

# SNP genotypes around the *SHOX* gene of the Xp/Yp pseudoautosomal region

**Table 1: 99 unrelated UK Caucasian semen donors**  
(NOTE: donors 1-50 have been used for the MHC projects)

All SNPs were discovered by resequencing semen donors 1, 2, 4, 5, 6, 7, & 86. Each SNP is classified by type:

- \* CTi: transition at a CpG doublet
- \* Ti: non-CpG transition
- \* Tv: transversion
- \* ID: indel

The location of each SNP is given relative to Genbank entry U82668. Genotypes of each SNP were established by ASO hybridisation of genomic PCR products and are given as single allele letters for homozygotes and **H** for heterozygotes. Uncertain genotypes are marked "?" and undetermined genotypes indicated with a dot.

SNP	location	type	1-10	11-20	21-30	31-40	41-50	51-60	61-70	71-80	81-90	91-99
+6/597C/T	4557	CTi	CCCCC <b>H</b> CHH	TCCCCCCCC	CCCC <b>H</b> CCCC	TCCC <b>HHH</b> CCH	CCCC <b>T</b> CC <b>H</b> CC	C <b>H</b> CC <b>H</b> CTCC	HCC <b>CH</b> HCCCC	CCCCCCCC <b>H</b> C	C <b>H</b> CCCCC <b>H</b>	CCCCCCCC <b>H</b>
+6/1323C/G	5880	Tv	GGGGG <b>H</b> GHG	GGGGGGGGG	GGGGGGGGG	GGGG <b>H</b> GGGG	GGGG <b>H</b> GGGG	G <b>H</b> GGGGGGG	GGGG <b>H</b> GGGG	GGGGGGGGG	GGGGGGGGG	GGGGGGGG <b>H</b>
+4/165A/G	36312	CTi	AHAGAA <b>HHHH</b>	GHG <b>AA</b> HHHH	HA <b>AAAA</b> AAH	HA <b>H</b> GGGA <b>HH</b>	A <b>HA</b> HHH <b>AA</b> HG	A <b>H</b> GA <b>HH</b> A <b>HA</b>	HA <b>AA</b> HHHH <b>GA</b>	HA <b>HHH</b> A <b>AAA</b>	HAG <b>GA</b> HH <b>HA</b> H	HAG <b>AA</b> HH <b>HA</b>
+4/223C/G	36370	Tv	<b>H</b> GH <b>G</b> CH <b>GH</b>	GHG <b>HH</b> CH <b>GH</b>	H <b>C</b> GH <b>HH</b> CH <b>C</b> G	H <b>CG</b> GH <b>G</b> GH <b>H</b>	H <b>H</b> GH <b>HHH</b> CH <b>G</b>	H <b>GG</b> H <b>CH</b> HH <b>HH</b>	H <b>G</b> HH <b>HHH</b> HH <b>C</b>	H <b>HHH</b> GH <b>G</b> CC	H <b>CG</b> GH <b>HHH</b>	GH <b>G</b> CC <b>GH</b> HH

