

	gene/locus ID	Associated gene	approx dist	rpt unit	Strain				class		
					Rd	2866	2846	86-026			
mononucleotides	NON-CODING REGION ASSOCIATED REPEATS										
	2866 (404270)	tatA	HI_0187(pseudo in Rd)	83	A	(A) ₆	(A) ₉	(A) ₆	(A) ₆	2	
	Rd (134961)	hypo/hypo	near 3' end of HI_0119/HI_0120	n/a	T	(T) ₉	(T) ₄ C(T) ₃ G	(T) ₄ C(T) ₃ G	(T) ₄ C(T) ₃ G	2	
	2866 (450059)	N/A	dwnstrm of omp2	n/a	A	(A) ₁₀	(A) ₉	(A) ₇	(A) ₇	2	
	Rd (581844)	hypo/hypo	HI_0561/HI_0562	206/98	T	(A) ₉	(A) ₈	(A) ₈	(A) ₈	2	
	86-028NP (232482)	acpP	NTHI0243	230	C	(C) ₅	(C) ₅	(C) ₅	(C) ₁₁	2	
	Rd (723771)	ilvY/ilvC	HI_0681/HI_0682	528/139	A	(A) ₉	(A)C(A) ₇	(A)C(A) ₇	(A)C(A) ₇	2	
	Rd (881589)	transglycosylase	HI_0831	58	T	(T) ₉	(T) ₉	(T) ₂ G(T) ₆	(T) ₉	2	
	86-028NP (1145509)	hypo	NTHI1201	122	C	no match	(C) ₂ A(C)A(C) ₃	(C) ₂ A(C)A(C) ₃	(C) ₉	2	
	Rd (1062153)	tbp2/hypo	HI_0995/HI_0996	44/43	T	(T) ₁₀	(T) ₂ C(T) ₇	(T) ₁₀	(T) ₂ C(T) ₇	2	
	86-028NP (1518695)	hypo	NTHI1636	50	T	no match	*see 66-8	(T) ₁₀	(T) ₁₀	1	
	Rd (1408920)	dacB/greA	HI_1330/HI_1331	22/132	T	(T) ₉	(T) ₉	(T) ₉	(T) ₉	1	
	2866 (982298)	fnr	HI_1425	17	A	(A) ₇	(A) ₉	(A) ₇	(A) ₇	2	
	2866 (1173753)	hifA/B	r2866v6.1191/r2866v6.1190c	95/123	T	no match	(T) ₉	no match	no match	1*	
	2866 (1343902)	ABC trans prfC (oligopeptidaseA)	HI_1080	55	T	(T) ₉	(T) ₉	(T) ₉	(T) ₉	1	
	Rd (229573)		HI_0213/HI_0214	90/24	T	(T) ₇	(T) ₇	(T) ₉	(T) ₇	2	
	Rd (153937)	ompP2	HI_0139	100	A	(A) ₈ T	(A) ₈ T	(A) ₉	(A) ₉	2	
	2846 (1225346)	hypo	HI_1176	27	A	(A) ₆ C(A) ₂	(A) ₈	(A) ₉	(A) ₉	2 ⁽²⁾	
	86-028NP (1706204)	hypo	NTHI1853	10	A	no match	no match	no match	(A) ₁₀	1*	
	2846 (1561562)	trmA	HI_0848	101	A	(A) ₂ C(A) ₅	(A) ₂ C(A) ₅	(A) ₉	(A) ₂ C(A) ₅	2	
	Rd (1415504)	hypo	HI_1339	185	T	(T) ₉	(T) ₇	(T) ₇	(T) ₇	2	
	Rd (15406098)	hypo	HI_1462.1	164	A	(A) ₉	(A) ₇	(A) ₇	(A) ₇	2	
	Rd (1677208)	tyrS	HI_1610	62	A	(A) ₉	(A) ₈	(A) ₈	(A) ₈	2	
	di-	2866(723452)	hia	HI_1732 Hia pseudogene	110	T	no match	(T) ₃₄	no match	no match	1*
		2866 (923693)	hypo	2866v6.923	47	A	no match	(A) ₉	no match	no match	1*
		2866 (82131)	potD2/ordL	HI_0498/HI_0499	48/27	GC	(GC) ₅	(GC) ₅	(GC) ₄ AC	(GC) ₃ AC(GC)	2
		86-028NP (167686)	chypo/htpG	HI_0104/HI_0105	54/147	TA	(TA)TG(TA) ₃	(TA)TG(TA) ₃	(TA)TG(TA) ₃	(TA) ₅	2
