

# **Genetic structure of Indian Jewish Diaspora and their genetic affinity with rest of the Jews from the world**

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***By***

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## **Contributions of the Authors:**

**Manvendra Singh- Performed Experiments, Data collection, data analysis and paper writing.**

Mini kariappa- Provided the Jews samples

Lalji Singh and Kumarasamy Thangaraj- sample collections, and correspondent of the paper.

## **Abstract:**

India is known for its highest level of human genetic diversity. India is inhabited by several indigenous populations and there have been several historic migrations into India. Jews are one of the recent migrants and they are inhabited in various parts of India. There have been several views about the arrival of Jews in India. One of the evidence suggests that traders from Judea had arrived to Cochin in 562 BC, another evidences suggest that additional Jews came to India as exiles from Israel after the destruction of second temple. Other view is that some of the paradise Jews, descendent of Sephardic, came to Calicut when they were expelled from Spain in 1492.

The Jews belong to 12 tribes-each a descendent of one of the 12 sons of Jacob. A few years ago a research was made in Israel for members of the 12 tribes but only descendents of 4 were found. We are still looking for the lost 8. Christianity came to Kerala long before they went to Europe; there is a chance that Syrian Christians of Kerala can be among the lost tribes.

We have analyzed the HVS and few coding regions of mtDNA of 275 samples and Y chromosomal SNPs from non coding region of 175 individuals of Jews population inhabited in Kerala, India. We have observed the mitochondrial haplogroups B, D, F, G, H, HV, J, K, M, Q, R, U, V, W and Z; suggesting that Jews from Kerala are exceptionally diverse population with high level of genetic admixture with local and non local populations. Y-Chromosomal haplogroups have limited and defined haplogroups. About 30% of Jews consists of haplogroups which are specific to East European Ashkenazims and about 40% are Indian specific, moreover the rest is either East Asian or containing new sub haplogroups. Our observation is extremely interesting, as the Jews from other part of world are highly endogamous and show high level of bottleneck; whereas the Kerala Jews are most diverse. This information is extremely useful to understand their health profile, particularly the breast cancer, although the prevalence of breast cancer among the any of Indian population is not known yet.

## **Introduction:**

Jewish populations represent low-end estimates of the worldwide population, accounting for around 0.2% of the world's population i.e. 13,156,500 individuals (census 2009). Country India harbors < .5% of world Jews. The Christian community of Kerala traces back its origin to the

advent of St. Thomas, the apostle. With the migration of these Christians from Syria in A.D.345 the early Christian converts as well as new Christians (the Knanaya Christians) came to be known as Syrian Christians. Both the Jewish as well as the local converts were in the beginning mentioned as St.Thomas Christians or Nazarinnes, being followers of Jesus who was a native of Nazareth. On seeing the sad condition of the Syrian Christians after the death of St.Thomas –the church Synod of Jerusalem sent a delegation to Malabar (Kerala) and in A.D. 345, around 72 families comprising men, women and children reached Kodungallore under the leadership of Thomas of Cana who was a blood relative of Jesus. (Varghese J. History of Christianity in India [www.Indianwomenonline.com/womenhome/meltingpot/philosophy/hischris/bottom.asp](http://www.Indianwomenonline.com/womenhome/meltingpot/philosophy/hischris/bottom.asp)). The Jews belong to 12 tribes-each a descendent of one of the 12 sons of Jacob. A few years ago a research was made in Israel for members of the 12 tribes but only descendents of 4 were found.

Amidst claims and counter claims by the various Christian groups regarding their ancestry, tracing their origin through the molecular analysis might give us clues, which are unbiased and foolproof. Hence, century old speculation about the origin of the Syrian Christian population can be solved. In addition, this study would help in understanding the molecular basis of various diseases for which these populations are prone. Results obtained from this study would help in genetic counseling and career planning. In our study we estimated the ages of diversion using Y-STRs and entire mtDNA associated with the several key lineages present at frequencies >5% in our various samples of Sephardic, Ashkenazim, cohanim and Siberian Christians. India is known for its highest level of human genetic diversity. India is inhabited by several indigenous populations and there have been several historical migrations. Jews are one of the recent migrants and they have been found in various part of India. The true origin of lineages of Jews is poorly understood. Jews diasporas across the world are having very much specific to Europeans. Most of the European haplogroups are Caucasoid specific. One of the views is that ten Jewish Families released from Persian Jail by the king in BC605 have arrived Kodungallore, Kerala, India. However, their arrival in India has not been well documented. The classification of most of Jewish mtDNA variation in the number of well defined haplogroups could provide the additional insights about the origin and relationships of Jewish population with Caucasians, Caucasoid indicus (Hindu kush) and south Asians, and moreover the process of Jewish colonization in India. As the evidence say that Jews in India are mainly migrants from East & Middle East Europe, which are highly endogamous population and hence susceptible for many

disease like Tay-Sacs and Breast Cancer. Now we need to get the information which can be useful to understand their health profile, particularly breast cancer, although the prevalence of breast cancer among the Kerala Jews are not Known. Jews in India are genetically admixed with their surrounding population (Behar 2010), so we may find the genetic factors responsible for diseases in the neighbour population as well. The study of the geographic distribution and diversity of genetic variation, known as the “phylogeographic approach” (Avice et al. 1987; Templeton et al. 1995), is emerging as a useful tool for the investigation of range expansions, migrations, and other forms of gene flow during prehistory. It is specifically suits to the study of nonrecombining-marker systems such as mtDNA and Y chromosomal SNPs, which is inherited down the female line and evolves rapidly, so that, provided that sufficient characters are assayed, the maternal genealogy can be well resolved. It’s contentious, colloquially, irreconcilable differences between Jewish and other populations. Every reported thing about Jews in India is a paradox of speculation due to the fact i.e. since the data which is generated on very less and insignificant number of samples so it is deficient in revealing appropriate information. We also need to generate a programme for elucidating the time of their admixture with neighbor populations.

## **MATERIALS AND METHODS**

### **Samples**

In total, 373 Indian Jews mtDNAs, 256 Indian Jews Y chromosomes and 747 Indian Jews and non-Jews RAD51 gene profiles were used in this study. Samples were obtained with informed consent. We compared the mtDNA diversity in Indian Jews with 15 949 mtDNA profiles from Indian non-Jews, 17–19 as well as from Jews of rest world (Behar et al. 2010, Nature). We used 3696 previously published Y-chromosomal haplotypes of populations from India, and the Y-Chromosomal haplotypes of the Jews from rest of the world to compare with the studied Indian Jews Y chromosomes.

### **mtDNA typing:**

The first hypervariable segment (HVS-I) of mtDNA was sequenced directly in all samples and variable positions were determined from nps 16 001 to 16 450. The second hypervariable segment (HVS-II) and haplogroup confirmatory diagnostic coding regions were sequenced for 373 samples on the basis of their haplotype information (Supplementary Table 1). In all, 56 samples were selected for whole mtDNA sequencing. The haplotypes defined by control region sequences and coding regions were haplogrouped by their mutational motifs (Supplementary Table 1), following previously published haplogroup trees.<sup>56</sup> Complete mtDNA genomes and segments including diagnostic positions were amplified using 24 sets of primers.<sup>40</sup> PCRs were carried out with 10 ng of template DNA in a 10 ml reaction volume with 10 pM of each primer, 100 mM dNTPs, 1.5mM MgCl<sub>2</sub> and 1U of Taq DNA polymerase. Thirty-five cycles were performed with 30-s denaturation at 94degree centigrade, 30-s annealing at 58degree centigrade and 2-min extension at 72degree centigrade. The annealing temperature and time were slightly modified for a few sets of primers. PCR products were directly sequenced using the BigDye Terminator cycle sequencing kit and an ABI Prism 3730XL DNA Analyzer (Applied Biosystems, Foster City, CA, USA), following the manufacturer's protocol. The individual mtDNA sequences were compared with rCRS41 using AutoAssembler – ver 2.1 (Applied Biosystems).

### **Y-chromosome typing:**

A total of 256 samples were typed with 23 Y-chromosomal markers (M89, YAP/M145, M96, M35, M78, M130, M356, M9, M45, M304, M172, M410, M69, M82, Apt, M170, M201, M173, M17, M124, M11, M214 and M175). The thermal cycling programs were set up with an initial denaturation at 95degree centigrade for 5min, followed by 30–35 cycles at 94 degree centigrade

for 30 s, at a primer-specific annealing temperature of 52–60 C for 30 s and 72.degree centigrade for 45s, followed by a final extension at 72 degree centigrade for 7min. PCR products were directly sequenced using the BigDye Terminator cycle sequencing kit (Applied Biosystems) and the ABI Prism 3730XL DNA Analyzer, following the manufacturer's protocol.

