

Supplemental Tables

Table S1. List of in-silico mixtures. A.) two person mixtures; B.) three person mixtures. Both tables list contributor ID, contributor haplogroup, the number of unique and shared haplogroup defining SNPs, and our determination of whether the mixture was considered to consist of similar or dissimilar haplotypes.

A.)

Contributor 1	Contributor 1 Haplogroup (Haplogrep2)	Contributor 2	Contributor 2 Haplogroup (Haplogrep2)	Unique Haplogroup Defining SNPs	Shared Haplogroup Defining SNPs	Percent Shared Haplogroup Defining SNPs	Similar (S) or Dissimilar (D) Haplotypes
20	K1a1b2a1a	235	L1c1d1	58	3	4.92	D
20	K1a1b2a1a	832	L1c2b1a'b	64	3	4.48	D
27	X2+225+@153	445	2b+226+16192	4	9	69.23	S
28	M7c1c2	776	Z4	26	4	13.33	S
45	D1	1219	D6a1a	15	7	31.82	S
51	J1c2	433	T2	25	4	13.79	S
51	J1c2	77	T1a1	29	4	12.12	S
57	G2a1c1	885	D1	20	5	20.00	S
97	V7	585	H7a1	9	0	0.00	D
97	V7	296	H1a3	9	1	10.00	S
97	V7	489	H3g1	11	0	0.00	D
97	V7	614	H4a1a1a	15	0	0.00	D
97	V7	516	H4a1a1a2	16	0	0.00	D
97	V7	1355	R11	17	0	0.00	D
234	L2a1a2	307	L2a1a2a1a	3	25	89.29	S
234	L2a1a2	471	L2a1c3b1	12	18	60.00	S
307	L2a1a2a1a	471	L2a1c3b1	16	18	52.94	S
351	B2r	1282	D1	34	0	0.00	D
433	T2	484	J1c3	23	5	17.86	S
787	B2o	832	L1c2b1a'b	53	1	1.85	D
399	A2g1	918	A2+64+16129	6	15	71.43	S

B.)

Contributor 1	Contributor 1 Haplogroup (Haplogrep2)	Contributor 2	Contributor 2 Haplogroup (Haplogrep2)	Contributor 3	Contributor 3 Haplogroup (Haplogrep2)	Unique Haplogroup Defining SNPs	Shared Haplogroup Defining SNPs	Percent Shared Across All Contributors Haplogroup Defining SNPs	Similar (S) or Dissimilar (D) Haplotypes
20	K1a1b2a1a	787	B	832	L1c2b1a'b	76	4	5.00	D
20	K1a1b2a1a	235	L1c1d1	471	L2a1c3b1	73	9	10.98	S
27	X2+225+@153	445	X2b+226+16192	489	H3g1	9	9	50.00	S
27	X2+225+@153	343	A	489	H3g1	25	2	7.41	D
27	X2+225+@153	97	V7	471	L2a1c3b1	35	2	5.41	D
45	D1	1219	D6a1a	1282	D1	10	12	54.55	S
45	D1	57	G2a1c1	1282	D1	16	12	42.86	S
45	D1	235	L1c1d1	787	B2o	60	2	3.23	D
51	J1c2	433	T2	484	J1c3	16	14	46.67	S
51	J1c2	77	T1a1	484	J1c3	20	14	41.18	S
51	J1c2	77	T1a1	433	T2	22	14	38.89	S
57	G2a1c1	1219	D6a1a	1282	D1	25	9	26.47	S
65	L	235	L1c1d1	787	B2o	64	4	5.88	D
97	V7	296	H1a3	585	H7a1	12	1	7.69	D
97	V7	489	H3g1	585	H7a1	14	0	0.00	D
97	V7	489	H3g1	614	H4a1a1a	18	1	5.26	D
97	V7	343	A	885	D1	31	1	3.13	D
97	V7	516	H	1355	R11	26	1	3.70	D
234	L2a1a2	307	L2a1a2a1a	471	L	8	25	75.76	S
235	L1c1d1	787	B2o	832	L	44	25	36.23	S
399	A2g1	886	A2+64+16129	918	A2ap	7	15	68.18	S

Table S2. List of in-silico mixture contributors with haplogrep2 generated haplogroup and GM HTS generated haplotype and heteroplasmy information. Heteroplasmy is presented as rCRS nucleotide-nucleotide position-alternative nucleotide- frequency (%).