+4/375C/T	36522	CTi	CCCCTHCHCH	CCCCHCCHCC	CHCHCCCCHC	CCCCCCCCHC	CHCHCCCCHC	CCCCHHCCCC	CCCCHHHCCC	CHCCCCCCCC	CTCCHCCHCH	CHCHCCCHC
+4/500L3/4	36649	ID	H3H34H3H3H	3H3HHHH33H	343H3HH?43	H333333H3H	??3HH3H33	H3334HH34H	333H3HHH3H	3HHH3H3H33	3433433HH3	3H3HH3HHH
+4/1063C/G	37210	Tv	HHHGGHHGHG	HHGGHGHHGH	HGCHHCCHGH	GGHGGGGHHG	HGCHGGHGGH	HGGHGGGHCG	GCHGGGGGGG	GHHGCCCHGG	GGGHGGHGHG	HHHHHHGHG
+701C/T	42851	CTi	HCCHHHCCHC	CHCHHHCCCC	CHCCCCHHCC	CCCCCHCHCC	CCCCHHCCCC	HCCCTCHCHC	CCCCCHHCHH	CCCCHHHCC	HCCCCCCCCC	CCHCHCHCH
+876A/G	43026	Ti	HGGHHAGGHG	GHGHHAGGGG	GHGGGAAGG	G?GGHHGHGG	GGGGHHHGGG	HGGHAGHGHG	GGHGGHHGHA	GHGGGHHAHG	HHGGGGGGGG	HGHGAGHGH
+1096A/G	43246	Ti	HGGHHHGGHG	GHGHHHGGGG	GHGGGGHHGG	GGGGGHGHGG	GGGGHHGGGG	HGGGAGHGHG	GGGGHHHGH	GGGGHHHGG	HGGGGGGGGG	GGHGHHGHG
+2190C/T	44340	CTi	HCCHHHTCCHC	CHCHHCCCCH	CHCCCCCHCC	CCCCHHCHCC	CCCCHHHCCC	HCCHTCHCHC	CCHHCHHCHT	CHHCCTHHHC	HHCCCCCCCC	HCHCHCHCH
+2378C/T	44528	CTi	TTTTHTTTTT	CHTTTTHTTH	CTHHHTTHT	TTTTTTHHCH	TTHHTTHTH	HTHTTTTTHH	TCTHTTTTT	HTHTCTTTHH	THCHTHCHHH	HHHHHHHT
+2784A/G	44934	Ti	GGGGHHGGG	GGGGHGGGG	GGGGGHGGG	GAGGGGGGGG	GGGGGGGGGG	GGGGGGGGGG	HGGGGHGGGH	GGGGGGGHG	GGGGGGGGH	GGHHGGGHG
+2900A/G	45050	Ti	HGGHHHGGHG	GHGHAHGGGG	GHGGGGHGG	GGGGHHGHGG	GGGGHHAGGG	HGGGAGHGHG	GGGHGGHGH	GGHGGHHHGH	HHGGGGGGGG	GGGGHGHGH
+3571C/T	45721	CTi	CHTHCCHHHH	CCHHCCCTHC	CHHHHHHCHT	TCTTHHHCCH	TTHHHHCCHH	CHTCCTHCC	HCHCTCHTHC	HHCTCCHCCC	HCCCTHCCCT	CHCCCHCCH
