

TABLE S1. The regions enriched by ChIP with GntR1 in the *C. glutamicum* genome

Peak start ^a	Peak end ^b	Peak#	Neighboring gene	Gene name	Enrichment factor ^c	Gene function
1676016	1676265	#132	<i>cgR_1513</i>	<i>gnd</i>	5.66	6-phosphogluconate dehydrogenase
1676016	1676265	#132	<i>cgR_1514</i>		5.66	uncharacterized protein, possibly involved in aromatic compounds catabolism
2635673	2635922	#196	<i>cgR_2397</i>	<i>gntV</i>	5.19	gluconate kinase
2172711	2172960	#157	<i>cgR_1973</i>	<i>pyk</i>	5.14	pyruvate kinase
1622834	1623083	#129	<i>cgR_1469</i>	<i>uspA2</i>	5.08	universal stress protein UspA or related nucleotide-binding protein
283508	283757	#020	<i>cgR_0261</i>	<i>iolT1</i>	5.06	metabolite transport protein
437450	437699	#030	<i>cgR_0402</i>	<i>bgIS</i>	5.01	putative beta-glucosidase
3047886	3048135	#224	<i>cgR_2751</i>	<i>pckA</i>	4.91	phosphoenolpyruvate carboxykinase
3186797	3187046	#238	<i>cgR_2868_(5sRNA)</i>		4.84	
2710180	2710429	#203	<i>cgR_2459</i>		4.76	putative glucuronide permease
2710180	2710429	#203	<i>cgR_2460</i>		4.76	SAM-dependent methyltransferase
1551313	1551562	#120	<i>cgR_1413</i>		4.72	hypothetical protein
1880912	1881161	#144	<i>cgR_1690</i>		4.72	coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductasetase or related flavin-depende
3211500	3211749	#240	<i>cgR_2895</i>	<i>maeB</i>	4.67	malic enzyme
2076208	2076457	#149	<i>cgR_1874</i>		4.65	hypothetical protein
2493581	2493830	#186	<i>cgR_2263</i>		4.64	bacterial regulatory proteins, TetR family
2493581	2493830	#186	<i>cgR_2262</i>	<i>mdh</i>	4.64	malate dehydrogenase
1566524	1566773	#124	<i>cgR_1425</i>	<i>ptsG</i>	4.54	phosphotransferase, glucose-specific enzyme II
1803976	1804225	#139	<i>cgR_1624</i>	<i>tkt</i>	4.46	transketolase

1803976	1804225	#139	<i>cgR_1623_5(sRNA)</i>		4.46
3115510	3115759	#233	<i>cgR_2806</i>	<i>gntP</i>	4.32 gluconate permease
3115510	3115759	#233	<i>cgR_2805</i>	<i>glpQI</i>	4.32 putative glycerophosphoryl diester phosphodiesterase
2758270	2758519	#208	<i>cgR_2497</i>	<i>dctA</i>	4.25 Na ⁺ /H ⁺ -dicarboxylate symporter
1822137	1822386	#140	<i>cgR_1636</i>	<i>gapA</i>	4.24 glyceraldehyde-3-phosphate dehydrogenase
2703949	2704198	#202	<i>cgR_2454</i>		4.20 sugar phosphate isomerase/epimerase
2703949	2704198	#202	<i>cgR_6140</i>		4.20 HYPOTHETICAL
479980	480229	#038	<i>cgR_6020</i>		4.18 HYPOTHETICAL
1145984	1146233	#087	<i>cgR_1038</i>	<i>gapB</i>	4.14 glyceraldehyde 3-phosphate dehydrogenase
2319038	2319287	#173	<i>cgR_2102</i>		4.09 permease of the major facilitator superfamily
2693878	2694127	#201	<i>cgR_2451</i>		3.91 Na ⁺ /H ⁺ -dicarboxylate symporter
1554912	1555161	#121	<i>cgR_6099</i>		3.82 HYPOTHETICAL
2428132	2428381	#182	<i>cgR_2199</i>		3.76 putative membrane protein
325095	325344	#023	<i>cgR_0299</i>		3.55 sodium:sulfate symporter transmembrane component
1082299	1082548	#084	<i>cgR_0973</i>		3.52 secreted protein related to metalloendopeptidases
1082299	1082548	#084	<i>cgR_0974</i>		3.52 membrane protein
2453906	2454155	#184	<i>cgR_2222</i>	<i>dctPI</i>	3.49 putative C4-dicarboxylate-binding protein
3106850	3107099	#229	<i>cgR_2798</i>		3.44 hypothetical protein
2217713	2217962	#162	<i>cgR_2015</i>		3.26 predicted Co/Zn/Cd cation transporter
2174407	2174656	#158	<i>cgR_1974</i>	<i>lgt</i>	3.24 putative prolipoprotein diacylglycerol transferase
3214457	3214706	#241	<i>cgR_2896</i>	<i>gntK</i>	3.18 putative gluconate kinase
2340750	2340999	#175	<i>cgR_2120</i>	<i>aceE</i>	3.09 pyruvate dehydrogenase
2752328	2752577	#207	<i>cgR_2493</i>	<i>purS</i>	3.06 phosphoribosylformylglycinamide synthase component

