SUPPLEMENTARY TABLES

Supplementary Table 1: Summary of sequence read count, length, coverage, and unmapped reads for *H. pylori* whole genome sequences.

	B128 single colonies			**7.13 single colonies**			**7.13 iron-depleted single colonies**									**7.13 iron-replete single colonies**									**Avg**
	a	**b**	**c**	**a**	**B**	**c**	**D1 a**	**D1 b**	**D1 c**	**D2 a**	**D2 b**	**D2 c**	**D3 a**	**D3 b**	**D3 c**	**R1 a**	**R1 b**	**R1 c**	**R2 a**	**R2 b**	**R2 c**	**R3 a**	**R3 b**	**R3 c**	
Total read count	117200	641486	799182	145512	477807	608988	732531	691805	525715	755068	710201	587631	926113	556882	739911	782071	665731	532379	839757	798556	636620	826301	494261	891463	645132
Mean read length	260	262	267	262	238	265	267	265	264	265	266	264	265	266	265	266	266	266	266	266	266	266	266	253	263
Minimum fold coverage	1	5	3	1	5	4	2	5	5	0	0	0	3	2	2	2	3	1	0	8	0	6	8	3	3
Maximum fold coverage	45	228	279	54	170	221	303	266	205	274	269	242	326	236	271	252	233	192	292	294	239	281	197	308	237
Average fold coverage	18	101	128	23	68	96	117	110	83	120	113	93	147	89	117	124	106	85	133	127	101	131	78	135	102
Standard deviation	4.8	13.8	15.6	5.3	11.6	13.6	16.6	16.2	13.8	17.2	17.0	14.8	20.0	14.3	16.3	18.3	14.9	12.3	17.6	17.2	15.3	15.8	11.3	17.2	14.6
Unmapped reads	5789	46287	55279	15978	38984	52756	46802	48374	33760	54295	45959	47217	60683	39326	51092	58633	45755	40762	47241	47787	39796	58373	41932	58569	45060
Percentage unmapped reads	4.7	6.7	6.5	9.8	7.5	7.9	6.0	6.5	6.0	6.7	6.0	7.4	6.1	6.6	6.4	6.9	6.4	7.1	5.3	5.6	5.8	6.6	7.8	6.1	6.6

All sequences covered the total length of the *H. pylori* reference strain B8 genome (1,673,997 base pairs) and all sequenced strains had a GC content of 38.8%. D1-3 and R1-3 designate independent gerbils maintained on either iron-depleted (N=3) or iron-replete (N=3) diets, respectively, while a-c designate independent single colonies isolated from each gerbil. Avg represents the average among all 24 single colony isolates.

Supplementary Table 2: Unique single nucleotide polymorphisms in *H. pylori* strains B128, 7.13, and *in vivo*-adapted strains isolated form gerbils maintained on iron-depleted or iron-replete diets, relative to *H. pylori* reference strain B8.

Location	Gene	HPB8 locus
B128 single colonies (N=26)		
17317	hypothetical	13
97985	intergenic	
132884	*tonB1*	138
132888	*tonB1*	138
132892	*tonB1*	138
132919	*tonB1*	138
237373	*purD*	270
308952	putative OMP	342
342359	*pal*	375
397298	*fucT1*	427
447957	intergenic	
559618	hypothetical	587
591318	putative OMP	626
616637	DNA methyl-transferase	642
628583	intergenic	
692324	*cagY*	716
727820	hypothetical	750
798239	glycosyltransferase	817
833169	*fucT7*	854
883216	*hyuA1*	895
883595	*hyuA1*	895
913806	*mesE*	927
1195655	*fliF*	1220
1197192	intergenic	
1221163	polysaccharide deacetylase	1252
1355221	ABC transporter	1382
7.13 single colonies (N=2)		
846179	*rnc*	865
1064308	*katA*	1087
7.13 iron-replete single colonies (N=29)		
102469	intergenic	
203750	*oppA*	228
210808	intergenic	
211182	*babB*	237
236057	hypothetical	268
264278	intergenic	
692170	*cagY*	716
692177	*cagY*	716
692240	*cagY*	716
692255	*cagY*	716
692262	*cagY*	716
692423	*cagY*	716
692426	*cagY*	716
692441	*cagY*	716
799893	glycosyltransferase	818
799896	glycosyltransferase	818
1001780	intergenic	
1064871	intergenic	
1098589	*hsdR5*	1120
1283634	conserved hypothetical OMP	1309
1289275	intergenic	
1369139	*prfB*	1395
1377466	*hcpD*	1405
1377469	*hcpD*	1405
1377477	*hcpD*	1405
1533078	predicted coding region	1561
1533082	predicted coding region	1561
1533085	predicted coding region	1561

