**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 | B3GALTLN=46 | IER3N=41 | SLC16A8N=44 | TIMP3N=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 |