

Table S16

#	Fragment	Code (1)	Length (2)	Tm (3)	Sequence (5'-3')
1	7, 8	hmtH112	20(10/10)	65.8	ACAGATACTGCGACATAGGG
2	8, 1	hmtL569	20(10/10)	65.8	AACCAAACCCCAAAGACACC
3	8, 1	hmtH626	20(10/10)	65.8	TTTATGGGGTGATGTGAGCC
4	1	hmtL1305	19(8/11)	65.8	GTAAGCGCAAGTACCCACG
5	1	hmtH1405	20(10/10)	65.8	ATCCACCTTCGACCCTTAAG
6	1	hmtL2070	20(10/10)	65.8	AATTTGCCACAGAACCCTC
7	1	hmtH2174	20(10/10)	65.8	ATTGGTGGCTGCTTTTAGGC
8	1, 2	hmtL2797	21(11/10)	67.3	GTCCTAAACTACCAAACCTGC
9	1, 2	hmtH2941	21(11/10)	67.3	GACTCTAGAATAGGATTGCGC
10	2	hmtL3568	20(10/10)	65.8	CGCTCTTCTACTATGAACCC
11	2	hmtH3733	20(10/10)	65.8	ATGATGGCTAGGGTGACTTC
12	2	hmtL4322	21(12/9)	65.8	ATAATAGGAGCTTAAACCCCC
13	2	hmtH4501	20(10/10)	65.8	TGTGCCCTGCAAAGATGGTAG
14	2, 3	hmtL5061	20(10/10)	65.8	AGCAGTTCTACCGTACAACC
15	2, 3	hmtH5193	20(12/8)	62.9	GTGTTAGTCATGTTAGCTTG
16	3	hmtL5828	20(9/11)	67.3	GAAAATCACCTCGGAGCTGG
17	3	hmtH5993	20(10/10)	65.8	TAAGGAGGCTTAGAGCTGTG
18	3	hmtL6563	20(10/10)	65.8	ACCTCAACACCACCTTCTTC
19	3	hmtH6753	20(10/10)	65.8	TGTGCTCACACGATAAACCC
20	3, 4	hmtL7336	21(11/10)	67.3	GATTTGAGAAGCCTTCGCTTC
21	3, 4	hmtH7497	21(12/9)	65.8	TTTGAAAAAGTCATGGAGGCC
22	4	hmtL8080	20(10/10)	65.8	TCTTGCACTCATGAGCTGTC
23	4	hmtH8251	20(10/10)	65.8	GCTATAGGGTAAATACGGGC
24	4	hmtL8815	20(10/10)	65.8	CTCATTTACACCAACCACCC
25	4	hmtH9030	21(11/10)	67.3	CCAATTAGGTGCATGAGTAGG
26	4, 5	hmtL9611	20(10/10)	65.8	TCCCACTCCTAAACACATCC
27	4, 5	hmtH9819	21(11/10)	67.3	GCCAATAATGACGTGAAGTCC
28	5	hmtL10380	20(10/10)	65.8	TCTGGCCTATGAGTGACTAC
29	5	hmtH10598	21(11/10)	67.3	GTTGAGGGTTATGAGAGTAGC
30	5	hmtL11107	21(12/9)	65.8	TTCACAGCCACAGAATAATC
31	5	hmtH11381	20(10/10)	65.8	AAGTGGAGTCCGTAAGAGAGG
32	5, 6	hmtL11727	17(6/11)	62.9	GCCACGGGCTTACATC
33	5, 6	hmtH12111	20(10/10)	65.8	AAACCCGGTAATGATGTCCGG
34	6	hmtL12640	21(12/9)	65.8	TCGTTACATGGTCCATCATAG
35	6	hmtH12862	20(10/10)	65.8	AAACCGATATCGCCGATACG
36	6	hmtL13389	21(12/9)	65.8	TCCATCATCCACAACCTTAAC
37	6	hmtH13627	20(10/10)	65.8	AAGCGAGGTTGACCTGTTAG
38	6, 7	hmtL14130	20(10/10)	65.8	TCTTCCCACTCATCCTAACC
39	6, 7	hmtH14559	20(9/11)	67.3	GATTGTTAGCGGTGTGGTCG
40	7	hmtL14838	20(10/10)	65.8	TCCAACATCTCCGCATGATG
41	7	hmtH15153	21(11/10)	67.3	CCCCTCAGAAATGATATTTGGC
42	7	hmtL15591	20(10/10)	65.8	TTCGCCTACACAATTCTCCG
43	7, 8	hmtH15912	20(10/10)	65.8	TCTCCGGTTTACAAGACTGG
44	7, 8	hmtL16365	20(9/11)	67.3	GTCAAATCCCTTCTCGTCCC

8 fragments for complete mtDNA

## primers for HVSI

- (1) human-mitochondrial-strand-3'.  
(2) Primer length (nt) and (A+T/G+C).  
(3) Melting Temperature =  $1.46x[(A+T)+2x(G+C)]+22$

To amplify the whole mtDNA in 8 fragment	Length	Sequencing primers for this fragment	Reactions
1- hmtL569/hmtH2941	2412bp	2, 4, 5, 6, 7, 9	6
2- hmtL2797/hmtH5193	2436bp	8, 10, 11, 12, 13, 15	6
3- hmtL5061/hmtH7497	2476bp	14, 16, 17, 18, 19, 21	6
4- hmtL7336/hmtH9819	2524bp	20, 22, 23, 24, 25, 27	6
5- hmtL9611/hmtH12111	2539bp	26, 28, 29, 30, 31, 33	6
6- hmtL11727/hmtH14559	2851bp	32, 34, 35, 36, 37, 39	6
7- hmtL14130/hmtH112	2590bp	38, 40, 41, 42, 43, 1	6
8- hmtL15591/hmtH626	1643bp	44, 3	2
		Total	44