1533088	predicted coding region	1561
7.13 iron-depleted single colonies (N=49)		
273162	hypothetical	303
273165	hypothetical	303
365607	intergenic	
563546	hypothetical	593
591626	putative OMP	626
591635	putative OMP	626
591638	putative OMP	626
591647	putative OMP	626
607701	intergenic	
666812	*nudT14*	691
692887	*cagY*	716
693420	*cagY*	716
693440	*cagY*	716
693451	*cagY*	716
693458	*cagY*	716
693460	*cagY*	716
693464	*cagY*	716
693465	*cagY*	716
693471	*cagY*	716
693476	*cagY*	716
693483	*cagY*	716
693488	*cagY*	716
693497	*cagY*	716
693503	*cagY*	716
693505	*cagY*	716
693508	*cagY*	716
693513	*cagY*	716
693539	*cagY*	716
819621	*oipA*	838
1084103	putative OMP	1104
1084106	putative OMP	1104
1084152	putative OMP	1104
1084170	putative OMP	1104
1084521	putative OMP	1104
1084524	putative OMP	1104
1084548	putative OMP	1104
1084553	putative OMP	1104
1084556	putative OMP	1104
1084577	putative OMP	1104
1084581	putative OMP	1104
1084587	putative OMP	1104
1117619	hypothetical	1139
1130504	*pepP*	1155
1171489	hypothetical	1200
1302387	*hcpE*	1328
1405574	hypothetical	1436
1414196	intergenic	
1445365	*hrgA*	1474
1477835	hypothetical	1508

Color-coded regions separate unique SNPs from *H. pylori* strains B128 (green), 7.13 (orange), or *in vivo*-adapted strains isolated from iron-depleted (blue) or iron-replete (red) diets. OMP=outer membrane protein.

Supplementary Table 3: Unique genetic loci with single and multinucleotide polymorphisms in *H. pylori* strains B128, 7.13, and *in vivo*-adapted strains isolated from gerbils maintained on iron-depleted or iron-replete diets.

Variant			B128 single colonies			7.13 single colonies			7.13 iron-depleted single colonies									7.13 iron-replete single colonies								
Location	**Gene**	**HPB8 locus**	**a**	**b**	**c**	**a**	**b**	**c**	**D1 a**	**D1 b**	**D1 c**	**D2 a**	**D2 b**	**D2 c**	**D3 a**	**D3 b**	**D3 c**	**R1 a**	**R1 b**	**R1 c**	**R2 a**	**R2 b**	**R2 c**	**R3 a**	**R3 b**	**R3 c**
17317	hypothetical	13	100	100	100																					
88333	intergenic								26	29	31	29	26	45	31	33	29	46	28	30		33	30	26	26	30
88334	intergenic			49			46							54							52					
97985	intergenic		47	54	48																					
102469	intergenic																				75					
118890	*fliI*	124							100	100	100	100	100	100	100	100	100	100	99	99	100	100	100	100	100	100
132300	intergenic						70			65				63				58	55		52			62	66	50
132884	*tonB1*	138		27	44.3 - 46.2																					
132888	*tonB1*	138		31																						
132892	*tonB1*	138		33																						
132919	*tonB1*	138		25																						
132926	*tonB1*	138							85	90	79.7 - 81.4	80.6 - 81.6	77	92					75	76						
203750	*oppA*	228																		100						
210808	intergenic																	50								
211182	*babB*	237																97								
211347	*babB*	237			28		40	28	37	26			28			26	32	30	29			27			26	
211415	*babB*	237		26	34		35	36	38	32						27	29		34			26				
211583	*babB*	237							38	45		38	47	38				98	44	39		39			38	
211592	*babB*	237	31	46	46	50	48	44	39	46		38	47	39				98	46	38		39			37	
211690	*babB*	237	35	42	45	65	61	47	42	43								97		40		44			47	
211694	*babB*	237							43	41								95		40		42			47	
211838	*babB*	237	40	40	47	67	53	43	56	45	52	52	49	52	38	43	49	97	50	51	45	39	50	45	54	48
211844	*babB*	237	33	39	47	73	52	43										99								
212150	*babB*	237							54	36	56	42	51	52	41	49	44	98	53	41	56	48	45		49	
212315	*babB*	237	69	42	48	40	55	49	46	44	58	45	46	55	43	50	50	98	47	41	61	53	43		49	
236057	hypothetical	268																			96					
237373	*purD*	270	100	100	100																					
263819	intergenic								100	100	100	100	100	99	100	100	100	100	100	100	99	100	100	100	100	100
263909	*rpsL*	294	100	97	99	93	99	97	98	98	97	99	98	99	97	97	95	96	99	97	98	97	97	98	98	97
263920	*rpsL*	294	100	100	100	100	100	100	100	100	100	100	100	100	100	100	99	100	100	100	99	100	99	100	100	100
263985	*rpsL*	294							100	100	98	100	99	98	99	97	98	98	96	98	100	100	99	99	99	98
264004	*rpsL*	294	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
264055	*rpsL*	294	100	99	100	100	100	99	100	100	100	100	100	100	100	100	100	100	100	99	99	100	99	100	100	100
264145	*rpsL*	294							100	99	100	100	99	99	99	100	99	100	100	100	99	100	100	99	100	100
264157	*rpsL*	294	100	99	100	100	100	100	100	100	98	100	100	100	99	100	99	99	100	100	99	100	100	99	100	100
264163	*rpsL*	294	100	100	100	100	100	100	100	100	99	100	100	100	100	100	100	100	99	100	100	100	100	99	100	99