### **Statistical analyses:**

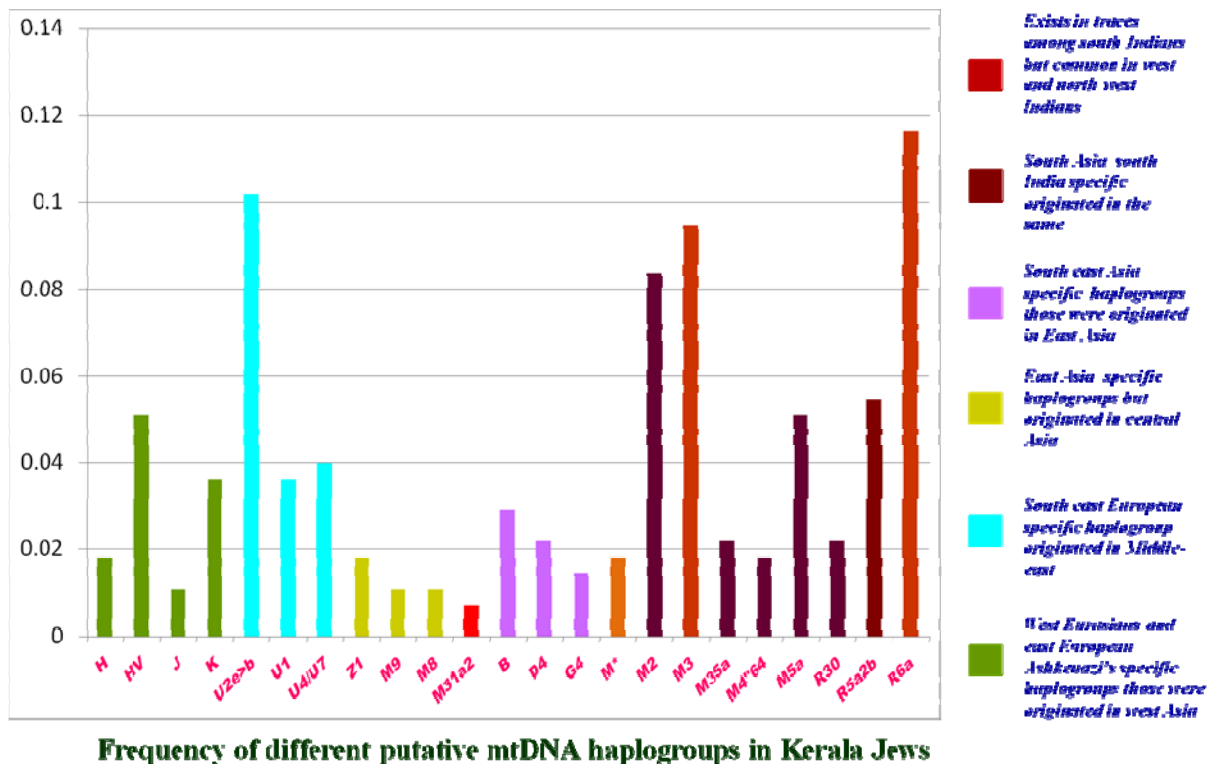
Phylogenetic trees were constructed using Network 4.2.0.1 ([www.fluxusengineering.com](http://www.fluxusengineering.com)).<sup>43</sup>,<sup>44</sup>. The program Admix2.0 ([http://web.unife.it/progetti/genetica/Isabelle/admix2\\_0.html](http://web.unife.it/progetti/genetica/Isabelle/admix2_0.html))<sup>45</sup> was used to calculate the admixture proportions of samples on the basis of the frequency of haplogroups. The age of the lineages was estimated on the basis of the molecular clock<sup>46,47</sup> based on synonymous mutation rate, given by Kivisild et al. and recalibrated by Soares et al assuming a mutation rate of one synonymous mutation per 7884 years. PC plots were generated with MVSP 3.1 (<http://www.kovcomp.co.uk/mvsp/index.html>).<sup>48</sup> Arlequin 3.1 (<http://cmpg.unibe.ch/software/arlequin3>)<sup>49</sup> was used to evaluate the genetic structure of the populations by performing analysis of molecular variance (AMOVA), as well as to calculate genetic diversities of mtDNA and the Y chromosome on the basis of haplogroup frequencies.

### **Autosomal markers typing:**

Twenty five nanograms of carefully chosen DNA sample (samples in which the paternal and maternal haplogroups are geographically distinct i.e. genetically admixed) was genotyped on Affymetrix 6.0 arrays containing one million SNPs. For some analysis we also intersected our data with Illumina 650Y genotyping of Human Genome Diversity panel (Li, J.L. *et al.Science*319, 1100-1104 (2008).

## Results:

### Unique Matrilineal genetic diversity of Jews diaspora in India:



### RESULTS:- Different from other Jews

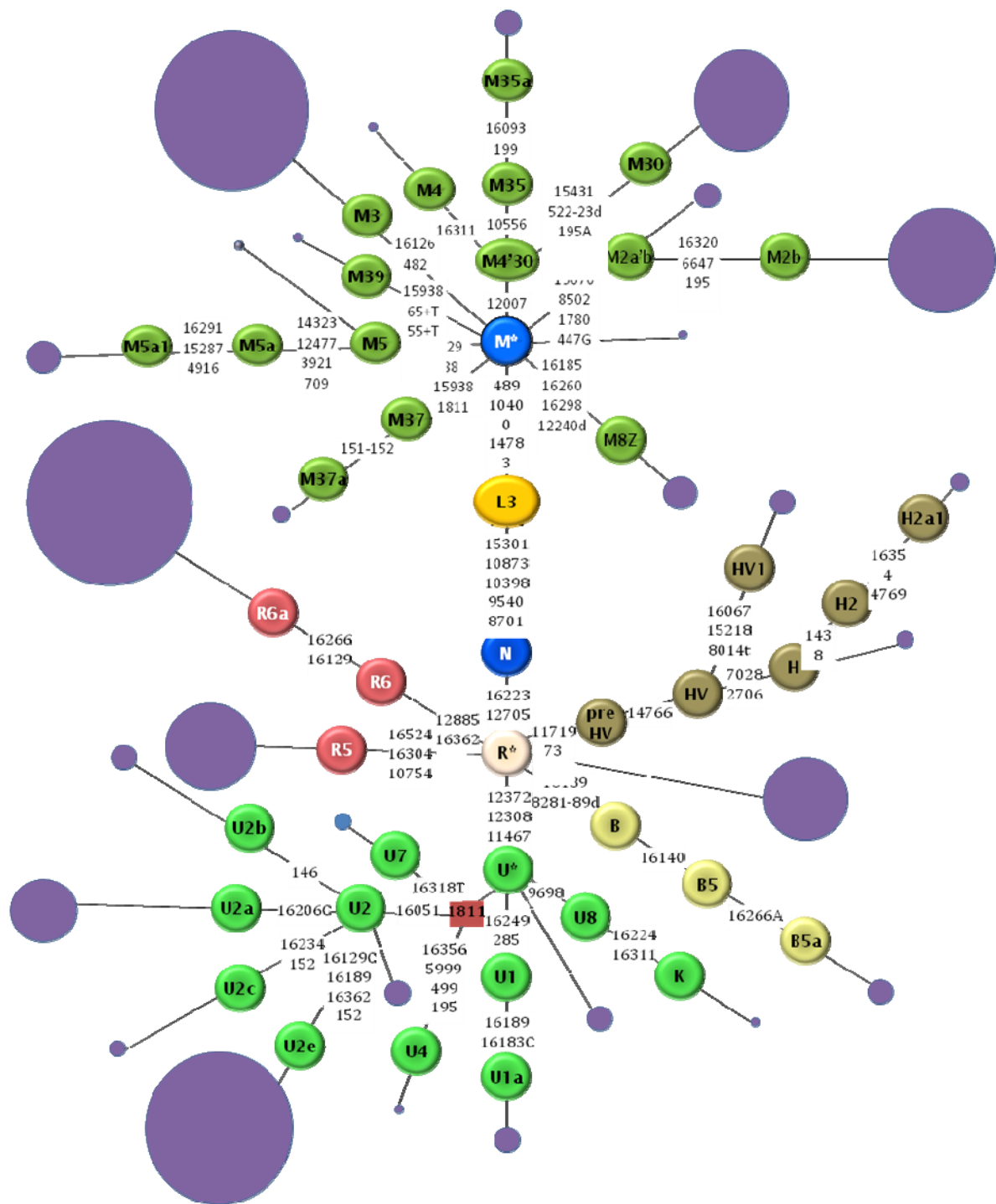
Y-SNP results with an elevated frequency of R1-M17(40%)-R1a1-M434-M458(12%) suggests possible gene flow from Eastern Europe.

Indian specific haplogroups like M82-H1, M11-L in significant frequencies suggests assimilation of Jews into the wider non-Jewish society around them.

Presence of haplogroup J2, which is very specific to the Jews population from the rest of world, though they are in low percentage.

Haplogroup H1 has been observed having low frequency of 12% which not very significant with Indian population.





