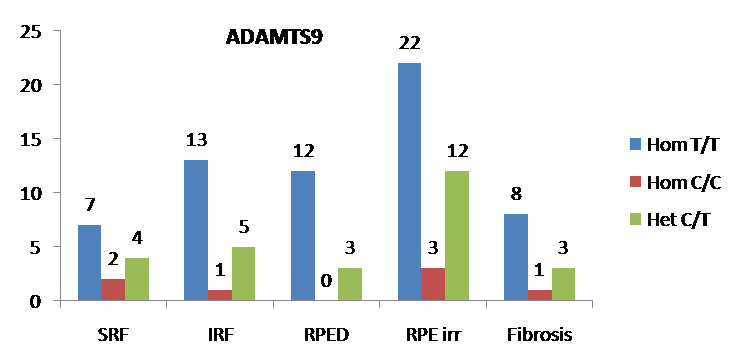
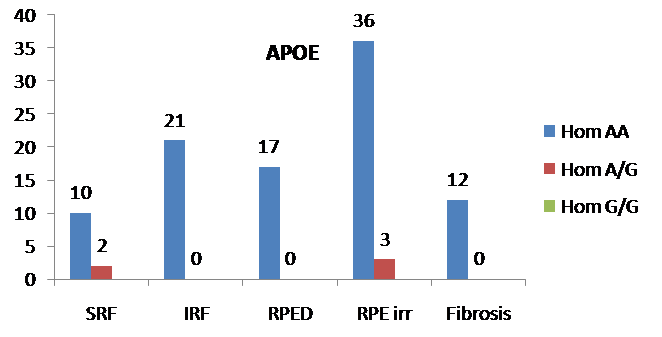
**Supplementary information**

**Results**

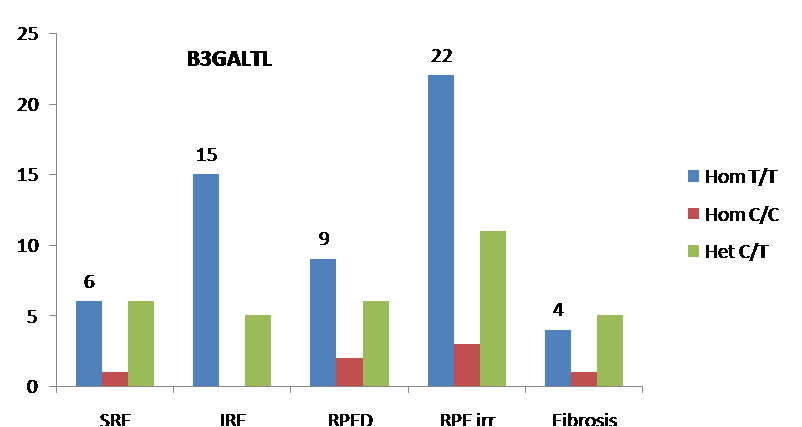
1. **Frequency of genotypes with clinical findings**

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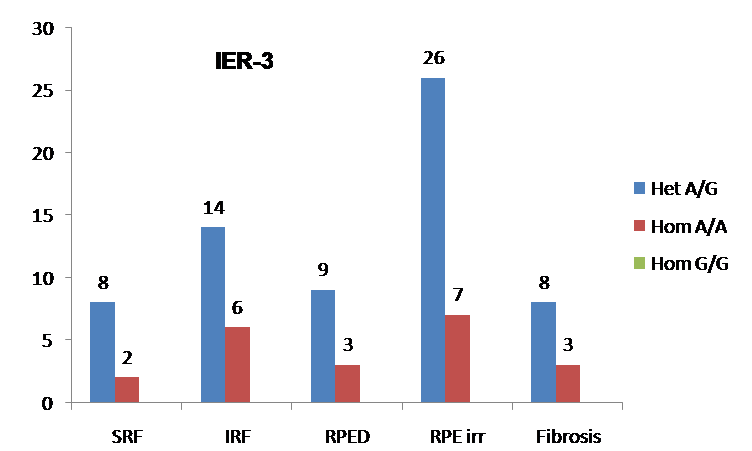
**Fig S1. Showing association of ADAMTS9 genotypes in different clinical findings.** X-axis represents clinical findings y axis represents number of individuals. Blue bar represents Hom T/T Genotype, Red bar represents Hom C/C and green bar represent Het C/T genotype respectively Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant.