	tri-	86-028NP (1145531)	hypo	NTHI1201	144	TC	(TC) ₅	(TC) ₅	(TC)TT(TC) ₃	(TC) ₅	2
		2866 (312999)	hxuC	HI_0262	45	ATA	(ATA) ₉	(ATA) ₉	degenerate	degenerate (24 bps not 27)	2
		2866 (1852642)	haemoglobin binding protein	HI_1565	6	ATT	(ATT) ₄	(ATT)AGT(ATT) ₂	(ATT) ₄	(ATT) ₄	2
	penta-	86-028NP (804379)	n/a	rRNA operon	181	AAT	(AAT) ₃	(AAT) ₅	(AAT) ₃	(AAT) ₄	2
		Rd (1369478)	hsdM/rbfA	HI_1287***		TCGTC	(TCGTC) ₄	(TCGTC) ₂	(TCGTC) ₄	TCGTC	2
		86-028NP (1596527)	hypo	NTHI1744	71	TGGCT	no match	no match	no match	(TGGCT) ₃	1*
hexa-	Rd(995716)	hypo	HI_0870.1	261	TTATT	(TTATT) ₃	region absent	region absent	region absent	1*	
	Rd (549556)	pgk	HI_0525	19	TTAAAA	(TTAAAA) ₃	(TTAAAA) ₂ TTGAA A	(TTAAAA) ₂ TTGA AA	(TTAAAA) ₂	2	
hepta-	86-028NP (624407)	rpoD/aspA	Rpt 3' end of both genes	92/199	CTTTTA	(CTTTTA) ₂	(CTTTTA) ₂	(CTTTTA) ₂	(CTTTTA) ₃	2	
	2866 (366328)	n/a	dwnstrm of HsdR2 Type I RE	n/a	TAATTCA	(TAATTCA) ₂	(TAATTCA) ₅	(TAATTCA) ₈	TAATTCA	2	
	2846 (737978)	hmw2A	2846.735c	109	TGAAAGA	no match	no match	(TGAAAGA) ₁₆	(TGAAAGA) ₂₃	2	
	2846 (1122093)	hmw1A	2846.1135	110	TGAAAGA	no match	no match	(ATCTTTC) ₁₇	(ATCTTTC) ₁₇	1	
ccta-	86-028NP (1636265)	hypo	NTHI1794	13	AACAACC	AACAACC	(AACAACC) ₆	AACAACC	(AACAACC) ₆	2	
	2866(816134)	chypo/cmK	HI_1646/HI_1647	12/80(400)	ATTATTTG	(ATTATTTG) ₂	(ATTATTTG) ₆	(ATTATTTG) ₄	(ATTATTTG)GTTA TTTG	2 ⁽²⁾	
nona-	86-028NP (141547)	hypo/hypo	NTHI0160/NTHI0161	1081/85	ATTAAGAC	no match	no match	no match	(ATTAAGAC) ₃	1*	
	86-028NP (1370900)	HMW2C	NTHI1448	92	GTTTTCTTA	no match	no match	no match	(GTTTTCTTA) ₁₉	1*	
	Rd (292209)	heme-hemopexin	HI_0262	43	ATTATTATT	(ATTATTATT) ₃	(ATTATTATT) ₃	TAATTATCATTAT T	TTATTATTATCAT C	2	
	Rd (1789537)	hypo	HI_1717	86	CGCCTTGTT	(CGCCTTGTT) ₄	region absent	region absent	region absent	1*	
mononucleotides	CODING REGION ASSOCIATED REPEATS										
	HI_0285	menF			A	(A) ₂ C(A) ₄	(A) ₁₀	(A) ₂ C(A) ₄	(A) ₂ C(A) ₄	2	
	HI_0021	citG			A	(A) ₉	(A) ₉	(A) ₉	(A) ₉	1	
	HI_0513	hindIIIM			A	(A) ₉	region absent	region absent	region absent	1*	
	HI_0648	mdaB			T	(T) ₉	(T) ₇	(T) ₆	(T) ₆	2 ⁽¹⁾	
	NTHI0546	smb			A	(A) ₂ G(A) ₃	(A) ₅ G(A) ₃	(A) ₂ G(A) ₃	(A) ₉	2	
	NTHI0694	hypo			G	region absent	region absent	region absent	(G) ₁₂	1*	
