATCCAG
	CmDown	CAGTACTGCGATGAGTGGCA
	PacUp	GTAGCTAATCTAACAGTAGG
	PacDown	GTCCTAGAACTTGGTGTATG
Primer extension reactions	PEmg236 (I)	[6-FAM] CACTTTAATAAAGCAATCCG
	PEmg236 (II)	[6-FAM] GGATCTACAAAGATGTTAATC
	PEmg235 (int)	[6-FAM] GTTAAGTCTCTGCCTATCTC
	PEmg233	[6-FAM] CAGCAAACAAAGCATGACCT
	PEmg232	[6-FAM] ATCACACAAACAACCTTAGC

Table S4. Differentially expressed genes in *M. genitalium* upon metal starvation with 2,2'-bipyridyl identified by RNA-Seq analysis. Cut off $\log_2 \pm 1$.

Up-regulated				
Locus tag	Gene	Gene product	log2 Fold Change	p-value
MG_355	<i>clpB</i>	Chaperone protein ClpB	3.84	2.09E-144
MG_241		Uncharacterized protein MG241	3.19	2.39E-98
MG_239	<i>lon</i>	Lon protease	2.84	9.87E-211
MG_242		Uncharacterized protein MG242	2.66	8.28E-60
MG_304		ABC transporter ATP-binding protein MG304	2.59	6.49E-94
MG_080	<i>oppF</i>	Oligopeptide transport ATP-binding protein OppF	2.47	2.23E-147
MG_303		ABC transporter ATP-binding protein MG303	2.42	7.56E-56
MG_244	<i>uvrD</i>	DNA helicase II homolog	2.33	5.32E-38
MG_302		Uncharacterized protein	2.22	5.71E-21
MG_079	<i>oppD</i>	Oligopeptide transport ATP-binding protein OppD	2.16	1.12E-79
MG_524		Uncharacterized protein MG384.1	2.14	1.71E-13
MG_078	<i>oppC</i>	Oligopeptide transport system permease protein OppC	2.12	2.60E-50
MG_149	<i>hrl</i>	Uncharacterized lipoprotein MG149	2.12	3.73E-113
MG_305	<i>dnaK</i>	Chaperone protein DnaK	2.01	8.67E-57
MG_439		Uncharacterized lipoprotein MG439	1.94	5.13E-31
MG_077	<i>oppB</i>	Oligopeptide transport system permease protein OppB	1.93	8.60E-51
MG_316		Uncharacterized protein MG316	1.85	7.12E-08
MG_192.1		Uncharacterized small protein MG192.1	1.74	6.27E-20
MG_321		Uncharacterized lipoprotein MG321	1.65	2.68E-55
MG_339	<i>recA</i>	Protein RecA	1.64	2.94E-43
MG_033	<i>glpF</i>	Glycerol uptake facilitator protein	1.60	1.21E-47
MG_083	<i>pth</i>	Peptidyl-tRNA hydrolase	1.53	2.49E-51
MG_084	<i>tilS</i>	tRNA(Ile)-lysidine synthase	1.50	9.12E-44
MG_085	<i>hprK</i>	HPr kinase/phosphorylase	1.49	5.32E-44
MG_384	<i>obg</i>	GTPase Obg	1.49	2.56E-37
MG_389		Uncharacterized protein MG389	1.47	5.86E-05
MG_390		ABC transporter ATP-binding protein MG390	1.37	5.37E-34
MG_282	<i>greA</i>	Transcription elongation factor GreA	1.36	4.84E-63
MG_478		Uncharacterized protein MG149.1	1.32	5.04E-17
MG_521		Uncharacterized protein MG350.1	1.31	0.017819 9
MG_081	<i>rplK</i>	50S ribosomal protein L11	1.31	9.44E-35
MG_098		Uncharacterized protein MG098	1.30	1.23E-22
MG_441		Uncharacterized protein MG441	1.29	0.000792 79
MG_245		5-formyltetrahydrofolate cyclo-ligase	1.28	9.94E-06
MG_012		Uncharacterized protein MG012	1.25	6.17E-10
MG_206	<i>uvrC</i>	UvrABC system protein C	1.21	6.69E-24
MG_074		Uncharacterized protein MG074	1.19	0.000382 07