In-silico Mixture Contributors	Haplogroup	Haplotype	Heteroplasmy
20	K1a1b2a1a	73G,114T,152C,263G,315.1C,497T,750G,1189C,1438G,1811G,2706G,3480G,3777C,4769G,7028T,7278C,7729G,8860G,9055A,9698C,9800C,10046C,10398G,10550G,11299C,11467G,11719A,11914A,12308G,12372A,13326C,14167T,14766T,14798C,15326G,15758G,15924G,16093C,16224C,16311C,16519C	T16093T 16.26
27	X2+225+@153	73G,195C,225A,263G,315.1C,750G,1438G,1719A,1888A,2706G,2772T,3483A,4769G,6221C,6371T,7028T,8860G,8966C,9438A,11293G,11719A,12705T,13966G,14470C,14766T,15326G,16182C,16183C,16189C,16223T,16248T,16278T,16519C	A153G 18.79 T11254C 19.72
45	D1	73G,196C,263G,315.1C,489C,729C,750G,1438G,2092T,2706G,3010A,3918A,4769G,4883T,5178A,7028T,8414T,8701G,8860G,9443C,9540C,9739T,10097G,10398G,10400T,10822G,10873C,11410C,11719A,12705T,14668T,14766T,14783C,15043A,15301A,15326G,16223T,16325C,16362C	none
51	J1c2	73G,185A,188G,228A,263G,295T,315.1C,462T,489C,750G,1438G,2706G,3010A,4216C,4769G,7028T,8860G,10398G,11251G,11719A,12612G,13708A,14766T,14798C,15326G,15452A,16069T,16126C	T152C 29.76
57	G2a1c1	73G,263G,309.1C,315.1C,489C,709A,750G,1438G,2706G,4769G,4833G,5021C,5108C,5601T,7028T,7600A,8701G,8860G,9377G,9540C,9575A,10398G,10400T,10873C,11719A,12705T,13563G,13780G,14200C,14569A,14766T,14783C,15043A,15301A,15326G,16093C,16183C,16189C,16194C,16195C,16223T,16227G,16278T,16362C,16519C	none
65	I2	73G,152C,199C,204C,207A,250C,263G,309.1C,315.1C,750G,1438G,1719A,2706G,4529T,4561C,4769G,7028T,8251A,8860G,10034C,10238C,10398G,11353C,11719A,12501A,12705T,13780G,14290C,14766T,15043A,15326G,15758G,15924G,16129A,16223T,16391A,16519C	none
77	T1a1	73G,152C,195C,263G,309.1C,309.2C,315.1C,524.1A,524.2C,709A,750G,1438G,1888A,2706G,4216C,4769G,4917G,7028T,8697A,8860G,9899C,10463C,11251G,11719A,12633A,13368A,14766T,14905A,15326G,15452A,15607G,15928A,16126C,16163G,16186T,16189C,16294T,16519C	none
97	V7	72A,93G,263G,309.1C,315.1C,750G,1438G,2706G,4580A,4769G,5054A,7028T,7444A,8860G,15326G,15904T,16298C	none
234	L2a1a2	73G,146C,152C,195C,263G,309.1C,309.2C,315.1C,750G,769A,1018A,1438G,2416C,2706G,2789T,3594T,3918A,4048A,4104G,4769G,5285G,7028T,7175C,7256T,7274T,7521A,7771G,8206A,8701G,8860G,9221G,9540C,10115C,10398G,10873C,11719A,11914A,11944C,12693G,12705T,13590A,13650T,14566G,14766T,15244G,15301A,15326G,15629C,15784C,16223T,16278T,16286T,16294T,16309G,16390A,16519C	T8908C 10.16 C16286C 6.39
