**Supplementary Table S1.** **Clinical characteristics of healthy subjects and colorectal cancer patients**

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Hong Kong** | **Hong Kong (subset with FIT)** | **Shanghai** |
| **Variables** | **Control****(n=200)** | **CRC****(n=170)** | ***P* value\*** | **Control****(n=119)** | **CRC****(n=111)** | ***P* value\*** | **Control****(n=36)** | **CRC****(n=33)** | ***P* value\*** |
| **Age**  | 59.3 ± 5.8 | 67.2 ± 11.6 | <0.001 | 59.1 ± 5.3 | 66.8 ± 11.4 | <0.001 | 53.2 ± 12.2 | 63.4 ± 9.6 | <0.001 |
| **Gender** | 　 | 　 | 　 |  |  | 　 |  |  |  |
| Male | 77 (38.5%) | 100 (58.8%) | <0.001 | 46 (38.7%) | 73 (65.8%) | <0.001 | 10 (27.8%) | 17 (51.5%) | <0.05 |
| Female | 123 (61.5%) | 70 (41.2%) | 73 (61.3%) | 38 (34.2%) |  | 26 (72.2%) | 16 (48.5%) |
| **BMI** | 23.4 ± 2.9 | 23.8 ± 3.4 | 0.443 | 23.1 ± 2.5 | 23.9 ± 3.3 | 0.228 |  |  |  |
| **Location** |  |  |  |  |  |  |  |  |  |
| Proximal |  | 40 (23.5%) |  |  | 22 (19.8%) |  |  | 7 (21.2%) |  |
| Distal |  | 126 (74.1%) |  |  | 89 (80.2%) |  |  | 26 (78.8%) |  |
| **TNM stage** |  |  |  |  |  |  |  |  |  |
| I |  | 27 (15.9%) |  |  | 17 (15.3%)  |  |  | 4 (12.1%) |  |
| II |  | 64 (37.6%) |  |  | 42 (37.8%) |  |  | 10 (30.3%) |  |
| III |  | 55 (32.4%) |  |  | 43 (38.7%) |  |  | 12 (36.4 %) |  |
| IV |  | 18 (10.6%) |  |  | 9 (8.1%) |  |  | 7 (21.2%) |  |

Notes: CRC, colorectal cancer; FIT, fecal immunochemical test; BMI, body mass index; TNM, tumor-node-metastasis.

\*Gender by Chi-square; Age and BMI by T-test.

#As the majority of CRC cases were moderately differentiated, differentiation status was not included in further analysis.

**Supplementary Table S2.** **Bacterial marker candidates identified by metagenome sequencing**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Species\*** | **Label** | **Control rank mean** | **CRC****rank mean** | **Enrichment** | **Wilcoxon rank-sum test** | **PCR target Gene ID/name** |
| **p-value** |  **q-value** |
| *Fusobacterium nucleatum* | *Fn* | 40.32407 | 82.1419 | CRC | 1.72E-10 | 7.48E-09 | *nusG* |
| *Clostridium hathewayi* | *Ch* | 46.77778 | 77.4324 | CRC | 2.12E-05 | 2.05E-04 | m2736705 |
| undefined species 'm7' | *m7* | na | na | CRC | 1.80E-07 | 3.24E-03 | m3246804 |
| *Bacteroides clarus* | *Bc* | 75.55556 | 56.4324 | Control | 1.29E-03 | 2.50E-03 | m370640 |
| *Roseburia intestinalis* | *Ri* | 76.99074 | 55.3851 | Control | 2.20E-03 | 3.58E-03 | m181682 |

Notes: \*MLG species associated with CRC at a significance level of q<0.05 according to Wilcoxon rank-sum tests with Benjamini-Hochberg adjustment. No species rank mean values could be calculated for the undefined species ‘m7’, so p-value and q-value shown were based on gene marker ‘3246804’.

