

Supplementary Table S1

mtDNA combined HVS1 and 2 and partial information on 3 SNPs from the mtDNA coding region in Gaspesian populations

Haplogroup	Haplotype	14766	7028	12308	Acadians (n=99)	French Canadians (n=104)	Channel Islanders (n=92)	Loyalists (n=91)	Gaspesians (n=388)
A	64,73,94,146,153,235,263,315.1,16111,16223,16290,16319,16325,16343,16362	T				1			1
A	64,73,94,146,153,235,263,315.1,16111,16223,16290,16319,16325,16362	T					3	1	4
C	73,150,152,249DELA,263,290DELA,291DELA,309.1,315.1,16223,16298,16325,16327	T			1	11	12	4	28
D	73,213,240,263,309.1,315.1,16223,16325,16362	T					2	1	3
D	73,213,263,309.1,315.1,16223,16325,16362	T				1			1
H	315.1	C	C		2				2
H	107,257,263,309.1,315.1,16183C,16189,16249,16362	C	C		1				1
H	107,257,263,309.2,315.1,16183C,16189,16249,16362	C	C		1				1
H	107,257,263,315.1,16183C,16189,16249,16362	C	C		2				2
H	111,263,309.1,315.1	C	C		3	2	1		6
H	111,263,309.2,315.1	C	C		1				1
H	131,195,263,315.1,16183C,16189	C	C					1	1
H	131,195,263,315.1,16189	C	C					1	1
H	146,195,263,315.1	C	C				1	4	5
H	146,263,309.1,315.1	C	C					1	1
H	146,263,309.1,315.1,16270	C	C		1				1
H	146,263,309.2,315.1,16264	C	C				1		1
H	146,263,309.2,315.1,16270	C	C					1	1

H	146,263,309.2,315.1,16302,16304	C	C				1		1
H	146,263,315.1,16129	C	C				1		1
H	150,263,309.1,315.1,16216,16311	C	C			1	1		2
H	150,263,309.2,315.1	C	C					2	2
H	150,263,315.1,16216,16311	C	C			1	1		2
H	151,263,315.1,16311	C	C		2	1			3
HV	152,263,309.1,315.1	C	T				2		2
HV	152,263,309.1,315.1,16186,16311	C	T					1	1
HV	152,263,309.1,315.1,16221,16291	C	T		1			1	2
H	152,263,309.1,315.1,16239G,16256,16311	C	C		1		1		2
H	152,263,309.1,315.1,16248,16354	C	C			1			1
H	152,263,309.1,315.1,16249	C	C			1		1	2
HV	152,263,309.2,315.1,16186,16311	C	T					1	1
HV	152,263,315.1,16221,16291	C	T		1				1
H	173,239,263,315.1,16188,16362	C	C					1	1
H	182,263,309.1,315.1	C	C		1				1
H	183,263,309.2,315.1,16302	C	C			1			1
H	194,263,309.1,315.1,16354	C	C		1				1
H	195,207,263,315.1,16293,16311	C	C				1		1
H	195,263,309.1,315.1	C	C		1				1
H	195,263,309.1,315.1,16092,16140,16293,16311	C	C					1	1
H	195,263,315.1	C	C					1	1
H	195,263,315.1,16286G	C	C			1	1	2	4
H	239,263,309.1,315.1,16129,16291,16362	C	C			1			1
H	239,263,309.1,315.1,16249,16362	C	C					2	4
H	239,263,309.1,315.1,16362	C	C		1				1
H	239,263,315.1,16362	C	C					1	1
H	263,291.1,315.1	C	C				3		3
H	263,309.1,315.1	C	C		11	4	2	2	19
HV	263,309.1,315.1	C	T		1				1
H	263,309.1,315.1,16093,16221	C	C					1	1
H	263,309.1,315.1,16093,16304,16352	C	C				2		2

H	263,309.1,315.1,16183C,16189	C	C			2			2	
H	263,309.1,315.1,16234	C	C				1		1	
H	263,309.1,315.1,16235	C	C					3	3	
H	263,309.1,315.1,16235,16291	C	C				1		1	
H	263,309.1,315.1,16239	C	C			1			1	
H	263,309.1,315.1,16261	C	C				1		1	
H	263,309.1,315.1,16269,16288	C	C					1	1	
H	263,309.1,315.1,16302	C	C					1	1	
H	263,309.1,315.1,16311	C	C			1			1	
HV	263,309.1,315.1,16311	C	T			1			1	
H	263,309.1,315.1,16362	C	C			3	1	1	5	
H	263,309.2,315.1	C	C			3	1		4	
H	263,309.2,315.1,16189	C	C					1	1	
H	263,309.2,315.1,16189,16356	C	C				1		1	
H	263,309.2,315.1,16304	C	C				1		1	
H	263,309.2,315.1,16319	C	C			1			1	
H	263,309.2,315.1,16362	C	C			1			1	
H	263,315.1	C	C			9	5	3	5	22
H	263,315.1,16093,16223	C	C			6	1			8
H	263,315.1,16093,16223,16311	C	C			2	2			4
H	263,315.1,16093,16311	C	C			8				8
H	263,315.1,16129	C	C			1				1
H	263,315.1,16148	C	C						2	2
H	263,315.1,16176,16311	C	C					3		3
H	263,315.1,16189	C	C				2			2
H	263,315.1,16189,16261,16362	C	C				1			1
H	263,315.1,16189,16356	C	C						1	1
H	263,315.1,16234	C	C				4	5	1	10
H	263,315.1,16263	C	C					1		1
H	263,315.1,16267	C	C			5	1			6
H	263,315.1,16291	C	C						1	1
H	263,315.1,16304	C	C						1	1