+3837C/T	45987	CTi	CCCCCHCCC	CCCCCHCCCC	CCCCCHHCC	CTCCCCCCCC	CCCCCCCCCC	CCCCCCCCCC	HCCCCCCCCC	CCCCCCCCCC	CCCCCCCCCC	CCCHCCCHC
+3955A/G	46105	Ti	AHGHHAHHHH	AAHHAAGGA	AHHHHHHAGG	GAGGHHAH	GGHHHAAGH	AHGHAGHHAH	HAGHGAHGH	HGAGAHHAAA	HAAAGHAAAG	HHAHHHAH
+3983A/G	46133	CTi	GHAAHHGHGH	GGHHGGGAHG	GHHHGHGAA	AGAAHHHGGH	AAHHHHGGHH	GHAGGAHGGH	HGHGAGHAHG	HHGAGGHGGG	HGGGAHGGGA	GHGGHHGGH
+3990A/T	46140	Tv	AHTHHAHHHH	AAHHAATHA	AHHHAHHATT	TATTHHHAH	TTHHHHAHH	AHTAATHAAH	HAHATAHTHA	HHATAAHAAA	HAAATHAAAT	AHAAHHAAH
+5053C/G	47203	Tv	HCHGCCHHGH	CCCCHHHGH	CCHHCHCCGC	CCCHCCHHCC	CHCCHHHHHC	HCCCCHCCH	CCCCHCCH	CCCCHHCHC	CCCCHCCHCC	CGHHHHCCC
+5683C/T	47833	Ti	THHCHHTTCC	THC?THCHTT	HTTHCCHCTH	TT?T?CTTT?	TTTTCHHCTH	HCTHTHTHTH	CHHTCTHTHC	CHHHCHHTHH	TCTHHHHHCT	HTHHHHHHH
+6085C/T	48235	Ti	HHHCCCCCCC	HCHHCHCCCC	CTHCCTCHCT	HCHTHCTCHH	???HCCCHCCH	HC?CCHCHCT	CHCCCCCHC	HHCHHHCCCC	CCCCCHHCC	TCCCCCHC
+6139A/G	48289	CTi	GGHHGGHGAH	HHAHAGHAG	GAAGAAGGGG	GHGGGAHHH	GHGGGHHHHA	HHHGGGHHHA	HAAGGHHHHH	GAGHHHHHAG	HGHGGGAHHG	AHHHHAGH
+6195C/T	48345	Ti	CCHHHCHCHH	CCCCCCCCHC	CCCHHCHHHC	CCCCCHCCCH	CCCCHHCCCC	CHCCCCHCCH	HCHCHCHCCC	CCHCCCCCTH	CHCCCCCHCC	CCCHHCCCH
+6211C/T	48361	Ti	CCCCCHCCC	CCCCCCCCHC	CCCCCHCCH	CCHCHCCCC	CHCCCCCH	CCCCCCCCHC	CCHHCCCC	CCCCCHCCC	CCCCCCCCCC	CCHCCCCC
+6236C/G	48386	Tv	CHHHCCCCCC	CCCCHCCHHC	CCHCHCHCGH	CHHCHCCCC	HHHHCHGHHC	CCCCGCHCC	CHCGCHCHC	CHCHCHCHCH	CCCCHCGCHC	CGHCHCCC
+6260A/C	48410	Tv	CCHHCCCCHC	CHCCHCAHHC	CCHCHCCCHC	CCCCCCCCCC	CHCCCCHHHC	CCCCCCCCCC	CHCCCCCCCC	CHCHCCCCCC	CCCCCHCHC	CHCCHCCCH

