

***Research article***

## Metagenomic analysis of fecal samples in colorectal cancer Egyptians patients post colectomy: A pilot study.

Rana H. Abo-Hammam<sup>1,†</sup>, Mohammed Salah<sup>2</sup>, Sarah Shabayek<sup>3</sup>, Amro Hanora<sup>3,\*</sup>, Samira Zakeer<sup>3</sup> and Randa H. Khattab<sup>4,†</sup>

<sup>1</sup> Forensic toxicologist and narcotics expert, Ministry of Justice, Tanta, Egypt

<sup>2</sup> Department of Microbiology and Immunology, Faculty of pharmacy, Port-Said University, Port-Said, Egypt

<sup>3</sup> Department of Microbiology and Immunology, Faculty of pharmacy, Suez Canal University, Ismailia, Egypt

<sup>4</sup> Department of Microbiology and Immunology, Al-Salam University, Tanta, Egypt

\* Correspondence: Email: a.hanora@pharm.suez.edu.eg.

† These Authors are equally contributed to this manuscript.

**Supplementary**

**Table S1.** The unique bacterial species in CRC patients' categories.

Category 1	Category 2
Acinetobacter townieri	Actinobaculum oral taxon 183
Actinomyces ICM 47	Actinomyces graevenitzii
Bifidobacterium adolescentis	Actinomyces odontolyticus
Bifidobacterium bifidum	Actinomyces oris
Bifidobacterium catenulatum	Actinomyces HMSC035G02
Bifidobacterium pseudolongum	Actinomycesoral taxon 181
Rothia aeria	Actinomycesoral taxon 448