235	L1c1d1	73G,151T,152C,182T,186A,189C,195C,198T,247A,263G,297G,309.1C,315.1C,316A,523del,524del,750G,769A,825A,1018A,1438G,2395del,2706G,2758A,2885C,3594T,3666A,3796T,3843G,4104G,4500C,4769G,5108C,5460A,5951G,6071C,7028T,7055G,7146G,7256T,7389C,7521A,7948T,8027A,8468T,8655T,8701G,8860G,9072G,9540C,10321C,10398G,10586A,10688A,10810C,10873C,11719A,11899C,11914A,11984C,12705T,12810G,13105G,13485G,13506T,13650T,13789C,14000A,14148G,14178C,14560A,14766T,14911T,15301A,15326G,15626T,16038G,16108T,16129A,16187T,16189C,16223T,16278T,16284G,16293G,16294T,16311C,16360T,16519C	C16108C 35.84
296	H1a3	56.1C,73G,263G,309.1C,309.2C,315.1C,750G,1438G,3010A,4769G,7444A,8860G,11242T,14560A,15326G,15757G,16051G,16162G,16288C	T16288T 23.84 T16519C 20.12
307	L2a1a2a1a	73G,146C,152C,195C,263G,315.1C,750G,769A,1018A,1438G,2416C,2706G,2789T,3594T,3918A,4104G,4769G,5285G,7028T,7175C,7256T,7274T,7521A,7771G,8206A,8701G,8860G,9211T,9221G,9540C,10115C,10398G,10454C,10873C,11719A,11914A,11944C,12693G,12705T,13590A,13650T,14566G,14766T,15211T,15244G,15301A,15326G,15421G,15629C,15784C,16092C,16223T,16278T,16286T,16294T,16309G,16390A,16519C	C16286C 11.83
343	A2	73G,146C,152C,153G,235G,263G,315.1C,523del,524del,663G,750G,1438G,1736G,2706G,4248C,4769G,4824G,7028T,8027A,8794T,8860G,11009C,11719A,12007A,12705T,14766T,15032T,15326G,16111T,16223T,16290T,16319A,16362C,16519C	none
351	B2r	73G,152C,189G,200G,263G,309.1C,315.1C,499A,750G,827G,960.1C,1438G,2706G,2833G,3547G,4769G,4820A,4977C,5492C,5899del,6473T,6752G,7028T,8281del,8282del,8283del,8284del,8285del,8286del,8287del,8288del,8289del,8860G,9950C,11177T,11719A,12372A,12904G,13590A,14374C,14766T,15326G,15535T,16183C,16189C,16217C,16278T,16456A,16519C	none
399	A2g1	64T,73G,146C,153G,235G,263G,309.1C,315.1C,523del,524del,663G,750G,1438G,1736G,2706G,4248C,4769G,4824G,4970G,7028T,7724T,8027A,8794T,8860G,11719A,12007A,12705T,13855T,14766T,15326G,16111T,16223T,16290T,16319A,16362C,16391A	none
433	T2	73G,146C,263G,309.1C,315.1C,709A,750G,1438G,1888A,2706G,4216C,4769G,4917G,7028T,8697A,8860G,10463C,11251G,11719A,11812G,13368A,14233G,14766T,14905A,15326G,15452A,15607G,15928A,16126C,16294T,16296T,16519C	T152C 11.5
445	X2b+22+16192	73G,153G,195C,225A,226C,263G,524.1A,524.2C,750G,1438G,1719A,2706G,4769G,6221C,6371T,7028T,7052G,8393T,8860G,11719A,12705T,13198A,13708A,13966G,14470C,14766T,15326G,15927A,16189C,16192T,16223T,16265G,16278T,16519C	16265A 47.02