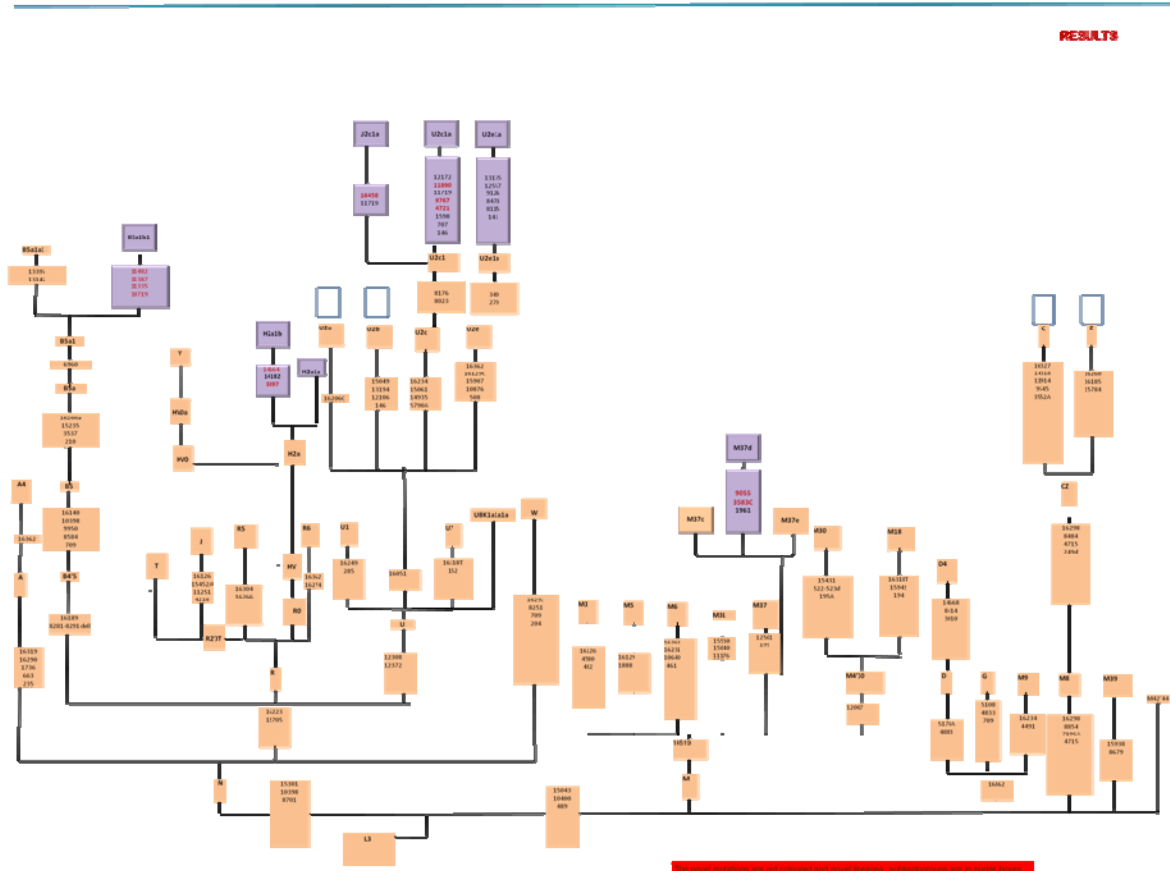
Tree drawn from Median joining network of Haplogroups observed in Indian Jewish population

Indian specific haplogroup R6a has surprisingly much elevated frequency which is reported to be found in North-West and Indus valley populations which includes Pakistan too.

Haplogroups HV1, H2a, H7, K, U2e and U4 which are having the West Eurasian origin gives an indication of West Eurasian maternal footprints in Indian Jewish maternal gene pool, supporting the fact that initial Jewish settlers included women also.

Presence of M8Z is also a surprising finding, which mostly confined predominantly in the Eastern India.

## Novel Mutations led the birth of new lineages in human phylogenetic tree



### Reconstructing the lineages of human phylogenetic tree based on complete mitochondrial DNA sequences of 56 samples

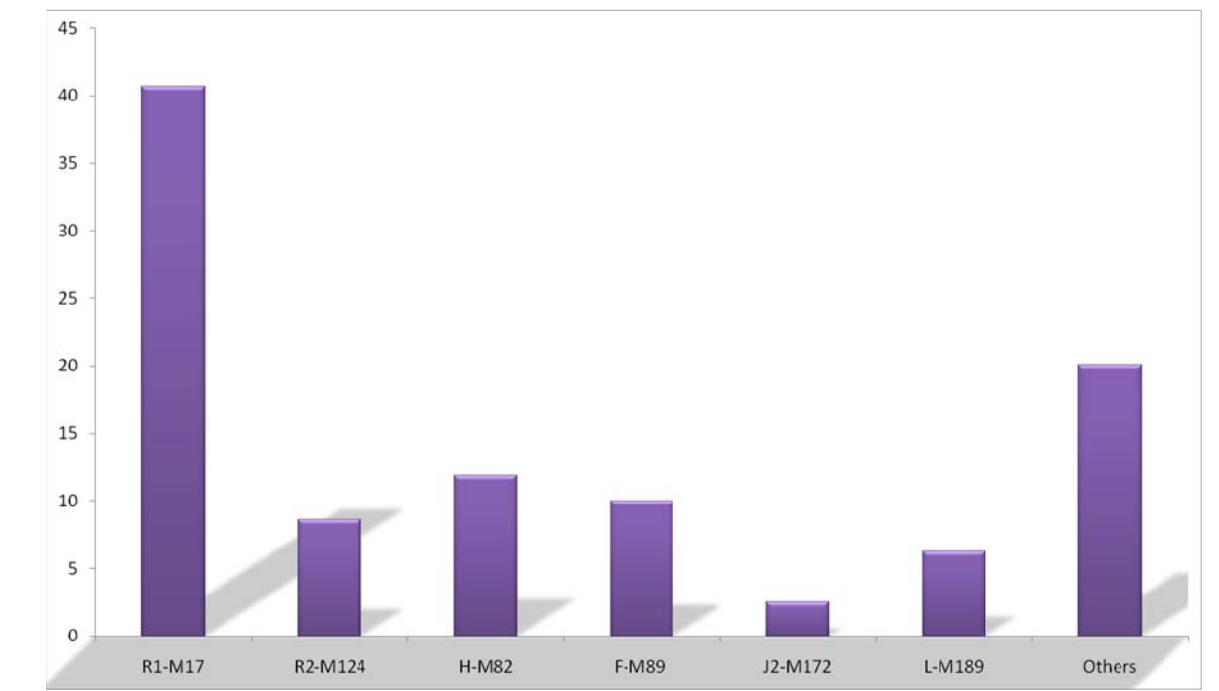
The novel lineages found exclusively in the Jewish specific haplogroups justifies the evidences of existence of the unknown tribes who were separated from their parental lineages approximately 18Kya back.

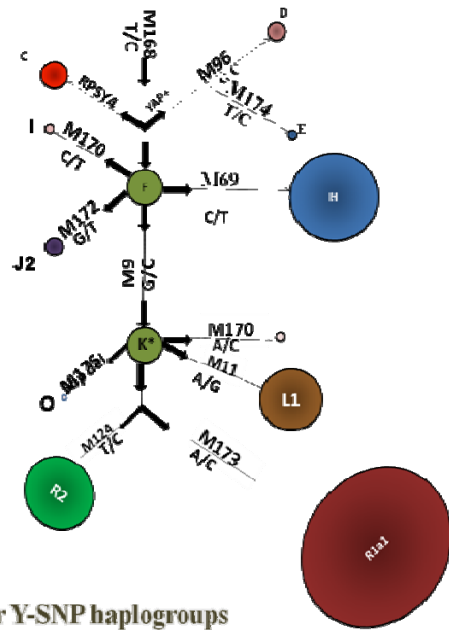
These lineages also suggest the eastward migration of early Jews.

Their genetic structure is very much admixed and shows affinity with Indian Jews and East European Jews

The Y- chromosomal haplogroups suggest that Jews in India are overwhelming patrilineally Indian specific

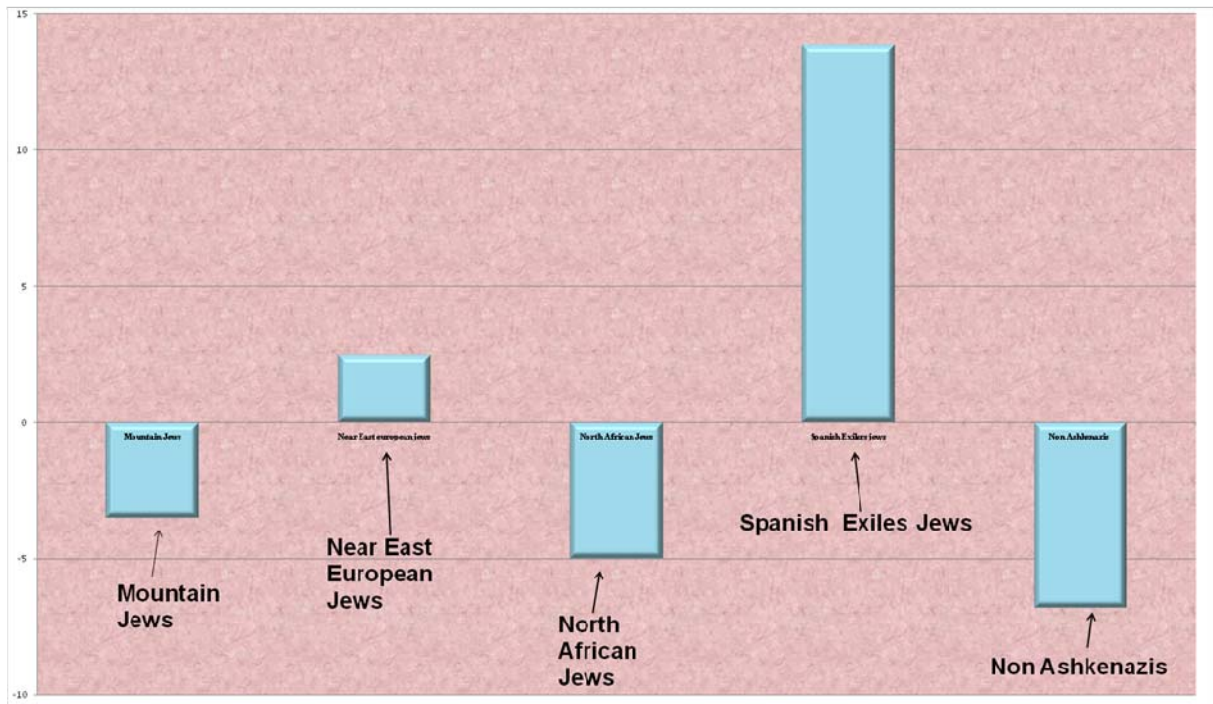
## Frequency of Y haplogroups in Indian Jews Population