**Supplementary Table S3.** **Primers and probes used in this study**

| **Targets** |  | **Nucleotide sequence (5'->3')** | **Size (bp)** |
| --- | --- | --- | --- |
| Internal control(16S rDNA) | Forward | CGTCAGCTCGTGYCGTGAG | 131 |
| Reverse | CGTCRTCCCCRCCTTCC |
| Probe | VIC-TTAAGTCCCRYAACGAGCGCAACCC-TAMRA |
| *Fusobacterium nucleatum* | Forward | TTCAATAAAAGTGGCAGGTCAAG | 100 |
| Reverse | TAACAACACATGCAGGTCAATGG |
| Probe | FAM-ACTCGAACCCCCAACCCTCGGTTT-TAMRA |
| *Clostridium hathewayi* | Forward | GGGCTGCGGAAGCAACTTA | 145 |
| Reverse | GATGACCTCGCCCTGATCAT |
| Probe | FAM-ACCACCACACAGGACGGAAAGATTCTCC-TAMRA |
| *m7* | Forward | TCGGCACGCTGATTATCACA | 119 |
| Reverse | CACACGCCGATCCATCTTC |
| Probe | FAM-ACCCACCTGGACGGCTCCGG-TAMRA |
| *Bacteroides clarus* | Forward | TCCATCCGCAAGCCTTTACT | 140 |
| Reverse | GCTTCCGGTGCCATTGACTA |
| Probe | FAM-TTCATCATCACAGCCGACAACGCA-TAMRA |
| *Roseburia intestinalis* | Forward | CGGATTTGCAGTGGCAAGTT | 140 |
| Reverse | TGATTGCAGACGCCAATGTC |
| Probe | FAM-CGTGAAAAATCCGCGCATCTGGC-TAMRA |