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**Fig S2. Showing Association of APOE genotypes in different clinical findings.** X-axis represents clinical findings and y axis represents number of individuals. Blue bar represents Hom AA Genotype and Red bar represents Hom A/G genotype and green bar represents G/G genotype respectively. Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant.



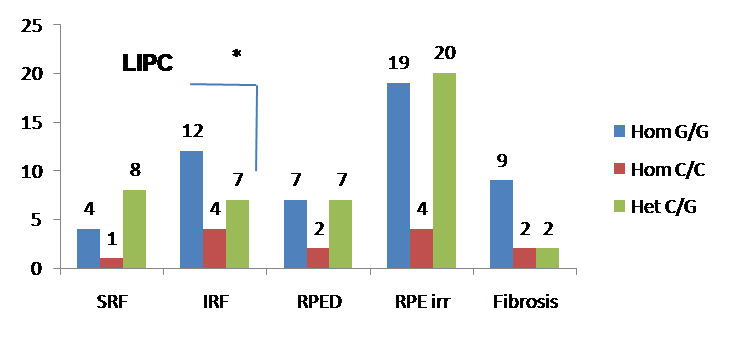
**Fig S3. Showing Association of B3GALTL genotypes in different clinical findings.** X-axis represents clinical findings and y axis represents number of individuals. Blue bar represents Hom T/T Genotype, Red bar represents Hom C/C and green bar represent Het C/T genotype respectively Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant



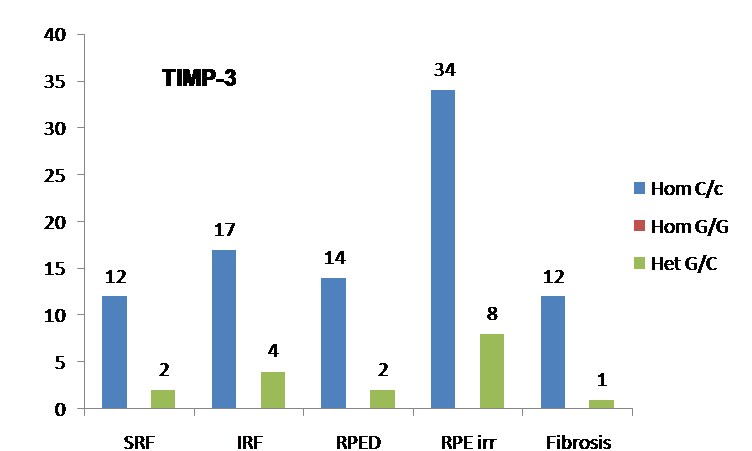
**Fig S4. IER-3 genotypes in different clinical findings.** X-axis represents clinical findings and y axis represents number of individuals. Blue bar represents Het A/G Genotype, Red bar represents Hom A/A and green bar represent Het G/G genotype respectively Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant.



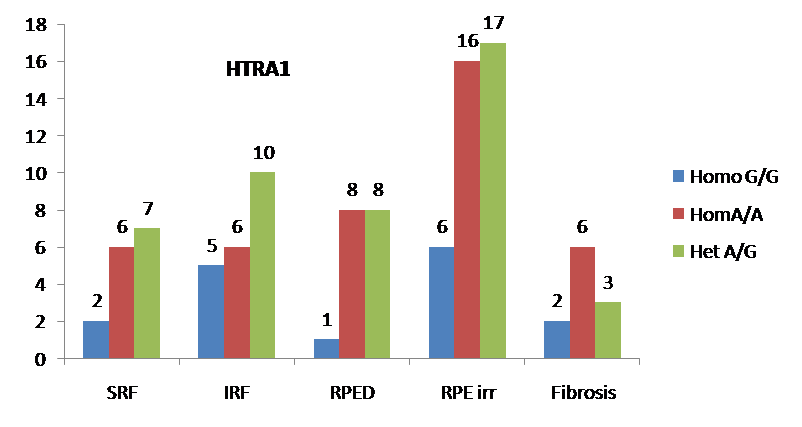
**Fig. S5. SLC16A8 genotypes in different clinical findings.** X axis represents clinical findings Blue bar represents Hom C/C Genotype, Red bar represents Hom T/T and green bar represent Het C/T genotype respectively Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant.



