

Table S2. For each bacterial strain on top distributions of genotype and allele frequencies, down haplotype analysis of SNPs VDR FokI (Rs2228570), VDR BsmI (Rs1577710), VDR ApaI (Rs7975232) and VDR TaqI (Rs731236) in health controls and periodontitis patients .

| Aggregatibacter Actinomycetemcomitans   |               |           |               |                |                 |
|---|---------------|-----------|---------------|----------------|-----------------|
|   |               |           | LOW<br>(N=36) | HIGH<br>(N=14) | P value         |
| <b>VDR FokI<br/>rs2228570</b><br>Exon2<br>c.2T>C ( <i>f&gt;F</i> )*<br><i>p.Met1Thr</i>   | Genotypes (%) | C/C (F/F) | 13 (36)       | 1 (7)          | <b>0.034708</b> |
|   |               | C/T (F/f) | 14 (39)       | 11 (79)        |                 |
|   |               | T/T (f/f) | 9 (25)        | 2 (14)         |                 |
|   | Alleles (%)   | C (F)     | 40 (56)       | 13 (46)        | 0.41            |
|   |               | T (f)     | 32 (44)       | 15 (54)        |                 |
|   | HW (p)        |           | 0.2           | 0.1            |                 |
| <b>VDR BsmI<br/>rs1544410</b><br>Intron 8<br>c.1024+283A>G( <i>B&gt;b</i> )*              | Genotypes (%) | A/A (B/B) | 1 (3)         | 0 (0)          | 0.75            |
|   |               | A/G (B/b) | 6 (17)        | 2 (14)         |                 |
|   |               | G/G (b/b) | 29 (81)       | 12 (86)        |                 |
|   | Alleles (%)   | A (B)     | 8 (11)        | 2 (7)          | 0.55            |
|   |               | G (b)     | 64 (89)       | 26 (93)        |                 |
|   | HW (p)        |           | 0.35          | 1              |                 |
| <b>VDR ApaI<br/>rs7975232</b><br>Intron 8<br>c.1025-49A>C( <i>A&gt;c</i> )*               | Genotypes (%) | A/A (A/A) | 5 (14)        | 0 (0)          | 0.28            |
|   |               | A/C (A/a) | 17 (47)       | 9 (64)         |                 |
|   |               | C/C (a/a) | 14 (39)       | 5 (36)         |                 |
|   | Alleles (%)   | A (A)     | 27 (38)       | 9 (32)         | 0.61            |
|   |               | C (a)     | 45 (62)       | 19 (68)        |                 |
|   | HW (p)        |           | 1             | 0.22           |                 |
| <b>VDR TaqI<br/>rs731236</b><br>Exon 9<br>c.1056T>C ( <i>T&gt;t</i> )<br><i>p.Ile352=</i> | Genotypes (%) | T/T (T/T) | 32 (89)       | 13 (93)        | 0.67            |
|   |               | T/C (T/t) | 4 (11)        | 1 (7)          |                 |
|   |               | C/C (t/t) | 0 (0)         | 0 (0)          |                 |
|   | Alleles (%)   | T (T)     | 68 (94)       | 27 (96)        | 0.68            |
|   |               | C (t)     | 4 (6)         | 1 (4)          |                 |
|   | HW (p)        |           | 1             | 1              |                 |

| Aggregatibacter Actinomycetemcomitans |                |                |                |                    |                              |       |              |                      |
|---------------------------------------|----------------|----------------|----------------|--------------------|------------------------------|-------|--------------|----------------------|
| Haplotype                             |                |                |                | Total<br>frequency | Clinical groups<br>frequency |       | p-value      | OR (95% CI)          |
| FokI                                  | BsmI           | ApaI           | TaqI           |                    | LOW                          | HIGH  |              |                      |
| T ( <i>f</i> )                        | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.287              | 0.247                        | 0.214 | 0.66         | 0.793 (0.277-2.266)  |
| C ( <i>F</i> )                        | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.260              | 0.266                        | 0.392 | <b>0.25</b>  | 1.702 (0.677-4.281)  |
| C ( <i>F</i> )                        | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.200              | 0.228                        | 0     | <b>0.005</b> | -                    |
| T ( <i>f</i> )                        | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.112              | 0.104                        | 0.287 | <b>0.029</b> | 3.322 (1.088-10.140) |
| C ( <i>F</i> )                        | A ( <i>B</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.05               | 0.04                         | 0.07  | 0.62         | 1.568 (0.255-9.648)  |

