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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. |