MG_082	<i>rplA</i>	50S ribosomal protein L1	1.16	4.78E-26
MG_385		Uncharacterized protein MG385	1.14	4.81E-18
MG_237		Uncharacterized protein MG237	1.13	7.28E-23
MG_064		Uncharacterized ABC transporter permease MG064	1.10	4.54E-24
MG_075		Uncharacterized protein MG075	1.08	5.38E-35
MG_365	<i>fmt</i>	Methionyl-tRNA formyltransferase	1.07	5.47E-08
MG_246		Putative phosphatase/phosphodiesterase MG246	1.06	1.08E-13
MG_236	<i>fur</i>	Ferric uptake regulation protein	1.03	5.40E-15
MG_358	<i>ruvA</i>	Holliday junction ATP-dependent DNA helicase RuvA	1.03	3.31E-13

Down-regulated

Locus tag	Gene	Gene product	log2 Fold Change	p-value
MG_189		ABC transporter permease protein MG189	-1.98	6.16E-46
MG_188		ABC transporter permease protein MG188	-1.73	1.85E-33
MG_511		tRNA-Val	-1.42	2.68E-04
MG_489		tRNA-Asp	-1.39	9.82E-05
MG_512		tRNA-Thr	-1.35	1.59E-05
MG_485		tRNA-Met	-1.34	3.23E-06
MG_112	<i>rpe</i>	Ribulose-phosphate 3-epimerase	-1.33	8.21E-15
MG_501		tRNA-Lys	-1.31	3.06E-04
MG_434	<i>pyrH</i>	Uridylate kinase	-1.31	1.68E-30
MG_350		Uncharacterized protein MG350	-1.29	1.77E-14
MG_187		ABC transporter ATP-binding protein MG187	-1.28	1.20E-29
MG_483		tRNA-Cys	-1.28	1.33E-04
MG_111	<i>pgi</i>	Glucose-6-phosphate isomerase	-1.27	8.22E-36
MG_453	<i>galU</i>	Glucose-1-phosphate uridylyltransferase	-1.23	5.48E-20
MG_500		tRNA-Leu	-1.22	1.50E-04
MG_132		Uncharacterized HIT-like protein MG132	-1.2	7.65E-14
MG_484		tRNA-Pro	-1.19	3.72E-03
MG_324	<i>pepP</i>	Putative Xaa-Pro aminopeptidase	-1.17	4.16E-21
MG_526		ABC transporter ATP-binding protein MG468.1	-1.13	6.15E-18
MG_510		tRNA-Thr	-1.13	5.44E-04
MG_513		tRNA-Glu	-1.11	1.26E-03
MG_186		Uncharacterized lipoprotein MG186	-1.11	4.12E-11
MG_507		tRNA-Ser	-1.09	1.21E-03
MG_515		Uncharacterized protein MG323.1	-1.08	4.21E-17
MG_024	<i>yhcF</i>	Ribosome-binding ATPase YhcF	-1.08	1.34E-19
MG_072	<i>secA</i>	Protein translocase subunit SecA	-1.08	5.23E-22
MG_514		tRNA-Asn	-1.07	1.32E-04
MG_488		tRNA-Met	-1.07	1.66E-03
MG_023	<i>fba</i>	Fructose-bisphosphate aldolase	-1.07	3.76E-20
MG_506		tRNA-Ser	-1.02	2.83E-02
MG_494		Uncharacterized protein MG255.1	-1.02	3.37E-03
MG_278	<i>relA</i>	Guanosine-3',5'-bis(diphosphate) 3'-	-1.02	3.18E-15

pyrophosphohydrolase

MG_190	<i>nrnA</i>	Bifunctional oligoribonuclease and PAP phosphatase NrnA	-1.02	9.17E-23
MG_435	<i>frr</i>	Ribosome-recycling factor	-1.01	1.05E-11
MG_262	<i>polA</i>	5'-3' exonuclease	-1	2.08E-07

Table S5. Differentially expressed genes in a *M. genitalium fur* mutant and the corresponding complemented strain derivative compared to the wild-type strain identified by RNA-Seq analysis. Cut off $\log_2 \pm 1$.

Locus tag	Gene	Gene product	<i>fur</i>		<i>fur</i> COM	
			log2 fold change	p-value	log2 fold change	p-value
MG_149	<i>hrl</i>	Uncharacterized lipoprotein MG149	2.45	2.09E-144	-0.95	1.87E-11
MG_304		ABC transporter ATP-binding protein MG304	2.2	9.87E-211	-0.35	0.10
MG_303		ABC transporter ATP-binding protein MG303	2.06	6.49E-94	-0.97	6.86E-05
MG_302		Uncharacterized protein MG302	1.45	7.56E-56	-0.37	0.47
MG_236	<i>fur</i>	Ferric uptake regulation protein	-5.77	3.13E-41	3.53	3.02E-293
MG_237		Uncharacterized protein MG237	-1.25	1.50E-05	-1.22	4.28E-14

Table S6. Differentially expressed genes in a *M. genitalium fur* mutant upon metal deprivation with 2,2'-bipyridyl identified by RNA-Seq analysis. Cut off $\log_2 \pm 1$.