**Fig. S6. LIPC genotypes in different clinical findings.** X axis represents clinical findings and y axis represents number of individuals. Blue bar represents Hom G/G Genotype, Red bar represents Hom C/C and green bar represent Het C/G genotype respectively. Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant

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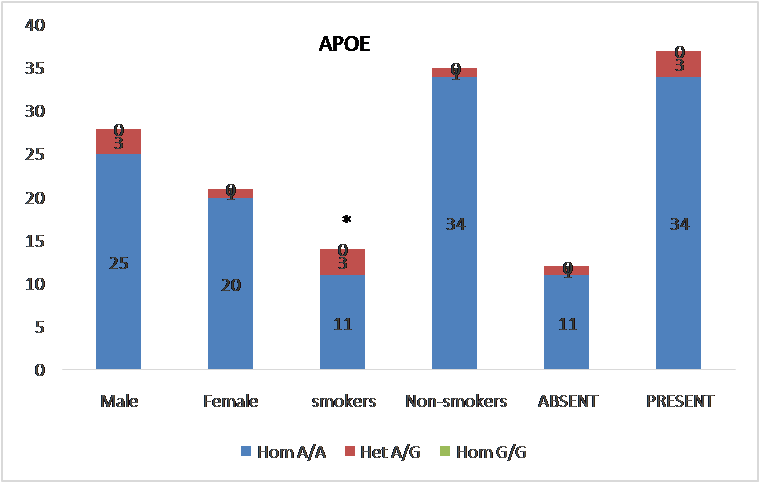
**Fig.S 7: TIMP3 genotypes in different clinical findings.** X-axis represents clinical findings and y axis represents number of individuals. Blue bar represents Hom C/C Genotype, Red bar represents Hom G/G and green bar represent Het G/C genotype respectively. Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant.



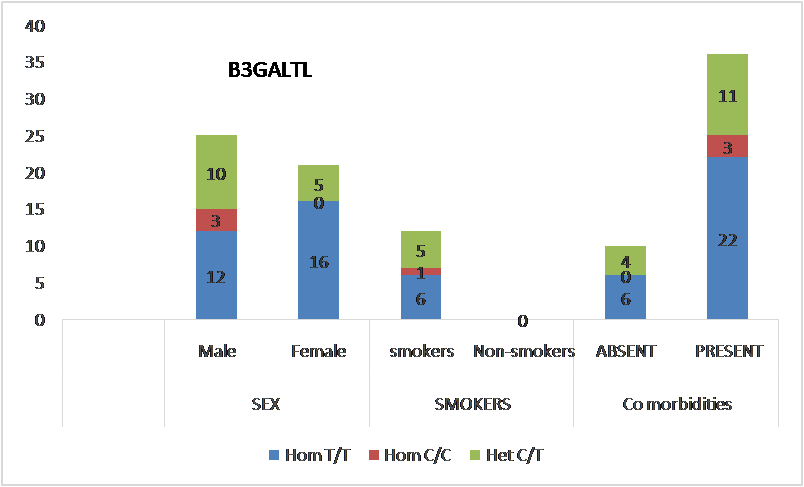
**Fig. S8. HTRA 1 genotypes in different clinical findings.** X-axis represents clinical findings and y axis represents number of individuals. Blue bar represents Hom G/G Genotype, Red bar represents Hom A/A and green bar represent Het A/G genotype respectively. Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant

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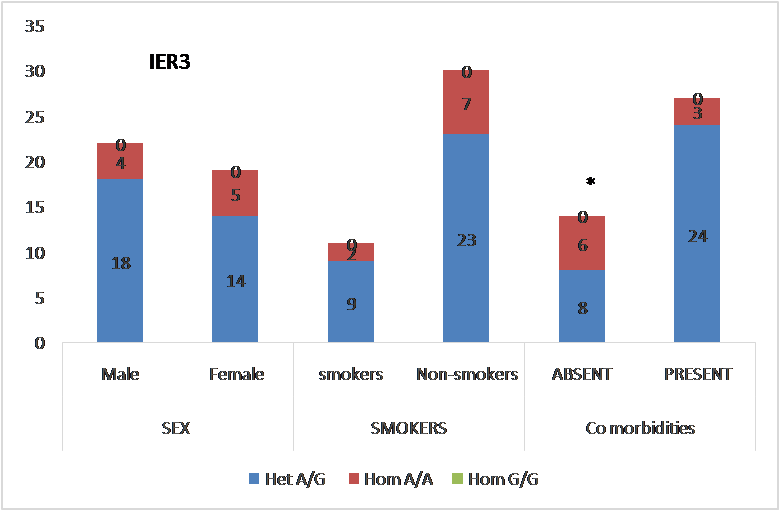
**Fig S 9: ADAMTS9 genotypes with socio­-demographic variables.** X-axis represents sociodemographic variables and y axis represents number of individuals .Green bar represents Het C/T red represents Hom C/C and Blue bar represents Hom T/T genotype respectively. Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant

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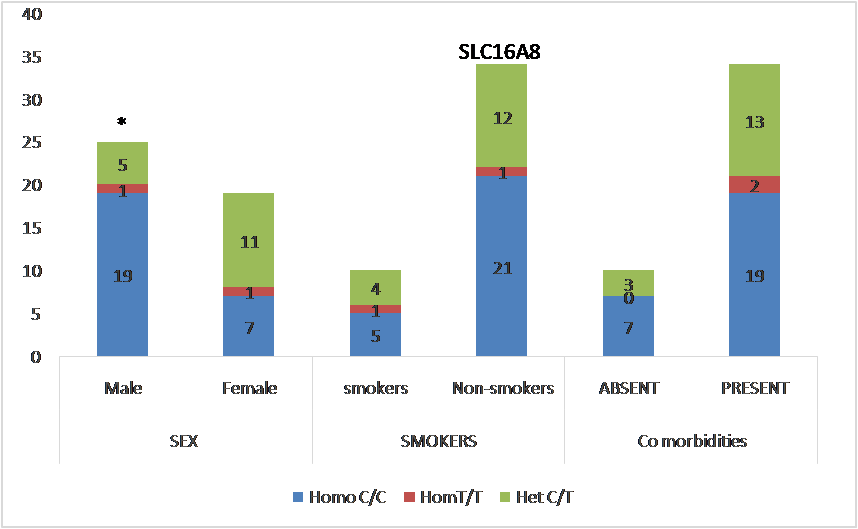
**Fig S10: APOE genotypes with sociodemographic variables.** X-axis represents sociodemographic variables and y axis represents number of individuals. Green bar represents Hom G/G red bar represents Het A/G , and Blue bar represents Hom A/A genotype respectively**.** Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant**.**



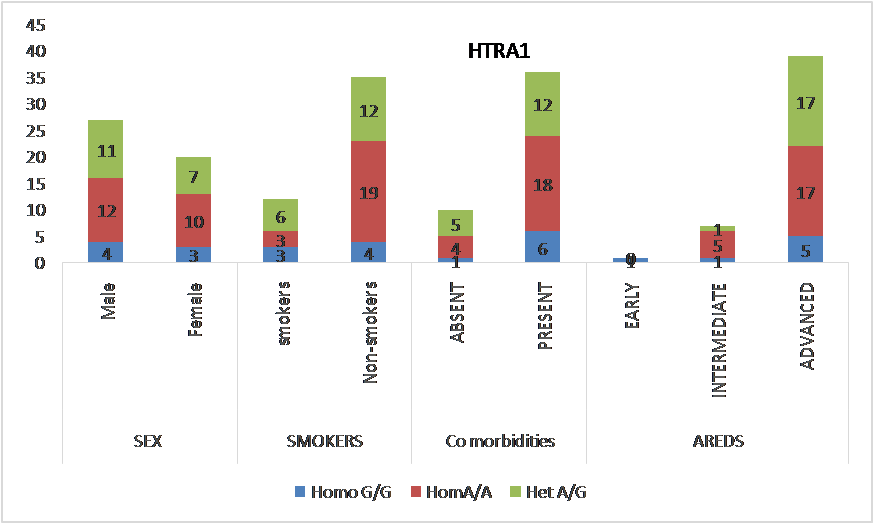
**Fig S11: B3GALTL genotypes with sociodemographic variables.** x axis represents sociodemographic variables and y axis represents number of individuals. Green bar represents Het C/T red bar represents Hom C/C , and Blue bar represents Hom T/T genotype respectively**.** Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant**.**