**Supplementary Table S4. Abundances of m1704941 (gene maker level, 99.13% identity) and *F. nucleatum* (species level) in fecal samples of CRC patients by metagenome sequencing**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#** | **CRC samples** | **m1704941 (\*10E-8)** | ***Fn* (\*10E-8)** |  | **#** | **CRC samples** | **m1704941 (\*10E-8)** | ***Fn* (\*10E-8)** |
| 1 | A10A | 119.103  | 770.962  |  | 22 | M2-Pk-014A | 6.780  | 1066.997  |
| 2 | M113A | 0.000  | 0.000  |  | 23 | M2-Pk-015A | 0.000  | 52.238  |
| 3 | M115A | 0.000  | 535.076  |  | 24 | M2-Pk-016A | 85.015  | 5278.599  |
| 4 | M116A | 12.186  | 1172.955  |  | 25 | M2-Pk-017A | 0.000  | 5.224  |
| 5 | M117A | 0.000  | 0.000  |  | 26 | M2-PK018A | 0.000  | 0.000  |
| 6 | M118A | 23.959  | 80.325  |  | 27 | M2-PK019A | 0.000  | 157.794  |
| 7 | M122A | 76.728  | 620.901  |  | 28 | M2-PK021A | 85.513  | 1903.679  |
| 8 | M123A | 0.000  | 211.109  |  | 29 | M2-PK022A | 4.441  | 847.987  |
| 9 | M2-Pk-001A | 0.000  | 68.787  |  | 30 | M2-PK023A | 4.883  | 11.652  |
| 10 | M2-PK002A | 0.000  | 251.341  |  | 31 | M2-PK024A | 0.000  | 120.104  |
| 11 | M2-PK003A | 0.000  | 66.039  |  | 32 | M2-PK026A | 0.000  | 417.015  |
| 12 | M2-Pk-004A | 0.000  | 33.969  |  | 33 | M2-PK027A | 0.000  | 144.897  |
| 13 | M2-Pk-005A | 0.000  | 12.579  |  | 34 | M2-PK029A | 211.346  | 5178.345  |
| 14 | M2-Pk-006A | 0.000  | 112.314  |  | 35 | M2-PK030A | 7.385  | 145.345  |
| 15 | M2-Pk-007A | 7.492  | 12.558  |  | 36 | M2-PK032A | 173.798  | 12597.161  |
| 16 | M2-Pk-008A | 0.000  | 87.967  |  | 37 | M2-PK037A | 4.656  | 77.877  |
| 17 | M2-Pk-009A | 0.000  | 6.170  |  | 38 | M2-PK038A | 5.344  | 87.607  |
| 18 | M2-Pk-010A | 24.677  | 351.666  |  | 39 | M2-PK041A | 0.000  | 75.317  |
| 19 | M2-Pk-011A | 0.000  | 10.725  |  | 40 | M2-PK042A | 0.000  | 0.000  |
| 20 | M2-Pk-012A | 0.000  | 0.000  |  | 41 | M2-PK043A | 0.000  | 80.437  |
| 21 | M2-Pk-013A | 0.000  | 0.000  |  | 42 | M2-PK045A | 8.567  | 407.051  |
| **#** | **CRC samples** | **m1704941 (\*10e-8)** | ***Fn* (\*10e-8)** |  | **#** | **CRC samples** | **m1704941 (\*10e-8)** | ***Fn* (\*10e-8)** |
| 43 | M2-PK046A | 6.250  | 647.331  |  | 64 | MSC1A | 134.217  | 3162.506  |
| 44 | M2-PK047A | 5.613  | 119.765  |  | 65 | MSC45A | 7.630  | 691.798  |
| 45 | M2-PK051A | 7.280  | 106.657  |  | 66 | MSC4A | 0.000  | 44.458  |
| 46 | M2-PK052A | 0.000  | 13.354  |  | 67 | MSC54A | 36.590  | 347.776  |
| 47 | M2-PK055A | 5.489  | 19.874  |  | 68 | MSC5A | 33.231  | 874.652  |
| 48 | M2-PK056B | 0.000  | 0.000  |  | 69 | MSC63A | 13.564  | 41.892  |
| 49 | M2-PK059A | 6.495  | 0.000  |  | 70 | MSC6A | 7.693  | 90.783  |
| 50 | M2-PK063A | 0.000  | 31.149  |  | 71 | MSC76A | 79.396  | 877.104  |
| 51 | M2-PK064A | 0.000  | 0.000  |  | 72 | MSC78A | 7.240  | 21.414  |
| 52 | M2-PK065A | 33.082  | 536.173  |  | 73 | MSC79A | 240.618  | 2072.609  |
| 53 | M2-PK066A | 0.000  | 0.000  |  | 74 | MSC81A | 8.325  | 79.723  |
| 54 | M2-PK067A | 7.238  | 127.253  |  |  | **Occurrence%** | **52.70%** | **83.80%** |
| 55 | M2-PK069B | 0.000  | 14.021  |  |  |  |  |  |
| 56 | M2-PK083B | 38.884  | 498.342  |  |  |  |  |  |
| 57 | M2-PK084A | 287.222  | 2738.321  |  |  |  |  |  |
| 58 | M2-PK085A | 0.000  | 0.000  |  |  |  |  |  |
| 59 | M84A | 19.101  | 176.928  |  |  |  |  |  |
| 60 | M89A | 0.000  | 0.000  |  |  |  |  |  |
| 61 | MSC103A | 27.599  | 1072.417  |  |  |  |  |  |
| 62 | MSC119A | 19.962  | 438.074  |  |  |  |  |  |
| 63 | MSC120A | 0.000  | 15.705  |  |  |  |  |  |

Note: The abundances of the gene marker and species are shown as relative abundances compared to all genes and species respectively in each sample.

