

# ***Helicobacter pylori* type 4 secretion systems as gastroduodenal disease markers**

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**Supplementary Material**

**Table S1: Assembly quality of 136 strains in this study**

Strain name	Number of contigs <sup>a</sup>	Largest contigs	Total length <sup>b</sup>	N50	N75	L50	L75	GC%	BUSCO	Accession
VN0211	28	337,040	1,630,376	154,782	59,734	4	9	38.67	88.5	BNNC01000001-BNNC01000034
VN0212	33	237,579	1,616,411	104,300	52,696	5	11	38.7	87.8	BNND01000001-BNND01000037
VN0219	32	434,738	1,686,404	218,516	57,859	3	7	38.57	87.2	BNNE01000001-BNNE01000044
VN0220	46	236,982	1,605,297	68,650	46,465	7	14	38.78	87.8	BNNF01000001-BNNF01000054
VN0223	30	330,397	1,582,744	167,078	74,463	3	7	38.85	87.8	BNNG01000001-BNNG01000031
VN0224	29	362,285	1,578,831	107,267	55,467	4	10	38.83	87.8	BNNH01000001-BNNH01000030
VN0227	39	297,830	1,588,929	106,597	53,568	5	11	38.73	88.5	BNNI01000001-BNNI01000041
VN0228	31	301,343	1,575,300	130,353	56,015	4	10	38.8	88.5	BNNJ01000001-BNNJ01000034
VN0229	42	447,435	1,660,119	87,401	53,729	4	10	38.6	87.2	BNNK01000001-BNNK01000052
VN0232	54	334,509	1,624,318	76,726	36,305	6	14	38.69	87.8	BNNL01000001-BNNL01000062
VN0235	25	430,471	1,567,205	144,419	70,040	3	7	38.85	87.2	BNNM01000001-BNNM01000025
VN0240	39	316,923	1,583,113	55,242	46,686	7	14	38.8	88.5	BNNN01000001-BNNN01000049
VN0244	37	288,499	1,612,297	75,303	52,933	5	12	38.12	87.2	BNNO01000001-BNNO01000044
VN0246	38	234,831	1,594,478	98,202	50,592	6	12	38.76	85.8	BNNP01000001-BNNP01000043
VN0264	38	217,643	1,628,795	79,438	51,971	6	13	38.68	87.8	BNNQ01000001-BNNQ01000046
VN0268	29	336,628	1,609,558	108,256	86,304	4	8	38.72	87.8	BNNR01000001-BNNR01000033
VN0271	34	676,484	1,625,401	184,705	53,219	2	7	38.72	87.8	BNNS01000001-BNNS01000038
VN0272	29	267,305	1,573,025	104,680	51,603	5	10	38.84	86.5	BNNT01000001-BNNT01000030
VN0274	46	336,085	1,580,312	72,729	46,828	4	11	38.81	87.2	BNNU01000001-BNNU01000053
VN0280	44	170,803	1,589,529	65,503	38,085	8	16	38.78	88.5	BNNV01000001-BNNV01000046
VN0283	46	129,057	1,603,717	53,616	39,968	10	18	38.79	88.5	BNNW01000001-BNNW01000058
VN0324	29	429,620	1,577,639	177,684	59,999	3	8	38.85	88.5	BNNX01000001-BNNX01000030
VN0338	43	234,055	1,642,070	109,182	51,935	6	12	38.64	87.8	BNNY01000001-BNNY01000049
VN0348	36	246,525	1,644,511	98,916	60,623	5	11	38.83	89.9	BNNZ01000001-BNNZ01000037
VN0352	23	370,752	1,586,424	211,641	68,205	3	7	38.83	87.2	BNOA01000001-BNOA01000028
VN0355	31	655,895	1,606,763	108,916	60,114	3	8	38.67	87.2	BNOB01000001-BNOB01000033
VN0361	45	321,825	1,637,587	82,853	53,790	5	11	38.66	87.8	BNOC01000001-BNOC01000054
VN0363	28	541,182	1,579,593	136,137	57,996	3	8	38.86	88.5	BNOD01000001-BNOD01000032
VN0366	35	330,120	1,573,206	107,419	65,919	4	8	38.8	87.8	BNOE01000001-BNOE01000036
VN0382	30	230,640	1,566,005	172,755	53,759	4	8	38.83	88.5	BNOF01000001-BNOF01000030
VN0390	29	432,180	1,574,742	124,862	53,167	3	10	38.8	87.8	BNOG01000001-BNOG01000037
VN0401	31	238,985	1,641,573	106,492	59,577	6	12	38.64	87.8	BNOH01000001-BNOH01000032
VN0403	33	232,881	1,559,731	66,989	54,639	7	13	38.87	88.5	BNOI01000001-BNOI01000035
VN0405	39	235,478	1,613,669	68,732	42,741	6	13	38.7	87.8	BNOJ01000001-BNOJ01000050
VN0406	27	648,464	1,573,126	178,717	58,002	2	7	38.77	87.8	BNOK01000001-BNOK01000027
VN0410	31	131,312	1,599,970	86,876	59,341	8	13	38.73	87.8	BNOL01000001-BNOL01000033

