Supplemental material:

Table S1. Demographic characteristics of the study population.

|  |  |  |
| --- | --- | --- |
| **Characteristic** | **Group** | ***p*-value** |
| **Periodontitis*****n* = 261** | **Reference group*****n* = 441** |
| Males, *n* (%) | 107 (41.0 %) | 213 (48.3 %) | 0.060 |
| Females, *n* (%) | 154 (59. 0 %) | 228 (51.7 %) |  |
| Age, median (IQR) | 70 (17) | 69 (18) | 0.173 |
| SmokersNon-smokers | 235 (90.0 %)26 (10. 0 %) |  |  |
|  |  |  |  |

*p-*value—significance level.

Table S2. Binomial logistic regression analysis of periodontitis and reference groups with age and gender as covariates.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Model** | **Genotype/allele** | **OR (95% CI) \*** | ***p*-value** | **AIC** |
| rs1570360 |  |  |  |  |
| Co-dominant | AG vs. GGAA vs. GG | 1.07 (0.76-1.50)0.69 (0.44-1.08) | 0.7000.102 | 920.4 |
| Dominant | AG+AA vs. GG | 0.93 (0.68-1.27) | 0.651 | 923.0 |
| Recessive | AA vs. GG+AG | 0.67 (0.44-1.02) | 0.059 | 918.5 |
| Over-dominant | AG vs. GG+AA | 1.18 (0.86-1.63) | 0.297 | 921.1 |
| Additive | A | 0.87 (0.71-1.63) | 0.202 | 920.5 |
| rs699947 |  |  |  |  |
| Co-dominant | AC vs. AACC vs. AA | 1.37 (0.94-1.98)1.32 (0.85-2.04) | 0.1000.223 | 921.3 |
| Dominant | AC+CC vs. AA | 1.35 (0.95-1.92) | 0.094 | 919.3 |
| Recessive | CC vs. AA+AC | 1.08 (0.75-1.54) | 0.700 | 922.0 |
| Over-dominant | AC vs. AA+AC | 1.20 (0.89-1.64) | 0.238 | 920.8 |
| Additive | C | 1.15 (0.93-1.43) | 0.199 | 920.5 |
| rs3025033 |  |  |  |  |
| Co-dominant | AG vs. AAGG vs. AA | 0.88 (0.63-1.23)0.26 (0.09-0.75) | 0.4430.013 | 916.0 |
| Dominant | AG+GG vs. AA | 0.79 (0.57-1.09) | 0.147 | 920.1 |
| Recessive | GG vs. AG+AA | 0.27 (0.09-0.78) | 0.016 | 914.6 |
| Over-dominant | AG vs. AA+GG | 0.93 (0.67-1.30) | 0.687 | 922.0 |
| Additive | G | 0.74 (0.56-0.98) | 0.034 | 917.6 |
| rs2146323 |  |  |  |  |
| Codominant | CA vs. CCAA vs. CC | 0.87 (0.63-1.21)0.67 (0.41-1.08) | 0.4120.101 | 921.4 |
| Dominant | CA+AA vs. CC | 0.82 (0.59-1.11) | 0.195 | 920.5 |
| Recessive | AA vs. CC+CA | 0.71 (0.45-1.13) | 0.147 | 920.0 |
| Over-dominant | CA vs. CC+AA | 0.96 (0.70-1.31) | 0.790 | 922.1 |
| Additive | A | 0.83 (0.67-1.04) | 0.102 | 919.5 |

OR – odds ratio; CI – confidence interval; *p*–value - significance level; AIC - Akaike information criteria.

\*Bonferroni-corrected significance threshold (p<0.0125).