Distribution of major Y-SNP haplogroups among the Jews populations of India

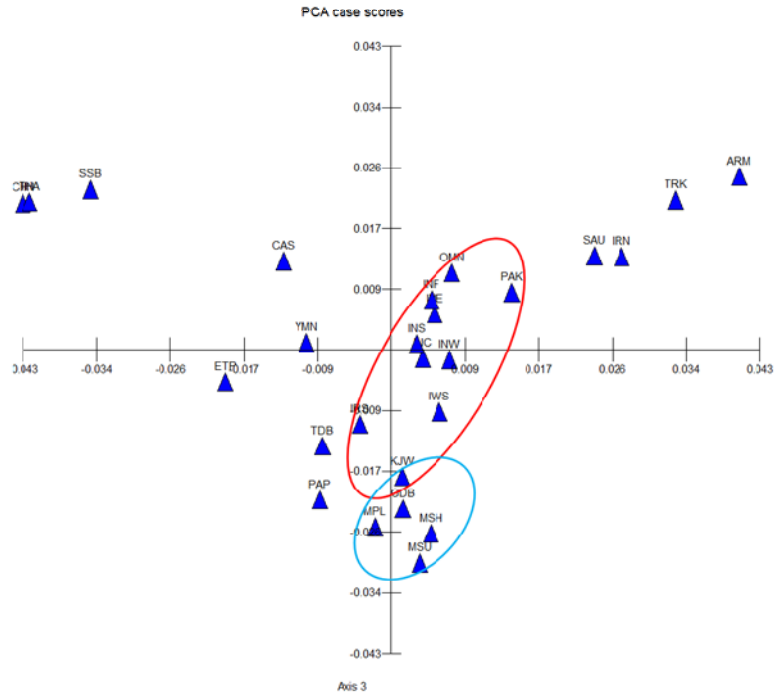
Admix 2.0 result of Kerala Jews population with other Jews



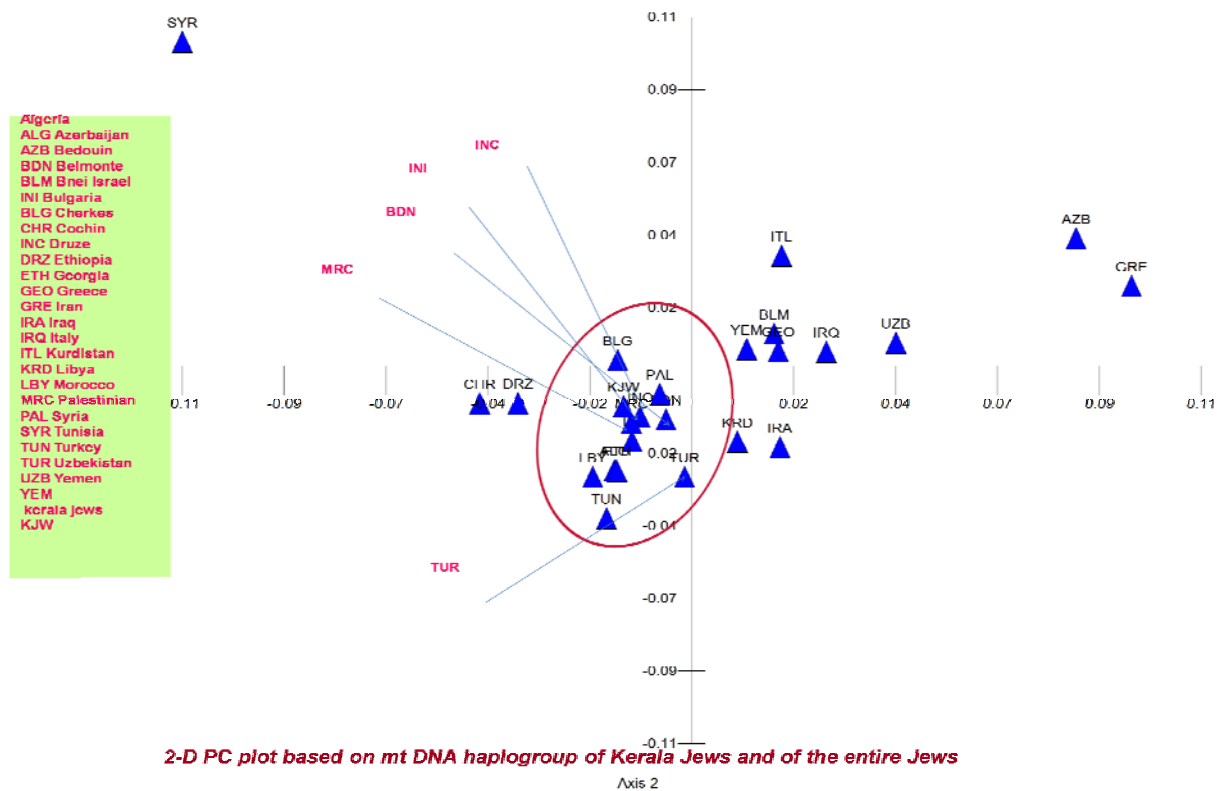
Picture showing the high genetic admixture of Indian Jews with Ashkenazis (Spanish exiles and East European Jews).

**The PC plot shows the genetic affinity of Kerala Jews with the major populations of India**

- Armenia - ARM
- CentralAsia- CAS
- China - CHN
- Ethiopia- ETH
- India Central- INS
- India East- INE
- India Far East- IFE
- India NW- INW
- India South- INS
- India West- INW
- Iran- IRN
- Oman- OMN
- Pakistan- PAK
- Papua- PAP
- Saudi- SAU
- South Siberia- SSB
- Turkey- TUR
- Yemen- YEM
- Shia Muslim- SHM
- Sunni Muslim- SUM
- TDawoodi Bohra- TDB
- GDawoodi Bohra- GDB
- Mappla- MPL
- Iranian Shia- IRS
- Kerala Jews- KJW



## PCA- Kerala Jews with the Jews population of world



We have observed the mitochondrial haplogroups B, D, F, G, H, HV, J, K, M, Q, R, U, V, W, and Z suggesting that Jews from Kerala are exceptionally diverse population.

They show high level of genetic admixture with the local population and North West Indian population and with the Eastern European Ashkenazis.

PC scale shows the genetic affinity of Indian Jews with the Indian Population and with the Jews from the rest of world e.g. Israel, Morocco and migrants from Israel (European).

Earlier reports suggest that a SNP i.e. 5' UTR RAD51 g.135:c>g is responsible for making East European Ashkenazis nearly five times more susceptible for Breast Cancer and SNP is found in Kerala Jews populations which is not ever reported in surrounding population.

### **Conclusions:-**

*In Y chromosome study elevated frequency of R1-M17(40%) and HV1, H2a, H7, K, U2e and U4 in mtDNA study gives a strong indication of both paternal and maternal West Eurasian gene flow.*

*In Y chromosome study the J1 and low frequency of **HI** has been observed which supports the theory significantly.*

*Presence of Indian specific haplogroups both in mtDNA and Y suggests the evident admixture with local population.*

*It is very much evident from the results that the gene flow is from West Eurasian but after the primary settlement the Jewish population has gone through the heavy admixture with local resident.*

*Time of admixture is yet to be concluded.*

*The Jews from other part of the world are highly endogamous and show high level of bottleneck, whereas the Kerala Jews are the most diverse. This information is useful to understand their health profile.*

*Our result shows the two major migrations of the Jews to India, first is from Israel and next is from Spain as the exiles.*

*Kerala Jews are very much contributing in the reconstruction of human phylogenetic tree. More samples of the same groups are sequenced in order to support the existence of novel lineages. This finding is very useful to present the Jews with different genetic structure, now we are running BATWING to calculate the coalescent times in order to investigate the lost lineages of ancient Jews.*

*The East European Ashkenazis immigration led the introduction of a SNP in Kerala Jews population, which is partially responsible for susceptibility of Breast Cancer; this is affecting the neighbor populations as well. We may find this SNP in most of the Indian population.*

## **Supplementary materials**

### **Table 1**

#### **Samples with their haplogroups based on mtDNA markers**

S.No.	hvr 1	18f	15f	22f-15326g	haplogroup
B86	129a-172c-234t-266t-274a-309g-362c	12285c-12705c	rCRS		R6a1a