	HI_1378	phoR			A	C(A) ₈	(A) ₉	(A) ₉	(A) ₉	2	
	HI_1588	purU			A	(A) ₉	(A) ₉	(A) ₉	(A) ₉	1	
	HI_1095	dsbE			A	(A) ₉	(A) ₉	(A) ₉	(A) ₉	1	
	HI_1060	lpxB			A	(A) ₂ G(A) ₄	(A) ₉	(A) ₂ C(A)G(A) ₄	(A) ₂ C(A)G(A) ₄	2	
	HI_0708	selA			A	(A) ₉	(A) ₇ CT	(A) ₉	(A) ₉	2	
	HI_1559	hemK			A	(A) ₉	(A) ₇ C(A)	(A) ₇ C(A)	(A) ₇ C(A)	2	
	dinucleotides	Integrated plasmid	hypo			A	region absent	(A) ₉	region absent	no match	1*
						A	region absent	(A) ₉	region absent	no match	1*
HI_0454		ycfH			GC	(GC) ₂ AC(GC)AC	(GC) ₅	(GC)AC(GC) ₃	(GC)ACGT(GC) ₂	2	
HI_0008		fdxI			AT	(AT) ₅	(AT) ₅	(AT) ₅	(AT) ₅	1	
n/a		lppL			GA	(GA) ₂ AA(GA)AA	(GA) ₅	(GA) ₅	(GA) ₅	2	
HI_0739		dnaE			CA	(CA) ₅	(CA)CG(CA) ₃	(CA) ₅	(CA) ₅	2	
	HI_0735	lpxH			AC	(AC) ₅	(CA) ₅ TACG	(AC) ₅	(AC) ₅	2	

trinucleotides	HI_0579	<i>fusA</i>			ACT	(ACT) ₄	(ACT) ₄	(ACT) ₄	ACC(ACT) ₃	2
	HI_0392	<i>putative acetylase</i>			ATT	(ATT) ₄	(ATT)ACT(ATT) ₂	(ATT)ACT(ATT) ₂	(ATT)ACT(ATT) ₂	2
	HI_0229	<i>prp</i>			CAA	(CAA) ₄	(CAA) ₄	(CAA) ₄	(CAA) ₄	1
	HI_0139	<i>omp2</i>			CAA	no match	(CAA) ₄	no match	no match	1*
	NTHI0694	<i>hypo</i>			GGG	no match	no match	no match	(GGG) ₄	1*
	HI_0738.1	<i>ilvA</i>			TGG	(TGG) ₄	(TGG)CGG(TGG) ₂	CGGCGG(TGG) ₂	CGG(TGG) ₃	2
	HI_1070	<i>hrpA</i>			CGT	(CGT) ₄	(CGT) ₃	(CGT) ₃	(CGT) ₃	2
	HI_1696	<i>lsgE</i>			GAT	(GAT) ₄	(GAT) ₄	(GAT) ₄	(GAT) ₄	1
	HI_1139	<i>murC</i>			TGT	(TGT) ₄	(TGT) ₄	(TGT) ₄	(TGT) ₄	1
	HI_0649	<i>rep</i>			CAA	(CAA) ₄	(CAA) ₄	(CAA) ₄	(CAA) ₄	1
	HI_0221	<i>guaB</i>			GCA	GCA(GCT) ₂ GCA	GCA(GCT) ₂ GCA	(GCA) ₄	(GCA) ₄	2
	HI_1663	<i>conserved hypothetical fbp</i>			TAT	(TAT) ₄	(TAT) ₃ TCT	(TAT) ₄	(TAT) ₃ TCT	2
	HI_1645				GAA	(GAA) ₄	(GAA) ₂ GAG(GAA)	(GAA) ₄	(GAA) ₂ GAG(GAA)	2
tetranucleotides	HI_0661	<i>haemoglobin binding protein</i>			ATT	(ATT) ₄	(ATT) ₄	(ATT) ₄	(ATT)AGT(ATT) ₂	2
	HI_1056	<i>hypothetical</i>			ATG	(ATG) ₂ ACG	ACG(ATG)ACG	(ATG) ₄	ACG(ATG)ACG	2
	HI_0258	<i>lgtC</i>			GACA	22	26	20	10	3
	HI_0352	<i>lic3A</i>			CAAT	33	20	26	19	3
	HI_0550	<i>lic2A</i>			CAAT	23	5	25	14	3
	HI_0635	<i>hgpC</i>			CCAA	37/21	28	25	20	3
	HI_0661	<i>hgpB</i>			CCAA	20	27	39/28	12	3
	HI_0687	<i>fusobacteria drug/metabolite exporter</i>			TTTA	6				1*
	HI_1058	<i>mod</i>				(TGAC) ₃₂	(AGCC) ₁₆			3*