1123410	1123659	#086	<i>cgR_1017</i>		2.98	hypothetical protein
1374000	1374249	#102	<i>cgR_1253</i>		2.80	hypothetical protein
1374000	1374249	#102	<i>cgR_1254</i>		2.80	bacterial regulatory proteins, crp family
1561578	1561827	#122	<i>cgR_1421</i>		2.79	hypothetical protein
113374	113623	#009	<i>cgR_0096</i>	<i>copO</i>	2.72	creatinine deaminase
2928826	2929075	#220	<i>cgR_2647</i>		2.68	Na ⁺ /phosphate symporter
2928826	2929075	#220	<i>cgR_2646</i>		2.68	permease of the major facilitator superfamily[nebacterium glutamicum]
773660	773909	#061	<i>cgR_0713</i>		2.64	hypothetical protein
1183886	1184135	#089	<i>cgR_1069</i>	<i>porB</i>	2.60	hypothetical protein
1183886	1184135	#089	<i>cgR_1070</i>		2.60	hypothetical protein
1859723	1859972	#143	<i>cgR_1674</i>		2.55	ABC-type cobalamin/Fe ³⁺ -siderophores transport system, permease component
868711	868960	#074	<i>cgR_0784</i>	<i>icd</i>	2.52	isocitrate dehydrogenase
26848	27097	#002	<i>cgR_0026</i>		2.49	5'-nucleotidase (putative pseudogene)
505522	505771	#044	<i>cgR_0453</i>	<i>mfsR</i>	2.46	Transcriptional regulator, TetR family
740086	740335	#060	<i>cgR_0682</i>	<i>rpsD</i>	2.41	30S ribosomal protein S4
449962	450211	#032	<i>cgR_0412</i>	<i>ushA</i>	2.29	probable 5'-nucleotidase precursor
2814253	2814502	#214	<i>cgR_2547</i>	<i>ptsS</i>	2.29	enzyme II sucrose protein
2124358	2124607	#152	<i>cgR_1934</i>	<i>pcaB2</i>	2.27	putative 3-carboxy-cis,cis-muconate cycloisomerase
2418995	2419244	#181	<i>cgR_2192</i>	<i>ptxB</i>	2.24	probable phosphite transport system binding protein
2626838	2627087	#194	<i>cgR_2388</i>	<i>betT</i>	2.22	high-affinity choline transport protein
2626838	2627087	#194	<i>cgR_6135</i>		2.22	HYPOTHETICAL
448074	448323	#031	<i>cgR_0412</i>	<i>ushA</i>	2.22	probable 5'-nucleotidase precursor
476055	476304	#036	<i>cgR_6017</i>		2.21	HYPOTHETICAL