VN0411	30	325,552	1,566,442	131,082	56,340	4	9	38.86	88.5	BNOM01000001-BNOM01000032
VN0418	30	235,227	1,668,999	172,176	77,198	4	8	38.6	87.8	BNON01000001-BNON01000030
VN0420	42	233,976	1,630,302	91,879	51,161	6	12	38.67	86.5	BNOO01000001-BNOO01000047
VN0431	32	423,191	1,566,026	108,091	55,116	4	9	38.84	88.5	BNOP01000001-BNOP01000033
VN0434	33	235,259	1,597,570	104,183	59,727	6	11	38.7	87.2	BNOQ01000001-BNOQ01000035
VN0438	25	362,194	1,571,559	199,187	58,533	3	8	38.83	87.8	BNOR01000001-BNOR01000026
VN0443	97	227,431	1,596,903	56,849	24,308	9	20	38.76	87.2	BNOS01000001-BNOS01000127
VN0448	41	334,954	1,600,753	107,589	42,908	5	13	38.71	87.2	BNOT01000001-BNOT01000047
VN0452	42	333,290	1,557,214	75,901	38,013	5	13	38.9	87.8	BNOU01000001-BNOU01000059
VN0453	61	237,246	1,595,496	65,116	42,898	8	16	38.78	85.8	BNOV01000001-BNOV01000082
VN0464	35	227,290	1,569,209	122,833	63,671	5	9	38.8	87.8	BNOW01000001-BNOW01000041
VN0472	39	400,244	1,599,160	67,410	52,635	5	12	38.75	87.8	BNOX01000001-BNOX01000046
VN0481	33	692,031	1,593,779	108,683	54,198	2	8	38.74	87.8	BNOY01000001-BNOY01000036
VN0484	129	100,573	1,606,762	45,923	20,959	12	25	38.84	87.9	BNOZ01000001-BNOZ01000173
VN0495	38	237,963	1,605,575	95,768	60,913	6	11	38.78	87.2	BNPA01000001-BNPA01000046
VN0511	40	393,223	1,643,921	207,635	67,493	3	7	38.66	88.5	BNPB01000001-BNPB01000047
VN0559	43	236,649	1,651,698	108,790	54,866	5	10	38.67	87.8	BNPC01000001-BNPC01000046
VN0754	31	318,655	1,605,059	95,059	65,816	5	10	38.74	87.2	BNPK01000001-BNPK01000036
VN0759	39	240,312	1,589,900	72,919	48,362	7	14	38.81	87.8	BNPL01000001-BNPL01000044
VN1154	29	313,196	1,573,179	107,557	65,489	4	9	38.77	89.2	BNPQ01000001-BNPQ01000031
VN1155	33	378,093	1,631,053	108,992	54,231	5	10	38.63	87.8	BNPR01000001-BNPR01000036
VN1156	30	231,954	1,574,628	70,526	58,237	5	11	38.84	87.8	BNPS01000001-BNPS01000034
VN1158	45	142,847	1,634,749	65,407	48,152	9	16	38.61	88.5	BNPT01000001-BNPT01000050
VN1161	36	242,737	1,585,941	74,033	53,617	6	12	38.73	87.2	BNPU01000001-BNPU01000045
VN1163	31	333,340	1,628,992	107,339	53,438	4	10	38.67	87.8	BNPV01000001-BNPV01000032
VN1165	33	459,318	1,595,474	111,244	54,119	3	10	38.68	87.8	BNPW01000001-BNPW01000034
VN1167	38	287,839	1,567,728	76,147	52,820	6	12	38.76	87.2	BNPX01000001-BNPX01000043
VN1169	41	234,189	1,607,416	72,653	48,808	6	13	38.67	88.5	BNPY01000001-BNPY01000045
VN1171	44	149,660	1,589,189	59,055	35,599	9	17	38.88	86.5	BNPZ01000001-BNPZ01000046
VN1172	53	173,717	1,645,458	77,084	38,972	8	16	38.91	87.2	BNQA01000001-BNQA01000059
VN1175	36	167,457	1,567,123	75,357	48,366	7	14	38.85	87.2	BNQB01000001-BNQB01000037
VN1176	56	111,892	1,568,799	59,099	36,227	10	18	38.89	88.5	BNQC01000001-BNQC01000068
VN1178	55	235,774	1,573,500	67,356	39,794	7	15	38.88	86.5	BNQD01000001-BNQD01000059
VN1180	38	467,285	1,621,371	74,667	52,428	5	12	38.73	86.5	BNQE01000001-BNQE01000041
VN1183	35	333,906	1,601,032	77,353	38,210	5	11	38.74	87.8	BNQF01000001-BNQF01000043
VN1184	42	226,656	1,683,321	109,600	60,695	5	11	38.69	89.2	BNQG01000001-BNQG01000049
VN1186	52	231,167	1,553,586	54,086	38,185	7	15	38.91	87.2	BNQH01000001-BNQH01000068
VN1192	37	246,754	1,625,927	76,918	46,809	6	13	38.75	87.8	BNQI01000001-BNQI01000051