| Porphyromonas Gingivalis  |               |           |            |             |                 |
|---|---------------|-----------|------------|-------------|-----------------|
|   |               |           | LOW (N=28) | HIGH (N=22) | P value         |
|   |               |           |            |             |                 |
| <b>VDR FokI<br/>rs2228570</b><br>Exon2<br>c.2T>C ( <i>f&gt;F</i> )*<br><i>p.Met1Thr</i>   | Genotypes (%) | C/C (F/F) | 12 (43)    | 2 (9)       | <b>0.022173</b> |
|   |               | C/T (F/f) | 10 (36)    | 15 (68)     |                 |
|   |               | T/T (f/f) | 6 (21)     | 5 (23)      |                 |
|   | Alleles (%)   | C (F)     | 34 (61)    | 19 (43)     | 0.081           |
|   |               | T (f)     | 22 (39)    | 25 (57)     |                 |
|   | HW (p)        |           | 0.23       | 0.19        |                 |
| <b>VDR BsmI<br/>rs1544410</b><br>Intron 8<br>c.1024+283A>G( <i>B&gt;b</i> )*              | Genotypes (%) | A/A (B/B) | 1 (4)      | 0 (0)       | 0.087           |
|   |               | A/G (B/b) | 7 (25)     | 1 (5)       |                 |
|   |               | G/G (b/b) | 20 (71)    | 21 (95)     |                 |
|   | Alleles (%)   | A (B)     | 9 (16)     | 1 (2)       | <b>0.022462</b> |
|   |               | G (b)     | 47 (84)    | 43 (98)     |                 |
|   | HW (p)        |           | 0.53       | 1           |                 |
| <b>VDR ApaI<br/>rs7975232</b><br>Intron 8<br>c.1025-49A>C( <i>A&gt;c</i> )*               | Genotypes (%) | A/A (A/A) | 4 (14)     | 1 (5)       | 0.22            |
|   |               | A/C (A/a) | 16 (57)    | 10 (45)     |                 |
|   |               | C/C (a/a) | 8 (29)     | 11 (50)     |                 |
|   | Alleles (%)   | A (A)     | 24 (43)    | 12 (27)     | 0.10            |
|   |               | C (a)     | 32 (57)    | 32 (73)     |                 |
|   | HW (p)        |           | 0.47       | 1           |                 |
| <b>VDR TaqI<br/>rs731236</b><br>Exon 9<br>c.1056T>C ( <i>T&gt;t</i> )<br><i>p.Ile352=</i> | Genotypes (%) | T/T (T/T) | 26 (93)    | 19 (86)     | 0.44            |
|   |               | T/C (T/t) | 2 (7)      | 3 (14)      |                 |
|   |               | C/C (t/t) | 0 (0)      | 0 (0)       |                 |
|   | Alleles (%)   | T (T)     | 54 (96)    | 41 (93)     | 0.45            |
|   |               | C (t)     | 2 (4)      | 3 (7)       |                 |
|   | HW (p)        |           | 1          | 1           |                 |

| Porphyromonas Gingivalis |                |                |                |                 |                           |       |               |                      |
|--------------------------|----------------|----------------|----------------|-----------------|---------------------------|-------|---------------|----------------------|
| Haplotype                |                |                |                | Total frequency | Clinical groups frequency |       | p-value       | OR (95% CI)          |
| FokI                     | BsmI           | ApaI           | TaqI           |                 | LOW                       | HIGH  |               |                      |
| T ( <i>f</i> )           | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.286           | 0.170                     | 0.464 | <b>0.0017</b> | 4.145 (1.658-10.361) |
| C ( <i>F</i> )           | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.260           | 0.258                     | 0.207 | 0.51          | 0.730 (0.284-1.279)  |
| C ( <i>F</i> )           | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.200           | 0.239                     | 0.202 | 0.62          | 0.788(0.302-2.058)   |
| T ( <i>f</i> )           | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.112           | 0.154                     | 0.036 | <b>0.04</b>   | 0.202(0.035-1.149)   |
| C ( <i>F</i> )           | A ( <i>B</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.05            | 0.09                      | 0.02  | 0.18          | 0.225 (0.036-1.423)  |