**Supplementary Table S5. Abundances of bacterial candidates in fecal samples of CRC patients and healthy control subjects**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Bacteria\*** | ***Fn*** | ***Ch*** | ***m7*** | ***Bc*** | ***Ri*** |
| **Group\*\*** | CRC | control | CRC | control | CRC | control | CRC | control | CRC | control |
| **Minimum** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **25% Percentile** | 0.0008 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| **Median** | 0.0288 | 8.1E-06 | 0 | 0 | 1.9E-07 | 0 | 0 | 0 | 0 | 0 |
| **75% Percentile** | 0.1011 | 0.0004 | 7.3E-07 | 0 | 0.0002 | 2.3E-06 | 0 | 0 | 6.4E-07 | 0.0004 |
| **Maximum** | 1.4960 | 0.5826 | 3.2500 | 0.0897 | 0.9900 | 0.1144 | 0.0047 | 0.3563 | 0.2324 | 0.2617 |
| ***P* value (Mann-Whitney test)** | <0.0001 | <0.0001 | <0.0001 | < 0.05 | < 0.05 |

Notes: \**Fn*, *Fusobacterium nucleatum*; *Ch*, *Clostridium hathewayi*; *m7*, in-house label for an unknown species; *Bc*, *Bacteroides clarus*; *Ri*, *Roseburia intestinalis*; \*\*n=370 (170 CRC and 200 healthy controls).

**Supplementary Table S6. Bivariate correlation analysis showing the correlation between bacterial candidates and CRC patients**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Bacteria\*** | ***Fn*** | ***Ch***  | ***m7***  | ***Bc***  | ***Ri***  |
| **Variable** | **Rho** | ***P* value** | **Rho** | ***P* value** | **Rho** | ***P* value** | **Rho** | ***P* value** | **Rho** | ***P* value** |
| **Age** | 0.301  | <0.001  | 0.143  | 0.006  | 0.110  | 0.035  | -0.053  | 0.310  | -0.091  | 0.081  |
| **Gender** | 0.105  | 0.044  | 0.097  | 0.062  | 0.041  | 0.429  | -0.008  | 0.877  | 0.050  | 0.335  |
| **CRC\*\*** | 0.636  | <0.001 | 0.350  | <0.001  | 0.208  | <0.001  | -0.128  | 0.014  | -0.143  | 0.006  |
| **TNM staging** | 0.042  | 0.589  | 0.012  | 0.877  | -0.056  | 0.475  | -0.057  | 0.465  | 0.077  | 0.327  |
| **Lesion location** | -0.023  | 0.769  | 0.029  | 0.709  | 0.008  | 0.915  | 0.020  | 0.796  | 0.068  | 0.386  |
| **BMI** | 0.069  | 0.432  | -0.020  | 0.819  | 0.003  | 0.976  | -0.088  | 0.315  | 0.076  | 0.386  |

Notes: \**Fn*, *Fusobacterium nucleatum*; *Ch*, *Clostridium hathewayi*; m7, in-house label for an unknown species; *Bc*, *Bacteroides clarus*; *Ri*, *Roseburia intestinalis*; \*\*n=170.

**Supplementary Table S7. The occurrence rates of bacterial candidates in fecal samples of CRC patients** **and healthy control subjects**

|  |  |  |  |
| --- | --- | --- | --- |
| **Bacteria** | **Occurrence in CRC** | **Occurrence in Control** | ***P* value (ᵡ2)** |
| ***F. nucleatum* (*Fn*)** | 98.2% | 72.0% | <0.0001 |
| ***C. hathewayi* (*Ch*)** | 35.3% | 8.0% | <0.0001 |
| ***m7*** | 53.5% | 37.0% | 0.001  |
| ***B. clarus* (*Bc*)** | 12.9% | 21.5% | 0.031  |
| ***R. intestinalis* (*Ri*)** | 22.9% | 36.0% | 0.006  |