B87	257t-266t-304c-309g-325c-335g-356c		rCRS	15385t	R5a2b
B102	051G-209C-239T-292T-352C-353T	12106a-308g-372a-705c	rCRS	rCRS	U2b2
B101	938t-223t-304c	12705t	10398g-400t	15043a-301a	M39b
B106	224t	12308g-372a-705c	rCRS	15355a	K1a4d
D1	040T-295T-311C	172t-12705c	10398g		N
D10	168T-172C-188g-239T	12705c	rCRS		B4f
D11	320T-356C	12308g-372a-705c	rCRS	15693c	U4
D3	223t	12007a 12172g-12308g-372a-705c	10398g-400t-556t	15043a-301a	M37
D4	051g-234t	12308g-372a-705c	rCRS	15214c	K1a4c
D5	189c-249c	12308g-372a-705c	rCRS	15217a	U1a3
D6	154t-354t	12127a-705c	rCRS		H2a1
D7	189c-240g-402g____2706	12705c 12308g-372a-618a-705c	rCRS		H
D8	16189c-270t	12705c	rCRS		U5b1b
D12	938t-223t-304c	rCRS	10398g-400t	15043a-301a	M39b
E5	223t-287t-304c	rCRS	10398g-400t	15043a-301a	M42
E6	082t-223t-311c	12414c	rCRS		W
E7	126c-154c-223t-354t	12467c	10398g-400t	15043a-301a	M3b
E8	354t	12705c	rCRS		H2a1
E9	126c-223t	rCRS	10398g-400t		M3
F10	184a-223t-260t-298c	12241del	10398g-400t	15043a-261a-301a-487(t)-784c926	Z1
F11	129a-172c-234t-266t-274a-309g-362c	12285c-705c	rCRS		R6a1a
F12	067t-182g-183g-327(A)	12705c	rCRS	15218g	HV1
F13	067t-182g-183g-327(A)	12705c	rCRS	15218g	HV1
F14	172c-192t	12133t-285c-705t	rCRS		HV5
F15	223t-257t	12477c-681c	10398g-400t		M5a
F16	067t-182g-183g-327(A)	12705c	rCRS	15218g	HV1
F17	458(a)	12705c	rCRS	15218g	HV1
G1	129a-291t	12477c	10398g-400t	15043a-287c-301a-379t	M5a1
G10	309g	12172g	10398g-400t	15043a-301a-670c	M50
G12	266t-274a-362c	12285c-705c	rCRS		R6a
G13	040-311c	12207a-705c	10142t		R30b
G14	042a-223t-274a-319a-320t-362c		10398g-400t	15043a-253g-301a-670c	M2
G15	924g-223t	12561g	10398g-400t	15043a-301a	M35a
G16	951g-126c-185t-223t-519c	rCRS	10398g-400t	15043a-257a-301a	M3
G17	954©-182©-183©-189C-249C	12308g-372a-705c	10253c 10398g-400t-670t	15217a	U1a3
G19	924g-093c-223t	12561g		15043a-301a	M35a
G2	093c-129a	12705c	rCRS	15326g	R
G20	257t-266t-304c-309g-325c-335g-356c	12705c	rCRS	15385t	R5a2b
G22	111t-187t-223t-274a-319a-320t-362c	12172g	10398g-400t	15043a-253g-301a-670c	M2
G23	111t-187t-223t-274a-319a-320t-362c	12172g	10398g-400t	15043a-253g-301a-670c	M2
G24	093c-129a-362c	12285t	rCRS		R6a



G26	140c-183©-189c-266(a)	705t	10398g	15235g	B5a
G25	111t-187t-223t-274a-319a-320t-362c	12172g	10398g-400t	15043a-253g-301a-670c	M2
G27	129a-172c-234t-266t-274a-309g-362c	12285c-705c	rCRS 10398g-400t- 556t	15043a-301a	R6a1a
G28	111t-184t-185t-186t-189c-223t-295t	12007a	10398g-400t	15043a-301a-431a	M37e
G29	223t	12007a	10398g-400t	15043a-301a-431a	M30
G3	951g-126c-185t-223t	rCRS	10398g-400t	15043a-301a	M3
G30	257t-266t-304c-309g-325c-335g-356c	12705c	rCRS	15385t	R5a2b
G31	951g-126c-185t-223t-	rCRS	10398g-400t	15043a-301a	M3
G32	129a-223t-291t	12477c	10398g-400t	15043a-287c-301a-379t	M5a1
G33	223t	12007a	10398g-400t	15043a-301a-431a	M30
G34	092c-111t-187t-189c-223t-274a-319a- 320t-362c	12172g	10398g-400t	15043a-253g-301a-670c	M2
G35	167t-172c-278t	12705c-714c	rCRS		R30a
G4	093c-176t-223t-362c	12007a-172g	10398g-400t	15043a-301a-431a	M30e
G40	167t-172c-176t-278t	12705c-714c	rCRS		R30a
G41	257t-266t-304c-309g-325c-335g-356c	12705c	rCRS	15385t	R5a2b
G42	954©-182©-183©-189t-249c	12308g-372a-705c	10253c	15217a	U1a3
G43	172c-278t	12705c-714c			R30a
G44	223t	12007a	10398g-400t	15043a-301a-431a	M30
G45	167t-172c-278t	12308a-372g	rCRS		U6a
G46	924g-266t-289g	rCRS	10398g-400t	15043a-301a	M35a
G47	266t-304c-309g-325c-356c	12705c	rCRS	15043a-226g-301a-385t	R5a2b
G48	924g-223t-266t-289g	12007a-618a	10398g-400t	15043a-301a	M4b1
G49	111t-223t-399g	12007a 12308g-372a--557c- 705c	10398g-400t	15043a-301a-314a-431a	M30e
G5	051g-129©-183©-189c-362C		rCRS		U2e
G6	051g-092c-129©-183©-189c-223t	12308g-372a-12414c	rCRS		U2e
G9	218t-309g-318©	12308g-372a-12705c	rCRS		U7
E1	927a-129a-223t	12477c	rCRS	15218g 15043a-261a-301a-487(t)- 784c926	HV1a1
G7	184a-223t-260t-298c	12241del	10398g-400t		Z1
D5	954©-182©-183©-189t	12308g-372a-12705c	rCRS		U1a3
D9	040t-295t-311c	12705c	rCRS		R30b
G37	951g-126c-185t-223t	rCRS	10398g-400t	15043a-301a	M3
G50	951g-126c-185t-223t	rCRS	10398g-400t	15043a-301a	M3
E3	126c-223t		10398g-400t		M3
E4	111t-223t-311c-357c		10398g-400t		M4
G8	218t-309g-318©	12308g-372a-12705c			U7
G10	218t-309g-318©	12308g-372a-12705c			U7
E2	189c-192t	12308g-372a-618a-705c			U5b1b
H26	126c	12308g-372a--557c-705c			U2e
18	051g-092c-129©-183©-189c-223t	12308g-372a-12705c			U2e
24	129a-172c-234t-266t-274a-309g-362c	705t			R6a1a
25	940c-051g-206©-230g-304c-311c-519c	12308g-372a-12705c			U2a
36	951g-126c-185t-223t-519c				M3

29a	051g-519c	12308g-372a-12705c	10253c	15217a	U1a3
19	257t-266t-304c-309g-325c-335g-356c				R5a2b
21	069t-274a-362c	12007a	10398g-400t	15043a-301a-431a	M30
H25	111t-144c-223t-224c-311c		10398g-400t		M4a
Z1	184a-223t-260t-298c		10398g-400t		M8a
Z2	224t	12308g-372a-705c	rCRS	15355a	K1a4d
Z3	184a-223t-260t-298c				M8a
Z4	224t	12308g-372a-705c	rCRS	15355a	K1a4d
83A	16274a-16301t		10398g	15301a	N1d
84	196a-203g-223t	705t		15904a	V5
D21	129A-519C	477c	10398g-400t		M5a
D25	129A-519C	477c	10398g-400t		M5a
HV 32	129A-265©-311c		10398g-400t		Q1
KH83	924G-093C-126C-290T		10398g-400t		M35a
KT001	15924-224t-234T-311c		10550t		K1a1b1a
NN94	928A-304C	12340g-561a	10398g-400t		M35b
RJ76	234T-249C	12308a-372g			U1
T21	126C-311C	rCRS	10398g-400t		M3
DG126	239T-298C-327T-357C	rCRS			C4a4a
2820	15924-224t-234T-311c		10550t		K1a1b1a
4335	129A	477c	10398g-400t		M5a
4355	129A	477c-705t	10398g-400t		M5a
4359	129A	477c	10398g-400t		M5a
5948	15924-224t-234T-311c		10550t		K1a1b1a
13	126C-311C	rCRS	10398g-400t		M3
4360	129a	477c-705t	10398g-400t		M5a
32TH	129A-172c-234T		10398g-400t		M12b
5923	909G-129A		10398g-400t		M5
D35	129A	477c			M5a
4366	172C-183©-189C-274A-319A-320T	705t	10398g-400t		M2a1a1a1
4367	172C-183©-189C-274A-319A-320T	705t	10398g-400t		M2a1a1a1
4362	172C-183©-189C-274A-319A-320T	705t	10398g-400t		M2a1a1a1
V07	145A-176T-234T-261T-311C	rCRS	10398g-400t		M4a
GD88	129A	477c	10398g-400t		M5a
AS90	129A-265©-390A	172A-477C			Q1b
53	223T-318(T)	498t	10398g-400t		M18
6021	172t-234T-270t-274a-319a-352c				M2a1a1a1
KT004	172t-234T-270t-274a-319a-352c				M2a1a1a1
T38	932+N-234T		10398g-10550t		K1a1b1a
D5	183©-189C-311C	705t			HV5
4338	129A	477c			M5a
R17	311C	705t			HV5