2092945	2093194	#150	<i>cgR_1893</i>		2.20	ClpP protease family protein
1350148	1350397	#099	<i>cgR_1235</i>		2.17	NTP pyrophosphohydrolase
416468	416717	#028	<i>cgR_0382</i>		1.97	putative serine protease, membrane protein
416468	416717	#028	<i>cgR_0383</i>		1.97	hydrolase or acyltransferase
2103149	2103398	#151	<i>cgR_1906</i>		1.94	putative single-strand binding protein
87275	87524	#006	<i>cgR_0076</i>		1.94	hypothetical protein
2312827	2313076	#171	<i>cgR_2094</i>		1.83	hypothetical protein
510201	510450	#045	<i>cgR_0457</i>	<i>deoC</i>	1.82	deoxyribose-phosphate aldolase
1543965	1544214	#117	<i>cgR_1409</i>	<i>int1</i>	1.80	probable phage-type integrase
2244607	2244856	#164	<i>cgR_2037</i>	<i>ftsZ</i>	1.79	cell division GTPase
1045645	1045894	#083	<i>cgR_0946</i>		1.74	hypothetical protein
1045645	1045894	#083	<i>cgR_0945</i>	<i>accDA</i>	1.74	acetyl-coenzyme A carboxylase carboxyl transferase
2795120	2795369	#212	<i>cgR_2529</i>	<i>thrE</i>	1.71	threonine export carrier
2352016	2352265	#177	<i>cgR_2130</i>		1.68	hypothetical protein
2352016	2352265	#177	<i>cgR_2130_5(sRNA)</i>		1.68	
1111039	1111288	#085	<i>cgR_1006</i>	<i>metS</i>	1.63	methionyl-tRNA synthetase
426543	426792	#029	<i>cgR_0394</i>	<i>cspA2</i>	1.63	cold-shock protein
821019	821268	#067	<i>cgR_0747</i>		1.60	nucleoside-diphosphate-sugar epimerase
2391628	2391877	#179	<i>cgR_2169</i>	<i>malQ</i>	1.60	4-alpha-glucanotransferase
473758	474007	#035	<i>cgR_0435</i>		1.57	hypothetical protein
1499429	1499678	#112	<i>cgR_1365</i>		1.57	putative aliphatic sulfonates uptake ABC transporter secreted solute-binding protein
1279187	1279436	#093	<i>cgR_1170</i>		1.56	putative membrane protein
2768358	2768607	#210	<i>cgR_2506</i>		1.54	SAM-dependent methyltransferase

2133493	2133742	#153	<i>cgR_1945</i>	<i>srp</i>	1.51	signal recognition particle GTPase
2284993	2285242	#168	<i>cgR_2070</i>	<i>nlpC</i>	1.49	hypothetical protein
112141	112390	#008	<i>cgR_0095</i>	<i>crnT</i>	1.48	permease of the major facilitator superfamily
1333476	1333725	#097	<i>cgR_1223</i>	<i>metE</i>	1.48	homocysteine methyltransferase
1333476	1333725	#097	<i>cgR_1224</i>		1.48	hypothetical protein
2204477	2204726	#159	<i>cgR_2005</i>		1.45	coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductasetase or related flavin-depende
541217	541466	#047	<i>cgR_5003</i>		1.45	hypothetical protein
471653	471902	#034	<i>cgR_0434</i>	<i>nrfC</i>	1.43	UDP-N-acetylglucosamine 2-epimerase
471653	471902	#034	<i>cgR_0433</i>	<i>cmtI</i>	1.43	trehalose corynomycolyl transferase
2676354	2676603	#200	<i>cgR_2434</i>	<i>gntRI</i>	1.39	bacterial regulatory proteins, GntR family
820275	820524	#066	<i>cgR_0746</i>		1.39	transcriptional regulator, MarR family
253339	253588	#019	<i>cgR_0235</i>		1.37	membrane protein
3235474	3235723	#243	<i>cgR_2915</i>	<i>trpP</i>	1.36	tryptophan-specific permease, 5-methyltryptophan resistance
2892243	2892492	#219	<i>cgR_2618</i>		1.35	hypothetical protein
898710	898959	#077	<i>cgR_0812</i>		1.35	cobalamin synthesis protein/P47K
898710	898959	#077	<i>cgR_0811</i>		1.35	secreted protein
2846057	2846306	#216	<i>cgR_2579</i>		1.34	uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides
618037	618286	#054	<i>cgR_0559</i>		1.31	probable DNA invertase
104577	104826	#007	<i>ribosomal</i>		1.26	
1600884	1601133	#128	<i>cgR_1449</i>	<i>ugpC</i>	1.22	ABC-type sugar transport systems, ATPase component
3112865	3113114	#232	<i>cgR_2803</i>		1.22	putative secreted protein
1361111	1361360	#100	<i>cgR_1244</i>		1.18	putative secreted lipoprotein
3105701	3105950	#228	<i>cgR_2797</i>		1.18	hypothetical protein

