

marker	P1
DYS456	17
DYS390	24
DYS389/II	29
DYS389/I	13
DYS458	17
DYS19	14
DYS385	11,14
GATA	12
DYS437	15
DYS438	12
DYS448	19
DYS393	13
DYS391	12
DYS439	12
DYS635	21
DYS392	13

Table S1. Y-STR typing results of sample P1 (Baron Revolt)

tella).

marker	RF2	LF2	Consensus D.P.R.	P1
D3S1358	16,17	16,17	16*,17*	16*,17*
TH01	8,9,3	8,9,3	8,9,3*	9,3,9,3*
D21S11	31,31	31,31	31,31*	29,31*
D18S51	14,15	14,15	14,15*	15,15*
D10S1248	13,16	13,16	13,16*	14,16*
D1S1656	14,15	14,15	14*,15	12,14*
D2S1338	17,20	17,17	/	17,20
D16S539	nt	11,12	/	11,13
D22S1045	16,16	16,16	16,16*	15,16*
VWA	16,17	16,17	16*,17	16*,18
D8S1179	14,15	14,15	14,15*	12,15*
FGA	25,25	20,25	/	21,25
D2S441	11,3,14	11,3,14	11,3,14*	14,14*
D12S391	17,18	18,20	/	17,20
D19S433	nt	12,13	/	12,14
SE33	28.2,28.2	17,28.8	/	17,31.2

Table S2. Autosomal
the consensus profile

al STR typing results of samples RF2, LF2 and P1. The alleles shared between
e of D.P.R. (Baron's mother) and P1 (Baron Revoltella) are shown by *.

sample	mapped reads	% on target	mean depth	uniformity
RF2	323,958	95.16%	2,400	67.53%
LF2_1	631,610	94.04%	4,786	69.31%
LF2_2	650,350	94.71%	4,935	70.40%
NEC	65,062	72.19%	49	3.87%

Table S3. Main sequencing parameters of libraries RF2, LF2_1, LF2_2 and the negative control (NEC) built with Precision ID Identity Panel.

extraction

Locus	RF2	LF2_1	LF2_2
rs1005533	AG	AG	AG
rs10092491	CC	CC	CC
rs1015250	GG	GG	GG
rs1024116	CC	CC	CC
rs1028528	AA	AA	AA
rs1031825	AC	AC	AC
rs10488710	CG	CG	CG
rs10495407	AG	AG	AG
rs1058083	AA	AA	AA
rs10773760	AG	AG	AG
rs10776839	TT	TT	TT
rs1109037	GG	GG	GG
rs12997453	AG	NN	NN
rs13218440	GG	GG	GG
rs1335873	AA	AA	AA
rs1355366	CT	CT	CT
rs1357617	AT	AT	AT
rs1360288	CC	CC	CC
rs1382387	AA	AA	AA
rs1413212	CT	CC	CC
rs1454361	TT	TT	TT
rs1463729	CT	CT	CT
rs1490413	GG	GG	GG
rs1493232	AC	AC	AC
rs1498553	TT	TT	TT
rs1523537	CT	CT	CT
rs1528460	CT	CT	CT
rs159606	AG	AG	AG
rs1736442	CT	TT	TT
rs1821380	CG	CG	CG
rs1872575	GG	GG	GG
rs1886510	AA	AA	AA
rs1979255	CG	CG	CG
rs2016276	TT	TT	TT
rs2040411	AA	AA	AA
rs2046361	AT	TT	TT
rs2056277	TT	CT	CT
rs2076848	AA	AA	AA
rs2111980	CC	CC	CC
rs214955	CT	CT	CT
rs221956	CT	CT	CT
rs2269355	CC	CC	CC
rs2292972	CT	CT	CT
rs2342747	GG	GG	GG
rs251934	GG	GG	GG
rs2830795	AA	AA	AA

rs2831700	AA	AA	AA
rs321198	TT	TT	TT
rs338882	AG	AG	AG
rs354439	TT	TT	TT
rs3780962	GG	GG	GG
rs4288409	AC	AC	AC
rs430046	CC	CC	CC
rs4364205	GT	GT	GT
rs445251	CG	CG	CG
rs4530059	GG	GG	GG
rs4847034	AG	AG	AG
rs560681	AG	AA	AA
rs576261	AA	AA	AA
rs6444724	CT	CT	CT
rs6811238	GG	GG	GG
rs6955448	CT	CT	CT
rs7041158	CC	CC	CC
rs717302	GG	GG	GG
rs719366	AG	AG	AG
rs722098	AA	AA	AA
rs722290	GG	CG	CG
rs727811	GT	GT	GT
rs729172	GG	GG	GG
rs733164	AG	AA	AA
rs735155	CT	CT	CT
rs737681	CT	CT	CT
rs740598	AG	AG	AG
rs740910	AG	AG	AG
rs7520386	GG	GG	AG
rs7704770	AA	AA	AA
rs826472	TT	TT	TT
rs873196	TT	TT	TT
rs876724	CC	CC	CC
rs891700	AG	AG	AG
rs901398	CT	CT	CT
rs907100	CG	CG	CG
rs914165	AG	AG	AG
rs917118	CT	CT	CT
rs938283	CT	TT	TT
rs964681	CT	TT	TT
rs987640	TT	TT	TT
rs9905977	AG	AG	AG
rs993934	AG	GG	GG
rs9951171	AA	AA	AA