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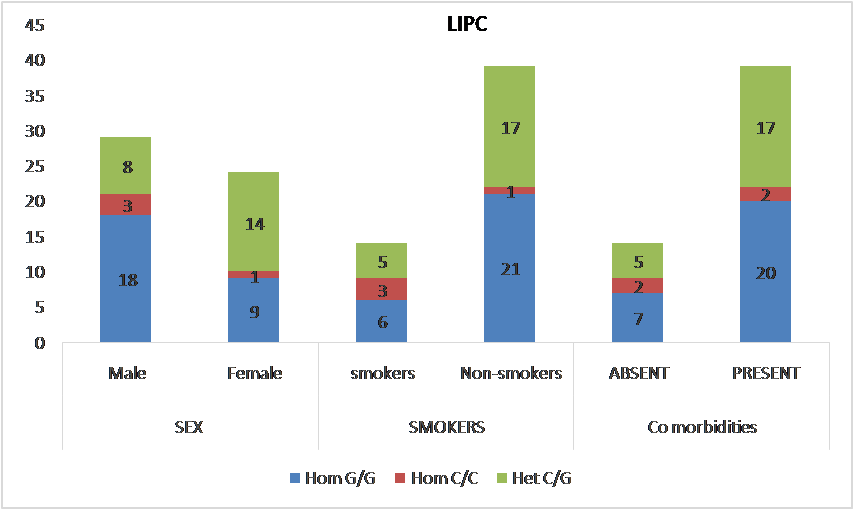
**Fig S12 :Association of IER-3 genotypes with sociodemographic variables.** X-axis represents sociodemographic variables and y axis represents number of individuals. Green bar represents Hom G/G red bar represents Hom A/A , and Blue bar represents Hom A/G genotype respectively. Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant**.**



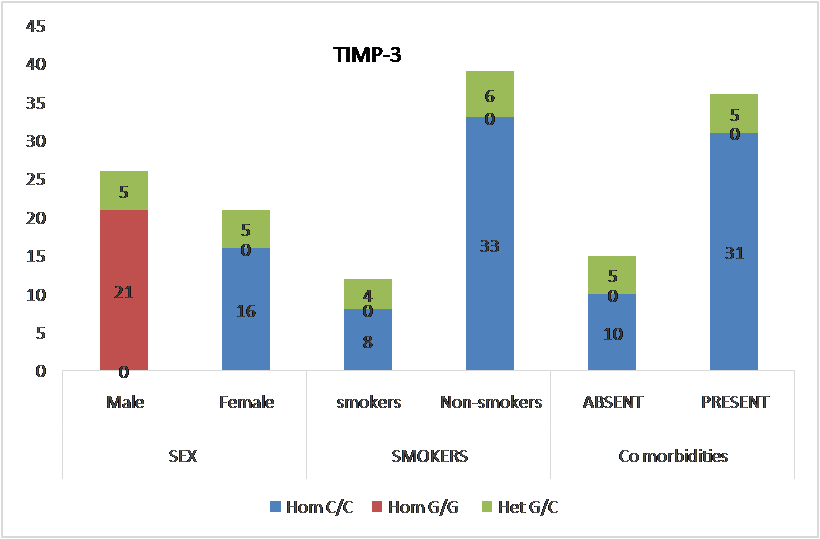
**Fig S13: Association of SLC16A8 genotypes with sociodemographic variables.** X-axis represents sociodemographic variables and y axis represents number of individuals. Green bar represents Het C/T red bar represents Hom T/T , and Blue bar represents Hom C/C genotype respectively**.** Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant**.**

