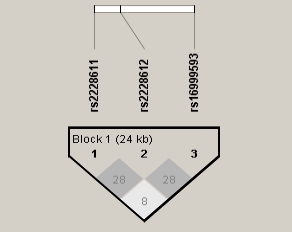
**Supplementary Figure 1 Linkage diaequillibrium(LD) pattern of DNMT1 SNPs by Haploview analysis.**



B

A

1. The schematic overview of linkage disequilibrium of the three studied SNPs. Numbers insides the boxes represent r2 values for LD

Shaded regions in the LD plot indicated the strength of LD between pair wise combinations of SNPs

1. Numbers behind the point show the frequent of the haplotype

**Supplementary Table 1 Odds ratio (OR) for case-control study of rs2228612 and rs16999593**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gender** | **Model type** | **Genotype** | **Control N (%)** | **Cases N (%)** | **OR(95% CI)** | **P-value** | **Adj OR(95% CI)** | **Adj P-value** |
| **rs2228612**  **(n=4078)** | **Codominant** | T/T | 327 (30.5%) | 939 (31.2%) | 1.00 | 1 | 1.00 | 1.00 |
| T/C | 524 (48.9%) | 1477 (49.1%) | 0.98 (0.84-1.15) | 0.82 | 1.02(0.85~1.22) | 0.86 |
| C/C | 221 (20.6%) | 590 (19.6%) | 0.93 (0.76-1.14) | 0.47 | 0.93(0.74~1.17) | 0.52 |
| **Dominant** | T/T | 327 (30.5%) | 939 (31.2%) | 1.00 | 1 | 1.00 | 1.00 |
| T/C-C/C | 745 (69.5%) | 2067 (68.8%) | 0.96 (0.83-1.12) | 0.66 | 0.99(0.83~1.18) | 0.92 |
| **Recessive** | T/T-T/C | 851 (79.4%) | 2416 (80.4%) | 1.00 | 1 | 1.00 | 1.00 |
| C/C | 221 (20.6%) | 590 (19.6%) | 0.94 (0.79-1.12) | 0.49 | 0.92(0.75~1.13) | 0.42 |
| **Overdominant** | T/T-C/C | 548 (51.1%) | 1529 (50.9%) | 1.00 | 1 | 1.00 | 1.00 |
| T/C | 524 (48.9%) | 1477 (49.1%) | 1.01 (0.88-1.16) | 0.89 | 1.05(0.89~1.23) | 0.59 |
| **rs16999593**  **(n=4089)** | **Codominant** | T/T | 697 (64.1%) | 1945 (64.8%) | 1.00 | 1 | 1.00 | 1.00 |
| T/C | 357 (32.8%) | 955 (31.8%) | 0.96 (0.83-1.11) | 0.58 | 1.01(0.85~1.20) | 0.89 |
| C/C | 34 (3.1%) | 101 (3.4%) | 1.07 (0.72-1.59) | 0.76 | 1.03(0.65~1.62) | 0.91 |
| **Dominant** | T/T | 697 (64.1%) | 1945 (64.8%) | 1.00 | 1 | 1.00 | 1.00 |
| T/C-C/C | 391 (35.9%) | 1056 (35.2%) | 0.97 (0.84-1.12) | 0.66 | 1.01(0.86~1.20) | 0.87 |
| **Recessive** | T/T-T/C | 1054 (96.9%) | 2900 (96.6%) | 1.00 | 1 | 1.00 | 1.00 |
| C/C | 34 (3.1%) | 101 (3.4%) | 1.08(0.73-1.6) | 0.7 | 1.02(0.65~1.61) | 0.93 |
| **Overdominant** | T/T-C/C | 731 (67.2%) | 2046 (68.2%) | 1.00 | 1 | 1.00 | 1.00 |
| T/C | 357 (32.8%) | 955 (31.8%) | 0.96 (0.82-1.11) | 0.55 | 1.01(0.85~1.2) | 0.90 |

OR, Odds ratio, N, number, Adj, adjust, 95%CI, 95% confidence interval .

1. value was the result from logistic regression analysis and OR and 95% CI were also the result from logistics.

Adj OR, P-values after adjusted for confounders (age, gender, BMI, heart rate, weight, height, TC, TG, HDL, LDL, HGB, GLU ).

**Supplementary Table 2 Multivariable adjusted haplotype analysis of DNMT1 gene and hypertension risk (n=3836)**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Haplotype1** | **Frequencies** | | | **OR(95%)** | **P -value** |
| **Total** | **Control** | **Case** |
| GTT | 0.276 | 0.286 | 0.272 | 1 | - |
| ATT | 0.275 | 0.26 | 0.28 | 1.15(1.00~1.32) | 0.05 |
| GCT | 0.252 | 0.259 | 0.25 | 1.02(0.89~1.17) | 0.79 |
| GCC | 0.189 | 0.188 | 0.189 | 1.06(0.9~1.23) | 0.49 |
| Rare | 0.009 | \* | \* | 1.08(0.55~2.12) | 0.82 |

1 Allele in haplotype were presented in order of polymorphisms rs2228611, rs2228612, rs16999593.

OR(95% Cl), P values were calculated after adjusted for age, gender and BMI

**Supplementary Table 3 Multivariable adjusted haplotype analysis of DNMT1 gene and hypertension risk (n=3836)**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Gender** | **Haplotype1** | **Frequencies** | | | **OR(95%)** | **P -value** |
| **Total** | **Control** | **Case** |
| Male | GTT | 0.280 | 0.282 | 0.279 | 1 | - |
| ATT | 0.275 | 0.256 | 0.281 | 1.11(0.9~1.38) | 0.33 |
| GCT | 0.246 | 0.256 | 0.244 | 0.97(0.78~1.21) | 0.8 |
| GCC | 0.190 | 0.195 | 0.187 | 0.95(0.75~1.20) | 0.65 |
| Rare | 0.009 | \* | \* | \* | \* |
| Female | GTT | 0.273 | 0.291 | 0.267 | 1 | - |
| ATT | 0.274 | 0.260 | 0.279 | 1.17(0.92~1.48) | 0.195 |
| GCT | 0.257 | 0.261 | 0.255 | 1.07(0.84~1.35) | 0.61 |
| GCC | 0.188 | 0.182 | 0.191 | 1.14(0.88~1.49) | 0.32 |
| Rare | 0.009 | \* | \* | \* | \* |

1 Allele in haplotype were presented in order of polymorphisms rs2228611, rs2228612, rs16999593.

OR(95% Cl), P values were calculated after adjusted for age and BMI