**Supplementary Table S8. Pairwise comparison of ROC curves**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Pair of criteria** | **Difference between AUROC** | **95% CI** | **SE** | ***P* value** |
| **4-bacteria *vs* *Fn*** | 0.0323 | 0.0087 to 0.056 | 0.0121 | **0.007** |
| **4-bacteria *vs* FIT** | 0.0813 | 0.0302 to 0.132 | 0.0261 | **0.002** |
| ***Fn* *vs* FIT** | 0.0489 | -0.0072 to 0.105 | 0.0286 | 0.087 |

Notes: A subset of 230 subjects (111 CRC and 119 healthy controls) with fecal immunochemical test (FIT) result was included. *Fn*, *Fusobacterium nucleatum*; 4-bacteria *includes Fn, Bacteroides clarus, Clostridium hathewayi and* an unknown species *m7*. 95% CI, 95% confidence interval; SE, standard error.

**Supplementary Table S9. Correlations of bacterial abundance, FIT with CRC diagnosis and staging**

|  |  |  |  |
| --- | --- | --- | --- |
|  | ***Fn*** | **4-bacteria** | **FIT** |
| **Variable** | **Rho** | ***P* value** | **Rho** | ***P* value** | **Rho** | ***P* value** |
| **CRC** | 0.685  | **<0.001** | 0.734  | **<0.001** | 0.720  | **<0.001** |
| **TNM staging** | 0.046  | 0.635  | 0.021  | 0.827  | 0.165  | 0.084  |
| **Lesion location** | 0.002  | 0.982  | -0.074  | 0.440  | 0.122  | 0.204  |

Notes: A subset of 230 subjects (111 CRC and 119 healthy controls) with fecal immunochemical test (FIT) result was included. *Fn*, *Fusobacterium nucleatum*; 4-bacteria *includes Fn, Bacteroides clarus, Clostridium hathewayi and* an unknown species *m7.*

**Supplementary Table S10. Univariate and multivariate logistic regression analyses of age, gender and bacterial abundances as risk factors for CRC**

|  |  |  |
| --- | --- | --- |
| **Variable\*** | **Univariate** | **Multivariate** |
| **Odds ratio** | **95% CI** | ***P* value** | **Odds ratio** | **95% CI** | ***P* value** |
| **Age** | 1.106  | 1.076 - 1.137 | <0.001 | 1.090  | 1.065 - 1.133 | <0.001 |
| **Gender** | 2.384  | 1.566 - 3.631 | <0.001 | 2.685  | 1.618 - 4.457 | <0.001 |
| ***Fn*** | 6.3E08 | 1.3E05 - 3.2E12 | <0.001 | 1.5E07 | 5.4E03 - 4.0E10 | <0.001 |
| **Age** | 1.106  | 1.076 - 1.137 | <0.001 | 1.093  | 1.059 - 1.127 | <0.001 |
| **Gender** | 2.384  | 1.566 - 3.631 | <0.001 | 2.650  | 1.589 - 4.420 | <0.001 |
| ***4-bacteria*** | 2.3E08 | 1.3E05 - 4.1E11 | <0.001 | 5.4E06 | 5.5E03 - 5.3E09 | <0.001 |

Notes: \**Fn*, *Fusobacterium nucleatum*; 4-bacteria *includes Fn, Bacteroides clarus, Clostridium hathewayi and* an unknown species *m7*; 95% CI, 95% confidence interval*.*

