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| **Table 1**. Taxa showing a significant different abundance between CRC with control in the gut microbiota. | | | | |
| Taxon | t-statistic | Unadjusted *p* value | Adjusted *p* value | Reference |
| Phylum Firmicutes |  |  |  |  |
| Family *Clostridiaceae 1* | -4.17 | <0.001 | **0.002** | (1) |
| Genus *Clostridium sensu stricto 1* | -4.17 | <0.001 | **0.004** |  |
| Family *Family XIII* | -3.73 | <0.001 | **0.004** | (2) |
| Genus *Family XIII AD 3011 group* | -3.73 | <0.001 | **0.008** |  |
| Family *Erysipelotrichaceae* | -3.50 | <0.001 | **0.016** | (1) |
| Genus *Erysipelotrichaceae UCG-003* | -3.50 | 0.001 | **0.042** |  |
| Genus *Turicibacter* | -2.89 | 0.004 | 0.129 | (1) |
| Family *Ruminococcaceae* |  |  |  | (1, 3) |
| Genus *Ruminococcus 1* | -5.81 | <0.001 | **0.004** | (4, 5) |
| Genus *Ruminococcaceae UCG-013* | -3.78 | <0.001 | **0.004** |  |
| Genus *Butyricicoccus* | -2.68 | 0.009 | 0.224 | (6) |
| Genus *Subdoligranulum* | -2.59 | 0.012 | 0.286 |  |
| Family *Lachnospiraceae* |  |  |  | (1, 4) |
| Genus *Blautia* | -4.27 | <0.001 | **0.009** | (5) |
| Genus *[Eubacterium] hallii group* | -3.82 | <0.001 | **0.003** | (7) |
| Genus *Lachnospiraceae NC2004 group* | -3.45 | <0.001 | **0.003** |  |
| Genus *[Eubacterium] ventriosum* | -3.08 | 0.004 | 0.117 | (7) |
| Genus *[Ruminococcus] torques group* | -2.15 | 0.037 | 0.553 |  |
| Family *Peptostreptococcaceae* | -2.80 | 0.008 | 0.128 | (1, 3) |
| Genus *Romboutsia* | -3.15 | 0.002 | 0.071 |  |
| Genus *Terrisporobacter* | -2.43 | 0.020 | 0.393 |  |
| Family *Christensenellaceae* | -2.76 | 0.007 | 0.124 | (1) |
| Genus *Christensenellaceae R-7 group* | -2.76 | 0.007 | 0.207 |  |
| Family *Leuconostocaceae* | -2.77 | 0.008 | 0.124 | (8) |
| Genus *Weissella* | -2.77 | 0.008 | 0.209 |  |
| Family *Lactobacillaceae* | -2.37 | 0.022 | 0.234 | (1) |
| Genus *Lactobacillus* | -2.37 | 0.022 | 0.405 |  |
| Phylum Bacteriodetes | 6.55 | <0.001 | **<0.001** |  |
| Family *Bacteroidaceae* | 5.26 | <0.001 | **0.002** |  |
| Genus *Bacteroides* | 5.26 | <0.001 | **0.004** | (4, 9) |
| Family *Marinifilaceae* | 2.69 | 0.009 | 0.128 |  |
| Genus *Odoribacter* | 2.69 | 0.009 | 0.227 | (1, 3, 4, 9) |
| Family *Rikenellaceae* | 2.47 | 0.015 | 0.185 | (1) |
| Genus *Alistipes* | 2.47 | 0.015 | 0.325 | (3, 4) |
| Family *Tannerellaceae* | 2.03 | 0.046 | 0.390 |  |
| Genus *Parabacteroides* | 2.03 | 0.046 | 0.613 | (4) |
| Phylum Actinobacteria | -5.82 | <0.001 | **<0.001** |  |
| Family *Bifidobacteriaceae* | -5.93 | <0.001 | **0.002** | (1) |
| Genus *Bifidobacterium* | -5.93 | <0.001 | **0.004** | (4, 5) |
| Family *Eggerthellaceae* | -2.52 | 0.014 | 0.185 |  |
| Genus *Eggerthella* | -2.52 | 0.014 | 0.321 | (3) |