| Porphyromonas Endodontalis  |               |           |            |             |                 |
|---|---------------|-----------|------------|-------------|-----------------|
|   |               |           | LOW (N=26) | HIGH (N=24) | P value         |
| <b>VDR FokI<br/>rs2228570</b><br>Exon2<br>c.2T>C ( <i>f&gt;F</i> )*<br><i>p.Met1Thr</i>   | Genotypes (%) | C/C (F/F) | 12 (46)    | 2 (8)       | <b>0.010462</b> |
|   |               | C/T (F/f) | 9 (35)     | 16 (67)     |                 |
|   |               | T/T (f/f) | 5 (19)     | 6 (25)      |                 |
|   | Alleles (%)   | C (F)     | 33 (63)    | 20 (42)     | <b>0.029180</b> |
|   |               | T (f)     | 19 (37)    | 28 (58)     |                 |
| HW (p)  |               | 0.22      | 0.11       |             |                 |
| <b>VDR BsmI<br/>rs1544410</b><br>Intron 8<br>c.1024+283A>G( <i>B&gt;b</i> )*              | Genotypes (%) | A/A (B/B) | 1 (4)      | 0 (0)       | 0.20            |
|   |               | A/G (B/b) | 6 (23)     | 2 (8)       |                 |
|   |               | G/G (b/b) | 19 (73)    | 22 (92)     |                 |
|   | Alleles (%)   | A (B)     | 8 (15)     | 2 (4)       | 0.06            |
|   |               | G (b)     | 44 (85)    | 46 (96)     |                 |
| HW (p)  |               | 0.47      | 1          |             |                 |
| <b>VDR ApaI<br/>rs7975232</b><br>Intron 8<br>c.1025-49A>C( <i>A&gt;c</i> )*               | Genotypes (%) | A/A (A/A) | 4 (15)     | 1 (4)       | 0.16            |
|   |               | A/C (A/a) | 15 (58)    | 11 (46)     |                 |
|   |               | C/C (a/a) | 7 (27)     | 12 (50)     |                 |
|   | Alleles (%)   | A (A)     | 23 (44)    | 13 (27)     | 0.07            |
|   |               | C (a)     | 29 (56)    | 35 (73)     |                 |
| HW (p)  |               | 0.69      | 0.64       |             |                 |
| <b>VDR TaqI<br/>rs731236</b><br>Exon 9<br>c.1056T>C ( <i>T&gt;t</i> )<br><i>p.Ile352=</i> | Genotypes (%) | T/T (T/T) | 24 (92)    | 21 (88)     | 0.57            |
|   |               | T/C (T/t) | 2 (8)      | 3 (12)      |                 |
|   |               | C/C (t/t) | 0 (0)      | 0 (0)       |                 |
|   | Alleles (%)   | T (T)     | 50 (96)    | 45 (94)     | 0.58            |
|   |               | C (t)     | 2 (4)      | 3 (6)       |                 |
| HW (p)  |               | 1         | 1          |             |                 |

| Porphyromonas Endodontalis |                |                |                |                 |                           |       |                |                       |
|----------------------------|----------------|----------------|----------------|-----------------|---------------------------|-------|----------------|-----------------------|
| Haplotype                  |                |                |                | Total frequency | Clinical groups frequency |       | p-value        | OR (95% CI)           |
| FokI                       | BsmI           | ApaI           | TaqI           |                 | LOW                       | HIGH  |                |                       |
| T ( <i>f</i> )             | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.287           | 0.133                     | 0.492 | <b>0.00009</b> | 6.427(2.395-17.249)   |
| C ( <i>F</i> )             | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.260           | 0.290                     | 0.162 | 0.12           | 0.464 (0.174-1.236)   |
| C ( <i>F</i> )             | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.200           | 0.261                     | 0.212 | 0.53           | 0.746 (0.294-1.897)   |
| T ( <i>f</i> )             | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.112           | 0.143                     | 0.02  | <b>0.04</b>    | 0.178 (0.028-1.140)   |
| C ( <i>F</i> )             | A ( <i>B</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.05            | 0.06                      | 0.04  | 0.61           | 0.634 0.(0.104-3.846) |