Table S3. Genotype and allele distribution of *VEGFA* (rs1570360, rs699947, rs3025033, and rs2146323) in males of periodontitis and reference groups.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype/Allele** | **Periodontitis** ***n* = 107****n (%)** | **Reference group*****n* = 213****n (%)** | ***p*-value** |
| rs1570360 |  |  |  |
| GG | 53 (49.5) | 93 (43.7) | 0.483 |
| AG | 38 (35.5) | 78 (36.6) |  |
| AA | 16 (15.0) | 42 (19.7) |  |
| Total | 107 (100) | 213 (100) |  |
|  |  |  |  |
| G | 144 (67.3) | 264 (62.0) | 0.187 |
| A | 70 (32.7) | 162 (38.0) |  |
| rs699947 |  |  |  |
| AA | 23 (21.5) | 64 (30.0) | 0.266 |
| AC | 56 (52.3) | 98 (46.0) |  |
| CC | 28 (26.2) | 51 (24.0) |  |
| Total | 107 (100) | 213 (100) |  |
|  |  |  |  |
| A | 102 (47.7) | 226 (53.1) | 0.198 |
| C | 112 (52.3) | 200 (46.9) |  |
| rs3025033 |  |  |  |
| AA | 77 (72.0) | 130 (61.0) | 0.120 |
| AG | 27 (25.2) | 70 (32.9) |  |
| GG | 3 (2.8) | 13 (6.1) |  |
| Total | 107 (100) | 213 (100) |  |
|  |  |  |  |
| A | 181 (84.6) | 330 (77.5) | 0.034 |
| G | 33 (15.4) | 96 (22.5) |  |
| rs2146323 |  |  |  |
| CC | 50 (46.7) | 97 (45.5) | 0.587 |
| CA | 44 (41.1) | 81 (38.0) |  |
| AA | 13 (12.1) | 35 (16.4) |  |
| Total | 107 (100) | 213 (100) |  |
|  |  |  |  |
| C | 144 (67.3) | 275 (64.6) | 0.492 |
| A | 70 (32.7) | 151 (35.4) |  |

*p*-value - significance level. Bonferroni-corrected significance threshold (p<0.0125).

Table S4. Genotype and allele distribution of *VEGFA* (rs1570360, rs699947, rs3025033, and rs2146323) in females of periodontitis and reference groups.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype/Allele** | **Periodontitis** ***n* = 154****n (%)** | **Reference group*****n* = 228****n (%)** | ***p*-value** |
| rs1570360 |  |  |  |
| GG | 67 (43.5) | 103 (45.2) | 0.160 |
| AG | 65 (42.2) | 78 (34.2) |  |
| AA | 22 (14.3) | 47 (20.6) |  |
| Total | 154 (100) | 228 (100) |  |
|  |  |  |  |
| G | 199 (64.6) | 284 (62.3) | 0.512 |
| A | 109 (35.4) | 172 (37.7) |  |
| rs699947 |  |  |  |
| AA | 40 (26.0) | 69 (30.3) | 0.664 |
| AC | 81 (52.6) | 111 (48.7) |  |
| CC | 33 (21.4) | 48 (21.1) |  |
| Total | 154 (100) | 228 (100) |  |
|  |  |  |  |
| A | 161 (52.3) | 249 (54.6) | 0.526 |
| C | 147 (47.7) | 207 (45.4) |  |
| rs3025033 |  |  |  |
| AA | 99 (64.3) | 144 (63.2) | **0.047** |
| AG | 54 (35.1) | 72 (31.6) |  |
| GG | 1 (0.6) | 12 (5.3) |  |
| Total | 154 (100) | 228 (100) |  |
|  |  |  |  |
| A | 252 (81.8) | 360 (78.9) | 0.330 |
| G | 56 (18.2) | 96 (21.1) |  |
| rs2146323 |  |  |  |
| CC | 72 (46.8) | 88 (38.6) | 0.235 |
| CA | 64 (41.6) | 104 (45.6) |  |
| AA | 18 (11.7) | 36 (15.8) |  |
| Total | 154 (100) | 228 (100) |  |
|  |  |  |  |
| C | 208 (67.5) | 280 (61.4) | 0.084 |
| A | 100 (32.5) | 176 (38.6) |  |

*p*-value - significance level; Bonferroni-corrected significance threshold (p<0.0125).