Up-regulated				
Locus tag	Gene	Gene product	log ₂ Fold Change	p-value
MG_355	<i>clpB</i>	Chaperone protein ClpB	4.33	2.35E-202
MG_241		Uncharacterized protein MG241	3.69	3.97E-99
MG_239	<i>lon</i>	Lon protease	3.02	3.42E-66
MG_079	<i>oppD</i>	Oligopeptide transport ATP-binding protein OppD	2.77	2.38E-90
MG_078	<i>oppC</i>	Oligopeptide transport system permease protein OppC	2.66	6.15E-63
MG_080	<i>oppF</i>	Oligopeptide transport ATP-binding protein OppF	2.58	7.58E-57
MG_083	<i>pth</i>	Peptidyl-tRNA hydrolase	2.57	1.53E-29
MG_242		Uncharacterized protein MG242	2.49	3.24E-33
MG_081	<i>rplK</i>	50S ribosomal protein L11	2.40	8.93E-31
MG_082	<i>rplA</i>	50S ribosomal protein L1	2.37	1.87E-36
MG_244	<i>uvrD</i>	DNA helicase II homolog	2.36	8.01E-51
MG_077	<i>oppB</i>	Oligopeptide transport system permease protein OppB	2.17	8.69E-64
MG_305	<i>dnaK</i>	Chaperone protein DnaK	2.09	6.78E-35
MG_321		Uncharacterized lipoprotein MG321	2.07	4.19E-48
MG_339	<i>recA</i>	Protein RecA	2.05	1.79E-22
MG_478		Uncharacterized protein MG149.1	1.91	1.78E-17
MG_084	<i>tilS</i>	tRNA(Ile)-lysidine synthase	1.88	1.64E-38
MG_012		Uncharacterized protein MG012	1.78	3.20E-15
MG_282	<i>greA</i>	Transcription elongation factor GreA	1.77	8.59E-20
MG_174	<i>rpmJ</i>	50S ribosomal protein L36	1.73	2.11E-09
MG_246		Putative phosphatase/phosphodiesterase MG246	1.72	4.62E-16
MG_384	<i>obg</i>	GTPase Obg	1.70	1.35E-17
MG_439		Uncharacterized lipoprotein MG439	1.70	3.08E-12
MG_085	<i>hprK</i>	HPr kinase/phosphorylase	1.61	3.06E-25
MG_098		Uncharacterized protein MG098	1.58	1.45E-29
MG_358	<i>ruvA</i>	Holliday junction ATP-dependent DNA helicase RuvA	1.57	3.59E-10
MG_393	<i>groES</i>	10 kDa chaperonin	1.56	1.54E-12
MG_206	<i>uvrC</i>	UvrABC system protein C	1.54	6.62E-14
MG_353		Uncharacterized protein MG353	1.52	1.18E-19
MG_142	<i>infB</i>	Translation initiation factor IF-2	1.46	4,36E-09
MG_521		Uncharacterized protein MG350.1	1.44	1.90E-02
MG_392	<i>groL</i>	60 kDa chaperonin	1.31	3.49E-19
MG_245		5-formyltetrahydrofolate cyclo-ligase	1.31	0.0003998 3
MG_149	<i>hrl</i>	Uncharacterized lipoprotein MG149	1.30	4.13E-14
MG_340	<i>rpoC</i>	DNA-directed RNA polymerase subunit beta'	1.28	6.92E-14
MG_440		Uncharacterized protein MG440	1.28	4,49E-12
MG_359	<i>ruvB</i>	Holliday junction ATP-dependent DNA helicase RuvB	1.24	2.22E-09