VN1193	33	356,367	1,569,529	68,996	52,407	6	12	38.83	87.2	BNQJ01000001-BNQJ01000038
VN1195	46	152,432	1,570,491	56,539	33,752	9	17	38.84	88.5	BNQK01000001-BNQK01000055
VN1196	32	232,509	1,607,485	101,854	55,504	5	11	38.68	87.8	BNQL01000001-BNQL01000037
VN1197	25	407,899	1,576,234	163,670	54,775	3	7	38.84	87.2	BNQM01000001-BNQM01000027
VN1199	53	143,730	1,552,412	59,597	33,798	9	18	39.01	89.9	BNQN01000001-BNQN01000062
VN1200	42	209,434	1,643,572	86,665	52,865	6	12	38.9	87.2	BNQO01000001-BNQO01000052
VN1202	40	289,939	1,577,348	68,022	44,967	6	13	38.88	88.5	BNQP01000001-BNQP01000046
VN1203	33	261,369	1,560,976	122,661	57,430	4	10	38.88	89.2	BNQQ01000001-BNQQ01000037
VN1204	49	182,970	1,632,040	81,209	51,237	7	13	38.72	88.5	BNQR01000001-BNQR01000055
VN1205	33	321,209	1,562,120	84,335	52,122	6	12	38.9	87.8	BNQS01000001-BNQS01000038
VN1210	45	276,005	1,593,975	66,469	39,206	7	15	38.8	87.8	BNQT01000001-BNQT01000053
VN1212	27	398,794	1,604,961	171,487	60,010	3	8	38.66	88.5	BNQU01000001-BNQU01000028
VN1213	39	178,751	1,570,582	88,158	53,625	7	13	38.85	87.2	BNQV01000001-BNQV01000043
VN1215	56	144,923	1,607,869	48,963	26,712	12	22	38.75	87.2	BNQW01000001-BNQW01000069
VN1217	33	240,457	1,568,845	105,419	55,487	5	11	38.82	89.2	BNQX01000001-BNQX01000040
VN1218	28	280,854	1,560,660	149,567	69,590	4	8	38.92	88.5	BNQY01000001-BNQY01000030
VN1219	32	332,612	1,570,697	106,558	65,316	4	9	38.82	88.5	BNQZ01000001-BNQZ01000034
VN1221	33	323,707	1,600,328	109,285	55,421	4	10	38.73	87.2	BNRA01000001-BNRA01000038
VN1222	56	186,146	1,599,128	48,846	34,306	11	21	38.75	87.8	BNRB01000001-BNRB01000061
VN1224	26	276,011	1,616,667	191,015	57,526	4	8	38.68	88.5	BNRC01000001-BNRC01000030
VN1225	38	189,394	1,598,103	68,942	50,912	6	13	38.74	87.8	BNRD01000001-BNRD01000046
VN1226	35	234,276	1,553,258	104,260	55,437	6	11	38.89	88.5	BNRE01000001-BNRE01000039
VN1227	33	180,950	1,555,386	60,109	44,050	8	15	38.88	87.8	BNRF01000001-BNRF01000037
VN1229	40	303,291	1,646,110	98,179	52,866	6	12	38.9	87.8	BNRG01000001-BNRG01000041
VN1230	47	141,656	1,554,919	54,711	38,825	11	19	38.91	87.8	BNRH01000001-BNRH01000052
VN1233	57	230,695	1,569,932	43,902	32,171	11	22	38.78	85.8	BNRI01000001-BNRI01000063
VN1235	42	225,514	1,614,913	75,785	50,743	7	14	38.72	87.8	BNRJ01000001-BNRJ01000048
VN1236	36	246,849	1,579,799	73,711	52,588	6	12	38.82	87.2	BNRK01000001-BNRK01000038
VN1237	33	308,768	1,595,658	99,493	60,995	5	10	38.76	88.5	BNRL01000001-BNRL01000042
VN1239	37	240,237	1,595,872	73,587	52,944	6	12	38.74	87.8	BNRM01000001-BNRM01000041
VN1240	59	172,603	1,572,062	61,599	30,075	9	18	38.85	86.5	BNRN01000001-BNRN01000087
VN1241	39	235,168	1,620,787	82,821	44,758	6	13	38.67	87.2	BNRO01000001-BNRO01000044
VN1244	53	233,128	1,628,617	61,073	38,865	8	16	38.75	87.8	BNRP01000001-BNRP01000061
VN1246	53	185,606	1,592,059	52,248	32,198	10	19	38.76	88.5	BNRQ01000001-BNRQ01000065
VN1247	36	176,140	1,576,733	61,302	48,389	7	14	38.83	86.5	BNRR01000001-BNRR01000041
VN1248	52	220,604	1,559,161	59,431	34,472	7	16	38.85	88.5	BNRS01000001-BNRS01000064
VN1249	37	235,148	1,617,478	75,863	48,228	6	13	38.77	87.8	BNRT01000001-BNRT01000039
VN1250	28	428,071	1,573,970	107,165	57,261	4	10	38.85	89.2	BNRU01000001-BNRU01000028