| Family *Actinomycetaceae* | -2.36 | 0.021 | 0.234 |  |
| Genus *Actinomyces* | -2.36 | 0.021 | 0.405 | (1) |
| The change of column (log2 fold) represents the multiplicative change in taxa abundance from CRC to control. | | | | |
| Negative numbers represent a trend of decreasing abundance in CRC group compared with control group. | | | | |

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| **Table 2.** Taxa showing a significant different abundance between CRC with control in the gut microbe-derived extracellular vesicles. | | | |
| Taxon | t-statistic | Unadjusted *p* value | Adjusted *p* value |
| Phylum Firmicutes | 3.16 | 0.002 | **0.008** |
| Family *Clostridiaceae 1* | -3.36 | 0.001 | **0.019** |
| Genus *Clostridium sensu stricto 1* | -3.36 | 0.001 | **0.003** |
| Family *Erysipelotrichaceae* | 3.28 | 0.001 | **0.019** |
| Genus *Catenibacterium* | 7.51 | <0.001 | **0.004** |
| Genus *Erysipelotrichaceae UCG-003* | 4.41 | <0.001 | **0.004** |
| Genus *Turicibacter* | -2.00 | 0.043 | 0.541 |
| Family *Ruminococcaceae* | 4.22 | <0.001 | **0.002** |
| Genus *Faecalibacterium* | 3.41 | <0.001 | **0.020** |
| Genus *Ruminococcus 1* | 2.96 | 0.004 | 0.089 |
| Genus *Ruminococcus 2* | 2.23 | 0.028 | **0.028** |
| Family *Lachnospiraceae* |  |  |  |
| Genus *Blautia* | 3.78 | <0.001 | **0.012** |
| Genus *[Eubacterium] hallii group* | 5.04 | <0.001 | **0.004** |
| Genus *[Ruminococcus] torques group* | 4.85 | <0.001 | **0.004** |
| Genus *Oribacterium* | 3.79 | <0.001 | **0.012** |
| Genus *Dorea* | 3.91 | 0.004 | **0.018** |
| Genus *Lachnospiraceae UCG-008* | 2.52 | 0.012 | 0.230 |
| Family *Peptostreptococcaceae* | -3.25 | 0.003 | **0.033** |
| Genus *Romboutsia* | -4.35 | <0.001 | **0.001** |
| Genus *Terrisporobacter* | -3.56 | <0.001 | **0.003** |
| Genus *Intestinibacter* | -3.07 | 0.004 | 0.092 |
| Family *Veillonellaceae* | -6.10 | <0.001 | **0.002** |
| Genus *Dialister* | -6.10 | <0.001 | **0.004** |
| Family *Staphylococcaceae* | -4.61 | <0.001 | **0.002** |
| Genus *Staphylococcus* | -4.61 | <0.001 | **0.004** |
| Family *Acidaminococcaceae* | -3.28 | 0.001 | **0.018** |
| Phylum Proteobacteria |  |  |  |
| Family *Moraxellaceae* |  |  |  |
| Genus *Enhydrobacter* | -2.15 | 0.034 | 0.476 |
| Phylum Actinobacteria |  |  |  |
| Family *Coriobacteriaceae* | 4.78 | <0.001 | **0.004** |
| Genus *Collinsella* | 4.78 | <0.001 | **0.007** |
| Phylum Verrucomicrobia | -3.77 | <0.001 | **0.002** |
| Family *Akkermansiaceae* | -3.77 | <0.001 | **0.004** |
| Genus *Akkermansia* | -3.77 | <0.001 | **0.012** |
| The change of column (log2 fold) represents the multiplicative change in taxa abundance from CRC to control. | | | |
| Negative numbers represent a trend of decreasing abundance in CRC group compared with control group. | | | |