MG_192.1		Uncharacterized small protein MG192.1	1.21	6.35E-07
MG_179	<i>ecfA1</i>	Energy-coupling factor transporter ATP-binding protein EcfA1	1.19	2.03E-09
MG_173	<i>infA</i>	Translation initiation factor IF-1	1.17	3.20E-06
MG_238	<i>tig</i>	Trigger factor	1.15	5.74E-08
MG_058	<i>prs</i>	Ribose-phosphate pyrophosphokinase	1.13	2.72E-09
MG_473	<i>rpmG2</i>	50S ribosomal protein L33 2	1.12	7.99E-07
MG_161	<i>rplN</i>	50S ribosomal protein L14	1.12	3.06E-05
MG_011		Uncharacterized protein MG011	1.06	1.93E-04
MG_164	<i>rpsN</i>	30S ribosomal protein S14 type Z	1.06	1.16E-04
MG_100	<i>gatB</i>	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B	1.05	2.17E-12
MG_237		Uncharacterized protein MG237	1.05	4.53E-06
MG_158	<i>rplP</i>	50S ribosomal protein L16	1.05	1.53E-05
MG_180	<i>ecfA2</i>	Energy-coupling factor transporter ATP-binding protein EcfA2	1.03	1.41E-10
MG_316		Uncharacterized protein MG316	1.02	9.22E-02
MG_160	<i>rpsQ</i>	30S ribosomal protein S17	1.00	3.38E-04

Down-regulated

Locus tag	Gene	Gene product	log2 Fold Change	p-value
MG_452		Uncharacterized protein MG452	-2.31	3.56E-09
MG_505		Putative pre-16S rRNA nuclease	-1.93	3.97E-03
MG_007		Uncharacterized protein MG007	-1.91	1.05E-03
MG_494		Uncharacterized protein MG255.1	-1.87	4.82E-04
MG_522	<i>rpsT</i>	30S ribosomal protein S20	-1.86	6.78E-06
MG_039		Uncharacterized protein MG039	-1.73	9.02E-18
MG_189		ABC transporter permease protein MG189	-1.71	4.90E-21
MG_453	<i>galU</i>	Glucose-1-phosphate uridylyltransferase	-1.7	4.92E-16
MG_350		Uncharacterized protein MG350	-1.68	9.45E-10
MG_409		Uncharacterized protein MG409	-1.53	1.42E-04
MG_435	<i>frr</i>	Ribosome-recycling factor	-1.51	1.39E-07
MG_188		ABC transporter permease protein MG188	-1.5	5.10E-16
MG_437	<i>cdsA</i>	Phosphatidate cytidylyltransferase	-1.48	4.61E-11
MG_010		Uncharacterized protein MG010	-1.48	1.24E-02
MG_001	<i>dnaN</i>	Beta sliding clamp	-1.44	9.69E-03
MG_380	<i>rsmG</i>	Ribosomal RNA small subunit methyltransferase G	-1.42	9.40E-03
MG_515		Uncharacterized protein MG323.1	-1.41	3.17E-07
MG_526		ABC transporter ATP-binding protein MG468.1	-1.41	3.02E-12
MG_071	<i>pacL</i>	Cation-transporting P-type ATPase	-1.38	1.23E-14
MG_429	<i>ptsI</i>	Phosphoenolpyruvate-protein phosphotransferase	-1.34	1.89E-19
MG_255		Uncharacterized protein MG255	-1.31	5.66E-14
MG_495		tRNA-Arg	-1.3	1.74E-04
MG_431	<i>tpiA</i>	Triosephosphate isomerase	-1.26	1.96E-09
MG_428		Alternative sigma factor σ 20	-1.26	4.96E-05