Consensus D.P.R.	P1	match
AG	GG	yes
CC	CC	yes
GG	GG	yes
CC	CC	yes
AA	AA	yes
AC	AC	yes
CG	CG	yes
AG	GG	yes
AA	AG	yes
AG	AG	yes
TT	GT	yes
GG	GG	yes
n.r.	AG	inc.
GG	AG	yes
AA	AA	yes
CT	TT	yes
AT	TT	yes
CC	CT	yes
AA	AA	yes
n.r.	CC	inc.
TT	AT	yes
CT	CT	yes
GG	GG	yes
AC	AC	yes
TT	CT	yes
CT	CT	yes
CT	CT	yes
AG	GG	yes
n.r.	TT	inc.
CG	CG	yes
GG	GG	yes
AA	AA	yes
CG	GG	yes
TT	TT	yes
AA	AG	yes
n.r.	TT	inc.
CT	CC	yes
AA	AA	yes
CC	CT	yes
CT	CC	yes
CT	TT	yes
CC	CC	yes
CT	TT	yes
GG	AG	yes
GG	AG	yes
AA	AG	yes

Table S4. SNP typin sharing between the inconclusive.

AA	AG	yes
TT	CT	yes
AG	AG	yes
TT	AT	yes
GG	GG	yes
AC	CC	yes
CC	CC	yes
GT	GT	yes
CG	CC	yes
GG	AG	yes
AG	AA	yes
n.r.	AA	inc.
AA	AA	yes
CT	TT	yes
GG	GT	yes
CT	TT	yes
CC	CT	yes
GG	AG	yes
AG	AA	yes
AA	AA	yes
CG	CC	yes
GT	GT	yes
GG	GG	yes
n.r.	AG	inc.
CT	CT	yes
CT	CT	yes
AG	AA	yes
AG	AA	yes
n.r.	AG	inc.
AA	AG	yes
TT	CT	yes
TT	CT	yes
CC	CC	yes
AG	GG	yes
CT	CC	yes
CG	CG	yes
AG	AG	yes
CT	CT	yes
n.r.	TT	inc.
n.r.	CT	inc.
TT	TT	yes
AG	GG	yes
n.r.	AG	inc.
AA	AG	yes

ng results of libraries RF2, LF2_1, LF2_2. Column G (match) indicate the allele
consensus profile of D.P.R. (Baron's mother) and sample P1. n.r.: no result; inc:

Marker	typing
rs2534636	C
rs35284970	C
rs9786184	A
rs9786139	G
rs16981290	C
rs17250845	G
rs372687543	T
P256	G
rs369616152	T
rs17306671	T
rs4141886	A
rs2032595	T
rs2032599	T
rs20320	G
rs2032602	T
rs8179021	C
rs2032624	C
rs2032636	G
rs9341278	G
rs2032658	G
rs2319818	G
rs17269816	C
rs17222573	A
rs372157627	C
rs3848982	C
rs3900	G
rs3911	A
rs2032631	A
rs2032673	T
rs2032652	T
rs16980426	T
rs13447443	A
rs17842518	G
rs2033003	C

Table S5. Y-SNP typing of sample P1 (obtained by Precisio

n ID Identity Panel).

sample	mapped reads	% on target	mean depth	uniformity
P1	26,769	98.46	2,019	82.03
P2	45,897	99.48	3,823	74.39
LF2	88,565	99.30	7,389	88.61

Table S6. Main sequencing parameters of libraries P1, P2 and LF2 built with the mtDNA Control Region Panel.

ie Precision ID

Method	Sample	Mitochondrial Position								hg
		HVR II					HVR III	HVR I		
PCR-CE (Sanger)	RF2	72C	263G	309.1C*	309.2C**	315.1C*	NS		16298C	HV0
	P1	72C	263G	309.1C*	309.2C**	315.1C*	NS		16298C	HV0
PCR-MPS	LF2	72C	263G	309.1C*		315.1C*	508G	16168Y	16298C	V18
	P1	72C	263G	309.1C*		315.1C*	508G		16298C	V18
	P2	72C	263G	309.1C*		315.1C*	508G		16298C	V18

Table S7. Mitochondrial typing of samples P1, P2, LF2 and RF2. Length Heteroplasmy: dominant variant (*), visible variant (**); NS: not sequenced.