3255486	3255735	#244	<i>cgR_2937</i>		1.18	putative oxidoreductase protein
1562548	1562797	#123	<i>cgR_1422</i>	<i>dkgX</i>	1.17	putative 2,5-diketo-D-gluconic acid reductasetase
466096	466345	#033	<i>cgR_0426</i>		1.16	hypothetical protein
1155037	1155286	#088	<i>cgR_1046</i>		1.16	putative multicopper oxidase
2742260	2742509	#206	<i>cgR_2485</i>		1.15	conserved hypothetical protein-fragment
487766	488015	#043	<i>cgR_0436</i>		1.15	putative glycosyltransferase
1378484	1378733	#104	<i>cgR_1257_5(sRNA)</i>		1.14	
779669	779918	#062	<i>cgR_0720</i>		1.13	hypothetical protein
2557253	2557502	#188	<i>cgR_2324</i>		1.11	putative transposase
2557253	2557502	#188	<i>cgR_2323</i>		1.11	putative transposase
610643	610892	#053	<i>cgR_0551</i>		1.08	hypothetical protein
884827	885076	#076	<i>cgR_0800</i>	<i>dac</i>	1.08	D-alanyl-D-alanine carboxypeptidase
1584006	1584255	#127	<i>cgR_1436</i>	<i>qor2</i>	1.06	NADPH-dependent quinone oxidoreductase
1584006	1584255	#127	<i>cgR_1435</i>	<i>qorR</i>	1.06	transcriptional regulator, HxIR family
209335	209584	#015	<i>cgR_0190</i>	<i>panB</i>	1.05	3-methyl-2-oxobutanoate hydroxymethyltransferase
17147	17396	#001	<i>cgR_0016</i>	<i>maoN</i>	1.04	monoamine oxidase N
2397039	2397288	#180	<i>cgR_2173</i>	<i>dcp</i>	1.03	probable peptidyl-dipeptidase A protein
2273010	2273259	#166	<i>cgR_2060</i>	<i>aroG</i>	1.03	phospho-2-dehydro-3-deoxyheptonate aldolase
2576410	2576659	#190	<i>cgR_2342</i>		1.02	hypothetical protein
2576410	2576659	#190	<i>cgR_2341</i>		1.02	ABC transporter, substrate-binding protein
1452713	1452962	#111	<i>cgR_1321</i>	<i>ligA</i>	1.01	DNA ligase
1041954	1042203	#082	<i>cgR_0942</i>		0.99	phosphoserine aminotransferase
1041954	1042203	#082	<i>cgR_0943</i>	<i>gltA</i>	0.99	citrate synthase

1041954	1042203	#082	<i>cgR_0942_3(sRNA)</i>		0.99	
2883015	2883264	#218	<i>cgR_2612</i>		0.99	rhodanese-related sulfurtransferase
2348740	2348989	#176	<i>cgR_2128</i>	<i>nagD</i>	0.99	putative phosphatase in N-acetylglucosamine metabolism
2348740	2348989	#176	<i>cgR_2127</i>		0.99	acyl carrier protein (ACP)
2348740	2348989	#176	<i>cgR_2126</i>		0.99	predicted hydrolase or acyltransferase
1916459	1916708	#147	<i>cgR_1724</i>	<i>ribD</i>	0.99	riboflavin specific deaminase
557436	557685	#050	<i>cgR_0499</i>		0.98	uroporphyrinogen III synthase/methyltransferase
557436	557685	#050	<i>cgR_0498</i>		0.98	iron/thiamine transport system, secreted component
557436	557685	#050	<i>cgR_0498_5(sRNA)</i>		0.98	#N/A
1543144	1543393	#116	<i>cgR_1408</i>		0.97	putative membrane protein
2225433	2225682	#163	<i>cgR_2021</i>	<i>lspA</i>	0.96	lipoprotein signal peptidase
2634588	2634837	#195	<i>cgR_2396</i>		0.96	putative glucuronide carrier protein
323144	323393	#022	<i>cgR_0298</i>	<i>mgtE2</i>	0.94	Mg ²⁺ transporter
323144	323393	#022	<i>cgR_0297</i>	<i>pat</i>	0.94	phenylalanine aminotransferase
1793427	1793676	#138	<i>cgR_1617</i>	<i>mptB</i>	0.93	putative membrane protein
1793427	1793676	#138	<i>cgR_1616</i>	<i>sufR</i>	0.93	transcriptional regulator, ArsR family
192770	193019	#014	<i>cgR_0174</i>		0.93	putative oxidoreductase
1338479	1338728	#098	<i>cgR_1228</i>		0.92	predicted hydrolase or acyltransferase (alpha/beta hydrolase superfamily)
1338479	1338728	#098	<i>cgR_1229</i>		0.92	non-ribosomal peptide synthetase module and related proteins
222754	223003	#016	<i>cgR_0204</i>		0.92	ABC-2 type transporter
1548568	1548817	#119	<i>cgR_5025</i>		0.91	hypothetical protein
1501139	1501388	#113	<i>cgR_1367</i>	<i>dnaQ</i>	0.91	DNA polymerase III, epsilon subunit, putative
2161986	2162235	#155	<i>cgR_1965</i>	<i>glxK</i>	0.90	putative glycerate kinase