+6485A/C	48625	Tv	AHCCCCHAHC	CAC?HHACCH	HCCHCCCHCCH	CCHHCCHCCC	CHCHCCCCC	CCHACHHCCC	CHCCCCHCCH	CCHCCHHCC	CCCACACCC	CCHHCCHHC
+6630G/T	48770	Tv	TTTTHHTTTT	HTHHTTTTTH	TTTTHTTTTT	HTTTTHTTTT	TTTTTTTTTT	HTTTTTTTHH	TTTTTTTTTT	THHHTTTTTT	THHTGTTTTT	TTTTTHTTT
+7445C/G	49585	Tv	CHCCCCCCCC	CCCCCCCCHC	CCCCCHCCH	CHHCCCCCCC	CCCHCCHCCH	CCCCCHCCHC	CCCHCCHCCC	CCCHCCHCCC	CCCCCHCCHC	CCCCCCCC
+7982A/C	50132	Tv	AHHAAAAAAA	AAAAAAHA	AAAAAAHAH	AHHHAAAAHA	HAHAHAHA	AAAAHAHA	AHACAAHA	AAHAHAHA	HAAHAHAHA	AAAAAAAH
+8965C/G	51115	Tv	GGGGHGGGG	GGHHGHGGH	GHHGHGCGH	HHHGHCCHH	GGGGHGHGH	GGCGGGGH	HGHGGGHGH	HGGGHGHGH	HGHGGGHGH	CHHHHCGHG
+9177C/T	51327	CTi	CHCCCCCCCC	CCCCC?C?C	CCCHCCHCC	CHCCCCCCC	CCCHCCHC	CCCCCHCCC	CCCHCCHCCC	CCHCCHCCH	CCCCCHCCH	CCCCCCCC
+9595C/T	51745	CTi	CCTHCHCCH	CCHHCCHTC	HCHCTHCTH	CCHCCHHC	THHCTHCH	CTCCHCTCH	HHHHTCHHC	HHCTCCCTC	HHCCCCHHH	CHCCCCCH
+9697G/T	51847	Tv	GHGGHGGGH	HGHGHGGT	GTHGHHTGH	HTHGHTHH	GGHHGHHT	GGTGGGHGH	HGHGHGHGH	HHHGHGHGH	HGHGHGHGH	THHHTGHG
+3/341A/T	61494	Tv	HHH?HTTTT	HTHHTHTHT	HATHTTTTT	HHTTTTAAAT	HHTHHHTHT	THHTTTTTT	HHHATHHHH	AHHHTHTHT	AATHTHTTT	HHHTTATHT
+3/663C/G	61817	Tv	CHGCGHHHH	HCCHHHHGCC	HHGHGHGCC	CCCCGHCHH	HCHCHHHCG	CHCCCH?HCH	HHCHCHCCC	HHCHHHH?H	CCCCHCHGH	HHCHCCHC
+3/849C/T	62003	CTi	TTTTHHHTT	TTHTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT
+3/1035A/G	62189	Ti	GHA?HHGHG	GGGGHGGGG	HGAGAGGGG	GGGAHGH	HGHHHHHGG	GGGGH?GGG	HHGHGHGGG	HGGHGGHGH	GHGHGGHHH	HGGGG?GG
+3/1239C/G	62393	Tv	GHG?HGHGH	HCHGHGGHC	HGGGGHGGH	?HCHHGGGH	GCHHGGHGH	CHHGH?GH	??HGHGHGH	GGH?HGHGG	HHCGHGGH	??HHC?HHH
+3/1248A/G	62401	CTi	GAGGHAHAH	HAHGHGHHA	AGHGAHAHA	GHAHAHGH	GAHAHGAH	AHHHHGHGH	GHHGHGHGH	HGHGAGAGG	HHAHAHAH	GGHAGAHA
+35/1652C/G	62931	Tv	HHCCCHHH	HGHCHCGGG	HCHCHHGH	HHGHCHCC	HGHCHCHGH	GHHHHCHH	HHHHHCGH	CCHCHCCH	HHHHGGHH	HHHGHCH
+35/2287A/G	63568	CTi	HHHHCHCCH	CCCCCACCC	CCCCACCC	CHHCHHHH	HCHHCHACCA	HCCCCCHCC	CCCCHHHCC	CCCHACHC	CHCHCHCH	HHCCCHCC
+35/2637A/G	63917	CTi	HHHAAGHH	GHAGAGGGG	HAGAGHGH	GHAAHGH	GHGHAGAG	HGHHAHAH	AGAGHHGH	AHHGAHGA	AHHHHHGH	HGHGHGA
+35/3390C/G	64671	Tv	GGGGGCGGG	HGGGHGCGH	GGGHGGCGG	HCGGGHGGG	CGGGGCGGH	GGGGGCGG	GGHHGG?GG	GGGG?GGH	GGGHGGHGH	GGHGC
+35/4673A/G	65954	Ti	GHGHAHGH	HAAHGHGH	AAHAG?GAG	HGGAAGHHA	GHAHGHGH	AAHAGHGH	AAHAG?AA	HHHGAHGA	HAAG?HGH	AHGHAGAA
+35/6219C/T	67500	Ti	HHHTHTHT	TTTCCHTTH	TTCTCCCT??	HTHTT?HHH	HTHTHTCTH	HHHTCHHHH	CCTHTTTTH	HTHTHTHT	H?HCHCTT	HHTHTCTH
+35/6445C/T	67725	CTi	HTHTHTHT	TTTTCHHTT	TTTTHTHT	HTHTHTTT	HHTHTCTH	TTTTHTTT	HCTHTHTH	TTTTTTTT	HTTTTTHT	TTTTCTT
+35/6978A/G	68259	Ti	HAHAHAHA	AAAGAAAH	AAHAHHAA	AAAAAAHA	AAAAAAHA	AAAAHHHA	HAAAAAAH	HAHAHAHA	AAHGAHHA	AHAHAHA
+5/507A/G	69507	Ti	GGGGHGGGH	GGGAGGGH	GGHGAGGH	HGGGGHGH	HGHGGGH	HHGHGHGG	HGHGGGH	GGGHGHGG	GHHGHGHGG	HHGGHGH