264229	*rpsL*	294							99	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
264278	intergenic																				99					
264279	intergenic		100	100	100	100	100	100	100	99	100	100	100	100	100	100	100	100	99	100		99	100	100	100	100
264349	*rpsG*	295	100	99	100	100	100	100	99	99	100	99	99	100	99	100	99	99	100	100	99	98	100	100	100	99
264366	*rpsG*	295							97	100	99	100	100	100	100	100	100	99	99	98	100	100	99	100	100	100
264374	*rpsG*	295	100	100	100	100	98	100	99	100	100	100	100	100	100	100	100	100	100	100	99	99	100	100	100	100
264391	*rpsG*	295	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
273162	hypothetical	303										26														
273165	hypothetical	303										26														
293971	intergenic						93	93	95	91	94	94	96	93	96	93	92	96	96	95	93	95	97	95	92	95
308952	putative OMP	342	94	100	99																					
342359	*pal*	375	100	100	100																					
365607	intergenic												94													
397298	*fucT1*	427	25	35	26																					
447957	intergenic			100	98																					
471641	intergenic		100	95	97	81	97	93	95	92	92	93	98	93	95	94	95	90	94	95	94	93	94	86	93	91
559618	hypothetical	587	95	100	100																					
563546	hypothetical	593													99	100	100									
591318	putative OMP	626		100	100																					
591626	putative OMP	626										32.5 - 32.7	30													
591635	putative OMP	626										33	30													
591638	putative OMP	626										31	27													
591647	putative OMP	626										30	27													
607701	intergenic										63															
616637	DNA methyl-transferase	642	100	99	100																					
628583	intergenic			29																						
629024	*babA*	657							83	84	33	80	80	78	83	78	87	96	88	86	79	78	77	85	83	79
629189	*babA*	657		68	81	61	50	74	66	80	29	70	70	65	69	63	76	72	74	61		68			68	
629257	*babA*	657	33	69	74	69	54	69	65	72					65	57	76		70			66				
629425	*babA*	657							47	47		58	51	43				99	53	39		52			52	
629434	*babA*	657	29	51	56	46	45	55	47	43		57	47	42				99	52	39		52			53	
629532	*babA*	657		45	60	42	41	51	53	47								96		46		56			42	
629536	*babA*	657							52	48								96		43		53			41	
629680	*babA*	657	33	39	49	44	65	42	53	52	42	47	43	47	44	41	59	100	44	41	39	51	51	45	52	51
629686	*babA*	657	33	39	48	52	63	41										98								
629992	*babA*	657							48	47	64	48	46	49	44	57	53	100	49	42	44	42	53		50	
630157	*babA*	657	56	54	41	59	47	44	43	47	51	44	42	42	45	55	60	100	44	45	48	41	40		48	
630946	*babA*	657		59	67		47	61	77	52	61	64	50	81	75	59	54	69	66	61	63	61	84	68	50	53
630951	*babA*	657							80	58	60	66	50	81	77	59	57	71	65	61	64	64	84	68	52	54

630954	*babA*	657		59	64		47	63	83	58	60	63	50	81	77	62	59	76	68	61	66	64	84	68	53	54
630975	*babA*	657		54	65		48	55	79	57	58	64	48	81	75	60	60	80	71	64	64	59	88	69	55	58
630987	*babA*	657		47	63		39	58	81	50	63	60	47	79	71	59	46	74	67	65	55	58	92	64	55	44
630989	*babA*	657		50	63		39	58	81	50	63	63	42	79	75	59	50	74	67	60	58	58	83	64	55	44
630991	intergenic			50	63		39	58	81	53	63	63	50	79	79	63	60	74	67	65	58	61	92	64	55	44
631022	intergenic				85		69	82		77	84		85		96	91	93		89	94	81	79	100	84	76	78
631027	intergenic			73	86		78	86	89	78	90	91	84	84	97	100	91	88	90	90	86	82	100	94	80	79
631033	intergenic			90	80		77	83	95	27	73	96	86	78	89	87	87	75	87	78	82	78	96	91	79	84
666812	*nudT14*	691										94	93	99												
692170	*cagY*	716																						96.9 - 98.5		
692177	*cagY*	716																						95		
692240	*cagY*	716																						28		
692255	*cagY*	716																						42		
692262	*cagY*	716																						48		
692324	*cagY*	716		98	98																					
692423	*cagY*	716																			99					
692426	*cagY*	716																			99					
692441	*cagY*	716																			92					
692493	*cagY*	716	93	98	98	100	100	98	99	100	92	99	98	100	97	97	97	97	100	91	98	99	98	98	97	99
692498	*cagY*	716	87	94	90	100	98	100	89	95	89	95	91	92	95	92	90	94	94	87	89	90	87	100	95	95
692887	*cagY*	716										100	100	100												
693420	*cagY*	716											100													
693440	*cagY*	716										100	100													
693451	*cagY*	716										100	100													
693458	*cagY*	716										100	88													
693460	*cagY*	716										100	94													
693464	*cagY*	716										70	60	44												
693465	*cagY*	716										70	56	56												
693471	*cagY*	716										100	100	100												
693476	*cagY*	716										100	100	100												
693483	*cagY*	716										100	100	100												
693488	*cagY*	716										100	93	100												
693497	*cagY*	716										100	100	100												
693503	*cagY*	716										92	94	100												
693505	*cagY*	716										96	91	100												
693508	*cagY*	716										100	100	100												
693513	*cagY*	716										96	100	100												
693539	*cagY*	716										98	100	100												
727820	hypothetical	750	94	100	100																					
759720	intergenic								68			66	65			74	72			74			63	63		70
798239	glycosyl-transferase	817	100	100	99																					
799893	glycosyl-transferase	818																51	45				34			