2161986	2162235	#155	<i>cgR_1964</i>	<i>gdh</i>	0.90	NADP-specific glutamate dehydrogenase
2660543	2660792	#198	<i>cgR_2417</i>	<i>murI</i>	0.89	glutamate racemase
2660543	2660792	#198	<i>cgR_2418</i>		0.89	putative secreted protein
180364	180613	#012	<i>cgR_6006</i>		0.89	HYPOTHETICAL
180364	180613	#012	<i>cgR_0164</i>		0.89	transcriptional regulator, MerR family
2806302	2806551	#213	<i>cgR_2539</i>		0.89	hypothetical protein
2336764	2337013	#174	<i>cgR_2114</i>		0.89	hypothetical protein
852307	852556	#072	<i>cgR_0773</i>		0.89	putative peptidase
3099717	3099966	#227	<i>cgR_2792</i>		0.89	hypothetical protein
3163789	3164038	#236	<i>cgR_2852</i>	<i>uspA3</i>	0.88	universal stress protein family
1891024	1891273	#145	<i>cgR_1699</i>	<i>rel</i>	0.88	PPGPP synthetase, PPGPP pyrophosphorylase
3111763	3112012	#231	<i>cgR_2803</i>		0.88	putative secreted protein
799705	799954	#063	<i>cgR_0734</i>		0.88	hypothetical protein
799705	799954	#063	<i>cgR_6048</i>		0.88	HYPOTHETICAL
799705	799954	#063	<i>cgR_6047</i>		0.88	HYPOTHETICAL
3095328	3095577	#226	<i>cgR_2789</i>		0.87	putative type 1 fimbrial major subunit
2653569	2653818	#197	<i>cgR_6137</i>	<i>mepA</i>	0.87	HYPOTHETICAL
2653569	2653818	#197	<i>cgR_2409</i>		0.87	hypothetical protein
860606	860855	#073	<i>cgR_0778</i>	<i>prpB2</i>	0.85	2-Methylisocitrate lyase
2973547	2973796	#223	<i>cgR_2686</i>	<i>ald</i>	0.85	aldehyde dehydrogenase
1669257	1669506	#131	<i>cgR_1506</i>		0.84	putative secreted protein
2308318	2308567	#170	<i>cgR_2091</i>		0.84	predicted permease
1688874	1689123	#133	<i>cgR_1526</i>	<i>ndh</i>	0.84	NADH dehydrogenase

1688874	1689123	#133	<i>cgR_1527</i>	<i>ufaA</i>	0.84	putative cyclopropane fatty acid synthase (cyclopropane-fatty-acyl-phospholipid synthase)
2673169	2673418	#199	<i>cgR_2431</i>	<i>ctaD</i>	0.84	cytochrome aa3 oxidase, subunit I
484049	484298	#040	<i>cgR_0436</i>		0.83	putative glycosyltransferase
1582484	1582733	#126	<i>cgR_6104</i>		0.83	HYPOTHETICAL
527904	528153	#046	<i>cgR_0472</i>	<i>fadD5</i>	0.83	long-chain-fatty-acid-CoA ligase
40518	40767	#003	<i>cgR_0034</i>		0.83	probable glycosyltransferase
2596203	2596452	#191	<i>cgR_2359</i>		0.82	putative membrane protein
2596203	2596452	#191	<i>cgR_2360</i>	<i>phoB</i>	0.82	alkaline phosphatase precursor
929314	929563	#080	<i>cgR_0839</i>		0.82	hypothetical protein
1422319	1422568	#109	<i>cgR_1293</i>		0.82	hypothetical protein
486966	487215	#042	<i>cgR_0436</i>		0.81	putative glycosyltransferase
2366789	2367038	#178	<i>cgR_2143</i>	<i>glmS</i>	0.81	probable glucosamine--fructose-6-phosphate aminotransferase
824663	824912	#069	<i>cgR_6058</i>		0.81	HYPOTHETICAL
244523	244772	#017	<i>cgR_0229</i>		0.81	hypothetical protein
726651	726900	#058	<i>cgR_0668</i>	<i>secY</i>	0.81	preprotein translocase subunit
726651	726900	#058	<i>cgR_0667</i>		0.81	bacterial regulatory proteins, IclR family
1252924	1253173	#092	<i>cgR_1143</i>		0.81	PEP phosphonmutase or related enzyme
1574218	1574467	#125	<i>cgR_1430</i>	<i>uriT</i>	0.80	uridine transporter
573998	574247	#051	<i>cgR_0513</i>		0.80	ABC transporter permease protein
2441431	2441680	#183	<i>cgR_2212</i>	<i>aceA</i>	0.79	isocitrate lyase
2441431	2441680	#183	<i>cgR_2211</i>	<i>aceB</i>	0.79	malate synthase
737010	737259	#059	<i>cgR_0677</i>		0.78	putative cellulose synthase protein
86355	86604	#005	<i>cgR_0076</i>		0.78	hypothetical protein