471	L2a1c3b1	73G,146C,195C,263G,309.1C,315.1C,750G,769A,1018A,1438G,2416C,2706G,2789T,3010A,3594T,4104G,4769G,6663G,7028T,7175C,7256T,7274T,7521A,7771G,8206A,8701G,8860G,9221G,9540C,9824C,9932A,10115C,10398G,10410C,10873C,11719A,11914A,11944C,12693G,12705T,13203G,13590A,13650T,14566G,14766T,15301A,15326G,15784C,15924G,16093C,16148T,16223T,16278T,16294T,16355T,16390A,16519C	none
484	J1c3	73G,185A,263G,295T,309.1C,315.1C,462T,489C,750G,1438G,2706G,3010A,4216C,4769G,5530T,7028T,7855T,8860G,10398G,11251G,11719A,12063T,12612G,13708A,13934T,14766T,14798C,15326G,15452A,16069T,16126C	none
489	H3g1	152C,263G,315.1C,750G,1438G,3992T,4418C,4769G,6776C,7967T,8860G,10235C,10754C,15326G,16223T,16325C,16519C	none
516	H4a1a1a2	73G,228T,263G,309.1C,315.1C,523del,524del,750G,1438G,3992T,4024G,4688C,4769G,5004C,5618C,8185C,8269A,8348G,8860G,9123A,10044G,11173T,13545T,14325C,14365T,14582G,15326G	none
585	H7a1	263G,309.1C,315.1C,750G,1438G,1719A,4769G,4793G,8860G,12063T,15326G,16261T,16519C	T152C 9,16
614	H4a1a1a	73G,263G,309.1C,315.1C,523del,524del,750G,1438G,3992T,4024G,4769G,5004C,8269A,8860G,9123A,10044G,14365T,14582G,15326G	A215G 29.56
787	B2o	73G,159C,263G,315.1C,499A,750G,827G,1438G,2706G,2804G,3547G,4769G,4820A,4977C,6473T,6647C,7028T,8281del,8282del,8283del,8284del,8285del,8286del,8287del,8288del,8289del,8292A,8860G,9950C,11177T,11719A,13590A,13879A,14766T,15326G,15535T,16092C,16182C,16183C,16189C,16217C,16519C	none
832	L1c2b1a'b	73G,150T,151T,152C,182T,186A,189C,195C,198T,247A,263G,297G,315.1C,316A,750G,769A,825A,1018A,1438G,2220G,2395del,2706G,2758A,2885C,3591A,3594T,3666A,4104G,4769G,5495C,5899.1C,5951G,6071C,6150A,6253C,7028T,7055G,7064C,7076G,7146G,7256T,7337A,7389C,7521A,8027A,8468T,8655T,8701G,8784G,8860G,8877C,9072G,9540C,9861C,10031C,10321C,10398G,10586A,10589A,10688A,10792G,10793T,10810C,10873C,11164G,11654G,11719A,12049T,12477C,12705T,12810G,13105G,13149G,13485G,13506T,13650T,13789C,14000A,14178C,14560A,14766T,14911T,15067C,15326G,16129A,16166G,16187T,16189C,16223T,16230G,16265C,16278T,16284G,16286A,16294T,16311C,16519C,16527T	none
885	D1	73G,263G,315.1C,489C,750G,1438G,2092T,2706G,3010A,3816G,4659A,4769G,4883T,5178A,7028T,8414T,8701G,8860G,9540C,10398G,10400T,10873C,11719A,12705T,12771A,13320T,14668T,14766T,14783C,15043A,15217A,15301A,15326G,16223T,16325C,16362C	none
886	A2+(64)+16129	64T,73G,146C,153G,235G,263G,309.1C,315.1C,499A,523del,524del,663G,750G,1438G,1736G,2706G,4248C,4310G,4769G,4824G,6249A,7028T,8027A,8794T,8860G,10045C,10373A,11719A,12007A,12705T,14766T,15326G,16111T,16129A,16223T,16290T,16319A,16354T,16362C,16519C	T16093C 25.94
918	A2ap	64T,73G,146C,153G,235G,263G,309.2CC,315.1C,523del,524del,663G,750G,1438G,1736G,2706G,4248C,4769G,4824G,7028T,8027A,8794T,8860G,9809G,11719A,12007A,12705T,14766T,15326G,16111T,16189C,16223T,16290T,16319A,16362C	none
1219	D6a1a	73G,263G,315.1C,489C,709A,750G,1438G,1719A,2706G,3714G,4769G,4883T,5178A,6701G,7028T,7424G,7879G,8020A,8618C,8701G,8860G,8895C,9540C,10398G,10400T,10873C,11719A,12654G,12705T,13194A,14766T,14783C,15043A,15301A,15326G,15553A,16182C,16183C,16189C,16223T,16274A,16362C	none
1282	D1	5C,61T,73G,131C,146C,263G,309.1C,309.2C,315.1C,489C,524.1A,524.2C,750G,1438G,2092T,2706G,3010A,4769G,4883T,5178A,7028T,8414T,8775T,8860G,9540C,10398G,10400T,10873C,11719A,11830C,12705T,14668T,14766T,14783C,15043A,15301A,15326G,15924G,16223T,16325C,16362C	none
1355	R11	73G,185A,189G,263G,309.1C,315.1C,709A,750G,1438G,2706G,4706G,4769G,5186C,5301G,6338G,7028T,8860G,9071T,10031C,10398G,10978G,11061T,11719A,12358G,12950G,13681G,14696G,14766T,15326G,16183C,16189C,16311C,16519C	none