H	263,315.1,16304,16362	C	C			1	1	1	3
H	315.1,16195	C	C				1	2	3
H	64,152,263,309.2,315.1,16126	C	C		1				1
H	72,263,309.1,315.1	C	C					1	1
H	73,152,263,315.1,16162,16209	C	C				2		2
H	73,263,315.1,16311	C	C					1	1
H	73,263,315.1,16162,16209	C	C					1	1
H	73,263,315.1,16183C,16189	C	C				1		1
H	93,263,309.1,315.1	C	C		1				1
H	93,263,315.1,16184,16284	C	C				1		1
I	73,152,199,204,207,239,250,263,309.1,315.1,16086,16129,16223,16319	T						1	1
I	73,152,199,204,207,250,263,309.1,315.1,16129,16223	T				1			1
I	73,152,199,204,207,250,263,315.1,16129,16223	T				1			1
I	73,152,199,204,207,250,263,315.1,16129,16223,16248	T				2	3		5
I	73,199,203,204,250,263,309.1,315.1,16129,16172,16223,16311	T						3	3
J	73,146,185,228,263,295,315.1,16069,16092,16126,16261	T					1	1	2
J	73,150,152,195,215,263,295,310.1,315.1,319,16069,16126,16145,16231,16261	T						1	1
J	73,150,152,195,215,263,295,310.1,315.1,321,16069,16126,16145,16231,16261	T						1	1
J	73,150,152,263,295,309.1,315.1,16069,16126,16193,16278	T			1				1
J	73,150,185,228,263,295,309.1,315.1,16069,16126,16213,16261	T				1		1	2
J	73,152,185,228,263,295,309.1,315.1,16069,16126	T						1	1
J	73,152,185,228,263,295,315.1,16069,16126	T					1		1
J	73,185,188,228,263,295,309.1,315.1,16069,16126,16163	T						1	1
J	73,185,188,228,263,295,309.1,315.1,16069,16126,16266	T						1	1
J	73,185,228,263,295,16069,16126	T				1			1
J	73,185,228,263,295,315.1,16069,16126	T				2			2
J	73,185,228,263,295,315.1,16069,16126,16319	T						1	1
J	73,185,263,295,309.1,315.1,16069,16126	T					1		1
J	73,185,263,295,315.1,16069,16126	T				1	1		2
J	73,228,263,295,309.1,315.1,16069,16126	T			1				1
J	73,263,295,315.1,16069,16126	T			1				1
J	73,263,295,315.1,16069,16126,16145,16222,16261	T					2		2

K	73,146,152,263,315.1,16189,16224,16311,16320	T		G		1			1
K	73,146,152,263,315.1,16224,16311	T		G			1		1
K	73,146,152,263,315.1,16224,16311,16320	T		G			1		1
K	73,146,263,315.1,16224,16245,16311	T		G				2	2
K	73,146,263,315.1,16224,16311	T		G				1	1
K	73,195,263,309.1,315.1, 16093, 16224, 16311	T		G		1			1
K	73,195,263,315.1,16093,16126,16224,16311	T		G				4	4
K	73,195,263,315.1,16093,16224,16291,16311	T		G				1	1
K	73,195,263,315.1,16093,16224,16311	T		G				1	1
K	73,195,263,315.1,16187,16224,16311	T		G			1		1
K	73,263,309.1,315.1,16224,16311	T		G	1	1	1		3
K	73,263,309.2,315.1,16224,16311	T		G		1			1
K	73,263,315.1,16093,16224,16311	T		G				1	1
K	73,263,315.1,16224,16265C,16311	T		G		1			1
N1b1	73,152,263,309.1,315.1,16145,16176G,16223	T				1	1		2
T	72,73,217Y,263,309.1,315.1,16126,16294,16325	T					1		1
T	72,73,263,309.1,315.1,16126,16294,16325	T				4	3		7
T	73,150,263,309.1,315.1,16126,16153,16207T,16294	T						1	1
T	73,150,263,309.1,315.1,16126,16294,16296,16304	T					1		1
T	73,151,263,309.1,315.1,16126,16294,16296,16304	T			1	5	2		8
T	73,152,195,263,309.1,315.1,16126,16163,16186,16189,16294	T			1				1
T	73,152,195,263,309.1,315.1,16126,16163,16186,16189,16294,16354	T				2	1		3
T	73,152,195,263,315.1,16126,16163,16186,16189,16234,16294	T					1	1	2
T	73,152,263,309.1,315.1,16126,16189,16294,16296	T					1		1
T	73,152,263,309.1,315.1,16126,16278,16294,16296,16304,16362	T				1			1
T	73,198,263,309.1,315.1,16126,16294,16304	T						1	1
T	73,263,309.1,315.1,16126,16183C,16189,16294,16296	T				1			1
T	73,263,309.1,315.1,16126,16239,16294,16296,16304	T			2				2
T	73,263,309.1,315.1,16126,16294	T			1	1			2
T	73,263,315.1,16126,16239,16294,16296,16304	T			1				1
T	73,263,315.1,16126,16294,16296,16304	T				1			1
T	73,263,315.1,16126,16294,16304	T				1			1

Source : Moreau C, Vézina H, Yotova V, Hamon R, de Knijff P, Sinnett D and Labuda D. Genetic Heterogeneity in Regional Populations of Quebec - Parental Lineages in the Gaspé Peninsula. *Am J Phys Anthropol.* 2009; 139(4):512-22.