| Treponema Denticola   |               |           |            |             |                 |
|---|---------------|-----------|------------|-------------|-----------------|
|   |               |           | LOW (N=22) | HIGH (N=28) | P value         |
| <b>VDR FokI<br/>rs2228570</b><br>Exon2<br>c.2T>C ( <i>f&gt;F</i> )*<br><i>p.Met1Thr</i>   | Genotypes (%) | C/C (F/F) | 10 (45)    | 4 (14)      | <b>0.045747</b> |
|   |               | C/T (F/f) | 9 (41)     | 16 (57)     |                 |
|   |               | T/T (f/f) | 3 (14)     | 8 (29)      |                 |
|   | Alleles (%)   | C (F)     | 29 (66)    | 24 (43)     | <b>0.021908</b> |
|   |               | T (f)     | 15 (34)    | 32 (57)     |                 |
|   | HW (p)        |           | 0.65       | 0.47        |                 |
| <b>VDR BsmI<br/>rs1544410</b><br>Intron 8<br>c.1024+283A>G( <i>B&gt;b</i> )*              | Genotypes (%) | A/A (B/B) | 0 (0)      | 1 (4)       | 0.60            |
|   |               | A/G (B/b) | 3 (14)     | 5 (18)      |                 |
|   |               | G/G (b/b) | 19 (86)    | 22 (79)     |                 |
|   | Alleles (%)   | A (B)     | 3 (7)      | 7 (12)      | 0.34            |
|   |               | G (b)     | 41 (93)    | 49 (88)     |                 |
|   | HW (p)        |           | 1          | 0.35        |                 |
| <b>VDR ApaI<br/>rs7975232</b><br>Intron 8<br>c.1025-49A>C( <i>A&gt;c</i> )*               | Genotypes (%) | A/A (A/A) | 1 (4)      | 4 (18)      | 0.14            |
|   |               | A/C (A/a) | 14 (50)    | 12 (55)     |                 |
|   |               | C/C (a/a) | 13 (46)    | 6 (27)      |                 |
|   | Alleles (%)   | A (A)     | 20 (45)    | 16 (29)     | 0.08            |
|   |               | C (a)     | 24 (55)    | 40 (71)     |                 |
|   | HW (p)        |           | 1          | 0.38        |                 |
| <b>VDR TaqI<br/>rs731236</b><br>Exon 9<br>c.1056T>C ( <i>T&gt;t</i> )<br><i>p.Ile352=</i> | Genotypes (%) | T/T (T/T) | 20 (91)    | 25 (89)     | 0.84            |
|   |               | T/C (T/t) | 2 (9)      | 3 (11)      |                 |
|   |               | C/C (t/t) | 0 (0)      | 0 (0)       |                 |
|   | Alleles (%)   | T (T)     | 42 (95)    | 53 (95)     | 0.85            |
|   |               | C (t)     | 2 (5)      | 3 (5)       |                 |
|   | HW (p)        |           | 1          | 1           |                 |

| Treponema Denticola |                |                |                |                 |                           |       |               |                      |
|---------------------|----------------|----------------|----------------|-----------------|---------------------------|-------|---------------|----------------------|
| Haplotype           |                |                |                | Total frequency | Clinical groups frequency |       | p-value       | OR (95% CI)          |
| FokI                | BsmI           | ApaI           | TaqI           |                 | LOW                       | HIGH  |               |                      |
| T ( <i>f</i> )      | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.287           | 0.129                     | 0.431 | <b>0.0009</b> | 5.259 (1.865-14.823) |
| C ( <i>F</i> )      | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.260           | 0.416                     | 0.165 | <b>0.004</b>  | 0.267 (0.105-0.683)  |
| C ( <i>F</i> )      | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.200           | 0.187                     | 0.168 | 0.79          | 0.869 (0.308-2.454)  |
| T ( <i>f</i> )      | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.112           | 0.176                     | 0.05  | <b>0.05</b>   | 0.278 (0.070-14.823) |
| C ( <i>F</i> )      | A ( <i>B</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.05            | 0                         | 0.05  | 0.17          | -                    |