799896	glycosyl-transferase	818																50	45				34			
819621	*oipA*	838												93												
833169	*fucT7*	854	63	66	65																					
846179	*rnc*	865						68																		
883216	*hyuA1*	895	93	99	98																					
883595	*hyuA1*	895	100	96	97																					
913806	*mesE*	927	69	51	42																					
919030	*sabA*	930	92	91	87								91	88												
1001780	intergenic																							100	100	100
1064308	*katA*	1087				100																				
1064871	intergenic																							99	100	100
1065100	intergenic			25		44																				
1082193	DNA methyl-transferase	1103									92												97			
1084103	putative OMP	1104										100	100	100												
1084106	putative OMP	1104										100	100	100												
1084152	putative OMP	1104										100	100	100												
1084170	putative OMP	1104										96	100	100												
1084521	putative OMP	1104										92	100	100												
1084524	putative OMP	1104										92	100	100												
1084548	putative OMP	1104										96	100	100												
1084553	putative OMP	1104										97	100	100												
1084556	putative OMP	1104										94	94	96												
1084577	putative OMP	1104										93	100	100												
1084581	putative OMP	1104										93	100	100												
1084587	putative OMP	1104										96	100	100												
1098589	*hsdR5*	1120																96								
1117619	hypothetical	1139													99	100	99									
1122559	*fur*	1145					98		100	99	100	100	100	99	100	100	100	100	100	100						
1130504	*pepP*	1155														100										
1171489	hypothetical	1200							99					97												
1195655	*fliF*	1220	100	100	99																					
1197192	intergenic		42	26	49																					
1197193	intergenic			50		59	57	59	56	48	57	51	52	54	52	55	55		57	51	57	62			55	62
1217501	intergenic												53				46	44				53				

1221163	poly-saccharide deacetylase	1252	100	100	100																								
1283634	conserved hypothetical OMP	1309																			100							
1289275	intergenic																									100		99
1302387	*hcpE*	1328										100	99	100														
1316726	*radA*	1343		32	31		38			29	29		32	26	36				28		32		26	28	38	
1332440	intergenic								45	50			44	48	47		50	46				48	53	57		44
1332612	*rfaJ*	1358				79	69	83.7 - 84.8	75	80	77	71.6 - 72.5	74	63	77	79	74.4 - 75.6	81	87	80	84	73	85	66	73	75
1355221	ABC transporter	1382	100	100	100																					
1369139	*prfB*	1395																98								
1377466	*hcpD*	1405																			100					
1377469	*hcpD*	1405																			100					
1377477	*hcpD*	1405																			100					
1405574	hypothetical	1436							100	99	100															
1414196	intergenic													87												
1445365	*hrgA*	1474							78																	
1477835	hypothetical	1508										99														
1533078	predicted coding region	1561																85								
1533082	predicted coding region	1561																85								
1533085	predicted coding region	1561																76.9 - 84.6								
1533088	predicted coding region	1561																85								
1566403	intergenic									38	36	43		38	48		37				37				44	
1566404	intergenic								59	46	45	53	55	55		47	44	57	51	49	47	58	57	39	59	53
1584758	*hopZ*	1616							90	81	90	89			90		86			89	90		87	86	88	89
1584759	*hopZ*	1616											89	97		90		91	88			93				
1621918	hypothetical	1665							98	96	97	98		98	97	99	94		96	98	99	98	97	99	99	98
1621919	hypothetical	1665											83					99								
1640821	*pcrA*	1681							100	100	98	100	100	99	100	100	100	100	99	100	100	100	100	100	100	99
1657270	intergenic												65	80	62				73		61			72		
1657271	intergenic								76	63	60	70			70	67	60	68		70		63	62		60	69

D1-3 and R1-3 designate independent gerbils maintained on either iron-depleted (N=3) or iron-replete (N=3) diets, respectively, while a-c designate different single colonies isolated from each gerbil. Color-coded regions within each single colony represent single nucleotide polymorphisms (SNPs) that were present in each isolate, and the number in each box represents the percentage of reads that contained each SNP. When a percentage range is shown, this represents multinucleotide polymorphisms present. OMP=outer membrane protein.