Table S5. Genotype and allele distribution of *VEGFA* (rs1570360, rs699947, rs3025033, and rs2146323) in males of periodontitis and reference groups.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Model** | **Genotype/allele** | **OR (95% CI) \*** | ***p*-value** | **AIC** |
| **Periodontitis** |  |  |  |  |
| rs1570360 |  |  |  |  |
| Co-dominant | AG vs. GGAA vs. GG | 0.86 (0.51-1.43)0.67 (0.34-1.30) | 0.5500.237 | 410.4 |
| Dominant | AG+AA vs. GG | 0.79 (0.50-1.26) | 0.320 | 408.8 |
| Recessive | AA vs. GG+AG | 0.12 (0.38-1.34) | 0.298 | 408.7 |
| Over-dominant | AG vs. GG+AA | 0.95 (0.59-1.55) | 0.846 | 409.8 |
| Additive | A | 0.83 (0.60-1.13) | 0.232 | 408.4 |
| rs699947 |  |  |  |  |
| Co-dominant | AC vs. AACC vs. AA | 1.59 (0.89-2.84)1.53 (0.79-2.97) | 0.1160.210 | 409.1 |
| Dominant | AC+CC vs. AA | 1.57 (0.91-2.71) | 0.106 | 407.1 |
| Recessive | CC vs. AA+AC | 1.13 (0.66-1.92) | 0.663 | 409.6 |
| Over-dominant | AC vs. AA+AC | 1.29 (0.81-2.05) | 0.286 | 408.7 |
| Additive | C | 1.23 (0.89-1.70) | 0.207 | 408.2 |
| rs3025033 |  |  |  |  |
| Co-dominant | AG vs. AAGG vs. AA | 0.65 (0.39-1.10)0.39 (0.09-1.41) | 0.1100.151 | 407.4 |
| Dominant | AG+GG vs. AA | 0.61 (0.37-1.01) | 0.055 | 406.0 |
| Recessive | GG vs. AG+AA | 0.44 (0.12-1.59) | 0.213 | 408.0 |
| Over-dominant | AG vs. AA+GG | 0.69 (0.41-1.16) | 0.162 | 405.8 |
| Additive | G | 0.64 (0.42-0.98) | 0.041 | 405.4 |
| rs2146323 |  |  |  |  |
| Codominant | CA vs. CCAA vs. CC | 1.05 (0.64-1.74)0.72 (0.35-1.48) | 0.8380.374 | 410.7 |
| Dominant | CA+AA vs. CC | 0.95 (0.60-1.52) | 0.840 | 409.8 |
| Recessive | AA vs. CC+CA | 0.70 (0.36-1.39) | 0.313 | 408.8 |
| Over-dominant | CA vs. CC+AA | 1.14 (0.71-1.83) | 0.593 | 409.5 |
| Additive | A | 0.90 (0.65-1.25) | 0.520 | 409.4 |

OR – odds ratio; CI – confidence interval; *p*–value - significance level; AIC - Akaike information criteria. \*Bonferroni-corrected significance threshold (p<0.0125).

Table S6. Genotype and allele distribution of *VEGFA* (rs1570360, rs699947, rs3025033, and rs2146323) in females of periodontitis and reference groups.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Model** | **Genotype/allele** | **OR (95% CI) \*** | ***p*-value** | **AIC** |
| **Periodontitis** |  |  |  |  |
| rs1570360 |  |  |  |  |
| Co-dominant | AG vs. GGAA vs. GG | 1.286 (0.82-2.01)0.72 (0.40-1.30) | 0.2810.276 | 515.4 |
| Dominant | AG+AA vs. GG | 1.07 (0.71-1.62) | 0.747 | 517.0 |
| Recessive | AA vs. GG+AG | 0.64 (0.37-1.12) | 0.117 | 514.6 |
| Over-dominant | AG vs. GG+AA | 1.40 (0.92-2.14) | 0.114 | 514.6 |
| Additive | A | 0.92 (0.70-1.21) | 0.549 | 516.8 |
| rs699947 |  |  |  |  |
| Co-dominant | AC vs. AACC vs. AA | 1.26 (0.78-2.04)1.19 (0.66-2.14) | 0.3510.571 | 518.3 |
| Dominant | AC+CC vs. AA | 1.24 (0.78-2.96) | 0.363 | 516.3 |
| Recessive | CC vs. AA+AC | 1.02 (0.62-1.69) | 0.930 | 515.1 |
| Over-dominant | AC vs. AA+AC | 1.17 (0.78-1.76) | 0.453 | 516.6 |
| Additive | C | 1.10 (0.82-1.47) | 0.524 | 516.7 |
| rs3025033 |  |  |  |  |
| Co-dominant | AG vs. AAGG vs. AA | 1.09 (0.71-1.68)0.12 (0.02-0.95) | 0.6960.044 | 511.6 |
| Dominant | AG+GG vs. AA | 0.95 (0.62-1.46) | 0.822 | 517.1 |
| Recessive | GG vs. AG+AA | 0.12 (0.02-0.91) | 0.041 | 509.8 |
| Over-dominant | AG vs. AA+GG | 1.17 (0.76-1.80) | 0.477 | 516.6 |
| Additive | G | 0.83 (0.57-1.20) | 0.322 | 514.1 |
| rs2146323 |  |  |  |  |
| Codominant | CA vs. CCAA vs. CC | 0.75 (0.48-1.17)0.61 (0.32-1.17) | 0.2050.135 | 516.2 |
| Dominant | CA+AA vs. CC | 0.72 (0.47-1.08) | 0.113 | 514.6 |
| Recessive | AA vs. CC+CA | 0.71 (0.39-1.30) | 0.261 | 515.8 |
| Over-dominant | CA vs. CC+AA | 0.85 (0.56-1.28) | 0.434 | 516.5 |
| Additive | A | 0.77 (0.57-1.04) | 0.092 | 514.3 |

