

Suppl. Table 5. *Haloferax volcanii* main chromosome base substitution and inserion-deletion (indel) summary statistics

MA Line	Substitutions											Indels				Total sites	Gen.	Base- sub Rate	Indel Rate	
	Transitions						Transversions					Ins.	Del.							
	GC>AT	AT>GC	AT>TA	GC>TA	AT>CG	GC>CG														
Hv1	1	2.53E-10	0	0	0	0	1	3E-10	0	0	0	0	0	0	1	0	2E+06	3384	3E-10	2E-10
Hv2	1	2.48E-10	2	9.3E-10	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3456	5E-10	0
Hv4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3456	0	0
Hv5	1	2.48E-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3456	2E-10	0
Hv7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2E+06	3072	0	2E-10
Hv8	2	5.06E-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3384	3E-10	0
Hv16	1	2.44E-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3504	2E-10	0
Hv17	0	0	0	0	0	0	1	2E-10	0	0	0	0	0	0	0	0	2E+06	3528	2E-10	0
Hv18	1	2.58E-10	0	0	1	5E-10	1	3E-10	0	0	0	0	0	0	2	0	2E+06	3312	5E-10	3E-10
Hv19	1	2.6E-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3288	2E-10	0
Hv20	0	0	1	5.1E-10	1	5E-10	1	3E-10	0	0	0	0	0	0	0	0	2E+06	3168	5E-10	0
Hv21	1	2.77E-10	0	0	1	5E-10	1	3E-10	0	0	0	0	0	0	0	0	2E+06	3096	5E-10	0
Hv22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	2832	0	0
Hv23	1	2.64E-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3240	2E-10	0
Hv25	2	3.19E-10	0	0	0	0	1	2E-10	0	0	0	0	0	0	1	0	3E+06	3360	3E-10	1E-10
Hv26	0	0	1	4.8E-10	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3360	2E-10	0
Hv29	1	2.7E-10	0	0	0	0	1	3E-10	0	0	1	3E-10	0	0	0	0	2E+06	3168	5E-10	0
Hv30	1	2.55E-10	0	0	1	5E-10	0	0	0	0	0	0	0	0	0	0	2E+06	3360	2E-10	0
Hv32	0	0	1	4.8E-10	1	5E-10	1	3E-10	0	0	0	0	0	0	0	0	2E+06	3312	5E-10	0
Hv33	3	7.93E-10	0	0	2	1E-09	1	3E-10	0	0	0	0	0	0	1	0	2E+06	3240	1E-09	2E-10
Hv34	0	0	0	0	1	5E-10	0	0	0	0	0	0	0	0	1	0	2E+06	3336	2E-10	2E-10
Hv35	0	0	0	0	0	0	1	3E-10	0	0	0	0	0	0	1	0	2E+06	3288	2E-10	2E-10
Hv41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3216	0	0
Hv42	1	2.68E-10	0	0	1	5E-10	0	0	0	0	0	0	0	0	0	0	2E+06	3192	3E-10	0
Hv43	3	7.64E-10	0	0	1	5E-10	0	0	0	0	0	0	0	0	0	0	2E+06	3360	7E-10	0
Hv44	1	2.95E-10	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2E+06	2904	2E-10	2E-10
Hv45	2	5.49E-10	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2E+06	3120	4E-10	2E-10
Hv46	1	2.6E-10	0	0	1	5E-10	1	3E-10	0	0	0	0	0	0	0	0	2E+06	3288	3E-10	0
Hv47	1	2.51E-10	2	9.4E-10	1	5E-10	0	0	0	0	0	0	0	0	0	0	2E+06	3408	5E-10	0
Hv48	0	0	0	0	0	0	0	0	0	0	1	3E-10	0	0	0	0	2E+06	3312	2E-10	0
Hv49	1	2.57E-10	2	9.6E-10	0	0	2	5E-10	0	0	0	0	0	0	0	0	2E+06	3336	8E-10	0
Hv50	1	2.51E-10	0	0	1	5E-10	1	3E-10	0	0	0	0	0	0	0	0	2E+06	3408	5E-10	0
Hv51	0	0	0	0	1	5E-10	1	3E-10	0	0	0	0	0	0	0	0	2E+06	3288	3E-10	0
Hv52	0	0	0	0	0	0	1	1E-10	0	0	0	0	0	0	0	0	3E+06	3600	1E-10	0
Hv53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3456	0	0
Hv54	3	7.28E-10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3528	5E-10	0
Hv65	1	2.53E-10	1	4.7E-10	0	0	1	3E-10	0	0	0	0	0	0	0	0	2E+06	3384	5E-10	0
Hv66	0	0	0	0	1	5E-10	0	0	0	0	0	0	0	0	0	0	2E+06	3336	2E-10	0
Hv67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3168	0	0

Hv68	0	0	0	0	1	5E-10	0	0	0	0	0	0	0	0	0	0	2E+06	3216	0	0
Hv69	0	0	1	4.8E-10	1	5E-10	0	0	0	0	0	0	0	0	0	0	2E+06	3336	3E-10	0
Hv73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3096	0	0
Hv74	1	2.68E-10	0	0	0	0	1	3E-10	0	0	0	0	0	0	0	0	2E+06	3192	2E-10	0
Hv75	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3192	0	0
Hv76	2	5.4E-10	0	0	2	1E-09	1	3E-10	0	0	0	0	0	0	0	0	2E+06	3168	7E-10	0
Hv77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3144	0	0
Hv79	2	5.4E-10	0	0	1	5E-10	0	0	0	0	0	0	0	0	0	0	2E+06	3168	5E-10	0
Hv80	2	5.71E-10	1	5.3E-10	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3000	6E-10	0
Hv85	2	3.46E-10	0	0	0	0	1	2E-10	0	0	0	0	0	0	0	0	3E+06	3096	3E-10	0
Hv86	1	2.77E-10	0	0	1	5E-10	0	0	0	0	0	0	0	0	0	0	2E+06	3096	4E-10	0
Hv87	2	5.17E-10	1	4.8E-10	0	0	0	0	0	0	0	0	1	0	1	0	2E+06	3312	5E-10	3E-10
Hv88	1	2.49E-10	1	4.7E-10	0	0	0	0	0	0	0	0	0	0	0	0	2E+06	3432	3E-10	0
Hv90	3	8.17E-10	0	0	1	5E-10	0	0	0	0	0	0	0	0	1	0	2E+06	3144	7E-10	2E-10
Hv98	3	7.75E-10	0	0	1	5E-10	0	0	1	4.8E-10	0	0	0	0	0	0	2E+06	3312	8E-10	0
	51		14		23		20		1		2		2		11					
Overall mut ra	2.39E-10			1.2E-10		2E-10		9E-11		8.8E-12		9E-12		0		0			3E-10	4E-11
lower limit	1.78E-10			6.8E-11		1E-10		6E-11		2.2E-13		1E-12		0		0			3E-10	2E-11
upper limit	3.14E-10			2.1E-10		3E-10		1E-10		4.9E-11		3E-11		0		0			4E-10	7E-11
SEM*	3.35E-11			3.6E-11		4E-11		2E-11		9E-12		7E-12		0		0			3E-11	3E-10

* SEM is the standart error.