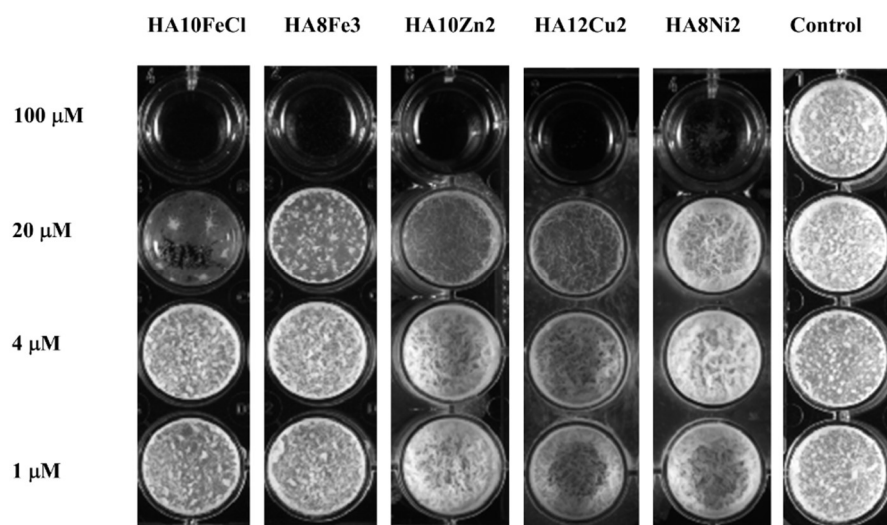


## Supplementary Figure



**Figure S1.** Representative *M. bovis* BCG biofilm formation assay. The *M. bovis* BCG was grown in Sauton's medium in the presence or absence (control) of various compounds (1-100  $\mu$ M) for 24 days.

## Supplementary Table

**Table S1.** Differential protein amounts identified by comparing HA10FeCl treated and untreated *M. bovis* BCG.

Index	Protein name	Gene name	Molecular Weight (kDa)	LFQ intensity		Fold change HA10FeCl /BCG	t test <i>p</i> value
				HA10FeCl	BCG		
1	HTH tetR-type domain-containing protein	<i>BCG_2177c</i>	21.614	14520.95	164180	0.0884	0.0002
2	Conserved hypothetical proline and threonine rich protein	<i>BCG_0352</i>	64.129	765540	634273.3	1.207	0.0032
3	UPF0353 protein BCG_1543	<i>BCG_1543</i>	36.03	12012667	12857333	0.9343	0.0032
4	Transcriptional activator protein	<i>BCG_2384c</i>	48.381	1981267	3505300	0.5652	0.0034
5	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE	<i>BCG_3492c</i>	18.214	1522100	1278200	1.1908	0.0039
6	Probable methylmalonyl-CoA mutase large subunit mutB	<i>mutB (BCG_1556)</i>	80.603	17600000	16619667	1.059	0.0042
7	DNA topoisomerase 1	<i>topA (BCG_3704c)</i>	102.37	44207667	39517000	1.1187	0.0044
8	Cyclic pyranopterin monophosphate synthase	<i>moaC3 (BCG_3390c)</i>	18.555	950413.3	783746.7	1.2127	0.0047
9	Large ribosomal subunit protein uL2	<i>rplB (BCG_0754)</i>	30.576	74363000	68214000	1.0901	0.0054
10	Indole-3-glycerol phosphate synthase	<i>trpC (BCG_1649)</i>	28.023	34303000	32548333	1.0539	0.0057
11	NADH-dependent glutamate synthase (Small subunit) gltD	<i>gltD (BCG_3921c)</i>	53.401	18078000	15521000	1.1647	0.0059
12	Thiazole synthase	<i>thiG (BCG_0456)</i>	25.894	865536.7	1122833	0.7709	0.0071
13	NADH-quinone oxidoreductase subunit A	<i>nuoA (BCG_3168)</i>	13.975	4408700	4133400	1.0666	0.0072
14	Probable integral membrane protein	<i>BCG_3545c</i>	23.793	607810	509986.7	1.1918	0.01
15	Probable transcriptional regulatory protein (Probably tetR-family)	<i>BCG_1076</i>	21.701	1806133	2037933	0.8863	0.01
16	Small ribosomal subunit protein bS6	<i>rpsF (BCG_0084)</i>	10.935	39701000	44250333	0.8972	0.0101
17	Calcineurin-like phosphoesterase domain-containing protein	<i>BCG_2813c</i>	37.6	5039900	4367967	1.1538	0.0114
18	Probable polyketide synthase pks12	<i>pks12 (BCG_2067c)</i>	431.54	78558333	71357333	1.1009	0.0127
19	Possible transcriptional regulatory protein (Probably tetR-family)	<i>BCG_0702c</i>	24.727	715100	694466.7	1.0297	0.0134
20	Rubredoxin	<i>BCG_3279c</i>	6.7974	70134.5	31983	2.1929	0.0141
21	Phosphate transport system permease protein	<i>pstC2(BCG_0981)</i>	34.261	87300.33	40007.33	2.1821	0.0143
22	Probable mutator protein mutT2	<i>mutT2 (BCG_1222)</i>	15.16	1039500	922426.7	1.1269	0.0157
23	DUF427 domain-containing protein	<i>BCG_1708</i>	13.11	18771.5	15052.67	1.2471	0.0158
24	Ribonuclease P protein component	<i>rnpA_2 (BCG_3981c)</i>	13.942	1077833	976606.7	1.1037	0.0162
25	Probable cytochrome P450 124 CYP124	<i>cyp124 (BCG_2283)</i>	47.824	90852.33	262460	0.3462	0.0162
26	Possible adenylate cyclase	<i>BCG_1381c</i>	61.934	3759367	4121333	0.9122	0.0167
27	Large ribosomal subunit protein uL4	<i>rplD (BCG_0752)</i>	23.743	28623667	26318000	1.0876	0.0182