546114	546363	#048	<i>cgR_0490</i>		0.78	hypothetical protein
1690801	1691050	#134	<i>cgR_1528</i>		0.77	permease of the major facilitator superfamily
407684	407933	#027	<i>cgR_0371</i>		0.77	putative transcription regulator protein, MarR fam
407684	407933	#027	<i>cgR_0372</i>		0.77	3-oxoacyl-(acyl-carrier protein) reductase
407684	407933	#027	<i>cgR_0373</i>		0.77	metal-dependent hydrolase of the TIM-barrel fold
635804	636053	#055	<i>cgR_0576</i>	<i>ispB</i>	0.76	putative octaprenyl-diphosphate synthase protein
635804	636053	#055	<i>cgR_0577</i>	<i>secE</i>	0.76	SecE subunit of protein translocation complex
2150598	2150847	#154	<i>cgR_1953</i>		0.76	putative membrane protein
1507612	1507861	#114	<i>cgR_1373</i>		0.75	putative membrane protein
1908293	1908542	#146	<i>cgR_1714</i>	<i>pgsA1</i>	0.74	phosphatidylglycerophosphate synthase
651467	651716	#056	<i>cgR_0590</i>		0.74	secreted protein
2622613	2622862	#193	<i>cgR_2386</i>	<i>lppS</i>	0.74	secreted lipoprotein ErfK/YbiS/YcfS/YnhG family
1189224	1189473	#090	<i>cgR_1076</i>	<i>ripA</i>	0.73	AraC-type DNA-binding domain-containing protein
1286119	1286368	#094	<i>cgR_1180</i>		0.73	putative secreted protein
1692420	1692669	#135	<i>cgR_1528</i>		0.73	permease of the major facilitator superfamily
1243746	1243995	#091	<i>cgR_1132</i>		0.72	Major facilitator superfamily permease
1243746	1243995	#091	<i>cgR_1133</i>		0.72	putative transcriptional regulator
1243746	1243995	#091	<i>cgR_1134</i>		0.72	hypothetical protein
361172	361421	#024	<i>cgR_0324</i>		0.72	hypothetical protein
1305982	1306231	#096	<i>cgR_1201</i>	<i>glgA</i>	0.71	glycosyl transferase
1305982	1306231	#096	<i>cgR_1202</i>	<i>glgC</i>	0.71	ADP-glucose pyrophosphorylase
3206177	3206426	#239	<i>cgR_2890</i>		0.71	hypothetical protein
822520	822769	#068	<i>cgR_0747</i>		0.71	nucleoside-diphosphate-sugar epimerase