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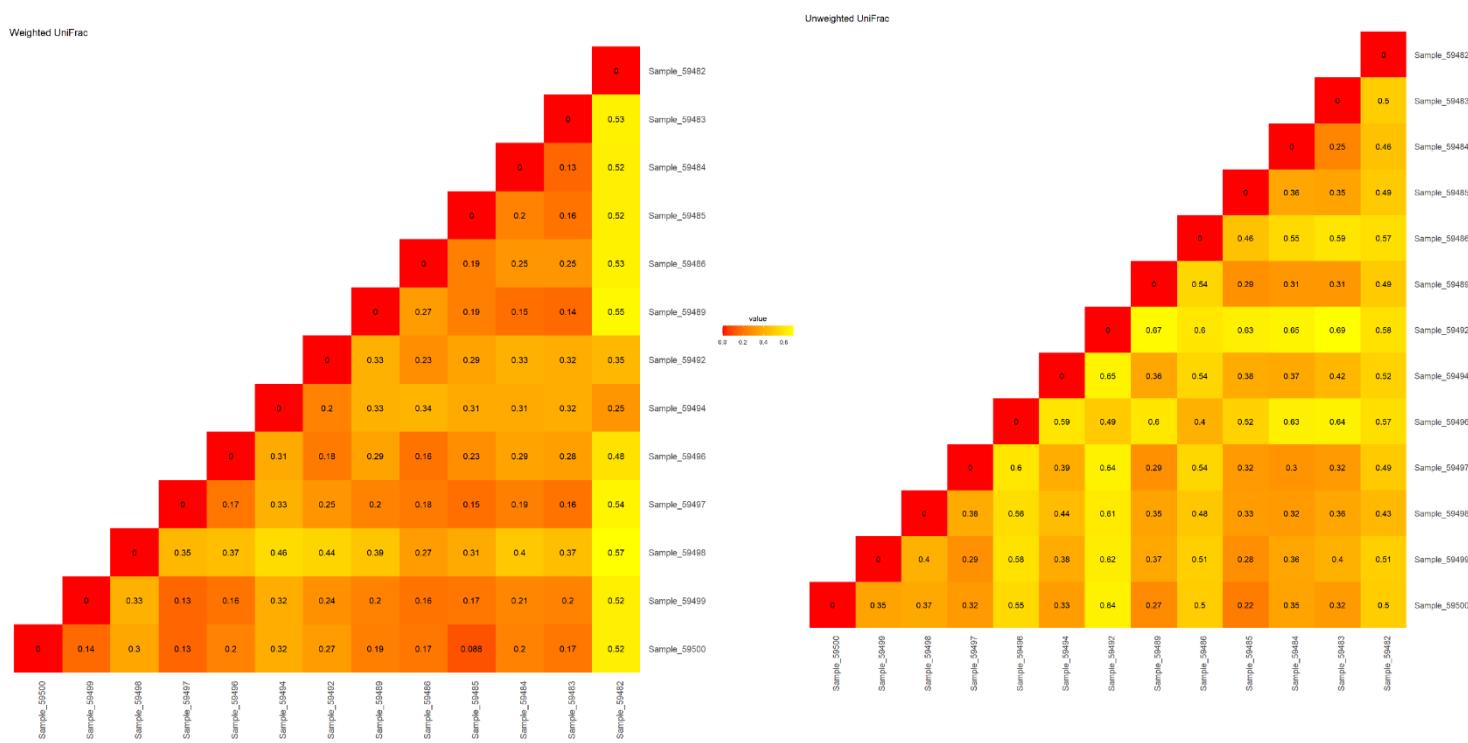
Category 1	Category 2
<i>Rothia mucilaginosa</i>	<i>Bifidobacterium_minimum</i>
<i>Collinsella intestinalis</i>	<i>Bifidobacterium_mongoliense</i>
<i>Adlercreutzia equolifaciens</i>	<i>Scardovia wiggiae</i>
<i>Bacteroides clarus</i>	<i>Corynebacterium_amycolatum</i>
<i>Bacteroides faecis</i>	<i>Corynebacterium_HMSC08A12</i>
<i>Bacteroides faecis CAG 32</i>	<i>Cutibacterium acnes</i>
<i>Bacteroides galacturonicus</i>	<i>Propionibacterium freudenreichii</i>
<i>Bacteroides CAG 927</i>	<i>Bacteroides nordii</i>
<i>Porphyromonas gingivalis</i>	<i>Coprobacter_fastidiosus</i>
<i>Alistipes inops</i>	<i>Prevotella_sp_885</i>
<i>Alistipes onderdonkii</i>	<i>Prevotella AM42 24</i>
<i>Parabacteroides goldsteinii</i>	<i>Prevotella stercorea</i>
<i>Parabacteroides johnsonii</i>	<i>Gemella_haemolysans</i>
<i>Phascolarctobacterium CAG 266</i>	<i>Lactobacillus_agilis</i>
<i>Enterococcus avium</i>	<i>Lactobacillus fermentum</i>
<i>Enterococcus faecalis</i>	<i>Lactobacillus helveticus</i>
<i>Enterococcus gallinarum</i>	<i>Lactobacillus_mucosae</i>
<i>Enterococcus hirae</i>	<i>Lactobacillus_paragasseri</i>
<i>Lactobacillus ruminis</i>	<i>Lactobacillus_pontis</i>
<i>Streptococcus thermophilus</i>	<i>Lactobacillus_rossiae</i>
<i>Clostridium bolteae CAG 59</i>	<i>Weissella confusa</i>
<i>Clostridium CAG 253</i>	<i>Lactococcus chungangensis</i>
<i>Clostridium ventriculi</i>	<i>Streptococcus milleri</i>
<i>Bacteroides pectinophilus</i>	<i>Streptococcus mitis</i>
<i>Lawsonibacter asaccharolyticus</i>	<i>Streptococcus pasteurianus</i>
<i>Eubacterium CAG 251</i>	<i>Streptococcus vestibularis</i>
<i>Eubacterium OM08 24</i>	<i>Clostridium bolteae CAG 59</i>
<i>Blautia CAG 257</i>	<i>Eisenbergiella massiliensis</i>
<i>Clostridium aldenense</i>	<i>Clostridium_citroniae</i>
<i>Clostridium asparagiforme</i>	<i>Clostridium_lavalense</i>
<i>Clostridium clostridioforme</i>	<i>Romboutsia ilealis</i>
<i>Roseburia CAG 182</i>	<i>Anaerotruncus colihominis</i>
<i>Roseburia CAG 303</i>	<i>Flavonifractor An10</i>
<i>Sellimonas intestinalis</i>	<i>Catenibacterium mitsuokai</i>
<i>Clostridioides difficile</i>	<i>Coprobacillus cateniformis</i>
<i>Paenibacillus sordellii</i>	<i>Firmicutes bacterium CAG 110</i>
<i>Anaeromassilibacillus An250</i>	<i>Phascolarctobacterium succinatutens</i>
<i>Pseudoflavonifractor An184</i>	<i>Veillonella parvula</i>
<i>Ruminococcaceae bacterium D5</i>	<i>Methylobacterium_frigidaeris</i>
<i>Ruminococcus obeum CAG 39</i>	<i>Achromobacter xylosoxidans</i>
<i>Ruminococcus CAG 403</i>	<i>Desulfovibrio_fairfieldensis</i>
<i>Ruminococcus CAG 488</i>	<i>Haemophilus parainfluenzae</i>
<i>Holdemaniella biformis</i>	<i>Proteobacteria bacterium_CAG 139</i>
<i>Firmicutes bacterium CAG 94</i>	<i>Akkermansia muciniphila</i>
<i>Mitsuokella jalaludinii</i>	<i>Candida albicans</i>
<i>Mitsuokella multacida</i>	<i>Candida dubliniensis</i>
<i>Dialister invisus</i>	<i>Candida tropicalis</i>
<i>Dialister succinatiphilus</i>	<i>Saccharomyces cerevisiae</i>
<i>Megasphaera hexanoica</i>	<i>Fusobacterium varium</i>
<i>Veillonella dispar</i>	
<i>Veillonella infantium</i>	
<i>Veillonella T11011 6</i>	