Table S3. List of biological mixture contributors with haplogrep2 generated haplogroup and GM HTS generated haplotype and heteroplasmy information. Heteroplasmy is presented as rCRS nucleotide-nucleotide position-alternative nucleotide- frequency (%).

Biological Mixtures Contributor ID	Haplogroup	Haplotype	Heteroplasmy
1J	J1c8a	A73G,G185A,G228A,A263G,C295T,C315insC,C462T,T489C,C524insAC,A750G,A1438G,A2706G,G3010A,T4216C,A4769G,C7028T,A8860G,T10084C,A11251G,G11719A,A12612G,G13708A,C14766T,T14798C,A15326G,C15452A,C16069T,T16126C,G16319A,T16368C	none
2K	K1a1b2a1a	A73G,T152C,A263G,C315insC,C497T,C524insAC,A750G,C770T,T1189C,A1438G,A1811G,A2706G,A3480G,T3777C,A4769G,C7028T,T7278C,A7729G,A8860G,G9055A,T9698C,T9800C,A10398G,A10550G,A11053G,T11299C,A11467G,G11719A,G11914A,A12308G,G12372A,T13326C,C14167T,C14766T,T14798C,A15326G,A15758G,A15924G,T16093C,T16224C,T16311C,T16519C	16093 11.77
3K	K2a	A73G,T146C,T152C,A263G,C315insC,G709A,A750G,A1438G,A1811G,A2706G,A3480G,T4561C,A4769G,C7028T,A8860G,G9055A,T9698C,T9716C,A10550G,T11299C,A11467G,G11719A,A12308G,G12372A,C14167T,C14766T,T14798C,A15326G,T16224C,T16311C,T16519C	234G 7.53 7050G 34.5
4D	D4e2	A73G,A263G,C315insC,T489C,A523del,C524del,A750G,A1438G,A2706G,G3010A,A4769G,C4883T,C5178A,C7028T,C8414T,A8701G,A8860G,T9540C,A10398G,C10400T,T10873C,C11215T,G11719A,C12705T,C14668T,C14766T,T14783C,G15043A,G15301A,A15326G,A15874G,C16223T,T16362C	none
5U	U5a1a1	A73G,A263G,C309insC,C315insC,A750G,A1438G,T1700C,A2706G,T3197C,A4769G,T5495C,T6351C,C7028T,A8860G,G9477A,A11467G,G11719A,A12308G,G12372A,T13617C,C14766T,A14793G,A15218G,A15326G,A15924G,C16256T,C16270T,A16399G	251A 3.23 6351T 41.12
6J	J1c2c2	A73G,T146C,G185A,A188G,G228A,A263G,C295T,C315insC,C462T,T489C,A750G,A1438G,A2706G,G3010A,T4216C,A4769G,C7028T,A8860G,G8865A,A10398G,G10685A,A11251G,G11719A,A12612G,T13281C,G13708A,A13933G,C14766T,T14798C,A15326G,C15452A,C16069T,T16126C,T16519C	16286T 15.0
7D	D4b2a1	A73G,A263G,C280T,C315insC,T489C,A523del,C524del,A750G,A1382C,A1438G,C1662T,A2706G,G3010A,A4769G,C4883T,C5178A,C7028T,G8020A,C8414T,A8701G,A8860G,C8964T,T9540C,T9824A,A10398G,C10400T,T10873C,G11719A,C12705T,G13708A,C14668T,C14766T,T14783C,G15043A,G15301A,A15326G,A15524G,C16223T,C16355T,T16362C	200G 4.66 4883C 2.42
8J	J1c4	A73G,G185A,A263G,C295T,C315insC,C462T,T489C,A750G,A1438G,A2706G,G3010A,T4216C,A4769G,A6503G,C7028T,A7271G,A8860G,A9632G,A10398G,A11251G,G11719A,T12083G,A12612G,T13641C,G13708A,C14766T,T14798C,A15326G,C15452A,C16069T,T16126C	none
9A	A2ac1	A73G,T146C,A153G,A235G,A263G,C309insC,C315insC,A523del,C524del,A663G,A750G,A1438G,A1736G,A2706G,T3083C,T4248C,A4769G,A4824G,C7028T,G8027A,C8794T,A8860G,G9055A,A9377G,A9473C,G11719A,G12007A,C12705T,A14687G,C14766T,T15074C,A15326G,C16111T,G16213A,C16223T,C16290T,G16319A,T16362C	none
10U	U5a1a2a1	A73G,A263G,C309insC,C315insC,C573insCC,A750G,A1438G,T1700C,A2706G,T3197C,A4769G,A5319G,T6293C,A6629G,T6719C,C7028T,A8860G,G9477A,T11152C,A11467G,G11719A,A12308G,C12346T,G12372A,T13617C,C14766T,A14793G,A15218G,A15326G,C16256T,C16270T,A16399G	none
11A	A2k1a	C64T,A73G,T146C,A153G,A235G,A263G,C309insC,C315insC,A523del,C524del,A663G,A750G,A1438G,A1736G,A2706G,T3202C,T4248C,A4769G,A4824G,C7028T,G8027A,A8460G,C8794T,A8860G,G11719A,G12007A,C12705T,C14766T,A15326G,A15924G,C16111T,C16223T,C16290T,G16319A,T16362C	none