| Tannerella Forsythia  |               |                             |         |             |                 |
|---|---------------|-----------------------------|---------|-------------|-----------------|
|   |               | LOW (N=33)                  |         | HIGH (N=17) | P value         |
| <b>VDR FokI<br/>rs2228570</b><br>Exon2<br>c.2T>C ( <i>f</i> > <i>F</i> )*<br><i>p.Met1Thr</i>   | Genotypes (%) | C/C ( <i>F</i> / <i>F</i> ) | 13 (39) | 1 (6)       | <b>0.034969</b> |
|   |               | C/T ( <i>F</i> / <i>f</i> ) | 13 (39) | 12 (71)     |                 |
|   |               | T/T ( <i>f</i> / <i>f</i> ) | 7 (21)  | 4 (24)      |                 |
|   | Alleles (%)   | C ( <i>F</i> )              | 39 (59) | 14 (41)     | 0.08            |
|   |               | T ( <i>f</i> )              | 27 (41) | 20 (59)     |                 |
|   | HW (p)        |                             | 0.29    | 0.14        |                 |
| <b>VDR BsmI<br/>rs1544410</b><br>Intron 8<br>c.1024+283A>G( <i>B</i> > <i>b</i> )*              | Genotypes (%) | A/A ( <i>B</i> / <i>B</i> ) | 1 (2)   | 0 (3)       | 0.26            |
|   |               | A/G ( <i>B</i> / <i>b</i> ) | 7 (16)  | 1 (21)      |                 |
|   |               | G/G ( <i>b</i> / <i>b</i> ) | 25 (82) | 16 (76)     |                 |
|   | Alleles (%)   | A ( <i>B</i> )              | 9 (14)  | 1 (3)       | 0.09            |
|   |               | G ( <i>b</i> )              | 57 (86) | 33 (97)     |                 |
|   | HW (p)        |                             | 0.47    | 1           |                 |
| <b>VDR ApaI<br/>rs7975232</b><br>Intron 8<br>c.1025-49A>C( <i>A</i> > <i>a</i> )*               | Genotypes (%) | A/A ( <i>A</i> / <i>A</i> ) | 4 (12)  | 1 (1)       | 0.41            |
|   |               | A/C ( <i>A</i> / <i>a</i> ) | 15 (45) | 11 (52)     |                 |
|   |               | C/C ( <i>a</i> / <i>a</i> ) | 14 (42) | 5 (38)      |                 |
|   | Alleles (%)   | A ( <i>A</i> )              | 23 (35) | 13 (38)     | 0.73            |
|   |               | C ( <i>a</i> )              | 43 (65) | 21 (62)     |                 |
|   | HW (p)        |                             | 1       | 0.3         |                 |
| <b>VDR TaqI<br/>rs731236</b><br>Exon 9<br>c.1056T>C ( <i>T</i> > <i>t</i> )<br><i>p.Ile352=</i> | Genotypes (%) | T/T ( <i>T</i> / <i>T</i> ) | 31 (94) | 14 (82)     | 0.19            |
|   |               | T/C ( <i>T</i> / <i>t</i> ) | 2 (6)   | 3 (18)      |                 |
|   |               | C/C ( <i>t</i> / <i>t</i> ) | 0 (0)   | 0 (0)       |                 |
|   | Alleles (%)   | T ( <i>T</i> )              | 64 (97) | 31 (91)     | 0.20            |
|   |               | C ( <i>t</i> )              | 2 (3)   | 3 (9)       |                 |
|   | HW (p)        |                             | 1       | 1           |                 |

| Tannerella Forsythia |                |                |                |                 |                           |       |              |                     |
|----------------------|----------------|----------------|----------------|-----------------|---------------------------|-------|--------------|---------------------|
| Haplotype            |                |                |                | Total frequency | Clinical groups frequency |       | p-value      | OR (95% CI)         |
| FokI                 | BsmI           | ApaI           | TaqI           |                 | LOW                       | HIGH  |              |                     |
| T ( <i>f</i> )       | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.287           | 0.221                     | 0.465 | <b>0.009</b> | 3.183(1.2977-8.11)  |
| C ( <i>F</i> )       | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.260           | 0.309                     | 0.09  | <b>0.02</b>  | 0.248(0.071-0.859)  |
| C ( <i>F</i> )       | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.200           | 0.184                     | 0.283 | 0.24         | 1.786 (0.673-4.738) |
| T ( <i>f</i> )       | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.112           | 0.133                     | 0.03  | 0.12         | 0.237 (0.033-1.699) |
| C ( <i>F</i> )       | A ( <i>B</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.05            | 0.08                      | 0     | 0.08         | -                   |