OR – odds ratio; CI – confidence interval; *p*–value - significance level; AIC - Akaike information criteria. Bonferroni-corrected significance threshold (p<0.0125).

Table S7. Genotype and allele distribution of *VEGFA* (rs1570360, rs699947, rs3025033, and rs2146323) in >70 years old periodontitis and reference group subjects.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype/Allele** | **Periodontitis** ***n* = 130****n (%)** | **Reference group*****n* = 189****n (%)** | ***p*-value** |
| >70 years |
| rs1570360 |  |  |  |
| GG | 54 (18.5) | 84 (44.4) | 0.767 |
| AG | 52 (40.0) | 68 (36.0) |  |
| AA | 24 (18.5) | 37 (19.6) |  |
| Total | 130 (100) | 189 (100) |  |
|  |  |  |  |
| G | 160 (61.5) | 236 (62.4) | 0.819 |
| A | 100 (38.5) | 142 (37.6) |  |
| rs699947 |  |  |  |
| AA | 32 (24.6) | 56 (29.6) | 0.557 |
| AC | 69 (53.1) | 90 (47.6) |  |
| CC | 29 (22.3) | 43 (22.8) |  |
| Total | 130 (100) | 189 (100) |  |
|  |  |  |  |
| A | 133 (51.2) | 202 (53.4) | 0.570 |
| C | 127 (48.8) | 176 (46.6) |  |
| rs3025033 |  |  |  |
| AA | 88 (67.7) | 115 (60.8) | 0.202 |
| AG | 40 (30.8) | 65 (34.4) |  |
| GG | 2 (1.5) | 9 (4.8) |  |
| Total | 130 (100) | 189 (100) |  |
|  |  |  |  |
| A | 216 (83.1) | 295 (78) | 0.118 |
| G | 44 (16.9) | 83 (22) |  |
| rs2146323 |  |  |  |
| CC | 60 (46.2) | 86 (45.5) | 0.687 |
| CA | 55 (42.3) | 75 (39.7) |  |
| AA | 15 (11.5) | 28 (14.8) |  |
| Total | 130 (100) | 189 (100) |  |
|  |  |  |  |
| C | 175 (67.3) | 247 (65.3) | 0.607 |
| A | 85 (32.7) | 131 (34.7) |  |

*p-*value - significance level; Bonferroni-corrected significance threshold (p<0.0125).

Table S8. Binary logistic regression analysis of *VEGFA* (rs1570360, rs699947, rs3025033, and rs2146323) in >70 years old periodontitis and reference group subjects.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Model** | **Genotype/allele** | **OR (95% CI) \*** | ***p*-value** | **AIC** |
| rs1570360 |  |  |  |  |
| Co-dominant | AG vs. GGAA vs. GG | 1.190 (0.723-1.956)1.009 (0.544-1.879) | 0.4940.977 | 434.7 |
| Dominant | AG+AA vs. GG | 1.126 (0.717-1.769) | 0.607 | 433.0 |
| Recessive | AA vs. GG+AG | 0.930 (0.526-1.645) | 0.803 | 433.2 |
| Over-dominant | AG vs. GG+AA | 1.186 (0.749-1.879) | 0.466 | 432.7 |
| Additive | A | 1.032 (0.767-1.389) | 0.834 | 433.2 |
| rs699947 |  |  |  |  |
| Co-dominant | AC vs. AACC vs. AA | 1.342 (0.785-2.292)1.180 (0.622-2.240) | 0.2820.612 | 434.1 |
| Dominant | AC+CC vs. AA | 1.289 (0.777-2.140) | 0.325 | 432.3 |
| Recessive | CC vs. AA+AC | 0.975 (0.571-1.664) | 0.926 | 433.2 |
| Over-dominant | AC vs. AA+AC | 1.244 (0.795-1.946) | 0.338 | 432.3 |
| Additive | C | 1.096 (0.799-1.504) | 0.570 | 432.9 |
| rs3025033 |  |  |  |  |
| Co-dominant | AG vs. AAGG vs. AA | 0.804 (0.497-1.302)0.290 (0.061-1.378) | 0.3750.120 | 431.8 |
| Dominant | AG+GG vs. AA | 0.742 (0.464-1.186) | 0.212 | 431.7 |
| Recessive | GG vs. AG+AA | 0.313 (0.066-1.471) | 0.141 | 430.6 |
| Over-dominant | AG vs. AA+GG | 0.848 (0.526-1.368) | 0.499 | 432.8 |
| Additive | G | 0.716 (0.473-1.083) | 0.113 | 430.7 |
| rs2146323 |  |  |  |  |
| Codominant | CA vs. CCAA vs. CC | 1.051 (0.651-1.698)0.768 (0.378-1.559) | 0.8380.465 | 434.5 |
| Dominant | CA+AA vs. CC | 0.974 (0.622-1.525) | 0.909 | 433.2 |
| Recessive | AA vs. CC+CA | 0.750 (0.383-1.467) | 0.401 | 432.5 |
| Over-dominant | CA vs. CC+AA | 1.115 (0.708-1.755) | 0.639 | 433.0 |
| Additive | A | 0.922 (0.669-1.271) | 0.622 | 433.0 |