+5/772G/T 69772 Tv GGGGGHGGG HGGGGHGHG GHHHGGTHG HHGGHGHG HTGGHGGH GHHGGGGHGG GGCHGGHHGG GGGHGGGHGG GHHHGHGHTGH GGHTHGGGH

+5/934A/C 69935 Tv HCAHCHAHCA HCCAAHACA CCAHAAAH HHHCHAAA AHHAACAA HHCHAHHAH AACAHHAHA HCHAHHHHC HHAACAACA AAHHACHH

+35/375A/G 71375 CTi GGGGAHGGH HGHGGGAGG HGGHHGHGG GGGAGHGHG GGGGHGHGG GGGGGHGGG HAHGGGGHH HGGGGHGGG GGGGHGGH GHHGGGGG

+35/520C/T 71520 Ti TTTTCHHTH HTHHTTCTT HTTHHTHTT TTTCTHTHT TTTHTHTT TTTTHTTT HCHTTTTTH HTTTHTTT THTTHTHT TTTTTTTT

+35/801C/T 71801 CTi CCCCCHHCH HCHCCHCC HCHCCHCC CCCCCCCC CCCCCHCCC CCCCCCCC HCCCCCCC HCCCCCHC CCCCCCHC CHCCCCC

+35/939A/G 71939 CTi GGGHAGGAG HAHGGHGHG GAHHGGAGH AAHHGGGG GGGGHGHGG GHAAHGHHA HHHHHGHGG GAGHHHAGA HHHHGHGGH GAHHHAH

+35/151A/G 72151 CTi GGGGGHGHG HGHGGGHGG HGGGGGGH GGGGGHGG GGGGHGGGG GGGGGHGGG HHGGGGGGH HGGGGGGH GGGGGGGH GHHGGGGG

+35/329A/G 72329 CTi HHGHGGHHG GGGAAHGGG GGGHGGHG GHGGHGHG AAHGGHGGH GHGGGGGGG GGGHAGGH GGHGGGGH GGHGHAGA GGGGHGHG

+7/1400C/T 78440 CTi CCCTHTHTT HHTTHCHCH HHTHTTTTH CTCTHHCH CHCTTHHCH H?TTTCHC HHTHTHTHC TTHCCTCH CHCCHHHH THHTHTT

+7/1593C/T 78633 CTi CHCCHCCCC CCCCCCCCC CCCCCCCCC CCCCCCCCC CCCCCCCCC CCCCCCCCC CCCCCCCCC CCCCCCCCC CCCCCCCCC CCCCCCCCC

+7/1985A/G 79025 Ti GGGHAGGG GGHHHGGG GHGGHGGG GGGHGGHG GGGGGHGG GGHGGGGG GHGHGGGG HHGGGGGG GGGGHGGG GHGGHGH

**Table 2: 40 unrelated Saami (see Sajantila et al 1995)**

SNP	location	type	S1-10	S11-20	S21-30	S31-40
+6/597C/T	4557	CTi	.....	.....	.....	.....
+6/1323C/G	5880	Tv	.....	.....	.....	.....
+4/165A/G	36312	CTi	.....	.....	.....	.....
+4/223C/G	36370	Tv	.....	.....	.....	.....
+4/375C/T	36522	CTi	.....	.....	.....	.....
+4/500L3/4	36649	ID	.....	.....	.....	.....