Supplementary Table 4: Single nucleotide polymorphisms, multinucleotide polymorphisms, insertions and deletions in *H. pylori* B128 and 7.13 single colony isolates.

Variants	**B128 single colonies**				**7.13 single colonies**			
	a	**b**	**c**	**Avg**	**a**	**b**	**c**	**Avg**
Transitions (SNP)	74	88	84	**98**	33	43	42	**47**
Transversions (SNP)	11	14	13		5	5	7	
Substitutions (MNP)	2	3	3		1	2	2	
Insertions	8	15	13	**12**	6	12	9	**9**
Deletions	6	16	14	**10**	4	4	2	**3**
Synonymous	24	33	30	**29**	11	17	17	**15**
Non-synonymous	55	58	60	**58**	26	29	29	**28**

Number of single nucleotide polymorphisms (SNPs), multinucleotide polymorphisms (MNPs), insertions, and deletions relative to the reference *H. pylori* B8 genome sequence. a-c designate individual single colonies isolated from a single gerbil. Avg represents the average number of variants among all three single colony isolates.

Supplementary Table 5: Single nucleotide polymorphisms, multinucleotide polymorphisms, insertions and deletions in *in vivo*-adapted *H. pylori* 7.13 single colony isolates harvested from gerbils maintained on iron-depleted or iron-replete diets.

Variants	**7.13 iron-depleted single colonies**										**7.13 iron-replete single colonies**									
	D1 a	**D1 b**	**D1 c**	**D2 A**	**D2 b**	**D2 c**	**D3 a**	**D3 b**	**D3 c**	**Avg**	**R1 a**	**R1 b**	**R1 c**	**R2 a**	**R2 b**	**R2 c**	**R3 a**	**R3 b**	**R3 c**	**Avg**
Transitions (SNP)	40	41	31	55	56	51	31	37	36	**52**	46	39	37	35	42	31	30	38	27	**43**
Transversions (SNP)	6	6	4	12	10	8	4	3	3		6	4	7	4	6	4	4	6	4	
Substitutions (MNP)	2	2	2	9	9	7	2	2	2		3	2	2	2	2	2	4	2	2	
Insertions	10	12	12	11	14	14	11	10	12	**12**	11	10	10	13	14	11	11	10	12	**11**
Deletions	6	5	5	6	8	9	3	3	2	**5**	3	4	3	3	2	3	3	2	3	**3**
Synonymous	17	17	17	32	32	28	8	18	18	**21**	19	18	18	22	17	18	20	17	17	**18**
Non-synonymous	27	27	16	40	39	34	2	20	19	**25**	32	23	24	15	28	15	12	23	10	**20**

Number of single nucleotide polymorphisms (SNPs), multinucleotide polymorphisms (MNPs), insertions, and deletions relative to the reference *H. pylori* B8 genome sequence. D1-3 and R1-3 designate independent gerbils maintained on either iron-depleted (N=3) or iron-replete (N=3) diets, respectively, while a-c designate different single colonies isolated from each gerbil. Avg represents the average among all nine single colony isolates.

Supplementary Table 6: Common single nucleotide polymorphisms between *in vivo*-adapted *H. pylori* strain 7.13 isolated from gerbils maintained on high salt or iron-depleted diets.

Variant			**7.13 high-salt single colonies**				**7.13 iron-depleted single colonies**								
Location	**Gene**	**HPB8 locus**	**H1 a**	**H1 b**	**H1 c**	**H1 d**	**D1 a**	**D1 b**	**D1 c**	**D2 a**	**D2 b**	**D2 c**	**D3 a**	**D3 b**	**D3 c**
563546	hypothetical	593	100	100	100	100							99	100	100
693488	*cagY*	716	25							100	93	100			
693539	*cagY*	716	25							98	100	100			
1117619	hypothetical	1139	100	100	100	100							99	100	99
1122559	*fur*	1145	100	100	100	100	100	99	100	100	100	99	100	100	100

H1 and D1-3 designates independent gerbils maintained on a high salt (N=1) or iron-depleted (N=3) diets, respectively, while a-d designate different single colonies isolated from each gerbil. Color-coded regions within each single colony represent single nucleotide polymorphisms (SNPs) that were present in each isolate, and the number in each box represents the percentage of reads that contained each SNP.

Supplementary Table 7: Summary of clinical information pertaining to *H. pylori* strains isolated from three independent and well-defined patient cohorts.