5923	15909g-129a-223t-519c	477c	10398g-400t		M5a
DG119	1303a-1438g-1888a	477c			M5a1b
4344	1438g-1888a-4454c-	477c			M5a2
B67	126C-129(c)223T	11985g-285c	rCRS		U2e
B69	051G-092c-129©-183©-189c-362C	308g-372a-557t	10101t	018a-326g	U2e
B52	223T-368C	rCRS	10398g-400t		D4I
B55	187T-189C-207G-309G-318(T)	308g-372a-557t			U7
B64	187T-189C-207G-309G-318(T)	308g-372a-557t			U7
B63	051G-234T-247G-254G-311C	308g-372a-557t	rCRS		U2c
B68	051G	308g-372a	10253c	15217a	U1a3
B76	223T-311C	12007a-705t	10398g-400t		M4
B77	217G-325C	12705t			HV2
B56a	189C-224C-311C	12308g-372a-12705c			K2
B57	186T-189C-223T-270T-319A-352C		10398g-400t	15043a-301a-326g-670	M2a
B74	266t-304c-309g-325c-356c				R5a2b
B76	266T-318G-320T-362C	12285t	10084c		R6a1a
B84	147T-189C-217G-235G			rCRS	B4c2
B51	223T-311C		10398g-400t		M3
B53	223T-311C		10398g-400t	043a-301A-326g-431a	M30
B73	266t-304c-309g-325c-356c				R5a2b
B54	rCRS	12133t-705c			HV5
H36	183©-189c-266(a)-362c	12285c	10101c 10084c-398g-400t	rCRS	B5a
B103	126C-223T-309G	12705t		15043a-301a	M3
B104	129a-172c-234t-266t-274a-309g-362c	12106t	rCRS		R6a1a
B105	093C-223T-309G	12561g	10398g-400t	15043a-301a-326g-924g	M35a
B106"	223T-309G-318(t)	308g-372a-705t			U7
B3c	176T-223T-270T-274A-319A-352C	12705t 14985g-308g-372a-705t		018a-043a-301a-326g	M2a
B4	176T-291t-352C-353t		10084c	rCRS	U2a
B42	126A-185T-223T-309G	12705t	10398g-400t	018a-043a-301a-326g	M3
B43	223T-234t-362c	12705t	10398g-400t	043a-301A-326g-431a	M30
B52	051G-092c-129©-183©-189c-362C	12308g-372a-557t	rCRS	rCRS	U2e
B65	223T-320T	12007a-705t	10398g-400t		M3
B66	051r-223T-309G	12007a-705t	10398g-400t		M35a
B72	111t-187t-223t-274a-319a-320t-362c	12561g-	10556c	043a-253g-301a-326g-670c	M2b
B75	129a-172c-234t-266t-274a-309g-362c	12285c	rCRS		R6a1a
B85	111t-187t-223t-274a-319a-320t-362c	14985g-12172g-705t/	10398g-400t	018a-043a-130t-253g-301a-326g	M2b
B86	129a-172c-234t-274a-309g-362c	12285c			R6a1a
B87B	16189c-192t-270t	12308g-372a-618a-705c			U5b1b
C17	257T-304C-309G-335G-356C	705		15385t	R5a2b
C17b	257T-304C-309G-335G-356C	705	10443y	15385t	R5a2b
C36	309G	12172t	10398g-400t		M50
G20	257T-304C-309G-335G-356C	705		15385t	R5a2b

H32	129a-172c-234t-274a-309g-362c					R6a1a
K1	051G-209C-239T-292T-352C-353T	308g-372a-705t	rCRS			U2b2
K2	183©-189C-304C	705t		10310a-609c		F1
K3	051G-209C-239T-292T-352C-353T	308g-372a-705t	rCRS	rCRS		U2b2
K4	126A-223T	12285c-705c	398G-400T	043A-301A		M3
K5	181G-309G-318(t)	12172c				U7
B71	051g-092c-129©-183©-189c-223t	14985g-12007a-705t	10084c	018a-326g		U2e
B61	051G-092c-129©-183©-189c-362C	12308g-372a-557t	10101c	018a-326g		U2e
C21	rCRS	12133t				HV5
B51	223T		10398g-400t	043a-301A-326g-431a		M30
B56	185T-223T-260T-298C	12241d-705t				Z1
B67a	126C-223T	14985g-705t	10398g-400t	043A-301A		M3
B70	126C-223T	14985g-12705t	10398g-400t			M3
B79	129a-172c-234t-266t-274a-309g-362c	12285c		14990t-326g-385t		R6a1a
C1	223T-	12007a	10398g-400t	15043a-301a-326g-431a		M30
C2	111t-187t-223t-274a-319a-320t-362c	12172c-705t	10398g-400t			M2b
C3	104T-129A-223T	12477t				M5a
C4	111t-187t-223t-274a-319a-320t-362c	12172c-705t	10398g-400t	043a-253g-301a-326g-670c		M2b
C5	129a-172c-234t-266t-274a-309g-362c	12007(t)-133t-285c				R6a1a
C6	951g-126c-185t-223t-519c	12705t	10398g-400t	15043a-301a-326g		M3
C7	093C-129A-356C-362C	12007a-705t	10398g-400t	15043a-301a-326g		D4a3a
C8	951g-126c-185t-223t-519c		10398g-400t			M3
C9	16069a	12007a-705t				J1c2a
C10	185T-223T-260T-298C	12241d-705t		15043a-261a-301a-326g-486t-		Z1
C11	051G-187T-189C-206©-230g	308g-372a-705t	rCRS			U2a
C12	051G-092C-129©-183©-189©-362C	12308g-372a-557t				U2e
C13	017C-126C-145A-223T-	12705t				M31a2
c15	189c-249c-311c-327c	12308g-357g-372a-	rCRS			U1b
C14	940c-051g-206©-230g-304c-311c-519c	12308g-357g-372a-	rCRS			U2a
C16	940c-051g-206©-230g-304c-311c-519c	12308g-357g-372a-	rCRS	15049t		U2a
C17	111T-223T-274A	12285t	rCRS			R6a
C18	051g-234t	12172g-12308g-372a-705c	rCRS	15214c		K1a4c
C19	051G-092C-129©-362C	12308g-372a-705c	rCRS			U2e
C20	257t-266t-304c-309g-325c-335g-356c	12705t	rCRS	14990t-326g-385t		R5a2b
C21	051G-092C-129©-183©-189©-362C	308g-372a-705t				U2e
C22	954©-182©-183©-189C-249C	308g-372a-705t	10443y			U1b
C23	129a-172c-234t-274a-309g-362c	12285c	rCRS			R6a1a
C24	940c-051g-206©-230g-304c-311c-519c	12308g-357g-372a-	10084c	rCRS		U2a
C25	040T-295T-311C	172t-12705c	10398g	14990t-226a-301a-326g-385t		N
C26	940c-051g-206©-230g-304c-311c-519c	12308g-357g-372a-				U2a
C27	266t-304c-309g-325c-356c	12705t	rCRS	14990t-226a-301a-326g-385t		R5a2b
C28	067t-182g-183g-327(A)		rCRS	15218g		HV1

C29	954©-182©-183©-189C-249C	308g-372a-705t	rCRS		U1b
C30	051G-187T-189C-206©	12308g-372a-705t			U2a
C31	129a-172c-234t-266t-274a-309g-362c	12172c	rCRS	rCRS	R6a1a
C32	129h-234y-266y-309G-362C	12285t	10084c	rCRS	R6a1a
C33	051h-172y-234y-274A-309r-362C				R6a1a
C34	051G-187T-189C-206©				U2a
C35	951g-126c-185t-223t-519c				M3
C36	223T	007a-705t	10398g-400t	15043a-301a-326g	M4
C37	951g-126c-185t-223t-519c	12705t	10398g-400t	15043a-301a-326g	M3
C38	257t-266t-304c-309g-325c-335g-356c				R5a2b
H1	172c-183©-189C-274a-278t-319a	12285t	10398g-400t	15043a-301a-326g-670c	M2a1b
H2	187t-223t-270t-274a-291t-319a-320t-352c-362c	rCRS	10398g-400t	15043a-253g-301a-326g-670c	M2a1a
H3	129a-172c-223t-234t-266t-274a-309g-362c	12714c	10084c		R6a1a
H4	114(a)-129a-223t-362c				G4
H5	114(a)-129a-223t-362c	12285t	rCRS		G4
H6	051g-126c-185t-223t	rCRS	10398g-400t	15043a-301a-326g	M3
H7	129a-172c-234t-266t-274a-309g-362c				R6a1a
H8	126c-154c-223t-224c-311c	12308g-372a-705t	10084c	rCRS	K
H9	223t-234t-362c	12285t	10398g-400t	15043a-301a-326g	M9d
H10	129a-172c-234t-266t-274a-309g-362c	12285t	rCRS	rCRS	R6a1a
H11	129a-172c-234t-266t-274a-309g-362c	12714c	10084c	rCRS	R6a1a
H12	129a-167t-172c-234t-266t-274a-278t-309g-362c	285t	rCRS	rCRS	R6a1a
H13	257t-266t-304c-309g-325c-335g-356c	12007a-705t	rCRS	rCRS	R5a2b
H14	111t-223t-362c	12705t	rCRS	15385t	R5a2b
H15	951g-126c-185t-223t-519c	12133t-285c	10398g-400t	15043a-301a-314a-431a-478g	M3
H16	093c-129a-362c	12133t-12285t	10398g-400t	043a-130t-253g-301a-326g-670c	M8Z
H17	129a-172c-234t-266t-274a-309g-362c	133t-285c/007a-705t	rCRS		R6a1a
H18	951g-069-126c-185t-223t-519c	12705t	10084c		J1c8
H19	111t-187t-189c-223t-274a-319a-320t-362c				M2b
H20	092c-111t-187t-189c-223t-274a-319a-320t-362c				M2b
H21	951g-126c-185t-223t-519c	12705t	10398g-400t	15043a-253g-301a-326g-670	M3
H22	126c-154c-223t-224c	12705t	10398g-400t	15043a-301a-326g	M3b
H23	140c-183©-189c-266(a)	12705t	10398g	15235g	B5a
H24	111t-144c-223t-224c-311c	12308g-372a-557t	10443y	15119a	K
H25	051g-092c-129©-183©-189c-362C	013r-064y-189y-285y-290-705t	10321c	15119a	U2e
H26	951g-069-126c-185t-223t-519c	12705t	10013t-084c	rCRS	J1c8
H27	140c-183©-189c-266(a)	12705t	10398g	15235g	B5a
H28	rCRS	12285t	rCRS	15235g	J1c2a
H29	129a-172c-234t-266t-274a-309g-362c		rCRS		R6a1a
H30	051g-093c-153a-182©-183©-189c-218t-263c-292t	12285t	10084c	15148a	HV1
H31	051g	12070a-172c-308g-372a	rCRS	15148a	U1