+4/1063C/G	37210	Tv	.....	.....	.....	.....
+701C/T	42851	CTi	CCHHCCCCC	HCCHHCHCCT	??HHCC?HCC	CCCCC?HCC
+876A/G	43026	Ti	HGHHGGGGG	HGHHGHGGA	??AAGG?HHH	GGGGHG?HHG
+1096A/G	43246	Ti	GGHHGGGGG	HGGA?GA??A	??HHGG?AGG	GG?GGG?H??
+2190C/T	44340	CTi	?CHHCCCCC	HCCHHC????	H?HTCC?HCC	CHHCCC?H??
+2378C/T	44528	CTi	HHTHHHCTT	HTHTHTCCT	HTTTHH?THH	HTHTHCTH?C
+2784A/G	44934	Ti	?HGGGGGGHG	GHHGHGGGGH	GAAGGGGGHH	GGGGHHHGGG
+2900A/G	45050	Ti	?GHHGGGGHG	HGHHGGGGHG	H?GHGGGGHG	GGGGGGHHHG
+3571C/T	45721	CTi	HCCCCHCCT	CHHCCHHCC	CTHCCCCHHH	CHHTHCTCCH
+3837C/T	45987	CTi	CHCCCCCHC	CHCCCCCCC	CCCCCCCCC	CCCCCCCCC
+3955A/G	46105	Ti	HAAAAAAAAHG	AAAAAAAAAH	AGHHHHHHH	HGHGAGAAH
+3983A/G	46133	CTi	HGHHHHGHGA	GHHHHHGGH	GAHHHHHHH	HAAHAGAGGH
+3990A/T	46140	Tv	HAAAAAAAAHT	AAAAAAAAAH	ATHHHHHHH	HTHTATAAH
+5053C/G	47203	Tv	CCCCGCHCC	HCCHCCCCC	CCCCHHCCCH	HGCHCCCHC
+5683C/T	47833	Ti	HHHCCHCT	THCCHCTTH	HCHHTTTC	HHCCCTCCT
+6085C/T	48235	Ti	HCHCCHCCC	CCHCCCHCH	CTHTTHTHH	HTCTHCTCCH
+6139A/G	48289	CTi	HGHG?HHGGG	GHHGGHHHG	GAHHAAHHH	HAAHAGAGGH
+6195C/T	48345	Ti	CHHCCHCC	CHCCCCCCC	CCCCCCCCC	CCHCCCCC
+6211C/T	48361	Ti	CCCCCCCCC	HCCCCCCCC	CCCCCCCCC	CCCCCCCCC
+6236C/G	48386	Tv	CCCHCCCCCH	HCCCHCCCC	CCCCCCCCC	CCCCCCCCC
+6260A/C	48410	Tv	.....	.....	.....	.....
+6485A/C	48625	Tv	AAAAAAAAHH	HCAHHHCHAA	AAACHHCHAA	AHHHAAAHAA
+6630G/T	48770	Tv	?GGGGGGGGG	GGGGG????	??GGGG?GGG	?GGGG????

+7445C/G	49585	Tv	CCCHCCCCC	HCCCCCCCC	CCCCCCCCC	CCCCCCCCC
+7982A/C	50132	Tv	AAAHAAAAAH	HAAAHAAAA	AAAAAAAAA	AAAAAAAAA
+8965C/G	51115	Tv	HHGGGGGGHG	GCGHGHCHGG	HHGCHHHHGH	HHGHGGGHGG
+9177C/T	51327	CTi	CCCHCCCCC	HCCCCCCCC	CCCCCCCCC	CCCCCCCCC
+9595C/T	51745	CTi	HCHCHCCCCH	CCCHHCCCCH	HHCCCCHCCH	?CHCCCCC
+9697G/T	51847	Tv	HHGHGGGGHG	HHG?GHTHGG	HHGTHHHHGH	GHHGGGGHG?
+3/341A/T	61494	Tv	.....	.....	.....	.....
+3/663C/G	61817	Tv	.....	.....	.....	.....
+3/849C/T	62003	CTi	.....	.....	.....	.....
+3/1035A/G	62189	Ti	.....	.....	.....	.....
+3/1239C/G	62393	Tv	.....	.....	.....	.....
+3/1248A/G	62401	CTi	.....	.....	.....	.....
+35/1652C/G	62931	Tv	.....	.....	.....	.....
+35/2287A/G	63568	CTi	.....	.....	.....	.....
+35/2637A/G	63917	CTi	.....	.....	.....	.....
+35/3390C/G	64671	Tv	.....	.....	.....	.....
+35/4673A/G	65954	Ti	.....	.....	.....	.....
+35/6219C/T	67500	Ti	.....	.....	.....	.....
+35/6445C/T	67725	CTi	.....	.....	.....	.....
+35/6978A/G	68259	Ti	.....	.....	.....	.....
+5/507A/G	69507	Ti	.....	.....	.....	.....
+5/772G/T	69772	Tv	.....	.....	.....	.....
+5/934A/C	69935	Tv	.....	.....	.....	.....