Table S4. List of biological mixtures. A.) two-person mixtures; B.) three-person mixtures. Both tables list contributor ID, contributor haplogroup, the number of unique and shared haplogroup defining SNPs, and our determination of whether the mixture was considered to contain similar or dissimilar haplotypes.

A.)

Contributor 1	Contributor 1 Haplogroup (Haplogrep2)	Contributor 2	Contributor 2 Haplogroup (Haplogrep2)	Unique Haplogroup Defining SNPs	Shared Haplogroup Defining SNPs	Percent Shared Haplogroup Defining SNPs	Similar (S) or Dissimilar (D) Haplotypes
4D	D4e2	7D	D4b2a1	10	10	50.00	S
5U	U5a1a1	10U	U5a1a2a1	10	12	54.55	S
1J	J1c8a	6J	J1c2c2	11	14	56.00	S
6J	J1c2c2	8J	J1c4	11	14	56.00	S
1J	J1c8a	8J	J1c4	9	13	59.09	S
9A	A2ac1	11A	A2k1a	10	14	58.33	S
9A	A2ac1	10U	U5a1a2a1	39	0	0.00	D
5U	U5a1a1	7D	D4b2a1	32	0	0.00	D
7D	D4b2a1	10U	U5a1a2a1	38	0	0.00	D

B.)

Contributor 1	Contributor 1 Haplogroup (Haplogrep2)	Contributor 2	Contributor 2 Haplogroup (Haplogrep2)	Contributor 3	Contributor 3 Haplogroup (Haplogrep2)	Unique Haplogroup Defining SNPs	Shared Haplogroup Defining SNPs	Percent Shared Across All Contributors Haplogroup Defining SNPs	Similar (S) or Dissimilar (D) Haplotypes
3K	K2a	10U	U5a1a2a1	2K	K1a1b2a1a	32	14	30.43	S
10U	U5a1a2a1	2K	K1a1b2a1a	5U	U5a1a1	30	13	30.23	S
1J	J1c8a	6J	J1c2c2	8J	J1c4	12	15	55.56	S
4D	D4e2	5U	U5a1a1	9A	A2ac1	45	1	2.17	D
9A	A2ac1	10U	U5a1a2a1	4D	D4e2	50	1	1.96	D

Figure S1. Screen shot images of the MixtureAce MT™ user-friendly interface. A. Sample identification and run status, B. Data type selection, C. Data file upload, D. Advanced options, E. Contributor detection options.

A.

MixtureAce MT Live - Deconvolving mtDNA Mixtures by Expectation Maximization

MixtureAce MT Live is a program for forensic analysis of mitochondrial samples that have been target sequenced using commercial forensic kits. MixtureAce MT Live utilizes phylogenetically aware artificial intelligence to determine the identity and proportions of the haplogroups and the specific haplotypes of contributors present in a mixed sample.