***H. pylori* strain ID**	**Country**	**Age**	**Sex**	**Diagnosis**
PZ5001	Colombia	58	M	NAG
PZ5003	Colombia	44	M	NAG
PZ5004	Colombia	52	M	NAG
PZ5005	Colombia	53	M	NAG
PZ5006	Colombia	45	M	NAG
PZ5007	Colombia	58	M	NAG
PZ5008	Colombia	41	M	NAG
PZ5009	Colombia	53	M	NAG
PZ5010	Colombia	55	M	NAG
PZ5011	Colombia	56	M	NAG
PZ5014	Colombia	47	M	IM
PZ5015	Colombia	42	M	NAG
PZ5016	Colombia	40	M	MAG
PZ5017	Colombia	52	M	MAG
PZ5018	Colombia	50	M	NAG
PZ5019	Colombia	47	M	IM
PZ5021	Colombia	48	M	MAG
PZ5022	Colombia	54	M	IM
PZ5023	Colombia	48	M	IM
PZ5024	Colombia	47	M	NAG
PZ5025	Colombia	39	M	NAG
PZ5026	Colombia	47	M	DYS
PZ5028	Colombia	55	M	MAG
PZ5029	Colombia	43	M	NAG
PZ5031	Colombia	54	M	IM
PZ5032	Colombia	43	M	MAG
PZ5033	Colombia	57	M	IM
PZ5034	Colombia	44	M	IM
PZ5035	Colombia	45	M	NAG
PZ5036	Colombia	45	M	NAG
PZ5038	Colombia	39	M	MAG
PZ5039	Colombia	42	M	NAG
PZ5043	Colombia	40	M	DYS
PZ5044	Colombia	40	M	NAG
PZ5045	Colombia	44	M	NAG
PZ5047	Colombia	48	M	IM
PZ5051	Colombia	57	M	NAG
PZ5054	Colombia	47	M	NAG
PZ5055	Colombia	56	M	IM
PZ5056	Colombia	55	M	IM
PZ5057	Colombia	57	M	MAG
PZ5058	Colombia	60	M	IM
PZ5059	Colombia	55	M	NAG
PZ5060	Colombia	49	M	NAG
PZ5062	Colombia	48	M	MAG
PZ5064	Colombia	54	M	NAG
PZ5065	Colombia	52	F	NAG
PZ5066	Colombia	53	M	NAG
PZ5068	Colombia	51	M	IM
PZ5069	Colombia	46	M	IM
PZ5070	Colombia	54	M	IM
PZ5072	Colombia	49	M	MAG
PZ5074	Colombia	53	M	IM
PZ5075	Colombia	50	M	NAG
PZ5077	Colombia	53	M	IM
PZ5078	Colombia	47	M	IM
PZ5079	Colombia	46	M	MAG

PZ5080	Colombia	49	M	MAG
PZ5081	Colombia	45	F	IM
PZ5082	Colombia	51	M	IM
PZ5083	Colombia	51	M	NAG
PZ5084	Colombia	48	M	IM
PZ5085	Colombia	52	F	NAG
PZ5086	Colombia	54	M	IM
PZ5087	Colombia	47	M	MAG
PZ5088	Colombia	48	M	IM
PZ5090	Colombia	43	M	NAG
PZ5091	Colombia	46	M	IM
PZ5093	Colombia	46	M	IM
PZ5094	Colombia	40	M	IM
PZ5095	Colombia	31	M	NAG
PZ5096	Colombia	47	M	IM
PZ5097	Colombia	48	M	IM
PZ5098	Colombia	47	M	IM
PZ5099	Colombia	56	M	IM
PZ5100	Colombia	55	M	NAG
PZ5102	Colombia	48	M	IM
PZ5104	Colombia	45	M	MAG
PZ5105	Colombia	46	M	IM
PZ5111	Colombia	46	M	NAG
PZ5112	Colombia	41	M	IM
PZ5113	Colombia	50	M	NAG
PZ5114	Colombia	49	M	IM
NQ4001	Colombia	61	F	NAG
NQ4002	Colombia	62	M	IM
NQ4005	Colombia	58	M	IM
NQ4014	Colombia	71	M	IM
NQ4016	Colombia	63	M	DYS
NQ4017	Colombia	73	F	IM
NQ4018	Colombia	55	F	IM
NQ4019	Colombia	57	F	NAG
NQ4023	Colombia	69	F	IM
NQ4025	Colombia	64	M	IM
NQ4034	Colombia	57	F	IM
NQ4038	Colombia	64	F	IM
NQ4043	Colombia	61	M	IM
NQ4044	Colombia	66	F	IM
NQ4045	Colombia	67	M	IM
NQ4046	Colombia	64	M	MAG
NQ4048	Colombia	53	F	NAG
NQ4050	Colombia	66	F	MAG
NQ4051	Colombia	74	M	MAG
NQ4053	Colombia	59	M	IM
NQ4056	Colombia	55	F	DYS
NQ4060	Colombia	51	F	DYS
NQ4061	Colombia	53	M	IM
NQ4062	Colombia	45	F	IM
NQ4063	Colombia	56	F	IM
NQ4064	Colombia	57	F	IM
NQ4066	Colombia	76	F	IM
NQ4072	Colombia	70	M	DYS
NQ4073	Colombia	68	M	IM
NQ4075	Colombia	52	M	DYS
NQ4076	Colombia	57	M	MAG
NQ4077	Colombia	72	F	IM
NQ4078	Colombia	56	M	IM
NQ4080	Colombia	57	F	IM
NQ4081	Colombia	62	M	IM
NQ4084	Colombia	52	F	IM
NQ4085	Colombia	71	M	IM
NQ4094	Colombia	50	F	IM