+35/375A/G	71375	CTi	.....	.....	.....	.....
+35/520C/T	71520	Ti	.....	.....	.....	.....
+35/801C/T	71801	CTi	.....	.....	.....	.....
+35/939A/G	71939	CTi	.....	.....	.....	.....
+35/151A/G	72151	CTi	.....	.....	.....	.....
+35/329A/G	72329	CTi	.....	.....	.....	.....
+7/1400C/T	78440	CTi	.....	.....	.....	.....
+7/1593C/T	78633	CTi	.....	.....	.....	.....
+7/1985A/G	79025	Ti	.....	.....	.....	.....

**Table 3: 35 Vlax Romani (Kalderas and Lom gypsies - see Kalaydjieva et al 2001)**

SNP	location	type	B1-10	B11-20	B21-30	B31-35
+6/597C/T	4557	CTi	CHCHHCHHH	HCCHCCCC	CHCCHTCCHH	HCCTC
+6/1323C/G	5880	Tv	GGGGGGHHG	GGGGHGGGG	GGGGHGGGG	GGGGG
+4/165A/G	36312	CTi	AAAAHHAHGH	AAAAGHHAH	AAHAAGAAHH	AAHHH
+4/223C/G	36370	Tv	HCHCHGCHGH	CHCHGHGCC	CCHCC?HGHH	HHCHH
+4/375C/T	36522	CTi	HCCHHCCHCH	HCHCCHCTCC	TCCCCCCCC	CCTCC
+4/500L3/4	36649	ID	H4H4H34H3H	4H4H3H3H4H	4H344HH3HH	HH4HH
+4/1063C/G	37210	Tv	HGHGCCGGGG	GHGGGGGGGG	GGGGGHCGG	HHGGG

+701C/T	42851	CTi	HCCCCCCHCH	HCCCHHHHCC	THTCCHCCCH	CCTCC
+876A/G	43026	Ti	HGGGHGGHHA	?GGHHAAGH	AAAH?HGGGH	GGAGG
+1096A/G	43246	Ti	HGGGGGGHGH	HGGHGHGGGG	AHAGGHGGGH	GGAGG
+2190C/T	44340	CTi	HCCCCHCCHT	HCCCHTTHCH	THTCCHCCCH	CCTCC
+2378C/T	44528	CTi	HTTHHHTTTT	TTHTTTTTTT	TTTTTTHCTT	THTTH
+2784A/G	44934	Ti	GHGHGGAGGG	HHHGGGGGAG	GGGGHGGGHG	HGGHG
+2900A/G	45050	Ti	HGGGHGGHHA	HGGHHAAGH	AGAGGHGGGH	GHAGG
+3571C/T	45721	CTi	CHTCCCHCCH	CHCHCCCHCH	CHCTHHHHHC	HCCHH
+3837C/T	45987	CTi	CCCCCCCCC	CCCCCCCCC	CCCCCCCCC	CCCCC
+3955A/G	46105	Ti	HH?AAHAAHA	A?AHAAAH	AGAG??HHHA	HAAHH
+3983A/G	46133	CTi	HHAGGHGGHG	GHGHGGGGH	GHGAHHHHHG	HGGHH
+3990A/T	46140	Tv	HH?AAHAAHA	A?AHAAAH	AHAT??HHHA	HAAHH
+5053C/G	47203	Tv	HHHHCCHCHC	HHCHCCCCCH	CHHCHHHCHH	HHCHC
+5683C/T	47833	Ti	HCTHHCCHCH	HHHCHHTCH	TCHTHHHHHT	HHCHC
+6085C/T	48235	Ti	HHHHHTTHT	TTHCTHHHTH	HTCCHHCTTC	HTTTH
+6139A/G	48289	CTi	HGHHAAHHAA	HHHHHHHHAH	HANHHAGANH	HHAHA
+6195C/T	48345	Ti	CCCCCCCCC	CCCCCCCCC	CCCCCCHCC	CCCCC
+6211C/T	48361	Ti	HCCCCCCCC	CCHCCCCC	CCCCHCCCC	CCCCC
+6236C/G	48386	Tv	HCCCCCCHC	CCHCCCCC	CCHHCHHCHG	HCCCC
+6260A/C	48410	Tv	CCCCCCHC	CCCCCCCC	CCHCCHHCHH	HCCCH
+6485A/C	48625	Tv	CCHCCCCC	CCCHHHHCH	CCHCCCHCHC	CCCCH
+6630G/T	48770	Tv	.....	.....	.....	.....
+7445C/G	49585	Tv	HCC?CHCCCC	?CHHCCGCC	CCHHC?CCCG	?CCCC