| Prevotella Intermedia   |               |                             |         |             |                 |
|---|---------------|-----------------------------|---------|-------------|-----------------|
|   |               | LOW (N=27)                  |         | HIGH (N=23) | P value         |
| <b>VDR FokI<br/>rs2228570</b><br>Exon2<br>c.2T>C ( <i>f</i> > <i>F</i> )*<br><i>p.Met1Thr</i>   | Genotypes (%) | C/C ( <i>F</i> / <i>F</i> ) | 13 (48) | 1 (4)       | <b>0.002382</b> |
|   |               | C/T ( <i>F</i> / <i>f</i> ) | 9 (33)  | 16 (70)     |                 |
|   |               | T/T ( <i>f</i> / <i>f</i> ) | 5 (19)  | 6 (26)      |                 |
|   | Alleles (%)   | C ( <i>F</i> )              | 35 (65) | 18 (39)     | <b>0.010352</b> |
|   |               | T ( <i>f</i> )              | 19 (35) | 28 (61)     |                 |
|   | HW (p)        |                             | 0.2     | 0.074       |                 |
| <b>VDR BsmI<br/>rs1544410</b><br>Intron 8<br>c.1024+283A>G( <i>B</i> > <i>b</i> )*              | Genotypes (%) | A/A ( <i>B</i> / <i>B</i> ) | 1 (4)   | 0 (0)       | 0.066           |
|   |               | A/G ( <i>B</i> / <i>b</i> ) | 7 (26)  | 1 (4)       |                 |
|   |               | G/G ( <i>b</i> / <i>b</i> ) | 19 (70) | 22 (96)     |                 |
|   | Alleles (%)   | A ( <i>B</i> )              | 1 (2)   | 9 (17)      | <b>0.016089</b> |
|   |               | G ( <i>b</i> )              | 45 (98) | 45 (83)     |                 |
|   | HW (p)        |                             | 0.55    | 1           |                 |
| <b>VDR ApaI<br/>rs7975232</b><br>Intron 8<br>c.1025-49A>C( <i>A</i> > <i>a</i> )*               | Genotypes (%) | A/A ( <i>A</i> / <i>A</i> ) | 4 (4)   | 1 (15)      | 0.27            |
|   |               | A/C ( <i>A</i> / <i>a</i> ) | 15 (48) | 11 (56)     |                 |
|   |               | C/C ( <i>a</i> / <i>a</i> ) | 8 (48)  | 11 (30)     |                 |
|   | Alleles (%)   | A ( <i>A</i> )              | 23 (43) | 13 (36)     | 0.13            |
|   |               | C ( <i>a</i> )              | 31 (57) | 33 (64)     |                 |
|   | HW (p)        |                             | 0.7     | 0.63        |                 |
| <b>VDR TaqI<br/>rs731236</b><br>Exon 9<br>c.1056T>C ( <i>T</i> > <i>t</i> )<br><i>p.Ile352=</i> | Genotypes (%) | T/T ( <i>T</i> / <i>T</i> ) | 25 (93) | 20 (87)     | 0.50            |
|   |               | T/C ( <i>T</i> / <i>t</i> ) | 2 (7)   | 3 (13)      |                 |
|   |               | C/C ( <i>t</i> / <i>t</i> ) | 0 (0)   | 0 (0)       |                 |
|   | Alleles (%)   | T ( <i>T</i> )              | 52 (96) | 43 (93)     | 0.51            |
|   |               | C ( <i>t</i> )              | 2 (4)   | 3 (7)       |                 |
|   | HW (p)        |                             | 1       | 1           |                 |

| Prevotella Intermedia |                |                |                |                 |                           |       |                 |                      |
|-----------------------|----------------|----------------|----------------|-----------------|---------------------------|-------|-----------------|----------------------|
| Haplotype             |                |                |                | Total frequency | Clinical groups frequency |       | p-value         | OR (95% CI)          |
| FokI                  | BsmI           | ApaI           | TaqI           |                 | LOW                       | HIGH  |                 |                      |
| T ( <i>f</i> )        | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.287           | 0.125                     | 0.515 | <b>0.000022</b> | 7.463 (2.809-20.745) |
| C ( <i>F</i> )        | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.260           | 0.300                     | 0.144 | <b>0.05</b>     | 0.384 (0.139-1.056)  |
| C ( <i>F</i> )        | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.200           | 0.231                     | 0.224 | 0.91            | 0.950 (0.370-2.440)  |
| T ( <i>f</i> )        | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.112           | 0.157                     | 0.02  | <b>0.02</b>     | 0.156 (0.024-1.021)  |
| C ( <i>F</i> )        | A ( <i>B</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.05            | 0.09                      | 0.02  | 0.14            | 0.203 (0.032-1.283)  |