28	ESX-1 secretion-associated protein EspA/EspE-like domain-containing protein	<i>BCG_3927</i>	43.506	11706667	10565333	1.108	0.0199
29	thiosulfate sulfurtransferase	<i>BCG_0364</i>	24.091	809230	652393.3	1.2404	0.0205
30	Signal transduction histidine-protein kinase/phosphatase MprB	<i>mprB (BCG_1037)</i>	54.431	3165333	3524033	0.8982	0.0213
31	Uncharacterized protein	<i>BCG_2826</i>	9.8619	776093.3	648636.7	1.1965	0.0216
32	50S ribosomal protein L25	<i>rplY (BCG_1072c)</i>	22.441	28694667	26092000	1.0997	0.022
33	DUF222 domain-containing protein	<i>BCG_0128c</i>	29.034	234963.3	188753.3	1.2448	0.023
34	Putative S-adenosyl-L-methionine-dependent methyltransferase BCG_1935c	<i>BCG_1935c</i>	33.267	6691433	5960633	1.1226	0.0231
35	Probable oxidoreductase	<i>BCG_2793c</i>	33.517	304546.7	556953.3	0.5468	0.0237
36	Probable lipase/esterase lipG	<i>lipG (BCG_0695c)</i>	32.963	6949833	5992800	1.1597	0.0242
37	Probable beta-glucosidase bglS	<i>bglS (BCG_0223)</i>	73.552	669126.7	449480	1.4887	0.0249
38	Putative phthiocerol dimycocerosate transporter LppX	<i>lppX (BCG_2967c)</i>	24.14	55880000	53324000	1.0479	0.0268
39	Probable propionyl-CoA carboxylase beta chain 4 accD4	<i>accD4 (BCG_3861c)</i>	56.679	25602667	24137667	1.0607	0.0275
40	Transmembrane protein	<i>BCG_1127c</i>	64.357	6147900	5556067	1.1065	0.0293
41	tRNA pseudouridine synthase A	<i>truA (BCG_3520c)</i>	28.092	6145633	5449833	1.1277	0.0295
42	Thioredoxin	<i>trxC_1 (BCG_0020)</i>	12.544	16445000	17423000	0.9439	0.0301
43	Possible conserved membrane protein	<i>BCG_3932</i>	51.092	1164233	891630	1.3057	0.0306
44	Cell division protein CrgA	<i>crgA (BCG_0011c)</i>	10.43	928696.7	605450	1.5339	0.0327
45	Probable transmembrane protein	<i>BCG_1629</i>	23.183	2499733	2330567	1.0726	0.0331
46	Probable conserved transmembrane alanine rich protein	<i>BCG_2863</i>	17.767	810793.3	931126.7	0.8708	0.0348
47	Endolytic murein transglycosylase	<i>mltG (BCG_2576c)</i>	45.473	6583633	5878633	1.1199	0.0357
48	Glutamyl-tRNA amidotransferase	<i>BCG_3747c</i>	16.701	3316733	3643000	0.9104	0.0364
49	VOC domain-containing protein	<i>BCG_1384c</i>	16.626	1672967	1359033	1.231	0.0367
50	Probable conserved transmembrane transport protein mmpL4	<i>mmpL4 (BCG_0489c)</i>	105.23	9818967	9134000	1.075	0.0376
51	Small ribosomal subunit protein uS4	<i>rpsD (BCG_3523c)</i>	23.476	110000000	104000000	1.0604	0.0393
52	Possible conserved membrane protein	<i>BCG_1478</i>	16.383	1205787	623100	1.9351	0.0395
53	Phthiotriol/phenolphthiotriol dimycocerosates methyltransferase	<i>BCG_2973</i>	30.651	39149667	34174333	1.1456	0.0397
54	Dolichyl-phosphate-mannose--protein mannosyltransferase	<i>BCG_1059c</i>	55.544	749520	587350	1.2761	0.0401
55	Possible conserved membrane protein	<i>BCG_0582</i>	55.016	4408433	4119933	1.07	0.0457
56	Probable oxidoreductase	<i>BCG_0099</i>	32.413	4390933	3837100	1.1443	0.0469
57	Glycosyltransferase 2-like domain-containing protein	<i>BCG_1268</i>	34.379	1285367	1138700	1.1288	0.0473
58	Probable conserved membrane protein mmpS4	<i>mmpS4 (BCG_0490c)</i>	15.403	2704100	2379033	1.1366	0.0479

LFQ: protein quantification; HA10FeCl: HA10FeCl-treated *M. bovis* BCG.

**Table S2.** Differential protein amounts unidentified by comparing HA10FeCl treated and untreated *M. bovis* BCG.

Index	Protein name	Gene name	Molecular Weight (kDa)	LFQ intensity	
				Average HA10FeCl	Average BCG
1	IS like-2 transposase	<i>BCG_1100c</i>	15.189	69579	NA
2	Possible nitrate/nitrite transporter narK2	<i>narK2 (BCG_1776c)</i>	41.109	2638.747	NA
3	Probable aldehyde dehydrogenase	<i>BCG_0259c</i>	28.491	81704.5	NA
4	DUF732 domain-containing protein	<i>BCG_3092</i>	13.915	46762	NA
5	PE family protein	<i>PE15 (BCG_1447)</i>	9.862	NA	1619
6	Probable conserved transmembrane transport protein mmpL9a	<i>mmpL9a (BCG_2361)</i>	89.958	NA	169034.3

LFQ: protein quantification; HA10FeCl: HA10FeCl-treated *M. bovis* BCG; NA: unidentified with lower expression.