



		Fragsmen				
BATCH	Hg	D-loop	Length	Sequence	Notes	
<b>Amplification #1411</b>						
CA-SCL-38 B4 5/17/11 (RS)	1	C	1	16131C		
			1.3	16131C, 16164G, 16207T, 16223T, 16247T, 16244A, 16298C, 16325C, 16327T		
			1.4	16131C, 16164G, 16207T, 16223T, 16247T, 16244A, 16298C, 16325C, 16327T		
			1.5	16131C, 16164G, 16207T, 16223T, 16247T, 16244A, 16298C, 16325C, 16327T		
			1.6	16131C, 16164G, 16207T, 16223T, 16247T, 16244A, 16298C, 16325C, 16327T, 00073G		
			1.7	16131C, 16164G, 16207T, 16223T, 16247T, 16244A, 16298C, 16325C, 16327T, 00073G		
<b>Amplification #1711</b>						
CA-SCL-38 B4 1/10 5/17/11	1	C	1	16131C	read reverse sequence	
			1.2	16131C, 16164G, 16207T, 16223T		
			1.3	16131C, 16164G, 16207T, 16223T, 16247T, 16244A, 16298C, 16325C, 16327T		
			1.4	16131C, 16164G, 16207T, 16223T, 16247T, 16244A, 16298C, 16325C, 16327T		
CA-SCL-38 B8G (RS) 5/17/11	1	D	1	16084A		
			1.2	16084A, 16198T, 16223T, 16082T, 16084A, 16198T, 16223T, 16292C		
CA-SCL-38 B8E 1/10 5/17/11	1	D	1	16084A		
CA-SCL-38 B171 (RS) 5/17/11	1	D	1	CRS	Consistent with no D	
			1.2	16223T		
			1.3	16223T, 16325C		
			1.4	16223T, 16325C, 16390C		
			1.5	16223T, 16325C, 16390C		
			1.6	16223T, 16325C, 16390C, 00073G		
			1.7	16223T, 16325C, 16390C, 16416CT, 00073G		
			1.8	16193T, 16223T, 16325C, 16325C, 16327T, 00073G, 16193T, 00279C, 003151C	00279C could be damage (E's in Mitomap)	
CA-SCL-38 B171 1/10 5/17/11	1	D	1	CRS	read reverse sequence	
			1.2	16223T		
			1.3	16223T, 16325C		
			1.4	16223T, 16325C, 16390C		
			1.5	16193T, 16223T, 16325C, 16390C, 16408T		
			1.6	16044A, 16023T, 16325C, 16390C, 16515A, 00073G		
			1.7			
			1.8			
			1.9			
CRS 9 (RS) 5/17/11	1	B, non-B	1	16023A, 16065A	No B's like this in the database, no non-B's with both of these in the database both are not in mitdb, both are not in mtomap	
BMI1 C3 5/17/11 (UB)	1	D	1	CRS		
			1.2	16142T, 16223T		
BMI1 C3 5/17/11 (RS)	1	D	1	CRS		
			1.2	16142T, 16223T	These mutations were observed in the TFR study	
<b>Amplification #2211</b>						
BMI1 C7 5/17/11 1/10	1	B	1	16111T, 16120A	These mutations were observed in the TFR study	
BMI1 C7 5/17/11 (RS)	1	B	1	CRS	Conflicts with 1/10 dilution amplification, probably contamination could be heteroplasmic B	
Table 2 5/22/11 (RS)	2	B	1	CRS		
Table 3 5/22/11 (UB)	2	B	1	16170A, 16183C, 16189C, 16170T, 16207T	Because of poly-C sequence read is 16208-16212. Note three Navajo New 16170Aid, but they also have 16111T, 16223T, 16292C	
Table 3 5/22/11 (RS)	2	B, non-B	1	CRS	Consistent with heteroplasmic B	
			1.2	16051G, 16129C, 16180C, 16183C, 16189C	Because of Poly-C, sequence read 16032-16215 (KEMP)	
			1.5	16051G, 16129C, 16180C, 16183C, 16189C, 16296T, 16362C	Because of Poly-C, sequence read 16045-16052 (KEMP)	
			1.7	Lost amplicons		
CA-SCL-38 B 93 5/22/11 (RS)	2	D	1	CRS		
