**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 |