MixtureAce MT Live Results

Run Type	File1	File2	Status	Start Date	End Date		
Paired End FastQ	20_S9_L001_R1_001.fastq.gz	20_S9_L001_R2_001.fastq.gz	Complete	7/21/2022 1:11:51 PM	8/1/2022 10:13:44 PM	View Results	Delete
Single Direction FastQ	mix1.fastq		Complete	4/25/2022 9:31:39 PM	4/26/2022 1:33:41 PM	View Results	Delete
BAM	InputBAM.bam		Complete	3/30/2022 12:34:22 PM	3/30/2022 7:03:11 PM	View Results	Delete
Paired End FastQ	45_S5_L001_R1_001.fastq.gz	45_S5_L001_R2_001.fastq.gz	Complete	3/19/2022 12:35:49 PM	3/21/2022 12:44:20 AM	View Results	Delete
Paired End FastQ	45_S5_L001_R1_001.fastq.gz	45_S5_L001_R2_001.fastq.gz	Complete	3/19/2022 12:24:08 PM	3/20/2022 6:23:18 AM	View Results	Delete
Paired End FastQ	248_S2_L001_R1_001.fastq.gz	248_S2_L001_R2_001.fastq.gz	Complete	3/18/2022 6:37:45 PM	3/19/2022 2:05:14 AM	View Results	Delete
Paired End FastQ	248_S2_L001_R1_001.fastq.gz	248_S2_L001_R2_001.fastq.gz	Complete	3/18/2022 6:35:25 PM	3/19/2022 12:42:06 AM	View Results	Delete
Paired End FastQ	248_S2_L001_R1_001.fastq.gz	248_S2_L001_R2_001.fastq.gz	Complete	3/15/2022 9:47:53 PM	3/16/2022 7:40:18 AM	View Results	Delete
Paired End FastQ	28_S3_L001_R1_001.fastq.gz	28_S3_L001_R2_001.fastq.gz	Complete	3/15/2022 3:47:10 PM	3/15/2022 8:16:21 PM	View Results	Delete
Paired End FastQ	20_S9_L001_R1_001.fastq.gz	20_S9_L001_R2_001.fastq.gz	Complete	3/14/2022 2:13:31 PM	3/14/2022 6:24:39 PM	View Results	Delete
Paired End FastQ	20_S9_L001_R1_001.fastq	20_S9_L001_R2_001.fastq	Complete	3/10/2022 7:06:23 PM	3/10/2022 10:20:15 PM	View Results	Delete
Paired End FastQ	776_S13_L001_R1_001.fastq.gz	776_S13_L001_R2_001.fastq.gz	Complete	3/7/2022 12:30:10 PM	3/8/2022 2:10:38 AM	View Results	Delete
Paired End FastQ	776_S13_L001_R1_001.fastq.gz	776_S13_L001_R2_001.fastq.gz	Complete	3/7/2022 12:29:38 PM	3/7/2022 5:20:03 PM	View Results	Delete
Paired End FastQ	776_S13_L001_R1_001.fastq.gz	776_S13_L001_R2_001.fastq.gz	Complete	3/7/2022 12:29:04 PM	3/7/2022 5:21:42 PM	View Results	Delete
Paired End FastQ	sup_worm_dnc30_R1.fastq	sup_worm_dnc30_R2.fastq	Complete	12/28/2021 7:40:00 AM	12/29/2021 6:25:16 AM	View Results	Delete

Create new job

Refresh

B.

MixtureAce MT Live - Deconvolving mtDNA Mixtures by Expectation Maximization

MixtureAce MT Live is a program for forensic analysis of mitochondrial samples that have been target sequenced using commercial forensic kits. MixtureAce MT Live utilizes phylogenetically aware artificial intelligence to determine the identity and proportions of the haplogroups and the specific haplotypes of contributors present in a mixed sample.

Email:

Input data type:

Show Advanced Options	Reset Options	Submit	Display Previous Results
-----------------------	---------------	--------	--------------------------



C.

MixtureAce MT Live - Deconvolving mtDNA Mixtures by Expectation Maximization

MixtureAce MT Live is a program for forensic analysis of mitochondrial samples that have been target sequenced using commercial forensic kits. MixtureAce MT Live utilizes phylogenetically aware artificial intelligence to determine the identity and proportions of the haplogroups and the specific haplotypes of contributors present in a mixed sample.

Email:

Input data type:

FastQ 1: Sample_RX34_R1.fastq

FastQ 2: Sample_RX34_R2.fastq ☒ Seq error correction?

Use subset of reads?: ☐ Max Total Reads Max % Read

Show Advanced Options	Reset Options	Submit	Display Previous Results
-----------------------	---------------	--------	--------------------------



D.