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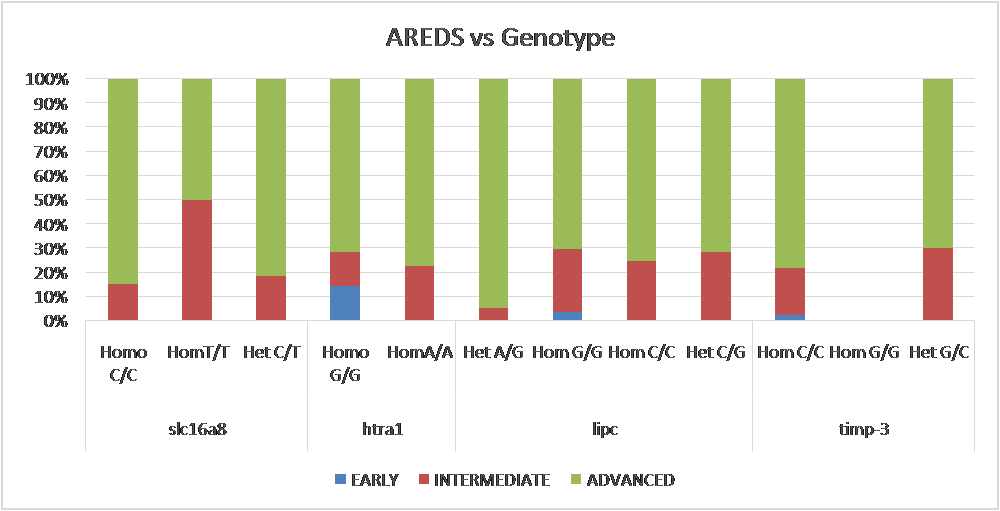
**Fig. S14: Association of HTRA1 genotypes with sociodemographic variables.** X-axis represents socio-demographic variables and y axis represents number of individuals. Green bar represents Het A/G genotype red bar represents Hom A/A , and Blue bar represents Hom G/G genotype respectively**.** Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant**.**



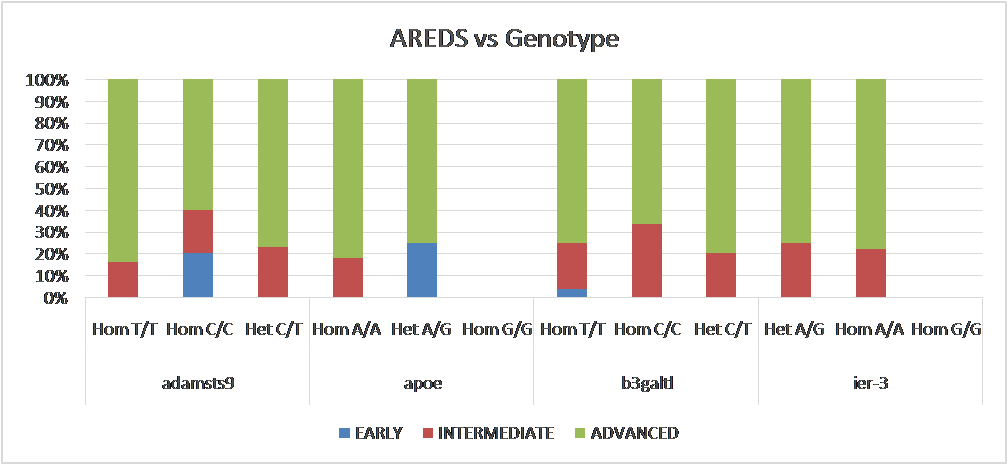
**Fig. S15: Association of LIPC genotypes with sociodemographic variables.** X-axis represents sociodemographic variables and y axis represents number of individuals. Green bar represents Het C/G genotype, red bar represents Hom C/C , and Blue bar represents Hom G/G genotype respectively**.** Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant.

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**Fig. S16: Association of TIMP3 genotypes with sociodemographic variables**. X-axis represents sociodemographic variables and y axis represents number of individuals. Green bar represents Het G/C genotype, red bar represents Hom G/G , and Blue bar represents Hom C/C genotype respectively**.** Statistical analysis was done by SPSS’s Pearson’s Chi Square test, (p≤0.05) was considered statistically significant.