1390691	1390940	#106	<i>cgR_1266</i>	<i>narJ</i>	0.70	nitrate reductasetase delta chain
2539501	2539750	#187	<i>cgR_2305</i>		0.70	hypothetical protein
1375608	1375857	#103	<i>cgR_1256</i>	<i>ctpC</i>	0.70	cation transport ATPase
2872834	2873083	#217	<i>cgR_2601</i>	<i>ppa</i>	0.69	inorganic pyrophosphatase
2872834	2873083	#217	<i>cgR_2600</i>	<i>dacB</i>	0.69	penicillin-binding protein, D-Ala-D-Ala carboxypeptidase
485333	485582	#041	<i>cgR_0436</i>		0.69	putative glycosyltransferase
2773807	2774056	#211	<i>cgR_2511</i>	<i>phoR</i>	0.68	two component response regulator
2280617	2280866	#167	<i>cgR_2066</i>	<i>plsC</i>	0.68	1-acyl-SN-glycerol-3-phosphate acetyltransferase
1545527	1545776	#118	<i>cgR_6092</i>		0.67	HYPOTHETICAL
2558213	2558462	#189	<i>cgR_2325</i>		0.66	putative transcription regulator
247890	248139	#018	<i>cgR_6011</i>		0.66	HYPOTHETICAL
848089	848338	#070	<i>cgR_0768</i>		0.65	putative membrane transport protein
963596	963845	#081	<i>cgR_0875</i>		0.65	hypothetical protein
2840810	2841059	#215	<i>cgR_2574</i>	<i>mutY</i>	0.65	A/G-specific adenine glycosylase
2840810	2841059	#215	<i>cgR_2573</i>	<i>cynT</i>	0.65	carbonic anhydrase
879311	879560	#075	<i>cgR_0795</i>		0.64	ABC-type cobalamin/Fe ³⁺ -siderophores transport system, ATPase component
2294023	2294272	#169	<i>cgR_2077</i>	<i>ltsA</i>	0.64	glutamine-dependent amidotransferase involved in formation of cell wall and L-glutamate biosynthesis
2725578	2725827	#205	<i>cgR_2469</i>	<i>sucC</i>	0.64	succinyl-CoA synthetase beta chain
1757074	1757323	#136	<i>cgR_1587</i>	<i>mcmB</i>	0.64	methylmalonyl-CoA mutase large subunit
916977	917226	#078	<i>cgR_0827</i>	<i>dtsR2</i>	0.63	acetyl/propionyl CoA carboxylase, beta subunit
123931	124180	#010	<i>cgR_0109</i>	<i>ureD</i>	0.63	urease accessory protein
1400438	1400687	#107	<i>cgR_1272</i>		0.63	membrane protein containing CBS domain
1849744	1849993	#142	<i>cgR_1661</i>	<i>pyrB</i>	0.63	aspartate carbamoyltransferase catalytic chain

607235	607484	#052	<i>cgR_0547</i>		0.63	hypothetical protein
2212106	2212355	#160	<i>cgR_2012</i>		0.63	similar to methionine synthase II (cobalamin-independent)
2317735	2317984	#172	<i>cgR_2101</i>		0.62	permease of the major facilitator superfamily
2317735	2317984	#172	<i>cgR_2100</i>		0.62	hypothetical protein
2317735	2317984	#172	<i>cgR_2099</i>	<i>thrC</i>	0.62	threonine synthase
52798	53047	#004	<i>cgR_0046</i>		0.61	probable ABC transport protein, ATP-binding component
2722540	2722789	#204	<i>cgR_2467</i>		0.61	hypothetical protein
1986263	1986512	#148	<i>cgR_1790</i>	<i>bioN</i>	0.61	predicted permease (cobalt permease subfamily)
928179	928428	#079	<i>cgR_0838</i>		0.61	short chain dehydrogenase, N-terminal fragment
928179	928428	#079	<i>cgR_6062</i>		0.61	HYPOTHETICAL
1424878	1425127	#110	<i>cgR_1297</i>		0.61	thioredoxin domain-containing protein
1424878	1425127	#110	<i>cgR_1295</i>		0.61	glyoxalase/bleomycin resistance/dioxygenase superfamily protein
1424878	1425127	#110	<i>cgR_1296</i>		0.61	hypothetical protein
1406925	1407174	#108	<i>cgR_1278</i>	<i>rho</i>	0.60	transcription termination factor Rho
2940619	2940868	#221	<i>cgR_2655</i>	<i>ackA</i>	0.60	acetate kinase
3061361	3061610	#225	<i>cgR_2760</i>	<i>pks</i>	0.60	polyketide synthase
131433	131682	#011	<i>cgR_0112</i>		0.59	putative heat shock protein (HSP90-family)
370112	370361	#026	<i>cgR_0330</i>		0.57	putative membrane protein
3109494	3109743	#230	<i>cgR_2801</i>		0.56	putative aminotransferase
3134797	3135046	#235	<i>cgR_2822</i>		0.56	putative GntR-family regulatory protein
3134797	3135046	#235	<i>cgR_2821</i>		0.56	putative amino acid symporter
1759494	1759743	#137	<i>cgR_1589</i>		0.56	putative membrane protein
1759494	1759743	#137	<i>cgR_1588</i>	<i>mcmA</i>	0.56	methylmalonyl-CoA mutase small subunit