VN1251	41	244,456	1,599,681	68,086	51,992	7	14	38.76	87.2	BNRV01000001-BNRV01000049
VN1258	23	675,092	1,587,516	174,398	53,829	2	7	38.78	87.8	BNRW01000001-BNRW01000026
VN1260	26	366,882	1,619,970	217,986	54,520	3	8	38.79	87.8	BNRX01000001-BNRX01000027
VN1261	29	436,746	1,647,578	107,386	55,364	4	9	38.62	87.8	BNRY01000001-BNRY01000032
VN1262	48	319,039	1,678,279	59,352	49,294	6	14	38.58	88.5	BNRZ01000001-BNRZ01000057
VN1263	30	433,970	1,618,364	170,034	69,125	3	7	38.68	88.5	BNSA01000001-BNSA01000031
VN1264	35	532,693	1,621,926	130,061	63,467	3	7	38.65	87.8	BNSB01000001-BNSB01000039
VN1266	26	371,650	1,607,715	206,830	64,795	3	7	38.71	88.5	BNSC01000001-BNSC01000027
VN1269	36	414,614	1,592,773	96,596	52,491	4	10	38.81	87.8	BNSD01000001-BNSD01000038
VN1270	34	235,450	1,606,632	133,890	51,325	5	10	38.76	87.2	BNSE01000001-BNSE01000035
VN1272	28	457,595	1,603,253	75,237	59,153	4	10	38.74	87.2	BNSF01000001-BNSF01000033
VN1274	33	235,483	1,587,600	104,717	59,526	5	10	38.77	88.5	BNSG01000001-BNSG01000036
VN1276	30	211,262	1,617,262	131,410	57,339	5	10	38.69	87.2	BNSH01000001-BNSH01000034
VN1277	43	246,971	1,570,223	76,213	37,505	7	15	38.85	87.2	BNSI01000001-BNSI01000047
VN1279	35	327,671	1,601,596	91,715	52,380	5	11	38.73	87.8	BNSJ01000001-BNSJ01000038
VN1280	27	434,171	1,583,722	156,037	55,363	3	9	38.86	87.2	BNSK01000001-BNSK01000029
VN1281	34	236,739	1,577,605	166,231	52,896	4	10	38.86	87.2	BNSL01000001-BNSL01000038
VN1283	64	138,799	1,611,849	47,867	30,988	11	21	38.68	87.2	BNSM01000001-BNSM01000077
VN1284	44	147,729	1,567,670	56,835	38,441	10	18	38.84	87.2	BNSN01000001-BNSN01000057
VN1286	62	117,495	1,629,874	61,406	35,038	10	19	38.66	87.8	BNSO01000001-BNSO01000074
VN1288	49	216,086	1,590,292	53,358	36,077	10	18	38.69	88.5	BNSP01000001-BNSP01000052
VN1289	49	204,476	1,598,138	50,184	28,401	8	18	38.8	87.8	BNSQ01000001-BNSQ01000052
VN1290	54	233,200	1,606,787	53,732	31,829	7	16	38.71	87.2	BNSR01000001-BNSR01000063
VN1291	81	201,587	1,672,214	47,413	26,793	10	23	38.57	87.8	BNSS01000001-BNSS01000093