**Supplementary Table S11. Combining bacterial markers and FIT in diagnosing CRC**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **TNM** | **#** | **Fn** | **4-Bac** | **FIT** | **&FIT** |
| I | 1 | 0.95580 | 0.96380 | 1 | 1 |
| 2 | 0.90263 | 0.90337 | 1 | 1 |
| 3 | 0.23575 | 0.23577 | 1 | 1 |
| 4 | 0.19319 | 0.19202 | 1 | 1 |
| 5 | 0.04631 | 0.04656 | 1 | 1 |
| 6 | 0.00965 | 0.00965 | 1 | 1 |
| 7 | 0.00128 | 0.00185 | 1 | 1 |
| 8 | 0.42338 | 0.42338 | 0 | 1 |
| 9 | 0.09616 | 0.09616 | 0 | 1 |
| 10 | 0.02638 | 0.02638 | 0 | 1 |
| 11 | 0.00791 | 0.99791 | 0 | 1 |
| 12 | 0.00185 | 0.00185 | 0 | 1 |
| 13 | 0.00085 | 0.00098 | 0 | 1/0 |
| 14 | 0.00000 | 0.00269 | 0 | 0/1 |
| 15 | 0.00058 | 0.00058 | 0 | 0 |
| 16 | 0.00001 | 0.00005 | 0 | 0 |
| 17 | 0.00000 | 0.00000 | 0 | 0 |
| II | 1 | 1.49632 | 1.49640 | 1 | 1 |
| 2 | 0.87787 | 0.87787 | 1 | 1 |
| 3 | 0.55448 | 0.55448 | 1 | 1 |
| 4 | 0.27088 | 0.27089 | 1 | 1 |
| 5 | 0.11118 | 0.11118 | 1 | 1 |
| 6 | 0.09866 | 0.09995 | 1 | 1 |
| 7 | 0.09256 | 0.09256 | 1 | 1 |
| 8 | 0.09236 | 0.09033 | 1 | 1 |
| 9 | 0.08412 | 0.08430 | 1 | 1 |
| 10 | 0.07488 | 0.07488 | 1 | 1 |
| 11 | 0.07170 | 0.07193 | 1 | 1 |
| 12 | 0.05593 | 0.05593 | 1 | 1 |
| 13 | 0.05478 | 0.05478 | 1 | 1 |
| 14 | 0.04136 | 0.04138 | 1 | 1 |
| 15 | 0.03991 | 0.04100 | 1 | 1 |
| 16 | 0.03721 | 0.03650 | 1 | 1 |
| 17 | 0.03675 | 0.03675 | 1 | 1 |
| 18 | 0.02761 | 0.02872 | 1 | 1 |
| 19 | 0.01574 | 0.01574 | 1 | 1 |
| 20 | 0.01401 | 0.01402 | 1 | 1 |
| 21 | 0.00783 | 0.00783 | 1 | 1 |
| 22 | 0.00354 | 0.00355 | 1 | 1 |
| 23 | 0.00313 | 0.00313 | 1 | 1 |
| 24 | 0.00079 | 0.00182 | 1 | 1 |
| 25 | 0.00079 | 0.00457 | 1 | 1 |
| 26 | 0.00076 | 0.00101 | 1 | 1 |
| 27 | 0.22595 | 0.22723 | 0 | 1 |
| 28 | 0.08132 | 0.08132 | 0 | 1 |
| 29 | 0.05251 | 0.05251 | 0 | 1 |
| 30 | 0.04693 | 0.04693 | 0 | 1 |
| 31 | 0.04509 | 0.04513 | 0 | 1 |
| 32 | 0.03386 | 0.03386 | 0 | 1 |
| 33 | 0.02126 | 0.02128 | 0 | 1 |
| 34 | 0.01812 | 0.01656 | 0 | 1 |
| 35 | 0.00247 | 0.00336 | 0 | 1 |
| 36 | 0.00059 | 0.00407 | 1 | 1 |
| 37 | 0.00030 | 0.04061 | 1 | 1 |
| 38 | 0.00011 | 0.50011 | 1 | 1 |

