Gene ID	Comments	Fold-difference in mRNA abundance for MGAS6180 relative to M28ΔRD2
M28_RS00290	Bifunctional cyclohydrolase	-11.64
M28_RS00280	Phosphoribosylformylglycinamidine cycloligase	-9.84
M28_RS00285	Phosphoribosylglycinamide formyltransferase	-8.82
M28_RS00305	5-(carboxyamino)imidazole ribonucleotide mutase	-8.04
M28_RS00275	Amidophosphoribosyltransferase	-7.68
M28_RS00295	Amidase	-7.02
M28_RS00310	5-(carboxyamino)imidazole ribonucleotide synthase	-6.46
M28_RS00265	Phosphoribosylaminoimidazolesuccinocarboxamide synthase	-6.45
M28_RS06825	rRNA	-6.43
M28_RS00270	Phosphoribosylformylglycinamidine synthase	-6.21
M28_RS03370	Virulence factor S5nA	-5.77
M28_RS04210	Guanosine monophosphate reductase	-5.68
M28_RS07230	Carbonate dehydratase	-5.33
M28_RS05660	MFS transporter	-5.08
M28_RS08590	PTS cellobiose transporter subunit IIC	-4.68
M28_RS00300	Phosphoribosylamine--glycine ligase	-4.58
M28_RS07330	NCS2 family permease	-4.28
M28_RS02120	Hypothetical	-4.17
M28_RS09130	Hypothetical	-4.10
M28_RS03950	Relaxase	-3.93
M28_RS07955	tRNA	-3.87
M28_RS05265	Hypothetical	-3.76
M28_RS07750	Hypothetical	-3.63
M28_RS03365	Peptide deformylase	-3.62
M28_RS05515	Virulence factor GRAB	-3.55
M28_RS09415	Transposase	-3.39
M28_RS07130	Hypothetical	-3.22
M28_RS07370	Acetyl-CoA carboxylase carboxyl transferase subunit beta	-3.15
M28_RS08110	PTS lactose transporter subunit IIA	-3.05
M28_RS07615	Fructokinase	-2.96
araD	AraD	-2.75
M28_RS05355	Hypothetical	-2.74
M28_RS06730	ABC transporter permease	-2.73
M28_RS06420	Dihydroneopterin aldolase	-2.70
M28_RS05325	PTS cellobiose transporter subunit IIA	-2.62
M28_RS05165	Hypothetical	-2.61
M28_RS08130	Galactose-6-phosphate isomerase	-2.61
M28_RS08485	Hypothetical	-2.60
M28_RS05140	Hypothetical	-2.59
M28_RS04815	Hypothetical	-2.57
M28_RS06860	Cysteine synthase A	-2.52
M28_RS00810	3-oxoacid CoA-transferase subunit A	-2.44
M28_RS03740	Hypothetical	-2.43
M28_RS02515	Energy-coupled thiamine transporter ThiT	-2.42
M28_RS00320	Adenylosuccinate lyase	-2.40
M28_RS07680	30S ribosomal protein S18	-2.36
M28_RS03315	N-acetylmuramidase	-2.36
M28_RS06740	6-phospho-beta-glucosidase	-2.35
M28_RS02615	PTS N-acetylgalactosamine transporter subunit IIC	-2.34
M28_RS08720	Formate--tetrahydrofolate ligase	-2.34
M28_RS03320	Pseudogene	-2.34
M28_RS07365	Acetyl-CoA carboxylase carboxyl transferase subunit alpha	-2.32
M28_RS05370	IS3 family transposase	-2.32
M28_RS02545	Phosphoenolpyruvate carboxylase	-2.32
M28_RS07625	PTS beta-glucoside transporter subunit EIIBCA	-2.32
M28_RS00315	Hypothetical	-2.31
M28_RS00960	L-xylulose 5-phosphate 3-epimerase	-2.29
M28_RS08890	Hypothetical	-2.24
M28_RS03970	L-antibiotic streptin	-2.21
M28_RS07320	N-acetyltransferase	-2.20
M28_RS08120	Tagatose-6-phosphate kinase	-2.19
M28_RS08240	Phosphoenolpyruvate-dependent sugar PTS family porter, EIIA 2 component	-2.19
M28_RS07620	Virulence factor EndoS	-2.17
M28_RS08115	tagatose-bisphosphate aldolase	-2.15
M28_RS05400	phosphorylase	-2.14

M28_RS00415	30S ribosomal protein S17	-2.14
M28_RS01625	Membrane protein	-2.13
M28_RS08540	Hypothetical	-2.12
M28_RS08910	Hypothetical	-2.11
M28_RS08975	ArpU family transcriptional regulator	-2.10
M28_RS06725	Sugar ABC transporter permease	-2.10
M28_RS08935	Hypothetical	-2.07
M28_RS03870	PTS mannose transporter subunit IIC	-2.06
M28_RS07780	Aquaporin	-2.06
M28_RS09195	Hypothetical	-2.06
M28_RS04285	NADH oxidase	-2.05
M28_RS08390	tRNA	-2.05
M28_RS01720	Hypothetical	-2.04
M28_RS02620	PTS N-acetylgalactosamine transporter subunit IIB	-2.04
M28_RS02235	Multidrug ABC transporter permease	-2.03
M28_RS08525	Hypothetical	2.01
M28_RS04410	Citrate transporter	2.03
M28_RS04940	Hypothetical	2.06
rpsN	RspN	2.11
M28_RS04465	Hypothetical	2.12
M28_RS09035	50S ribosomal protein L32	2.13
M28_RS06200	Hypothetical	2.14
secE	SecE	2.16
M28_RS01890	Exotoxin SpeJ	2.17
M28_RS06340	Hypothetical	2.19
M28_RS08835	Arsenate reductase	2.22
M28_RS06315	Hypothetical	2.23
M28_RS02070	Bacteriocin	2.28
M28_RS05425	Hypothetical	2.31
M28_RS08140	Hypothetical	2.36
M28_RS00235	tRNA	2.40
M28_RS04530	Hypothetical	2.64
M28_RS08475	Virulence factor Mrp	2.67
M28_RS06370	Hypothetical	2.76
M28_RS08980	Hypothetical	2.80
M28_RS00200	tRNA	2.81
M28_RS01815	Hypothetical	3.28
M28_RS07470	Hypothetical	3.41
M28_RS00925	Hypothetical	4.09
M28_RS02770	tRNA	4.79
M28_RS06495	tRNA	6.50
M28_RS02430	Hypothetical	7.68
M28_RS08630	Enamine deaminase RidA	7.97

Table S1
Genes differentially expressed two-fold or greater between strains MGAS6180 and M28ΔRD2.