a: The number of contigs ( $\geq 500$  bp)

b: Total length of contigs ( $\geq 500$  bp)

**Table S2: Annotation of *tfs* ICE genes in *H. pylori* genome**

<b>Annotation</b>	<b><i>tfs3</i> (India7)</b>	<b><i>tfs3</i> (Gambia94/24)</b>		<b><i>tfs4a</i> (P12)</b>	<b><i>tfs4b</i> (Shi470)</b>	<b><i>tfs4c</i> (R036d)</b>	
<i>xerT</i>	3725	7345	<b><i>tfs4</i> module</b>	<b>L</b>	437	4480	1010
<i>virB6</i>	3760	7375			439	4485	1008
<i>virD2</i>	3720	7340		451	4530	996	
<i>virD4</i>	3825	7455		454	4545	993	
<i>virB11</i>	3835	7465		<b>C</b>	458	4565	990
<i>virB10</i>	3855	7485			462	4590	986
<i>virB9</i>	3860	7490		463	4595	985	
<i>virB8</i>	3865	7495		464	4600	984	
<i>virB7</i>	3870	7500		465	4605	982	
<i>virB4</i>	3875	7505		<b>R</b>	467	4615	980
<i>virB3</i>	3885	7515			468	4620	979
<i>virB2</i>	3890	7520			469	4625	978

**Table S3: Pairwise sequence comparison of T4SS nucleotide sequences**Percentage sequence identity of nucleotide sequence from pairwise sequence comparison of *vir* homologous genes