| Fusobacter Nucleatum  |               |                    |         |             |          |
|---|---------------|--------------------|---------|-------------|----------|
|   |               | LOW (N=21)         |         | HIGH (N=29) | P value  |
| VDR FokI<br>rs2228570<br>Exon2<br>c.2T>C ( <i>f&gt;F</i> )*<br><i>p.Met1Thr</i> | Genotypes (%) | C/C ( <i>F/F</i> ) | 5 (24)  | 9 (31)      | 0.32     |
|   |               | C/T ( <i>F/f</i> ) | 13 (62) | 12 (41)     |          |
|   |               | T/T ( <i>f/f</i> ) | 3 (14)  | 8 (28)      |          |
|   | Alleles (%)   | C ( <i>F</i> )     | 23 (55) | 30 (52)     | 0.76     |
|   |               | T ( <i>f</i> )     | 19 (45) | 28 (48)     |          |
| HW (p)  |               | 0.39               | 0.46    |             |          |
| VDR BsmI<br>rs1544410<br>Intron 8<br>c.1024+283A>G( <i>B&gt;b</i> )*            | Genotypes (%) | A/A ( <i>B/B</i> ) | 1 (5)   | 0 (0)       | 0.049991 |
|   |               | A/G ( <i>B/b</i> ) | 6 (29)  | 2 (7)       |          |
|   |               | G/G ( <i>b/b</i> ) | 14 (67) | 27 (93)     |          |
|   | Alleles (%)   | A ( <i>B</i> )     | 8 (19)  | 2 (3)       | 0.010305 |
|   |               | G ( <i>b</i> )     | 34 (81) | 56 (97)     |          |
| HW (p)  |               | 0.56               | 1       |             |          |
| VDR ApaI<br>rs7975232<br>Intron 8<br>c.1025-49A>C( <i>A&gt;c</i> )*             | Genotypes (%) | A/A ( <i>A/A</i> ) | 0 (0)   | 5 (17)      | 0.10     |
|   |               | A/C ( <i>A/a</i> ) | 11 (52) | 15 (52)     |          |
|   |               | C/C ( <i>a/a</i> ) | 10 (48) | 9 (31)      |          |
|   | Alleles (%)   | A ( <i>A</i> )     | 11 (26) | 25 (43)     | 0.08     |
|   |               | C ( <i>a</i> )     | 31 (74) | 33 (57)     |          |
| HW (p)  |               | 0.26               | 1       |             |          |
| VDR TaqI<br>rs731236<br>Exon 9<br>c.1056T>C ( <i>T&gt;t</i> )<br>p.Ile352=      | Genotypes (%) | T/T ( <i>T/T</i> ) | 19 (90) | 26 (90)     | 0.92     |
|   |               | T/C ( <i>T/t</i> ) | 2 (10)  | 3 (10)      |          |
|   |               | C/C ( <i>t/t</i> ) | 0 (0)   | 0 (0)       |          |
|   | Alleles (%)   | T ( <i>T</i> )     | 40 (95) | 55 (95)     | 0.92     |
|   |               | C ( <i>t</i> )     | 2 (5)   | 3 (5)       |          |
| HW (p)  |               | 1                  | 1       |             |          |

| Fusobacter Nucleatum |                |                |                |                 |                           |       |               |                     |
|----------------------|----------------|----------------|----------------|-----------------|---------------------------|-------|---------------|---------------------|
| Haplotype            |                |                |                | Total frequency | Clinical groups frequency |       | p-value       | OR (95% CI)         |
| FokI                 | BsmI           | ApaI           | TaqI           |                 | LOW                       | HIGH  |               |                     |
| T ( <i>f</i> )       | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.287           | 0.403                     | 0.275 | 0.19          | 0.570 (0.245-1.329) |
| C ( <i>F</i> )       | G ( <i>b</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.260           | 0.204                     | 0.275 | 0.39          | 1.504 (0.583-3.880) |
| C ( <i>F</i> )       | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.200           | 0.162                     | 0.206 | 0.56          | 1.358 (0.481-3.843) |
| T ( <i>f</i> )       | G ( <i>b</i> ) | A ( <i>A</i> ) | T ( <i>T</i> ) | 0.112           | 0                         | 0.155 | <b>0.0071</b> | -                   |
| C ( <i>F</i> )       | A ( <i>B</i> ) | C ( <i>a</i> ) | T ( <i>T</i> ) | 0.05            | 0.08                      | 0     | <b>0.04</b>   | -                   |