Norm std		0.132	0.204	0.167	0.181	0.143	0.166	0.200	0.202	0.215	0.200
DEPTH		63.92	13.705	32.13	13.585	46.195	84.31	35.23	106.04	65.43	72.51
		aM P3 Hamster	aM P4 Hamster	ProM (A) R3	ProM (A) R10	ProM (P) Sandfly 1	ProM (P) Sandlfy 2	ProM (P) Sandfly 3	ProM (A) Sandfly 1	ProM (A) Sandfly 2	ProM (A) Sandfly 3
Library prep									N	N	N
H-locus	LdBPK_230007600: hypotheticalprotein,conserved	2.877	2.643	3.281	3	2.875	2.882	2.815	3.213	3.329	3.143
	LdBPK_230007700: terbinafineresistancelocusprotein_yip1_	3	2.571	2.781	2.652	2.694	2.669	2.741	2.567	2.572	2.766
	LdBPK_230007800: pentamidineresistanceprotein1	2.862	2.786	3.062	2.783	2.625	2.803	2.63	2.779	2.814	2.636
	LdBPK_230007900: argininosuccinatesynthase,putative	3.031	2.786	2.812	2.522	2.597	2.834	2.407	3.089	3.429	3.26
	Average for H-locus	2.9425	2.6965	2.984	2.73925	2.69775	2.797	2.64825	2.912	3.036	2.95125
M-locus	LdBPK_360076600: tartrate-sensitiveacidphosphataseacp-3.2,putative	3.892	4.643	4.367	4.727	4.273	5.458	4.625	6.699	7.622	6.708
	LdBPK_360076700: hypotheticalprotein,conserved	8.092	8.143	7.433	7.409	7.364	8.688	9.75	6.265	6.228	6.333
	LdBPK_360076800: mitogen-activatedproteinkinase	15.661	15.072	13.933	15.319	14.5	12.417	14.937	14.803	15.258	15.568
	LdBPK_360076900: histidinesecretoryacidphosphatase,putative	13.323	13.072	13.6	12.955	13.023	17.632	13.937	12.86	13.91	12.694
	LdBPK_360077000: hypotheticalprotein,conserved	7.538	7.786	7.233	7.591	7.932	8.093	9.937	6.133	6.319	6.444
	Average for M-locus	9.7012	9.7432	9.3132	9.6002	9.4184	10.4576	10.6372	9.352	9.8674	9.5494
Ch6 - Yeti amplicon	LdBPK_060014000: hypotheticalprotein,conserved	1.016	0.923	1.061	1.136	0.896	0.989	0.778	0.971	1	0.829
	LdBPK_060014100: hypotheticalprotein,conserved	0.984	0.923	1.03	1	0.917	1.119	0.944	0.853	0.839	0.843
	LdBPK_060014200: dihydrofolatereductase-thymidylatesynthase	0.984	0.769	0.909	0.955	0.937	0.989	0.944	0.961	0.968	0.986
	LdBPK_060014300: arginineN-methyltransferase,typeIII,putative	1.081	0.923	1.061	1	1.021	0.891	1.056	0.951	0.952	0.914
	LdBPK_060014400: acyl-coenzymeadehydrogenase,putative	0.871	0.846	0.849	0.955	0.812	0.848	0.778	0.922	1	0.943
	Average for Yeti amplicon	0.9872	0.8768	0.982	1.0092	0.9166	0.9672	0.9	0.9316	0.9518	0.903

Table S2A

Chr	Ld24		Ld32		Ld32		Ld35		Ld35	
Gene ID	LdBPK_240007400.1		LdBPK_320042200.1		LdBPK_320005900.1		LdBPK_350008700.1		LdBPK_350045600.1	
SNP position on the chromosome	Ld24:65742		Ld32:1398170		Ld32:32369		Ld35:108596		Ld35:1591295	
Protein	hypothetical, con		hypothetical, con		NLI interacting factor-like phosphatase		ATP-dependent DEAD-box RNA helicase%2C putative		4E-interacting protein	
Changes (REF/ALT)	T/G => Stop		C/G=> Ala/Gly		A/G => Cys/Arg		C/T => Ser/Phe		A/T => Stop	
	DNA seq	RNA seq	DNA seq	RNA seq	DNA seq	RNA seq	DNA seq	RNA seq	DNA seq	RNA seq
ProM (I) R22	8/0	-	13/0	-	2/0	-	5/4	-	16/0	-
ProM (P) Sandfly 1	39/0	-	56/0	-	52/0	-	41/0	-	49/0	-
ProM (P) Sandfly 2	65/0	-	95/0	-	44/0	-	66/0	-	108/0	-
ProM (P) Sandfly 3	16/0	6/0	13/0	43/0	14/0	98/0	17/0	260/1	14/0	22/0
ProM (P) Sandfly 3	16/0	6/0	13/0	43/0	14/0	98/0	17/0	260/1	14/0	22/0
aM (P/sf) P1 Hamster	2/0	14/0	./.	60/0	2/0	96/0	2/0	303/0	./.	25/0
ProM (I) R20	64/0	13/0	79/0	56/0	37/0	108/0	70/31	329/175	151/0	58/0
aM P3 Hamster	20/35	11/7	29/33	30/32	32/32	58/69	27/28	178/148	28/13	5/5
aM P4 Hamster	7/11	4/4	7/6	10/7	7/12	13/18	3/7	46/49	9/5	4/4
aM P4 Hamster	7/11	4/4	7/6	10/7	7/12	13/18	3/7	46/49	9/5	4/4
ProM (A) Sandfly 4	3/0	-	0/1	-	0/1	-	./.	-	0/2	-
ProM (A) Sandfly 5	2/0	-	1/2	-	2/2	-	1/0	-	2/2	-
ProM (A) Sandfly 6	5/1	1/1	2/6	2/2	1/1	3/10	5/2	26/25	4/3	0/3
aM P4 Hamster	7/11	4/4	7/6	10/7	7/12	13/18	3/7	46/49	9/5	4/4
ProM (A) R3	23/16	5/4	19/19	30/27	14/15	56/86	15/11	192/198	14/16	13/6
ProM (A) R10	8/10	3/3	19/8	20/22	8/10	58/74	8/7	137/134	11/10	9/7

Table S2B