MG_248		tRNA methyltransferase MG248	-1.25	3.30E-06
MG_262	<i>polA</i>	5'-3' exonuclease	-1.25	8.83E-08
MG_325	<i>rpmG1</i>	50S ribosomal protein L33 1	-1.24	1.07E-07
MG_112	<i>rpe</i>	Ribulose-phosphate 3-epimerase	-1.24	1.25E-05
MG_438		Type-1 restriction enzyme specificity protein MG438	-1.24	6.66E-14
MG_110	<i>rsgA</i>	Small ribosomal subunit biogenesis GTPase RsgA	-1.22	1.95E-04
MG_111	<i>pgi</i>	Glucose-6-phosphate isomerase	-1.2	1.11E-11
MG_422		Uncharacterized protein MG422	-1.2	5.02E-03
MG_447		Uncharacterized protein MG447	-1.19	1.45E-03
MG_507		tRNA-Ser	-1.19	2.37E-05
MG_470		ParA family protein MG470	-1.18	9.71E-11
MG_370		Uncharacterized RNA pseudouridine synthase MG370	-1.16	5.53E-03
MG_296		Uncharacterized protein MG296	-1.14	2.84E-03
MG_520		tRNA-Leu	-1.12	1.12E-04
MG_485		tRNA-Met	-1.12	1.50E-04
MG_463	<i>rsmA</i>	Ribosomal RNA small subunit methyltransferase A	-1.12	2.09E-04
MG_074		Uncharacterized protein MG074	-1.12	1.88E-03
MG_123		Uncharacterized protein MG123	-1.11	1.79E-07
MG_047	<i>metK</i>	S-adenosylmethionine synthase	-1.09	2.61E-10
MG_135		Uncharacterized protein MG135	-1.07	1.21E-05
MG_240		Uncharacterized protein MG240	-1.04	7.16E-06
MG_140		Uncharacterized ATP-dependent helicase MG140	-1.04	2.37E-15
MG_132		Uncharacterized HIT-like protein MG132	-1.04	5.33E-07
MG_372	<i>thil</i>	Probable tRNA sulfurtransferase	-1.04	7.28E-05
MG_324	<i>pepP</i>	Putative Xaa-Pro aminopeptidase	-1.02	2.60E-13
MG_382	<i>udk</i>	Uridine kinase	-1.01	2.31E-03
MG_343		Uncharacterized protein MG343	-1.01	1.21E-02

Table S7. Differentially expressed proteins observed in the DIGE proteomic analysis of the fur mutant.

Spot #	Id Score ¹	#Peptides ¹	% SC ¹	Accession ²	Entry Name ²	Protein	Locus	Gene	log2 FC	p-value
1766	460	10	54.1	P47648	MSRA_MYCGE	Peptide methionine sulfoxide reductase MsrA	MG408	<i>msrA</i>	2.49	1.60E-02
2076	314	6	28.0	P47648	MSRA_MYCGE	Peptide methionine sulfoxide reductase MsrA	MG408	<i>msrA</i>	2.42	6.00E-03
2065	116	2	12.1	P47648	MSRA_MYCGE	Peptide methionine sulfoxide reductase MsrA	MG408	<i>msrA</i>	2.23	3.00E-03
2118	167	5	14.4	P47515	ODPB_MYCGE	Pyruvate dehydrogenase E1 component E1, subunit beta	MG273	<i>pdhB</i>	2.64	2.26E-04
1771	84	3	23.2	P47334	RS7_MYCGE	30S ribosomal protein S7	MG088	<i>rpsG</i>	2.54	2.00E-03
2143	163	4	26.5	P47656	RS9_MYCGE	30S ribosomal protein S9	MG417	<i>rpsI</i>	2.19	2.60E-02
1838	114	3	21.2	P47656	RS9_MYCGE	30S ribosomal protein S9	MG417	<i>rpsI</i>	2.08	2.00E-03
2064	235	5	14.6	P47395	Y149_MYCGE	Uncharacterized lipoprotein MG149 - Histidine-rich lipoprotein	MG149	<i>hrl</i>	2.60	3.18E-04
1808	112	2	6.4	P47395	Y149_MYCGE	Uncharacterized lipoprotein MG149 - Histidine-rich lipoprotein	MG149	<i>hrl</i>	2.22	1.30E-02
1810	122	2	1.8	P47580	Y338_MYCGE	Uncharacterized lipoprotein MG338	MG338	MG_338	2.60	3.00E-03
2075	192	4	3.1	P47580	Y338_MYCGE	Uncharacterized lipoprotein MG338	MG338	MG_338	2.45	6.00E-03
1918									3.02	8.45E-04
2145									1.87	1.00E-02
2111									1.65	5.00E-03
1881									1.58	4.50E-02
2138									1.47	1.20E-02

¹ Protein Identification Score in Mascot MSMS search, number of unique peptides identified and % sequence coverage.

² UniProt/SwissProt identifiers

Table S8. Insertion site of the TnPacHrl_{wt}:*cat:mcherry* transposon in the genome of two different G37-Hrlwt:CatCh clones.

G37-Hrl_{wt}CatCh clone	Fluorescence	Insertion site (bp)	Gene truncated
C1	Marginal	430390	None
C5	Marginal	72884	<i>fruK</i>

Table S9. Concentration of some transition metals in the SP-4 medium determined by ICP-MS analysis (n=10).

Element	Mean ($\mu\text{g/L}$)	SD
Mn	27.1	2.47
Fe	691.3	33.55
Co	9.72	0.64
Ni	5.52	1.11
Cu	33.7	3.83
Zn	948.5	39.31

SD: Standard Deviation