H32	051g-234t	12308g-372a-557t	254h	rCRS	U2c
H33	093c-129a-224-311c362c	12308g-372a	rCRS		K1c
H34	954©-182©-183©-189C-249C	12308g-372a-557t	rCRS	rCRS	U1b
H35	051G-092c-129©-183©-189c-362C	12308g-372a-557t	10253c-561c	rCRS	U2e
H37	051g-129©-183©-189c-362C	12308g-372a-705c	rCRS	rCRS	U2e
H38	223t	12133t-285c-705t			HV5
H39	129a-172c-234t-266t-274a-309g-362c				R6a1a
H40	069t-126c-223t	705t	10084c	rCRS	J1c8
H42	270t-274a-291t-319a-352c	561a-705t	10398g-400t	15043a-301a-326g-497a-670c	M2a1a
H43	270t-274a-291t-319a-352c	705t	10398g-400t	15043a-301a-326g-497a-670c	M2a1a
H44	924g-223t	705t	10398g-400t	15043a-301a-326g	M35a
H45	270t-274a-291t-319a-352c	12007a-705t	10398g-400t	15043a-301a-326g-497a-670c	M2a1a
H46	172c-278t		10398g-400t	15043a-055c-241g-301a-562g	M33a2
H47	223t-295c	172g-705t			R12
h36b	172C-183©-189C-274A-319A-320T			15043a-301a-326g-670c	M2a1b
C32b	129a-172c-234t-266t-274a-309g-362c	12285t		rCRS	R6a1a
B	069t-274a-362c	rCRS	10398g-400t	15043a-301a-326g-431a	M30c1a1
89	223T		10398g-400t	15043a-301a-314a-431a	M30
DB43	940-051-206©-215-230-255-304-311				U2e
DB68	223-290-311-319-362				M9
DB46	150t--185t-223t-260t				Z1
DB51	093c-223t-289+t-293c-319a-362c				D401

**Table 2**

**Haplogroups based on Y chromosomal markers**

S.NO	C BATCH	M9	M45	M173	M82	M69	M172	M175	M11	M124	M17	M89	M189	H
1	C1	D	D	D										R
2	C2	A	0	0	A	A		0	0	0	0		0	
3	C3	A	0	0	A	A	A	0	0	0	0	D		F
4	C4	NA												
5	C5	NA												
6	C6	A	0	0	A	A	A	0	0	0	0		0	
7	C7			A										
8	C8	D	D	D	0	0	0	0	0		D	0	0	R
9	C9	D	0	0	A	A	A	0	0	0	0	0		
10	C10	D	D	D	0	0	0	0	0	0	D	0	0	R
11	C11	A	0	0	A	A		0	0	0	0		0	

12	C12	D	A	0	0	0	0	A	A				A	
13	C13	A	0	0	A	A		0	0	0	0		0	
14	C14	D	A	0	0	0	0	A	A					
15	C15	A	0	0	A	A	A	0	0	0	0	A	0	
16	C16	D	D	D	0	0	0							R
17	C17	D	D	D	0	0	0	0	0	0	D	0	0	R
18	C18	D	D	D										R
19	C19	D	D	D	0	0	0	0	0		D	0	0	R
20	C20	D	D	D	0	0	0	0	0		D	0	0	R
21	C21	A	0	0	A	A	A	0	0	0	0	D		F
22	C22	D	D	A	0	0	0	0						
23	C23	NA												
24	C24	A	0	0	A	A	A	0	0	0	0	D		F
25	C25	A	0	0				0	0	0	0		0	
26	C27	D												
27	C29	D	D	D										R
28	C30	D	D	D	0	0	0	0	0		D	0	0	R
29	C31	NA												
30	C32	A	0	0	A	D	0	0	0	0	0			H
31	C34	OVER												
32	C36	D	0	0	0	0								
33	C37	A	0	0	A	D	0	0	0	0	0			H
34	C20b	D												
35	C17b	D	D	D	0	0	0	0	0		D	0	0	R
36	C32b	OVER												
37	C35		A	0	0	0	0	A						
38	H1	A	0	0	A	A	D	0	0	0	0			J
39	H2	A	0	0	A	A	D	0	0	0	0			J
40	H3	A	0	0	A	A	A	0	0	0	0	D		F
41	H5	D												
42	H6	A	0	0	A	A	A	0	0	0	0		0	
43	H8	D	D	D	0	0	0	0	0		D	0	0	R
44	H9	A	0	0	A	D	0	0						H
45	H10	D	D	D	0	0	0	0	0			0	0	R
46	H11	A	0	0	A	D	0	0						H
47	H12	D	D	D	0	0	0	0	0		D	0	0	R
48	H13	D	D	A	0	0	0	0	0	D	0	0	0	R
49	H14	A	0	0	D	0	0	0						H
50	H15	D	D	D	0	0	0	0	0		D	0	0	R

51	H16	A	0	0	D	0	0	0						H
52	H17	A	0	0	0	0	0	A	A	0	0	D		F
53	H18	D	D	A	0	0	0	0	0	D	0	0	0	R
54	H21	A	0	0	A	D	0	0						H
55	H22	D	A	0	0	0	0	A	D					L
56	H23	D	D	A	0	0	0	0	0	A	0	0	0	
57	H24	A	0	0	D	0	0	0						H
58	H25	D	D	D	0	0	0	0	0	0	D	0	0	R
59	H26	D	D	D	0	0	0	0	0		D	0	0	R
60	H27	D	D	D							D			R
61	H28	A	0	0	A	A	A	0	0	0	0	D		F
62	H29	D	A	0	0	0	0	A	D					L
63	H30	D	D	D	0	0	0	0	0		D	0	0	R
64	H31	A	0	0	D	0	0	0						H
65	H32	D	D	D										R
66	H33	D	D	A	0	0	0	0	0	A	0	0	0	
67	H34	A	0	0	D	0	0	0						H
68	H35	D	A	0	0	0	0	A	A			A	A	
69	H36	D	D	D	0	0	0	0	0		D	0	0	R
70	H37	A	0	0	A	A								
71	H40	D	D	D	0	0	0	0	0		D	0	0	R
72	H42	D	D	D										R
73	H43	A	0	0	D	0	0	0						H
74	H44		A	0	0	0	0	A						
75	H45	A	0	0	D	0	0	0						H
76	H46	D	D	D	0	0	0	0	0	0	D	0	0	R
77	H36b	D	D	A	0	0	0	0	0	D	0	0	0	R
78	B3c	D	D	A	0	0	0	0	0	D	0	0	0	R
79	B4	D	D	D										R
80	B71	D	D	D	0	0	0	0	0		D	0	0	R
81	B79	D	D		0	0	0	0	0			0	0	
82	B69	D	D	D	0	0	0	0	0	0	D	0	0	R
83	B75		A	0	0	0	0	A	A				A	
84	B85	A	0	0	D	0	0	0						H
85	B52	A	0	0	D	0	0	0						H
86	B42		A	0	0	0	0	A	A					
87	B43	D	D	D	0	0	0	0	0					R
S.NO	DEFG BATCH	M9	M45	M173	M82	M69	M172	M175	M11	M124	M17	M189	M89	H
1	D1	D	D		0	0	0	0	0			0	0	R



2	D3	A	0	0	A	A	D	0	0	0	0	0		J2
3	D4	A	0	0	A	A	0	0	0	0	0	0	D	F2
4	D5	D	A	0	0	0	0	D	0					O
5	D6	f												
6	D7	D	D	D	0	0	0	0	0	0	D	0	0	R
7	D8	f												
8	D9	f												
9	D10	A	0	0	D	0	0	0	0	0	0	0		H
10	D11	D	A	0	0	0	0	A	D					L
11	D12	D	D	D										R
12	E2	D	A	0	0	0	0	A	A			A		N
13	E1	D	D	D	0	0	0	0	0	0	D	0	0	R
14	E3	D	D	A	0	0	0	0	0	D	0	0	0	R
15	E4	D	D	D	0	0	0	0	0	0	D	0	0	R
16	E5	A	0	0			D	0	0	0	0	0		J2
17	E6	D	A	0	0	0	0	A	D					L
18	E7	A	0	0	A	A	A	0	0	0	0	0	D	F2
19	E8	D	D	D	0	0	0	0	0	0	D	0	0	R
20	E9	D	A	0	0	0	0	A	D					L
21	F12	A	0	0	A	A	A	0	0	0	0	0	D	F2
22	F13	A	0	0	A	A	A	0	0	0	0	0	D	F2
23	F14	A	0	0	A	A	A	0	0	0	0	0	A	C
24	F15	A	0	0	A	A	A	0	0	0	0	0	D	F2
25	F16	A	0	0	A	A	A	0	0	0	0	0	D	F2
26	F17	A	0	0	A	A	D	0	0	0	0	0	0	J2
27	F10	D	D	D	0	0	0	0	0	0	D	0	0	R
28	F11	A	0	0	A	A	A	0	0	0	0	0	D	F2
29	G1	D	D	D	0	0	0	0	0	0	D	0	0	R
30	G2	f												
31	G3	D	A	0	0	0	0	A	D					L
32	G4	D	D	D	0	0	0	0	0	0	D	0	0	R
33	G5	D	D	D	0	0	0	0	0	0	D	0	0	R
34	G6	D	A	0				D						O
35	G7	D	D	D	0	0	0	0	0	0	D	0	0	R
36	G9	D	A	0	0	0	0	A	A			A		N
37	G10	A	0	0	A	A	A	0	0	0	0	0	D	F2
38	G11	A	0	0	A	A	D	0	0	0	0	0		J2
39	G12	D	D	D	0	0	0	0	0	0	D	0	0	R
40	G13	D	D	D	0	0	0	0	0	0	D	0	0	R