T4SS proteins	<i>A. tumefaciens</i> pTi plasmid <sup>1</sup>				comB <sup>2</sup>				cagPAI <sup>2</sup>			
	vs				vs				vs			
	<i>tfs3</i> (Gambia94/24)	<i>tfs4a</i> (P12)	<i>tfs4b</i> (Shi470)	<i>tfs4c</i> (R036d)	<i>tfs3</i> (Gambia94/24)	<i>tfs4a</i> (P12)	<i>tfs4b</i> (Shi470)	<i>tfs4c</i> (R036d)	<i>tfs3</i> (Gambia94/24)	<i>tfs4a</i> (P12)	<i>tfs4b</i> (Shi470)	<i>tfs4c</i> (R036d)
<b>VirB2</b>	38.5	41.9	42.2	35.6	61.0	47.6	47.4	46.9	45.3	41.8	45.5	39.9
<b>VirB3</b>	40.6	42.1	42.5	21.4	57.6	52.0	59.6	47.4	-	-	-	-
<b>VirB4</b>	43.6	45.5	43	44.8	56.5	52.3	53.2	49.8	46.2	45.8	45.7	45.5
<b>VirB6</b>	40.1	38.3	39.4	38.7	-	44.4	-	44.3	44.4	42.6	44.3	47.2
<b>VirB7</b>	44.2	33.7	42.7	-	50.7	54.6	53.5	-	<15	<15	<15	-
<b>VirB8</b>	37.7	35.5	41.6	42.2	42.3	37.9	43.1	49.2	44.4	38.4	44.1	48.1
<b>VirB9</b>	29.6	34.4	34.9	34.9	39.3	40.5	40.2	40.6	43.2	46.1	46.9	46.8
<b>VirB10</b>	42.5	42.3	43.2	42.1	59.9	54.2	53.9	53.1	38.4	43.2	41.6	37.9
<b>VirB11</b>	43.6	45.4	45.2	43.5	-	-	-	-	50.9	46.9	45	48.5
<b>VirD2</b>	-	-	-	-	-	-	-	-	-	-	-	-
<b>VirD4</b>	-	-	-	-	-	-	-	-	42.6	40.2	38.5	46.4

1: T4SS genes of *Agrobacterium tumefaciens* pTi plasmid strain C582: indicated cagPAI, comB and *tfs3/4a/4b/4c* were retrieved from the same strain background

**Table S4: Pairwise sequence comparison of T4SS nucleotide sequences of *tfs3*, *tfs4a*, *tfs4b*, *tfs4c* ICE**

<i>tfs</i> ICE genes	<i>tfs3</i> (Gambia94/24)			<i>tfs4b</i> (Shi470)	<i>tfs4a</i> (P12)		
	<i>tfs3</i> (India7)	<i>tfs4a</i> (P12)	<i>tfs4b</i> (Shi470)	<i>tfs4c</i> (R036d)	<i>tfs4a</i> (P12)	<i>tfs4c</i> (R036d)	
<i>xerT</i>	<b>91.2</b>	68	61.2	67.6	62.1	62.1	<b>98.2</b>
<i>virB2</i>	<b>91.6</b>	51.2	48.8	50.8	55.3	49.5	<b>83.5</b>
<i>virB3</i>	<b>89</b>	56.1	56.7	56.3	59.8	56.4	<b>96.3</b>
<i>virB4</i>	<b>91</b>	53.5	54.7	53.7	56.5	55.2	<b>96.5</b>
<i>virB6</i>	66.4	46.2	47.7	47.1	51.9	52.1	<b>93.7</b>
<i>virB7</i>	70.9	48.3	52.4	n.a	56.5	n.a	n.a
<i>virB8</i>	<b>86.8</b>	52.6	52.9	52.1	59	58.5	<b>96.3</b>
<i>virB9</i>	<b>83.3</b>	45.4	46.3	45.8	<b>95.8</b>	<b>96.3</b>	<b>96.5</b>
<i>virB10</i>	<b>91</b>	57.2	59.1	57.5	<b>82.5</b>	<b>82.3</b>	<b>98</b>
<i>virB11</i>	<b>93.9</b>	58.3	58.3	56.2	<b>98.4</b>	61.6	62
<i>virD2</i>	<b>87.9</b>	49.4	48.8	49.8	<b>95.5</b>	54.4	55.1
<i>virD4</i>	<b>82.6</b>	46.1	45.7	54.1	<b>98.8</b>	48.7	48.5