OR – odds ratio; CI – confidence interval; *p*–value - significance level; AIC - Akaike information criteria. Bonferroni-corrected significance threshold (p<0.0125).

Table S9. Genotype and allele distribution of *VEGFA* (rs1570360, rs699947, rs3025033, and rs2146323) in <=70 years old periodontitis and reference group subjects.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype/Allele** | **Periodontitis** ***n* = 131****n (%)** | **Reference group*****n* = 252****n (%)** | ***p*-value** |
| <=70 years |
| rs1570360 |  |  |  |
| GG | 66 (50.4) | 112 (44.44) | 0.050 |
| AG | 51 (38.9) | 88 (34.9) |  |
| AA | 14 (10.7)1 | 52 (20.6)1 |  |
| Total | 131 (100) | 252 (100) |  |
|  |  |  |  |
| G | 183 (69.8) | 312 (61.9) | 0.029 |
| A | 79 (30.2) | 192 (38.1) |  |
| rs699947 |  |  |  |
| AA | 31 (23.7) | 77 (30.6) | 0.364 |
| AC | 68 (51.9) | 119 (47.2) |  |
| CC | 32 (24.4) | 56 (22.2) |  |
| Total | 131 (100) | 252 (100) |  |
|  |  |  |  |
| A | 130 (49.6) | 273 (54.2) | 0.2317 |
| C | 132 (50.4) | 231 (45.8) |  |
| rs3025033 |  |  |  |
| AA | 88 (67.2) | 159 (63.1) | 0.105 |
| AG | 41 (31.3) | 77 (30.6) |  |
| GG | 2 (1.5) | 16 (6.3) |  |
| Total | 131 (100) | 252 (100) |  |
|  |  |  |  |
| A | 217 (82.8) | 395 (78.4) | 0.145 |
| G | 45 (17.2) | 109 (21.6) |  |
| rs2146323 |  |  |  |
| CC | 62 (47.3) | 99 (39.3) | 0.241 |
| CA | 53 (40.5) | 110 (43.7) |  |
| AA | 16 (12.2) | 43 (17.1) |  |
| Total | 131 (100) | 252 (100) |  |
|  |  |  |  |
| C | 177 (67.6) | 308 (61.1) | 0.079 |
| A | 85 (32.4) | 196 (38.9) |  |

*p-*value - significance level; Bonferroni-corrected significance threshold (p<0.0125).