Notes: The best cutoff values (Fn=0.0007072; 4-Bac=0.001774) that maximize sensitivity and specificity were determined in the larger cohort with 170 CRC and 200 controls. *Fn*, *Fusobacterium nucleatum*; 4-Bac *includes Fn, Bacteroides clarus, Clostridium hathewayi and* an unknown species *m7.*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **TNM** | **#** | **Fn** | **4-Bac** | **FIT** | **&FIT** |
| II | 39 | 0.00034 | 0.00034 | 1 | 1 |
| 40 | 0.00011 | 0.00011 | 1 | 1 |
| 41 | 0.00006 | 0.00006 | 1 | 1 |
| 42 | 0.00000 | 0.00001 | 1 | 1 |
| III | 1 | 0.97603 | 0.97735 | 1 | 1 |
| 2 | 0.60055 | 0.60055 | 1 | 1 |
| 3 | 0.35341 | 0.35340 | 1 | 1 |
| 4 | 0.24074 | 0.24078 | 1 | 1 |
| 5 | 0.18005 | 0.18006 | 1 | 1 |
| 6 | 0.11989 | 0.12005 | 1 | 1 |
| 7 | 0.08829 | 0.08829 | 1 | 1 |
| 8 | 0.08775 | 0.13142 | 1 | 1 |
| 9 | 0.07796 | 0.08425 | 1 | 1 |
| 10 | 0.07075 | 0.07075 | 1 | 1 |
| 11 | 0.06448 | 0.06448 | 1 | 1 |
| 12 | 0.06352 | 0.06352 | 1 | 1 |
| 13 | 0.04412 | 0.04413 | 1 | 1 |
| 14 | 0.03778 | 0.03807 | 1 | 1 |
| 15 | 0.03171 | 0.03171 | 1 | 1 |
| 16 | 0.02501 | 0.02501 | 1 | 1 |
| 17 | 0.02354 | 0.05623 | 1 | 1 |
| 18 | 0.02197 | 0.01819 | 1 | 1 |
| 19 | 0.01891 | 0.01899 | 1 | 1 |
| 20 | 0.01273 | 0.01285 | 1 | 1 |
| 21 | 0.01191 | 0.01245 | 1 | 1 |
| 22 | 0.00482 | 0.00482 | 1 | 1 |
| 23 | 0.00308 | 0.00308 | 1 | 1 |
| 24 | 0.00293 | 0.00293 | 1 | 1 |
| 25 | 0.00142 | 0.00212 | 1 | 1 |
| 26 | 0.75260 | 0.75261 | 0 | 1 |
| 27 | 0.74845 | 0.75812 | 0 | 1 |
| 28 | 0.65098 | 0.65098 | 0 | 1 |
| 29 | 0.04723 | 0.04723 | 0 | 1 |
| 30 | 0.04069 | 0.04069 | 0 | 1 |
| 31 | 0.03509 | 0.03510 | 0 | 1 |
| 32 | 0.01441 | 0.01441 | 0 | 1 |
| 33 | 0.01099 | 0.01099 | 0 | 1 |
| 34 | 0.00244 | 0.41495 | 0 | 1 |
| 35 | 0.00196 | 0.00210 | 0 | 1 |
| 36 | 0.00056 | 0.00056 | 1 | 1 |
| 37 | 0.00041 | 0.00092 | 1 | 1 |
| 38 | 0.00032 | 0.00032 | 1 | 1 |
| 39 | 0.00011 | 0.00014 | 1 | 1 |
| 40 | 0.00000 | 0.00011 | 1 | 1 |
| 41 | 0.00008 | 0.00008 | 0 | 0 |
| 42 | 0.00005 | 0.00005 | 0 | 0 |
| 43 | 0.00001 | 0.00001 | 0 | 0 |
| IV | 1 | 0.68858 | 0.68858 | 1 | 1 |
| 2 | 0.10827 | 0.10401 | 1 | 1 |
| 3 | 0.07293 | 0.07293 | 1 | 1 |
| 4 | 0.05502 | 0.12836 | 1 | 1 |
| 5 | 0.03396 | 0.03397 | 1 | 1 |
| 6 | 0.02643 | 0.03824 | 1 | 1 |
| 7 | 0.02457 | 0.02458 | 1 | 1 |
| 8 | 0.02429 | 0.02430 | 1 | 1 |
| 9 | 0.00000 | 0.00121 | 0 | 0 |