NQ4095	Colombia	59	F	IM
NQ4097	Colombia	53	M	IM
NQ4098	Colombia	65	M	MAG
NQ4099	Colombia	68	F	IM
NQ4100	Colombia	61	F	DYS
NQ4102	Colombia	66	F	MAG
NQ4103	Colombia	57	F	IM
NQ4104	Colombia	70	M	DYS
NQ4107	Colombia	64	M	MAG
NQ4108	Colombia	67	M	IM
NQ4110	Colombia	55	M	MAG
NQ4113	Colombia	75	F	IM
NQ4117	Colombia	73	F	MAG
NQ4122	Colombia	68	M	IM
NQ4124	Colombia	49	M	DYS
NQ4127	Colombia	60	F	MAG
NQ4130	Colombia	67	M	IM
NQ4134	Colombia	68	F	IM
NQ4135	Colombia	71	M	IM
NQ4137	Colombia	71	F	MAG
NQ4145	Colombia	71	F	IM
NQ4147	Colombia	61	F	IM
NQ4153	Colombia	62	M	IM
NQ4156	Colombia	72	F	IM
NQ4157	Colombia	55	M	IM
NQ4161	Colombia	67	F	MAG
NQ4162	Colombia	58	M	NAG
NQ4175	Colombia	48	F	IM
NQ4178	Colombia	84	M	MAG
NQ4185	Colombia	62	F	IM
NQ4187	Colombia	77	M	IM
NQ4191	Colombia	55	F	IM
NQ4194	Colombia	71	F	IM
NQ4195	Colombia	72	F	MAG
NQ4197	Colombia	60	M	IM
NQ4200	Colombia	62	F	IM
NQ4203	Colombia	59	M	NAG
NQ4207	Colombia	56	F	MAG
NQ4211	Colombia	68	F	IM
NQ4216	Colombia	78	M	DYS
NQ4217	Colombia	82	F	IM
NQ4223	Colombia	57	M	DYS
NQ4228	Colombia	65	F	IM
NQ4229	Colombia	76	F	IM
NQ4236	Colombia	76	M	IM
NQ4240	Colombia	60	F	IM
NQ4245	Colombia	58	M	IM
NQ4248	Colombia	75	F	IM
NQ4249	Colombia	65	F	IM
NQ4250	Colombia	76	F	IM
NQ4259	Colombia	67	F	NAG
NQ4261	Colombia	56	F	IM
NQ4262	Colombia	56	M	IM
NQ4264	Colombia	69	F	IM
NQ4265	Colombia	81	M	IM
NQ4269	Colombia	83	F	IM
NQ4270	Colombia	72	M	IM
NQ4271	Colombia	58	M	IM
NQ4275	Colombia	69	M	IM
NQ4277	Colombia	75	F	IM
NQ4281	Colombia	62	M	MAG
NQ4282	Colombia	73	M	MAG
NQ4287	Colombia	59	M	NAG
NQ4299	Colombia	56	F	NAG
NQ4303	Colombia	58	M	IM

NQ4304	Colombia	83	F	NAG
NQ4305	Colombia	66	M	DYS
NQ4307	Colombia	58	M	IM
NQ4309	Colombia	66	M	IM
NQ4311	Colombia	55	F	MAG
NQ4312	Colombia	72	F	IM
NQ4314	Colombia	68	M	IM
NQ4315	Colombia	57	F	NAG
NQ4318	Colombia	56	M	IM
NQ4319	Colombia	62	M	MAG
NQ4322	Colombia	58	M	IM
NQ4326	Colombia	73	F	NAG
NQ4328	Colombia	66	M	IM
NQ4330	Colombia	63	M	IM
NQ4331	Colombia	69	M	IM
NQ4332	Colombia	60	M	IM
NQ4335	Colombia	65	F	NAG
NQ4337	Colombia	56	M	IM
NQ4352	Colombia	67	F	NAG
NQ4356	Colombia	79	F	DYS
NQ4359	Colombia	61	M	IM
NQ4371	Colombia	65	M	MAG
NQ4373	Colombia	57	M	DYS
NQ4379	Colombia	64	M	IM
NQ4381	Colombia	62	M	IM
NQ4386	Colombia	78	M	DYS
NQ4387	Colombia	66	M	MAG
NQ4390	Colombia	77	F	IM
NQ4391	Colombia	54	F	IM
NQ4393	Colombia	62	M	IM
NQ4394	Colombia	72	M	MAG
NQ4395	Colombia	67	M	MAG
NQ4396	Colombia	50	F	DYS
NQ4400	Colombia	74	M	DYS
NQ4407	Colombia	72	M	IM
NQ4408	Colombia	77	F	IM
NQ4409	Colombia	70	M	IM
NQ4410	Colombia	64	F	DYS
NQ4412	Colombia	62	F	IM
NQ4416	Colombia	72	F	IM
NQ4421	Colombia	53	F	NAG
NQ4430	Colombia	57	F	IM
NQ4431	Colombia	59	M	MAG
NQ4432	Colombia	66	M	IM
NQ4433	Colombia	46	F	MAG
NQ4436	Colombia	72	F	DYS
NQ4438	Colombia	66	F	MAG
NQ4443	Colombia	57	M	IM
NQ4444	Colombia	72	F	DYS
NQ4445	Colombia	73	M	IM
NQ4446	Colombia	75	F	IM
NQ4447	Colombia	58	F	MAG
NQ4449	Colombia	57	M	IM
NQ4450	Colombia	66	M	IM
NQ4456	Colombia	50	M	DYS
93-6	United States	70	M	NAG
93-65	United States	40	M	NAG
93-66	United States	57	M	NAG
J44	United States	64	M	MAG
J39	United States	68	M	NAG
J54	United States	78	M	NAG
J58	United States	53	M	NAG
J63	United States	53	M	NAG
J68	United States	33	M	NAG