Table S10. Binary logistic regression analysis of *VEGFA* (rs1570360, rs699947, rs3025033, and rs2146323) in <=70 years old periodontitis and reference group subjects.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Model** | **Genotype/allele** | **OR (95% CI) \*** | ***p*-value** | **AIC** |
| rs1570360 |  |  |  |  |
| Co-dominant | AG vs. GGAA vs. GG | 0.983 (0.621-1.558)0.457 (0.235-0.887) | 0.9430.021 | 489.7 |
| Dominant | AG+AA vs. GG | 0.788 (0.516-1.203) | 0.269 | 492.8 |
| Recessive | AA vs. GG+AG | 0.460 (0.244-0.866) | 0.016 | 487.7 |
| Over-dominant | AG vs. GG+AA | 1.188 (0.768-1.838) | 0.439 | 493.5 |
| Additive | A | 0.744 (0.555-0.997) | 0.048 | 490.1 |
| rs699947 |  |  |  |  |
| Co-dominant | AC vs. AACC vs. AA | 1.419 (0.850-2.369)1.419 (0.777-2.592) | 0.1800.254 | 494.0 |
| Dominant | AC+CC vs. AA | 1.419 (0.875-2.303) | 0.156 | 492.0 |
| Recessive | CC vs. AA+AC | 1.131 (0.688-1.860) | 0.627 | 493.8 |
| Over-dominant | AC vs. AA+AC | 1.206 (0.791-1.841) | 0.384 | 493.3 |
| Additive | C | 1.196 (0.889-1.609) | 0.237 | 492.7 |
| rs3025033 |  |  |  |  |
| Co-dominant | AG vs. AAGG vs. AA | 0.962 (0.607-1.524)0.226 (0.051-1.005) | 0.8690.051 | 490.7 |
| Dominant | AG+GG vs. AA | 0.835 (0.535-1.304) | 0.429 | 493.4 |
| Recessive | GG vs. AG+AA | 0.229 (0.052-1.010) | 0.052 | 488.7 |
| Over-dominant | AG vs. AA+GG | 1.035 (0.656-1.634) | 0.881 | 494.0 |
| Additive | G | 0.759 (0.520-1.109) | 0.154 | 492.0 |
| rs2146323 |  |  |  |  |
| Codominant | CA vs. CCAA vs. CC | 0.769 (0.488-1.214)0.594 (0.308-1.145) | 0.2600.120 | 493.2 |
| Dominant | CA+AA vs. CC | 0.720 (0.470-1.103) | 0.131 | 491.8 |
| Recessive | AA vs. CC+CA | 0.676 (0.365-1.254) | 0.214 | 492.5 |
| Over-dominant | CA vs. CC+AA | 0.877 (0.571-1.347) | 0.549 | 493.7 |
| Additive | A | 0.770 (0.569-1.044) | 0.093 | 491.2 |

OR – odds ratio; CI – confidence interval; *p*–value - significance level; AIC - Akaike information criteria. Bonferroni-corrected significance threshold (p<0.0125).

Table S11. Genotype distribution and serum VEGFA levels.

|  |  |  |
| --- | --- | --- |
| **Genotype** | **VEGFA level (pg/mL)** | **p-value** |
| **Periodontitis group****Median (IQR)** | **Reference group****Median (IQR)** |
| rs1570360 |
| GG | 315.06 (297.64) | 508.64 (414.46) | 0.033 |
| AG | 737.42 (776.85) | 486.00 (531.62) | 0.551 |
| AA | 200.61 (488.32) | 479.73 (570.12) | 0.462 |
| rs699947 |
| AA | 713.93 (794.54)  | 479.73 (459.76) | 0.534 |
| AC | 388.54 (621.31) | 518.87 (445.33) | 0.335 |
| CC | 423.96 (390.50) | 487.08 (585.54) | 0.166 |
| rs3025033 |
| AA | 423.96 (609.57) | 428.96 (459.23) | 0.509 |
| AG | 526.99 (608.83) | 615.65 (363.08) | 0.661 |
| GG | - | - | NA |
| rs2146323 |
| CC | 423.96 (584.33) | 487.08 (457.28) | 0.240 |
| CA | 322.29 (538.85) | 491.15 (461.99) | 0.245 |
| AA | 819.93 (928.71) | 526.73 (461.32) | 0.251 |

\*Mann-Whitney U test was used

Table S12. Linkage disequilibrium between studied polymorphisms in patients with periodontitis.

|  |  |
| --- | --- |
| **SNPs** | **Periodontitis vs. Reference group** |
| **D’** | **r2** | ***p* Value** |
| rs1570360–rs699947 | 0.539 | 0.280 | <0.001 |
| rs1570360–rs3025033 | 0.042 | 0.006 | 0.0036 |
| rs1570360–rs2146323 | 0.012 | 0.011 | 0.0001 |
| rs699947–rs3025033 | <0.001 | <0.001 | 0.7396 |
| rs699947–rs2146323 | 0.930 | 0.460 | <0.001 |
| rs3025033–rs2146323 | 0.028 | 0.013 | <0.001 |

D': the deviation between the expected haplotype frequency and the observed frequency; r²: the square of haplotype frequency correlation coefficient.