+7982A/C	50132	Tv	HAAAAAAAAA AAHAAAAAAAA AAACHAAAAH ?AAAA
+8965C/G	51115	Tv	GHHCCCHHGG HCGHHHHGGG GCGGHGGCHG HHGCG
+9177C/T	51327	CTi	HCCCCCCCC CCHCCCCCCC CCHCCCCCH CHCCC
+9595C/T	51745	CTi	HHHCCCCHH HCCCHHHCH TCHHTTCCH ?CCCH
+9697G/T	51847	Tv	HHHTHTHHGG HHHHHHHGGG GTGHHGGHHH THTG
+3/341A/T	61494	Tv	TAHHAAAAHT HHTAHAHTTH HATHHHHAAT HTTAT
+3/663C/G	61817	Tv	HHCHHGHHHH CCHHGCHCGH CHHCCCCHHG CGGHG
+3/849C/T	62003	CTi	TTTTHTTTTT TTTTTTTTTT TTTTT?TTTT TTTTC
+3/1035A/G	62189	Ti	GHGGGAGHGG GHHHHGHGGG GGHGGGGHGA GGGHG
+3/1239C/G	62393	Tv	HGHGGGHHHC HHCCHGCCCH HHHGGHHHGG HCGCG
+3/1248A/G	62401	CTi	HHHGGHHAHA HAAHAGHAAH HHAGGHHAGH HHAHH
+35/1652C/G	62931	Tv	.....
+35/2287A/G	63568	CTi	.....
+35/2637A/G	63917	CTi	.....
+35/3390C/G	64671	Tv	.....
+35/4673A/G	65954	Ti	.....
+35/6219C/T	67500	Ti	.....
+35/6445C/T	67725	CTi	.....
+35/6978A/G	68259	Ti	.....
+5/507A/G	69507	Ti	HGHGHGHHHH GGHHAHGGA HHGGG?HHGG GGAHH
+5/772G/T	69772	Tv	GGHH?HHHHH GTHHTHHHTH GGGGG?GTGG GTTGG
+5/934A/C	69935	Tv	ACAHHAAAAA HAAAAHAAA AHHCC?HACC HAAHH
+35/375A/G	71375	CTi	.....

+35/520C/T	71520	Ti	.....
+35/801C/T	71801	CTi	.....
+35/939A/G	71939	CTi	.....
+35/151A/G	72151	CTi	.....
+35/329A/G	72329	CTi	.....
+7/1400C/T	78440	CTi	.....
+7/1593C/T	78633	CTi	.....
+7/1985A/G	79025	Ti	.....

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**References:**

- Kalaydjieva *et al* (2001) *European Journal of Human Genetics* **9**: 97-104.
- Sajantila *et al* (1995) *Genome Research* **5**: 42-52.