Table S5: Diversity of T4SS sequences of *tfs3*, *tfs4a/b/c*, *cagPAI*, and *comB* of *H. pylori* strains isolated from Vietnam

<i>tfs</i> ICE type (total number of Vietnam strains possessed)	T4SS genes	No. of strains possessing the corresponding <i>vir</i> gene with 80%< identity	Range of nucleotide identity to reference T4SS (%)	Reference strain	
<b><i>tfs3</i> (n=62)</b>	<i>xerT</i>	59	91–99	Gambia94/24 and India7	
	<i>virB2</i>	37	91–98		
	<i>virB3</i>	37	88–93		
	<i>virB4</i>	37	89–97		
	<i>virB6</i>	46	85–99		
	<i>virB7</i>	32	96–98		
	<i>virB8</i>	32	82–98		
	<i>virB9</i>	35	86–97		
	<i>virB10</i>	35	88–94		
	<i>virB11</i>	35	91–95		
	<i>virD4</i>	35	81–86		
<i>virD2</i>	45	86–97			
<b><i>tfs4</i> (n=105)</b>	<b>L1 (n=41)</b>	<i>xerT</i>	41	96-98	Shi470, P12, R036d
		<i>virB6</i>	41	96-98	
	<b>L2 (n=64)</b>	<i>xerT</i>	64	95-98	
		<i>virB6</i>	28	94-97	
	<b>C1 (n=40)</b>	<i>virD2</i>	40	92-100	
		<i>virD4</i>	30	97-98	
		<i>virB11</i>	25	94-99	
		<i>virB10</i>	27	80-98	
		<i>virB9</i>	27	92-98	
	<b>C2 (n=4)</b>	<i>virD2</i>	4	96-97	
		<i>virD4</i>	4	97-99	
		<i>virB11</i>	4	98	
		<i>virB10</i>	4	96	
		<i>virB9</i>	4	94-97	
	<b>R1 (n=27)</b>	<i>virB8</i>	26	97-100	
		<i>virB7</i>	27	92-100	
		<i>virB4</i>	21	96-99	
		<i>virB3</i>	21	98-100	
<i>virB2</i>		21	97-99		
<b>R2 (n=38)</b>	<i>virB8</i>	5	97-98		
	<i>virB7</i>	0			
	<i>virB4</i>	38	97-98		
	<i>virB3</i>	38	91-99		
	<i>virB2</i>	38	94-99		
<b><i>cagPAI</i> (n=130)</b>	<i>virB2</i>	129	93–98	26695	
	<i>virB4</i>	128	98–99		
	<i>virB5</i>	128	93–96		
	<i>virB6</i>	129	97–99		
	<i>virB7</i>	129	98–99		
	<i>virB8</i>	128	98–99		
	<i>virB9</i>	129	97–99		
	<i>virB10</i>	129	98		
	<i>virB11</i>	130	99		
	<i>virD4</i>	130	98		
<b><i>comB</i> (n=136)</b>	<i>virB2</i>	136	97–100	26695	
	<i>virB3</i>	136	95–97		
	<i>virB4</i>	136	97		
	<i>virB7</i>	136	91–100		
	<i>virB8</i>	136	98		
	<i>virB9</i>	136	92–97		
	<i>virB10</i>	136	98		



**Table S7: Distribution of *tfs3/4* ICE on geographical populations in Vietnam**

		hpEurope (%), n=6	hspEAsia (%), n=130
<i>tfs3</i>		6 (100)	56 (43)
<i>tfs4</i> module	L1	4 (66)	37 (28)
	L2	1 (16)	63 (48)
	C1	1 (16)	39 (30)
	C2	1 (16)	3 (23)
	R1	1 (16)	26 (20)
	R2	1 (16)	37 (28)
<i>tfs4</i>		5 (83)	100 (76)
<i>tfs</i> ICE positive		6 (100)	117 (90.0)