2609875	2610124	#192	<i>cgR_2373</i>	<i>cspB</i>	0.56	PS2 protein
2609875	2610124	#192	<i>cgR_2374</i>		0.56	hypothetical protein
3168341	3168590	#237	<i>cgR_6154</i>		0.56	HYPOTHETICAL
814365	814614	#065	<i>cgR_6056</i>	<i>crtYe</i>	0.56	C50 CAROTENOID EPSILON CYCLASE
1380692	1380941	#105	<i>cgR_1259</i>	<i>argS</i>	0.55	arginyl-tRNA synthetase
1380692	1380941	#105	<i>cgR_1258</i>		0.55	putative secreted hydrolase
555468	555717	#049	<i>cgR_0497</i>		0.55	ABC transport system permease protein
3274821	3275070	#245	<i>cgR_2951</i>		0.55	putative secreted protein
2216012	2216261	#161	<i>cgR_2013</i>	<i>dnaE1</i>	0.55	putative DNA polymerase III, alpha chain
295420	295669	#021	<i>cgR_0266</i>	<i>embC</i>	0.55	probable arabinosyltransferase, membrane protein
2957963	2958212	#222	<i>cgR_2672</i>	<i>sseA1</i>	0.55	probable thiosulfate sulfurtransferase protein
1655085	1655334	#130	<i>cgR_1494</i>		0.54	ABC-type multidrug/protein/lipid transport system, ATPase component
3126167	3126416	#234	<i>cgR_2813</i>		0.54	putative membrane protein
1368019	1368268	#101	<i>cgR_1249</i>		0.54	ATPase involved in DNA repair
1511958	1512207	#115	<i>cgR_1379</i>		0.53	putative ATP/GTP-binding protein
2266628	2266877	#165	<i>cgR_2056</i>		0.53	hypothetical protein
2266628	2266877	#165	<i>cgR_2057</i>	<i>pknL</i>	0.53	putative serine/threonine protein kinase
482380	482629	#039	<i>cgR_6021</i>		0.53	HYPOTHETICAL
2762230	2762479	#209	<i>cgR_2499</i>	<i>purC</i>	0.53	phosphoribosylaminoimidazole-succinocarboxamide synthase
2762230	2762479	#209	<i>cgR_2500</i>		0.53	hypothetical protein
478040	478289	#037	<i>cgR_6019</i>		0.53	HYPOTHETICAL
3215488	3215737	#242	<i>cgR_2897</i>		0.53	putative membrane protein
713581	713830	#057	<i>cgR_0657</i>	<i>paaZ</i>	0.52	phenylacetic acid degradation protein paaZ

713581	713830	#057	<i>cgR_0656</i>	<i>paaY</i>	0.52	hypothetical protein
807213	807462	#064	<i>cgR_0735</i>		0.52	hypothetical protein
2467834	2468083	#185	<i>cgR_2237</i>	<i>proA</i>	0.52	gamma-glutamyl phosphate reductasetase
2171110	2171359	#156	<i>cgR_1972</i>		0.52	hypothetical protein
184401	184650	#013	<i>cgR_0169</i>	<i>mcrB</i>	0.51	5-methylcytosine-specific restriction enzyme B
366079	366328	#025	<i>cgR_0326</i>		0.50	bacterial regulatory proteins, TetR family
849761	850010	#071	<i>cgR_0770</i>		0.50	hypothetical protein
1300033	1300282	#095	<i>cgR_1194</i>	<i>folP2</i>	0.50	dihydropteroate synthase
1840134	1840383	#141	<i>cgR_1653</i>	<i>dfp</i>	0.50	DNA/pantothenate metabolism flavoprotein

^a and ^b Peak start and end sites detected in ChIP-chip analysis in the *C. glutamicum* R genome (Yukawa et al., 2007) are indicated.

^c Relative peak height ratio of the array data in the ChIP-DNA to Input-DNA are shown in the base 2 logarithm.