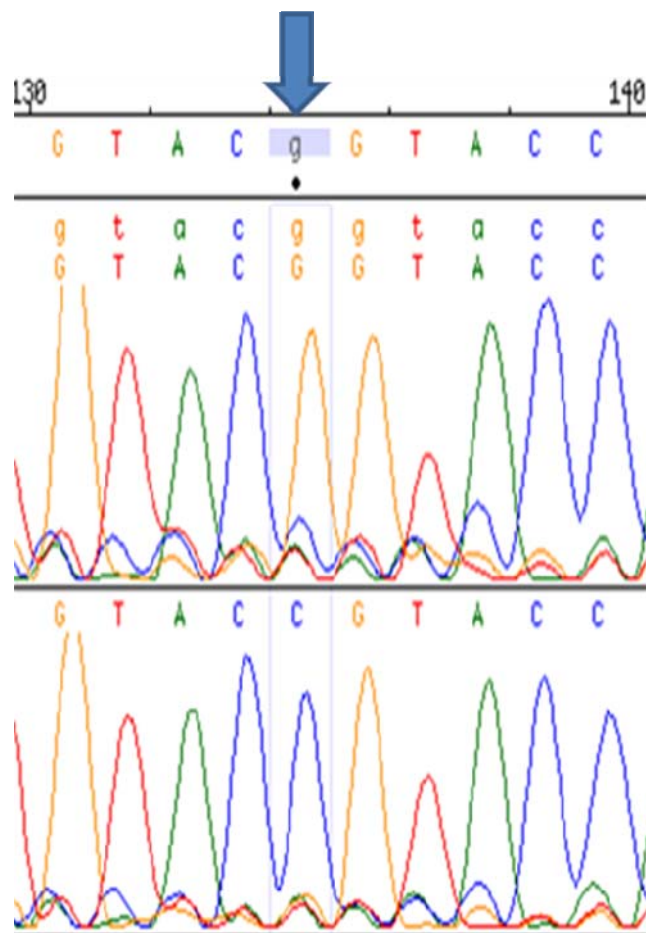


80	B72	f												
81	K1	D	D	D	0	0	0	0	0	0	D	0	0	R
82	K2	D	D	A	0	0	0	0	0	A	0	0	0	R
83	K3	D	D	D	0	0	0	0	0	0	D	0	0	R
84	K4	D	D	D	0	0	0	0	0	0	A	0	0	R
85	K5	A	0	0	A	A	D	0	0	0	0	0	0	J2
S.NO	DEFG BATCH	M9	M45	M173	M82	M69	M172	M175	M11	M124	M17	M189	M89	H
1	D1	D	D		0	0	0	0	0			0	0	R
2	D3	A	0	0	A	A	D	0	0	0	0	0		J2
3	D4	A	0	0	A	A	0	0	0	0	0	0	D	F
4	D5	D	A	0	0	0	0	D	0					O
5	D6	f												
6	D7	D	D	D	0	0	0	0	0	0	D	0	0	R
7	D8	f												
8	D9	f												
9	D10	A	0	0	D	0	0	0	0	0	0	0		H
10	D11	D	A	0	0	0	0	A	D					L
11	D12	D	D	D										R
12	E2	D	A	0	0	0	0	A	A			A		N
13	E1	D	D	D	0	0	0	0	0	0	D	0	0	R
14	E3	D	D	A	0	0	0	0	0	D	0	0	0	R
15	E4	D	D	D	0	0	0	0	0	0	D	0	0	R
16	E5	A	0	0			D	0	0	0	0	0		J2
17	E6	D	A	0	0	0	0	A	D					L
18	E7	A	0	0	A	A	A	0	0	0	0	0	D	F
19	E8	D	D	D	0	0	0	0	0	0	D	0	0	R
20	E9	D	A	0	0	0	0	A	D					L
21	F12	A	0	0	A	A	A	0	0	0	0	0	D	F
22	F13	A	0	0	A	A	A	0	0	0	0	0	D	F
23	F14	A	0	0	A	A	A	0	0	0	0	0	A	C
24	F15	A	0	0	A	A	A	0	0	0	0	0	D	F
25	F16	A	0	0	A	A	A	0	0	0	0	0	D	F
26	F17	A	0	0	A	A	D	0	0	0	0	0	0	J2
27	F10	D	D	D	0	0	0	0	0	0	D	0	0	R
28	F11	A	0	0	A	A	A	0	0	0	0	0	D	F
29	G1	D	D	D	0	0	0	0	0	0	D	0	0	R
30	G2	f												
31	G3	D	A	0	0	0	0	A	D					L
32	G4	D	D	D	0	0	0	0	0	0	D	0	0	R

33	G5	D	D	D	0	0	0	0	0	0	D	0	0	R
34	G6	D	A	0				D						O
35	G7	D	D	D	0	0	0	0	0	0	D	0	0	R
36	G9	D	A	0	0	0	0	A	A			A		N
37	G10	A	0	0	A	A	A	0	0	0	0	0	D	F
38	G11	A	0	0	A	A	D	0	0	0	0	0		J2
39	G12	D	D	D	0	0	0	0	0	0	D	0	0	R
40	G13	D	D	D	0	0	0	0	0	0	D	0	0	R
41	G14	D	A	0	0	0	0	A	A			A		N
42	G15	D	A	0	0	0	0	A	D					L
43	G16	D	D	A	0	0	0	0	0	D	0	0	0	R
44	G17	D	D	A	0	0	0	0	0	A	0	0	0	N
45	G19	D	A	0	0	0	0	A	A			A		N
46	G20	A	0	0	A	A	A	0	0	0	0	0	D	F
47	G21	D	D		0	0	0	0	0			0	0	R
48	G22	A	0	0	D	0	0	0	0	0	0	0	0	H
49	G23	A	0	0	D	0	0	0	0	0	0	0	0	H
50	G24	D	D	D	0	0	0	0	0	0	D	0	0	R
51	G25	D	A	0	0	0	0	A	D					L
52	G26	D	D	D	0	0	0	0	0	0	D	0	0	R
53	G27	A	0	0	A	A	A	0	0	0	0	0	D	F
54	G28	D	A	0	0	0	0	A	D					L
55	G29	A	0	0	A	D	0	0	0	0	0	0	0	H
56	G30	D	D	A	0	0	0	0	0	D	0	0	0	R
57	G31	D	D	D	0	0	0	0	0	0		0	0	R
58	G32	A	0	0	A	D	0	0	0	0	0	0	0	H
59	G33	D	A	0	0	0	0	A	D					L
60	G34	D	D	D	0	0	0	0	0	0		0	0	R
61	G35	D	A	0	0	0	0							O
62	G37	D	D	D	0	0	0	0	0	0	D	0	0	R
63	G40	D	D	D	0	0	0	0	0	0	D	0	0	R
64	G41	A	0	0	A	A	A	0	0	0	0	0	D	F
65	G42	D	D	A	0	0	0	0	0	A	0	0	0	R
66	G43	D	D	A	0	0	0	0	0	D	0	0	0	R
67	G44	D	D	A	0	0	0	0	0	A	0	0	0	Q
68	G45	D	D	A	0	0	0	0	0	A	0	0	0	Q
69	G46	D	D	D	0	0	0	0	0	0	D	0	0	R
70	G47	A	0	0			D	0	0	0	0	0		J2
71	G48	D	D	D	0	0	0	0	0	0	D	0	0	R

72	G49	F						0	0	0	0			
73	G50	D	D	D	0	0	0	0	0	0	D	0	0	R
74	B106	D	A	0	0	0	0	D				A		O
75	B105	D	D	A	0	0	0	0	0	D	0	0	0	R
76	B104	A	0	0	A		D	0	0	0	0	0		J2
77	B103	A	0	0	A	A	A	0	0	0	0	0	A	C
78	B87	D	D	D	0	0	0	0	0	0	D	0	0	R
79	B86	D	D	D										R
80	B72	f												
81	K1	D	D	D	0	0	0	0	0	0	D	0	0	R
82	K2	D	D	A	0	0	0	0	0	A	0	0	0	R
83	K3	D	D	D	0	0	0	0	0	0	D	0	0	R
84	K4	D	D	D	0	0	0	0	0	0	A	0	0	R
85	K5	A	0	0	A	A	D	0	0	0	0	0	0	J2

## Analysis of 5' UTR RAD 51 Gene



**g.135C>G mutation in 5' UTR RAD 51 gene**