			1.2	16223T		
			1.3	16223T, 16325C		
ATB 5 NEW 5/11/11	Liba	Extraction	A	16111T		
			1.2	16111T, 16223T		
			1.3	16111T, 16223T, 16290T, 16319A		
			1.4	16111T, 16223T, 16290T, 16319A		
			1.5	16111T, 16223T, 16290T, 16319A, 16362C		
			1.6	16111T, 16223T, 16290T, 16319A, 16362C, 00073G		
			1.7	16111T, 16223T, 16290T, 16319A, 16362C, 00073G, 00146C, 00150G		
ATB 5 OLD 5/11/11	Liba	Extraction	A	16111T		
			1.2	16111T, 16223T		
			1.3	16111T, 16223T, 16290T, 16319A		
EC 5/17/11	1		1	16051G, 16129C	Forward sequence only, read 16039-16131 (KEMP)	
			1.2	16183C, 16189C, 16180C, 16267T, 16325C, 16159C	Reverse sequence only, read 16182-00126 (KEMP)	
			1.3	00073G		
EC 5/22/11	2		1	16051G, 16129C	KEMP	
PCR NEG 1	ns		1	16051G, 16129C	KEMP	
<b>Amplification 161811</b>						
BMI1 C2 5/25/11	3	A	1	16051G, 16111T		
			1.2	16051G, 16111T, 16223T, 16051G, 16111T, 16223T, 16292T, 16319A		
			1.3	16292T, 16319A		
BMI1 C2 5/25/11 (RS)	3	A	1	16051G, 16111T		
			1.2	16051G, 16111T, 16223T, 16051G, 16111T, 16223T		
			1.3	16051G, 16111T, 16223T, 16292T, 16319A	read reverse, forward is empty miss	
NSRL 1209 OLD 6/3/11 (Z RS)	4	B	1	16111T		
			1.2	16111T, 16183C, 16189C	Because of Poly-C, sequence read 16038-16207	
			1.3	16180T, 16111T, 16183C, 16189C, 16210C	Because of Poly-C, sequence read 16038-16211	
NSRL 1308 OLD 6/3/11	4	C	1	16051G		
			1.2	16051G, 16223T, 16296C, 16311C, 16325C, 16327T		
			1.3	16051G, 16223T, 16296C, 16311C, 16325C, 16327T		
			1.5	16193C		
Scaple 66 6/3/11 (Z RS)	4	B	1	CRS	Consistent with heteroplasmic B	
Xoanel 94 OLD 6/3/11 (RS)	4	B	1	16111T	clean deletion	
			1.2	16111T, 16183C, 16189C	Because of Poly-C, sequence read 16041-16201	
			1.3	16051G, 16129C, 16180C, 16183C, 16189C, 16296T	Because of Poly-C and messy sequence read 16108-16443 (KEMP)	
			1.5	16292C, 16325C, 16327T		
NSRL 1288 6/3/11 NEW (ZRS)	5	D	1	CRS		
			1.2	16223T		
NSRL 1209 6/3/11 NEW (RS)	5	B	1	16107CT, 16111T	Because of Poly-C, sequence read 16037-16212	
			1.2	16111T, 16183C, 16189C		
NSRL 1308 6/3/11 NEW (ZRS)	5	C	1	CRS	Conflicts with NSRL 1308 OLD 6/3/11	
			1.2	16051G, 16223T		
			1.3	16051G, 16223T, 16296C, 16311C, 16325C, 16327T		
EC 6/3/11-2	5	ns	CRS			
Auyaveve 6/8/11	6	B	1	16085T, 16128T	read reverse, not in mitdb, 16128 not in mtomap	
			1.2	16183C, 16189C	Because of Poly-C, sequence read 16041-16205	
Punta Santana 6/8/11	6	C	1	16114T, 16223T	16114 observed before in this sample	
Z2 Bonifati B10 6/8/11	6	B	1	16111T, 16115T, 16115T	read sequence	
CA-SCL-38 B 102 6/8/11 (ZRS)	6	D	1	16092C		
			1.2	16092C, 16223T		
			1.3	16092C, 16223T, 16290CT, 16325C		
			1.5	16092C, 16223T, 16325C, 16362		
			1.6	16092C, 16223T, 16325C, 16362, 00073G		
CA-SCL-38 B 15F 6/8/11 (ZRS)	6	D	1	CRS		
			1.2	16223T, 16325C		
			1.3	16183T, 16223T, 16325C, 16362, 00073G		
			1.7			