J75	United States	62	M	NAG
J99	United States	48	M	MAG
J104	United States	65	M	IM
J117	United States	59	M	MAG
J133	United States	57	M	MAG
J134	United States	59	M	NAG
J150	United States	52	M	NAG
J154	United States	61	M	NAG
J166	United States	56	M	NAG
J170	United States	56	M	NAG
J174	United States	69	M	IM
J178	United States	61	M	IM
J182	United States	61	M	IM
J188	United States	54	M	IM
J190	United States	44	M	NAG
J195	United States	44	M	NAG
J198	United States	72	M	NAG
J226	United States	31	M	NAG
J238	United States	56	M	IM
J243	United States	73	M	NAG
J253	United States	48	M	NAG
J254	United States	45	M	NAG
J262	United States	63	M	MAG
J291	United States	27	M	NAG
A101	United States	33	M	NAG
B89	United States	76	M	IM
B93	United States	46	M	NAG
B96A	United States	32	M	NAG
B99A	United States	52	M	MAG
B105A	United States	44	M	IM
B107A	United States	60	M	NAG
B108A	United States	56	M	IM
B116A	United States	84	M	NAG
B119A	United States	65	M	MAG
B120A	United States	62	M	NAG
B127A	United States	69	M	NAG
B128A	United States	48	M	MAG
B130A	United States	62	M	IM
B134A	United States	58	M	NAG
B135A	United States	48	M	NAG
B136A	United States	67	M	MAG
B137A	United States	78	M	NAG
B140A	United States	31	M	NAG
B141A	United States	55	M	MAG
B146A	United States	67	M	MAG
B147A	United States	58	M	MAG
B148A	United States	59	M	IM
B151A	United States	84	M	MAG
B158A	United States	55	M	NAG
B166A	United States	61	M	NAG
B173A	United States	72	M	IM
B175A	United States	66	M	NAG
B177A	United States	64	M	NAG
B179A	United States	52	M	NAG
B181A	United States	40	M	NAG
B185A	United States	66	M	IM
B186A	United States	44	M	NAG
B194A	United States	74	M	NAG
B201A	United States	68	M	NAG
B202A	United States	63	M	NAG
B208A	United States	77	M	NAG
B211A	United States	39	M	NAG
B212A	United States	73	M	NAG
B213A	United States	66	M	IM
B215A	United States	69	M	MAG

B218A	United States	80	M	IM
B221A	United States	50	F	NAG
B223A	United States	75	M	NAG
B228A	United States	56	M	NAG
B234A	United States	69	M	NAG
B235A	United States	55	M	IM
B238A	United States	70	M	MAG
B240A	United States	48	M	MAG
B251A	United States	66	M	NAG
B253A	United States	71	M	NAG
B254A	United States	57	M	MAG
B255A	United States	66	M	IM
B256A	United States	66	M	MAG
B258A	United States	52	M	MAG
B263A	United States	51	M	NAG
B265A	United States	71	M	MAG
B266A	United States	60	M	NAG
B267A	United States	77	M	NAG
B268A	United States	74	M	MAG
B269A	United States	53	M	MAG
B277A	United States	56	M	NAG
B279A	United States	52	M	NAG
B284A	United States	67	M	IM
B291A	United States	67	M	NAG

H. pylori strain identification (ID) number, patient country of origin, age, sex, and histologic diagnoses are shown. NAG = non-atrophic gastritis alone; MAG = multifocal atrophic gastritis; IM = intestinal metaplasia; DYS = dysplasia. Samples highlighted in yellow designate clinical *H. pylori* strains harboring the *fur* SNP (FurR88H).