**Fig S17:** Frequency distribution genotypes of SLC16A8, HTRA1, LIPC and TIMP-3 variants among AMD subtypes.



**Figure S18:** Frequency distribution of genotypes of SNP variants of ADAMTS9, APOE, B3GALTL and IER3 among AMD subtypes

**Table S1.Describing association of Genotypes (B3GALTL, IER3, SLC16A8, TIMP3) and clinical findings.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | B3GALTL  N=46 | | | | IER3  N=41 | | | | SLC16A8  N=44 | | | | TIMP3  N=51 | | | |
| Oct findings | **TT**  **N=28** | **CC**  **N=3** | **CT**  **N=15** | **p** | **AG**  **N=32** | **AA**  **N=9** | **GG**  **N=0** | **P** | **CC**  **N=26** | **TT**  **N=2** | **CT**  **N=16** | **P** | **CC**  **N=41** | **GG**  **N=0** | **GC**  **N=10** | **P** |
| SRF | 6 | 1 | 6 | .427 | 8 | 2 | 0 | .864 | 8 | 0 | 2 | .287 | 12 | 0 | 2 | .556 |
| IRF | 15 | 0 | 5 | .129 | 14 | 6 | 0 | .224 | 10 | 1 | 7 | .911 | 17 | 0 | 4 | .933 |
| RPED | 9 | 2 | 6 | .478 | 9 | 3 | 0 | .762 | 9 | 0 | 4 | .517 | 14 | 0 | 2 | .387 |
| RPE Irr | 22 | 3 | 11 | .592 | 26 | 7 | 0 | .816 | 20 | 2 | 13 | .877 | 34 | 0 | 8 | .828 |
| Fibrosis | 4 | 1 | 5 | .311 | 8 | 3 | 0 | .618 | 6 | 0 | 4 | .727 | 12 | 0 | 1 | .210 |

**Table S2: Proteins levels with respect to their genotypes of studied SNP variants**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | ADAMTS9  (N=43) | | | | APOE  (N=49) | | | | B3GALTL  (N=46) | | | | IER-3  (N=41) | | | |
|  | **TT**  **(n=25)** | **CC**  **(N=5)** | **CT**  **(N=13)** | **P** | **AA**  **(N=45)** | **AG**  **(N=4)** | **GG** | **P** | **TT**  **(N=28)** | **CC**  **(N=3)** | **CT**  **(N=15)** | **P** | **AG**  **(n=32)** | **AA**  **(N=9)** | **GG** | **p** |
| Protein levels  (Mean±SD) | 2.43 ±  0.909 | 2.53 ±  1.098 | 2.83±  1.61 | 0.61 | 0.005±  0.0045 | 0.0057±  0.002 |  | 0.75 | 4.80 ±  3.31 | 3.72 ±  1.92 | 3.78±  2.09 | 0.51 | 1.45±  2.44 | 0.92±  2.05 |  |  |
|  | **SLC16A8**  **(N=44)** | | | | **HTRA1**  **(N=47)** | | | | **LIPC**  **(N=53)** | | | | **TIMP3**  **(N=51)** | | | |
|  | **CC**  **(N=26)** | **TT**  **(N=2)** | **CT**  **(N=16)** | **P** | **GG**  **(N=7)** | **AA**  **(N=22)** | **AG**  **(N=18)** | **P** | **GG**  **(N=27)** | **CC**  **(N=4)** | **CG**  **(N=22)** | **P** | **CC**  **(N=41)** | **GG**  **(N=10)** | **GC** | **p** |
| Protein levels  (Mean±SD) | 0.92 ±  1.01 | 0.86 ±  1.21 | 0.55 ±  0.80 | 0.47 | 1.7 ±  0.36 | 2.8 ±  1.4 | 4.12±  4.11 | 0.12 | 1.32 ±  1.4 | 1.98±  3.24 | 1.67 ±  1.67 | 0.66 | 0.042±  0.035 | 0.035±  0.020 |  | 0.48 |