Advanced Options

Basic options

Specify a reference sequence. The reference sequence must match the variants contained in the Phylotree input to avoid unexpected behavior.

Specify a Phylotree to use.

Customization options

Use the haplotypes described in the specified file along with the haplogroups from Phylotree. A haplotype file consists of lines representing haplotypes. Each line contains a distinct haplotype identifier, a tab character, and a comma-separated list of variants in the form [Ancestral/Reference Base][position][Derived/Variant Base] Positions that do not appear in the variant list are assumed to contain the reference base and positions that have been excluded from analysis are not used. Variants that appear at novel positions (i.e., no known variants in Phylotree) can be used, but it is assumed that all Phylotree haplogroups carry the reference base. Custom Haplotypes File: No file chosen

Excluded Ranges: Specify a comma-separated list of 1-based positions or 'start-end' ranges to be excluded from consideration.

Ignore Phylotree haplogroups without IDs: ☐ By default, a placeholder name is generated for these haplogroups using the parent haplogroup's ID and an integer number (e.g., **H1[2]** is a unnamed subgroup of haplogroup **H1**).

Ignore sites with variants listed as unstable in Phylotree: ☐

Quality filters

These options provide basic filtering of mapped sequences and base observations.

Ignore alignments with mapping quality less than this value.

Ignore bases with base quality scores less than this value.

Expectation-maximization

Options for setting the parameters used during the expectation-maximization step where the mixture proportions are inferred. The default values should work well most of the time, but adjusting these values may be useful in some situations.

Use this value to seed the random number generator that generates starting mixture proportions. Allows MixtureAce MT Live to be run multiple times using the same input and produce the same results each time. If unset, the starting mixture proportions will differ with each run.

Use parameter ALPHA to initialize haplogroup contributions from Dirichlet distribution.

Stop EM iteration when absolute difference between current and previous contribution estimates is less than this value.

Maximum of number of EM iterations to run.

Run EM until convergence multiple times and report the results averaged over all runs.

E.

Contributor detection options

Once the mixture proportions have been inferred, two filtering steps are applied to narrow the field of contributing to haplotypes to only the strongest candidates. First, we examine the read/haplogroup probabilities to find the haplogroup associated with the highest probability for each read. Haplogroups that have no or little read support are removed from consideration. Second, using the haplogroups that pass the previous filter, we verify that the variants that define each contributor are in fact present in the mixture. This step removes haplotype signals that are most likely driven by one or two private mutations.

Skip contributor detection step and use the specified comma-separated list of haplogroups instead.	
Haplogroup must have N reads to be considered a contributor. This value should be adjusted when coverage is high to avoid signals caused by sequencing errors and when coverage is low and allelic dropout may be likely.	10
Variant base must be found in n reads to be considered as present in sample. This value should be above the expected number of base errors given the sequence coverage.	3
Variant base must be found in fraction F of reads to be considered as present in sample. A minimum of reads can be set when this is low or can be low.	0.02
Fraction of unique defining variants that must be observed to call a haplogroup present. This value should be adjusted based on the likelihood of allelic dropout and the number of variant differences between contributors.	0.5
Call haplogroup a contributor if it has at least n unique variants observed in the sample, regardless of total number of defining variants. Use when allelic dropout is likely.	0
Disable requirement that the majority of contributors' unique defining variants are present in the sample. Use when coverage is very low and dropout is likely.	<input type="checkbox"/>
Skip contribution estimate refinement and report proportions from initial EM run.	<input type="checkbox"/>

Assembly options

Minimum odds ratio (probability between best and second best haplogroup) required to assign read to a contributor.	2
Attempt to extend haplotype assemblies iteratively by identifying novel variants from contributor consensus sequences assigning reads based off of them.	<input type="checkbox"/>
When extending assemblies, set the depth of coverage required to call a base for a contributor.	2

F.

MixtureKit RT-Live - Deconvolving mtDNA Mixtures by Expectation Maximization

MixtureKit RT-Live is a program for the analysis of individual samples that have been mixed together using commercial devices. MixtureKit RT-Live utilizes probabilistic models and artificial intelligence to determine the identity and proportions of the haplogroups and the specific haplogroups of contributors present in a mixed sample.

Host:

Panel 1: