SUPPLEMENTARY TABLES

Table S2. Himar insertion sites in *Ehrlichia* sp. HF genome

Isolate ID	Genomic Insertion Loci	Locus ID	Gene Product	Homologies in Rickettsiales
H5	98810	Intergenic	n/a	n/a
H19	245409	EHF_0231	Hypothetical protein	32% Eucl, 28% Emu
H34	580467	EHF_0522	RmuC family protein	96% Emu, 94% Eucl, 94% Emu, 89% Ech, 85% Eca, 85% Emin, 60% Ana
H35	364974	Intergenic	n/a	n/a
H43A	835933	EHF_0733	Hypothetical protein with GTA TIM-barrel-like domain protein	94% Emu, 94% Eucl, 83% Ech, 79% Eca, 77% Emin, 63% Eru, 40% Wol, 38% Ana
H43B	1050791	EHF_RS04100	Conserved hypothetical protein with SSL domain	62% Emu, 44% Ech, 37% Emin, 34% Eca, 25% Eru
H43F	133819	EHF_0135	trbC/VIRB2 family protein	90% Emu, 84% Eucl, 78% Ech, 74% Emin, 71% Eru, 74% Ana
H47	839819	Intergenic, 9 bp upstream of EHF_0735	Major facilitator superfamily protein	90% Emu, 90% Eucl, 83% Ech, 78% Eca, 76% Emin, 67% Eru, 36% Wol
H53C	252371	Intergenic, 343 up EHF_0242	Conserved hypothetical protein	n/a
H53D-1	371562	Intergenic	n/a	n/a
H53D-2	794748	EHF_0703	thiamine biosynthesis protein ThiC	95% Emu, 95% Eucl, 92%, Ech, 88% Eca, 88% Emin, 88% Eru, 75% Nlo, 73% Aov, 72% Ama, 69% Aph
H53E	150136	EHF_0140	Conserved hypothetical protein	72% Emu, 50% Ech, 46% Emin, 48% Eca, 41% Eru, 25% Ana
H53F	884488	Intergenic	n/a	n/a
H54	241428	Intergenic	n/a	n/a
H55	406316	EHF_0382	comEC/Rec2-related domain protein	93% Emu, 93% Eucl, 80% Ech, 74% Eca, 73% Emin, 63% Eru, 47% Nlo, 45% Wol, 42% Aov, 39% Ama, 40% Aph
H55E	973392	Intergenic, 376 bp up EHF_0841	COQ9 family protein	n/a
H56A	1143100	Intergenic, 157 bp up EHF_0993 and 126 bp up EHF_RS04480	120 kDa immunodominant surface protein, Ferredoxin	n/a
H56B	353657	EHF_0324	lipoate-protein ligase B (LipB)	95% Eucl, 95% Emu, 86% Ech, 80% Eca, 80% Emin,

				76% Eru, 60% Aph, 57% Wol, 59% Nlo
H56D	424981	Intergenic, 130 bp up EHF_0399 and 439 bp up EHF_0402	Polyprenyl synthetase protein, Ribonucleoside-diphosphate reductase subunit	n/a
H57A	695771	EHF_0623	Conserved hypothetical protein	47% Eucl, 46% Emu, 31% Ech, 24% Emin
H57B	1122448	Intergenic	n/a	n/a
H58A	908826	Intergenic	n/a	n/a
H58C	871479	EHF_0758	Hypothetical protein	43% Eucl, 44% Emu, 30% Eca, 30% Emin, 30% Ech
H58D	163171	Intergenic, 184 bp up EHF_0151	type I secretion outer membrane/TolC family protein	n/a
H59	1106870	EHF_0962	Conserved hypothetical protein	80% Emu, 80% Ech, 71% Eca, 62% Emin, 48% Eru
H60D	144692	Intergenic, 506 bp up EHF_0139	Conserved hypothetical protein	n/a
H60E	1142873	EHF_0993	120 kDa immunodominant surface protein	44% Emu, 38% Eucl, 41% Eca, 30% Ech
H62	1048515	Intergenic	n/a	n/a
H64A	163135	Intergenic, 148 bp up EHF_0151 and 411 bp up EHF_0152	type I secretion outer membrane/TolC family protein, ribosomal protein L13	n/a
H64C	341553	Intergenic	n/a	n/a
H64F-1	253435	EHF_0242	Hypothetical protein	78% Eucl, 78% Emu, 72% Ech, 51% Eca, 32% Eru
H64F-2	754040	EHF_0671	Conserved hypothetical protein	78% Eucl, 78% Emu, 72% Ech, 50% Eca, 31% Eru
H65A	117218	Intergenic	n/a	n/a
H65D	1018235	EHF_0880	Conserved hypothetical protein	72% Emu, 52% Eca, 55% Emin, 53% Ech
H66A	1074892	EHF_0933	Conserved hypothetical protein	92% Emu, 82% Eca, 80% Ech, 76% Emin, 77% Eru, 48% Anas, 54% Nlo, 44% Rick
H66C	357439	Intergenic, 289 bp up EHF_0326 and 78 bp up EHF_0328	DNA / pantothenate metabolism flavoprotein family protein, class II fumarate hydratase	n/a
H66F	364844	EHF_0332	Conserved hypothetical protein	74% Emu, 73% Eucl, 58% Ech, 45% Eca, 44% Emin, 38% Eru
H67A	309891	Intergenic, 560 bp up EHF_0288	Phosphoglycolate hydrolase	n/a
H67C	61587	EHF_0066	major outer membrane protein OMP1-2	93% Emu, 90% Eucl, 65% Ech, 56% Eca, 56% Emin, 45% Eru
H67E	1074820	Intergenic, 311 bp up EHF_0932	ATP synthase subunit delta	n/a

H67F	792889	EHF_0702	Smr domain-containing protein	87%. Emu, 87% Eucl, 76% Ech, 66% Eca, 64% Emin
H68B	593034	Intergenic, 199 bp up EHF_0532	gram-negative porin family protein	n/a
H68C-1	671520	Intergenic	n/a	n/a
H68C-2	269259	Intergenic, 254 bp up EHF_0253	Conserved hypothetical protein	n/a
H68E	1035030	Intergenic, 468 bp up EHF_0893	Hypothetical protein	n/a
H69C	569620	Intergenic, 272 bp up EHF_0515	Conserved hypothetical protein	n/a
H69E	810865	EHF_0717	major facilitator family transporter	96% Eucl, 94% Emu, 83% Ech, 74% Eca, 72% Emin, 68% Eru
H69F-1	579965	EHF_0522	DNA recombination protein RmuC	See H34
H69F-2	45987	EHF_0048	major outer membrane protein OMP1-17	94% Emu, 93% Eucl, 85% Ech, 79% Emin, 70% Eca, 68% Eru, 67% Eew
H72A-1	161141	EHF_0150	DUF2497 domain-containing protein	96% Eucl, 94% Emu, 85% Ech, 79% Eca, 78% Emin, 63% Eru, 35% Nlo, 30% Ana
H72A-2	1083158	307 bp up EHF_0939	citrate (Si)-synthase	n/a
H72B	1059627	EHF_0919	amidophosphoribosyltransferase ComF	93% Emu, 82% Ech, 80% Eca, 74% Eru, 54% Wol, 55% Nlo, 45% Aph, 41% Ama, 39% Aov
H72C	872359	EHF_0758	Hypothetical protein	See H58C
H72D	63069	Intergenic, 23 bp upstream of EHF_0067	major outer membrane protein OMP1-1	89% Emu, 88% Eucl, 80% Ech, 72% Eca, 71% Emin, 66% Eew, 60% Eru, 43% Nlo
H72E	248268	EHF_0237	DNA-3-methyladenine glycosylase	93% Emu, 87% Ech, 80% Eca, 78% Emin, 73% Eru, 63% Wol, 63% Nlo, 56% Ots
H73A-1	72763	EHF_0075	dethiobiotin synthase	91% Eucl, 92% Emu, 79% Ech, 72% Eca, 73% Emin, 70% Eru, 50% Ace, 50% Ama, 48% Aph
H73A-2	186084	Intergenic, 516 bp up EHF_0173	transcription termination factor Rho	n/a
H73B	308181	Intergenic, 390 bp up EHF_0286	pyruvate, phosphate dikinase	n/a
H73C	456831	Intergenic	n/a	n/a
H73D-1	21696	Intergenic	n/a	n/a
H73D-2	566454	EHF_0513	tellurium resistance protein TerC	91% Emu, 90% Eucl, 83% Ech, 82% Eca, 79% Emin, 72% Eru, 52% Nlo, 52% Wol, 44% Aov, 44% Ama, 43% Ace

H73E-1	490405	EHF_0445	trbL/VirB6 plasmid conjugal transfer family protein	77% Emu, 73% Eucl, 82% Ech, 51% Eca, 52% Emin, 70% Eru
H73E-2	1016610	EHF_0877	transcriptional regulator NrdR	99% Emu, 94% Ech, 89% Eca, 91% Emin, 88% Eru, 68% Nlo, 59% Ace, 58% Aov, 59% Aph
H73F	456831	Intergenic	n/a	n/a
H74A-1	47534	Intergenic, 188 bp up EHF_0050	P44/Msp2 family outer membrane protein	n/a
H74A-2	699943	Intergenic, 68 bp up EHF_0625 and 363 bp up EHF_0626	bifunctional FolC family protein, aspartyl/glutamyl-tRNA amidotransferase subunitA	n/a
H74B-1	366003	EHF_0333	dihydropteroate synthase	94% Emu, 94% Eucl, 71% Eru, 56% Ech, 56% Eca, 56% Emin
H74B-2	822691	Intergenic, 34 bp up EHF_0723 and 140 bp up EHF_0724	DNA mismatch repair protein MutS, aspartyl/glutamyl-tRNA amidotransferase subunitA	EHF_0723: 97% Eucl, 98% Emu, 93% Ech, 88% Emin, 89% Eca, 79% Eru, 67% Nlo, 63% Wol, 59% Aph, 57% Ama, 57% Aov, 57% Ace, 51% Rick
H74C	28140	EHF_0031	Chromosome partitioning ATPase ParA	97% Emu, 98% Eucl, 89% Eru, 95% Ech, 94% Eca, 93% Emin, 89% Nlo, 70% Aov, 70% Ama, 67% Wol, 66% Rick
H74D	1086516	EHF_0943	Hypothetical protein	63% Eucl, 59% Emu, 37% Emin, 33% Ech, 36% Eca
H74E	257823	Intergenic	n/a	n/a
H74F-1	470413	Intergenic, 16 bp up EHF_0435	tRNA-Arg	n/a
H74F-2	886486	EHF_0768	conserved hypothetical protein	61% Emu, 46% Ech, 32% Eru
H75A-1	354464	Intergenic	n/a	n/a
H75A-2	428707	Intergenic	n/a	n/a
H75A-3	188310	Intergenic	n/a	n/a
H75B-1	45586	EHF_0048	major outer membrane protein OMP1-17	See H69F-2
H75B-2	1028718	Intergenic, 319 bp up EHF_0885, 222 bp up EHF_0888	NADP-dependent malic enzyme, ABC transporter	n/a
H75C	308227	EHF_0287	RDD family protein	92% Emu, 90% Eucl, 81% Ech, 81% Eca, 80% Emin, 67% Eru, 35% Ana, 42% Wol, 33% Rick
H75D-1	838124	Intergenic	n/a	n/a
H75D-2	765049	Intergenic, 19 bp up EHF_0677,	RNA pseudouridylate synthase family protein, extragenic suppressor protein suhB (suhB)	EHF_0677: 92% Emu, 91% Eucl, 79% Ech, 76% Eca,

		502 bp up EHF_0678		74% Emin, 67% Eru, 49% Wol, 47% Ana, 39% Rick
H75E	939557	Intergenic, 99 bp up EHF_0812	patatin-like phospholipase family protein	n/a
H75F-1	869649	EHF_0758	hypothetical protein	See H58C
H75F-2	582106	Intergenic	n/a	n/a
H75F-3	364700	EHF_0332	conserved hypothetical protein	See H66E
H75F-4	831375	EHF_0732	phage conserved hypothetical BR0599 family protein	93% Emu, 83% Ech, 76% Emin, 77% Eca, 66% Eru, 49% Nlo, 40% Wol, 40% Ana
H76A-1	847362	EHF_0743	glutathione S-transferase	97% Emu, 97% Eucl, 94% Ech, 94% Emin, 95% Eca, 86% Eru, 68% Nlo, 63% Wol, 60% Ana, 48% Rick
H76A-2	273766	Intergenic	n/a	n/a
H76A-3	43980	Intergenic, 122 bp up EHF_0045	P44/Msp2 family outer membrane protein	n/a
H76B-1	1086497	EHF_0943	hypothetical protein	See H74D
H76B-2	517679	EHF_0470	conserved hypothetical protein	79% Emu, 73% Ech, 66% Eca, 66% Emin, 50% Eru, 30% Ana
H76C	1092639	Intergenic, 262 bp up EHF_0950, 121 up EHF_0951	protein translocase subunit SecF, archaeal holliday junction resolvase family protein	n/a
H76D-1	1112797	Intergenic, 183 bp up EHF_0967 AND 844 bp up EHF_0966	1-acyl-sn-glycerol-3-phosphate acyltransferase	n/a
H76D-2	376020	Intergenic, 142 bp up EHF_0341	SPFH domain / Band 7 family (membrane) protein	n/a
H76E-1	150664	EHF_0140	conserved hypothetical protein	See H53E
H76E-2	149069	Intergenic, 268 bp up EHF_0140	conserved hypothetical protein	n/a
H76F	179134	EHF_0167	aspartate kinase	96% Emu, 95% Eucl, 93% Ech, 93% Eca, 91% Emin, 81% Eru, 65% Nlo, 51% Ana
H77A-1	792823	EHF_0702	smr domain protein	See H67F
H77A-2	765387	Intergenic, 360 bp up EHF_0677	pseudouridine synthase	n/a
H77A-3	41666	Intergenic, 166 bp up EHF_0042	P44/Msp2 family outer membrane protein	n/a
H77A-4	43288	Intergenic	major outer membrane protein OMP1-19	
H77A-5	150664	EHF_0140	conserved hypothetical protein	See H53E
H77B-1	43813	EHF_0045	major outer membrane protein OMP1-19	See H77A-4
H77B-2	516921	Intergenic, 66 bp up EHF_0470	conserved hypothetical protein	n/a

H77B-3	46141	EHF_0048	major outer membrane protein OMP1-17	See H69F-2
H77C-1	516769	Intergenic, 218 bp up EHF_0470	conserved hypothetical protein	n/a
H77C-2	217716	Intergenic	n/a	n/a
H77D-1	1125230	Intergenic, 143 bp up EHF_0978 and 62 bp up EHF_0979	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase, hypothetical protein with MJ0042 family finger-like domain protein	n/a
H77D-2	525060	Intergenic	n/a	n/a
H77E-1	448957	Intergenic, 626 bp 425 bp up EHF_0423	Xaa-Pro aminopeptidase	n/a
H77E-2	753371	EHF_0671	Hypothetical protein	See H64F-2
H77F	936950	EHF_0810	BolA protein	83% Eucl, 94% Emu, 72% Ech, 73% Emin, 70% Eca, 64% Eru, 51% Wol, 40% Aph
H78	257958	Intergenic	n/a	n/a
H79A-1	1132802	Intergenic, 440 bp up EHF_0987	GTP cyclohydrolase	n/a
H79A-2	813074	EHF_0718	Major Facilitator Superfamily (MFS) transporter	94% Eucl, 95% Emu, 75% Ech, 75% Eca, 65% Eru, 37% Nlo, 35% Ana
H79A-3	64253	EHF_0069	nucleoside-diphosphate kinase	96% Eucl, 97% Emu, 94% Ech, 91% Eca, 88% Eru, 73% Nlo, 64% Ana, 69% Wol, 64% Nhe, 64% Nsen
H79C-1	870872	EHF_0758	hypothetical protein	See H58C
H79C-2	834447	EHF_0733	hypothetical protein with GTA TIM-barrel-like domain protein	See H43A
H79C-3	152197	Intergenic		n/a
H79C-4	62134	Intergenic, 438 bp up EHF_0066	P44/Msp2 family outer membrane protein	n/a
H79D-1	513076	EHF_RS02075	Hypothetical protein (pseudogene due to frameshift)	n/a
H79D-2	827624	Intergenic	n/a	n/a
H79E-1	946167	Intergenic	n/a	n/a
H79E-2	407501	EHF_0383	sodium:alanine symporter family protein	95% Eucl, 96% Emu, 90% Ech, 88% Emin, 87% Eca, 70% Eru, 60% Nlo, 57% Wol, 54% Ana, 39% Nhe, 37% Nri
H80A-1	42923	Intergenic, 246 bp up EHF_0044	major outer membrane protein OMP1-20	n/a
H80A-2	1061828	Intergenic, 83 bp up EHF_0922	n/a	n/a
H80B-1	1044678	EHF_0905	hypothetical protein	55 Eucl, 55% Emu, 36% Ech

H80B-2	1005383	Intergenic, 164 bp up EHF_0868	n/a	n/a
H80B-3	112044	EHF_0115	Gamma carbonic anhydrase family protein	92% Eucl, 95% Emu, 96% Ech, 80% Emin, 82% Eca, 64% Eru, 64% Nlo, 63% Wol, 63% Ana, 57% Nsen, 55% Nri
H80B-4	820620	EHF_0723	DNA mismatch repair protein MutS	See H74B-2
H80B-5	1008450	Intergenic	n/a	n/a
H80C-1	919082	986 bp up EHF_0795	n/a	n/a
H80C-2	1131409	EHF_0984	conserved hypothetical protein	88% Eucl, 85% Emu, 82% Ech72% Emin, 71% Eca, 62% Eru
H80C-3	382057	EHF_0346	cell division ZapA family protein	96% Eucl, 98% Emu, 88% Ech, 80% Emin, 80% Eca, 76% Eru, 40-50% Wo, 35% Aov, 33% Ama
H80D-1	763703	Intergenic	n/a	n/a
H80D-2	607098	139 bp up EHF_0545	conserved hypothetical protein - pseudogene	n/a
H80D-3	810577	EHF_0717	Major Facilitator Superfamily (MFS) transporter	See H69E
H80E	1018051	7 bp up EHF_0880	conserved hypothetical protein	79% Emu, 52% Eca, 55% Emin, 53% Ech
H80F	929685	8 bp up EHF_0806	3-phosphoshikimate 1-carboxyvinyltransferase	91% Eucl, 95% Emu, 74% Ech, 67% Emin, 67% Eca, 54% Eru, 37% Nlo
H81A-1	751268	Intergenic	n/a	n/a
H81A-2	897331	EHF_0775	putative membrane protein	65% Eucl, 69% Emu, 51% Ech, 53% Emin, 52% Eca, 48% Eru, 25% Ana
H81B-1	545195	EHF_0497	hypothetical protein	64% Emu, 36% Eucl, 30% Ech, 23% Emin
H81B-2	920774	182 bp up EHF_0796, 546 bp up EHF_0797	conserved hypothetical protein, tRNA-Leu	n/a
H81C-1	1013847	Intergenic, 160 bp up EHF_0874 and 109 bp up EHF_0875	hypothetical protein, conserved hypothetical protein	n/a
H81C-2	122477	EHF_0125	peptidase M16 family protein	93% Emu, 89% Ech, 85% Emin, 85% Eca, 68% Eru, 50% Nlo, 43% Aph, 40% Ana, 43% Wol
H81D	573935	EHF_0515	Chromosome segregation protein SMC (structural maintenance of chromosomes) archaeal type	56% Eucl, 56% Emu, 44% Ech, 34% Emin
H81E	1070542	Intergenic	n/a	n/a
H82A-1	448861	722 bp up EHF_0423	n/a	n/a

H82A-2	161191	EHF_0150	conserved hypothetical protein	96% Eucl, 94% Emu, 85% Ech, 79% Eca, 78% Emin, 63% Eru, 35% Nlo, 30% Ace
H82A-3	1098537	EHF_0956	octaprenyl-diphosphate synthase	98% Eucl, 96% Emu, 88% Ech, 87% Eca, 86% Emin, 74% Eru, 62% Nlo, 52% Ace, 53% Ama, 51% Aov, 50% Aph, 52% Wol
H82B-1	509073	343 bp up EHF_0462	n/a	n/a
H82B-2	45484	EHF_0048	major outer membrane protein OMP1-17	See H69F-2
H82C	491800	EHF_0446	DUF2460 domain-containing protein	95% Eucl, 95% Emu, 86% Ech, 83% Eca, 82% Emin, 76% Eru, 64% Nlo, 58% Wol, 49% Aph
H82D-1	737087	Intergenic, 87 bp up EHF_0656	bifunctional ADP-dependent NAD(P)H-hydratedehydratase/ NAD(P)H-hydrate epimerase	n/a
H82D-2	892485	EHF_0772	DNA mismatch repair protein MutL	93% Eucl, 92% Emu, 81% Ech, 76% Eca, 77% Emin, 66% Eru, 59% Nlo, 57% Wol, 51% Aph, 40% Ots
H82E-1	188165	Intergenic	n/a	n/a
H82E-2	753814	EHF_0671	Hypothetical protein	See H64F-2
H82E-3	999937	279 bp up EHF_0861	n/a	n/a

Abbreviations:

Up: upstream of ORFs; Ech: *E. chaffeensis*; Eca: *E. canis*; Emu: *E. muris*; Emin: *E. minasensis*; Eru: *E. ruminantium*; Eucl: *E. muris* subsp. *Eauclairensis*; Eew: *E. ewingii*; Nhe: *Neorickettsia helminthoeca*; Nri: *N. risticii*; Nlo: Candidatus *Neoehrlichia lotoris*; Nsen: *N. sennetsu*, Ana: several *Anaplasma* species; Aph: *A. phagocytophilum*; Ace: *A. centrale*; Aov: *A. ovis*; Ama: *A. marginale*; Wol: *Wolbachia*; Ots: *Orientia tsutsugamushi*; Rick: *Rickettsia* species