	Hi_1386 (upstream)	<i>putative glycosyltransferase</i>			CCAA	16	8	12	13	3
		<i>yadA</i>			CCAA	25	13	24	14	3
	HI_1537	<i>licA</i>			CAAT	17	36	7	15	3
	HI_1565	<i>hemoglobin binding</i>			CCAA	19				1*
	r2846v6.916	<i>pgt1</i>			GACA			16	14	3
	r2846v6.1528c	<i>lpt3 region</i>			AGTC			14		1*
	r2846v6.1683	<i>lex2A</i>			GCAA		24	17	14	3
	r2866v6.124c	<i>lav</i>			GCAA		20		30	3
	r2846v6.202	<i>oafA</i>			GCAA		9	14	8	3
pentanucleotides		<i>hgpD</i>			CCAA				17	1*
	NTHI1034	<i>lic3B</i>			CAAT				18	1*
	HI_1700	<i>lsgA</i>			TTATT	(TTATT) ₃	(TTATT) ₃	(TTATT) ₃	(TTATT) ₃	1
	HI_0936	<i>nrfE</i>			TTTAT	(TTTAT) ₃	(TTTAT) ₃	(TTTAT)CTTAT(TTAT)	(TTTAT) ₃	2
hexanucleotides	HI_1134	<i>murF</i>			TTACC	(TTACC) ₃	TTAGT(TTACC)TTATC	TTAGT(TTACC)TTATC	TTAGT(TTACC)TTATC	2
	HI_0867	<i>hmg</i>			TCAGC	(TCAGC) ₂	(TCAGC) ₃	(TCAGC) ₂	region absent	3
	2846.1264c				TCATT	TCATT	TCATT	(TCATT) ₇	TCATT	2 ⁽²⁾
	HI_0264	<i>hxA</i>			GAAAGA	no match	(GAAAGA) ₅	no match	no match	1*
	HI_0176	<i>rluD</i>			CGTTTA	(CGTTTA) ₃	(CGTTTA) ₃	(CGTTTA) ₃	(CGTTTA) ₃	1
	HI_1232	<i>aceF</i>			GCTTCA	GCATCAGCTCCA(GCTTCA)	(GCTTCA) ₃	GCATCAGATTCAGCATCA	GCATCA(GCTTCA)ACATCA	2
	HI_1264	<i>gyrA</i>			AGATGA	(AGATGA) ₂	(AGATGA) ₂	(AGATGA) ₃	(AGATGA)AGAA	2
	HI_0995	<i>tbp</i>			AAAAAG	no match	AAA(AAAAAG) ₂	(AAAAAG) ₃	no match	2 ⁽²⁾
	HI_0251	<i>tonB</i>			AGCCAG	(AGCCAG) ₄	(AGCCAG)AGCCTG(AGCCAG)	(AGCCAG)AGCCTG(AGCCAG)	(GACCGA)GTCCGA ₂	2
	HI_0264	<i>hxA</i>			AATGGC	(AATGGC) ₃	AAGGGC(AATGGC)AATAGC	(AATGGC)AATAGC ₂	(AATGGC) ₃	2
hepta-	HI_0917	<i>protective surface antigen D15</i>			ATGGTA	(ATGGTA) ₃	ATGATA(ATGGTA)ATAGTTCTGGTA	(ATGGTA)GCGGTA(ATGGTA)ATGGTG	(ATGGTA) ₃	2
nona-	HI_1042	<i>methH</i>			ACGGCTT	ACCGCTT(ACGGCTT)	ACCGCTT(ACGGCTT)	(ACGGCTT) ₃	region absent	2
	2846.733	<i>pseudo gene</i>			TTGCTTGGT	region absent	region absent	(TTGCTTGGT) ₁₂	TTGCTTGGT	2 ⁽²⁾
	2866 (1558354)	<i>hmg locus</i>			CTTGTTTTT	no match	(CTTGTTTTT) ₃	CTTCGCTTT(CTTGTTTTT)	region absent	2 ⁽²⁾
								class 1	did not vary in any only data on one strain change in repeat unlikely to lead to PV phenotype variability cannot say for sure non-PV phenotype change consistent with PV phenotype	
								class 1*		
								class 2		
								2(2)		
								class 3		