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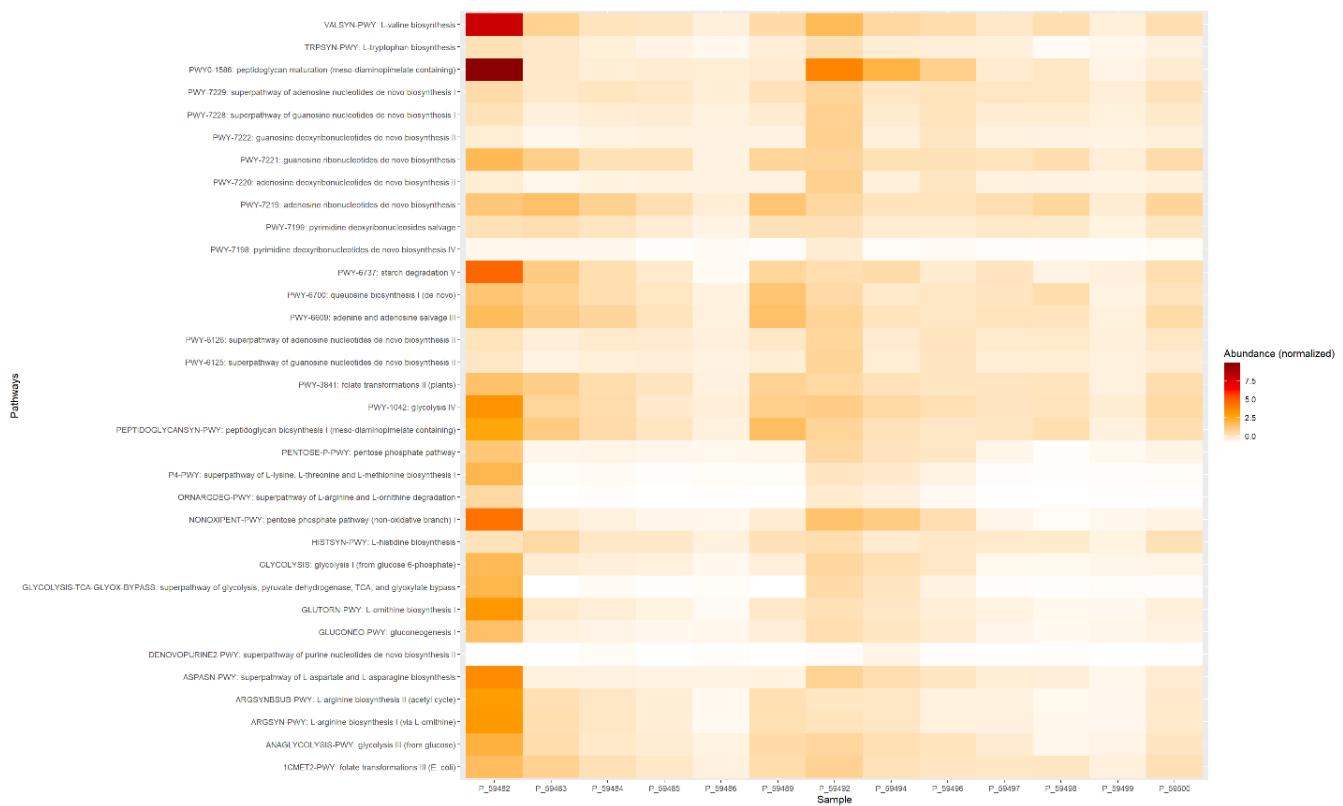
Category 1	Category 2
Tissierella P1	
Lautropia mirabilis	
Comamonas kerstersii	
Desulfovibrionaceae bacterium	
Desulfovibrio piger	
Morganella morganii	
Proteus mirabilis	
Acinetobacter baumannii	
Paraprevotella clara	

**Table S2.** Taxonomy for OTU correlated with samples.

NCBI_ID	Phylum	Class	Order	Family	Genus	Species
OTU48	Actinobacteria	Actinobacteria	Propionibacterales			
OTU75	Bacteroidetes	Bacteroidia	Bacteroidales			
OTU80	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides dorei
OTU98	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides vulgatus
OTU135	Bacteroidetes	Bacteroidia	Bacteroidales	Tannerellaceae		
OTU136	Bacteroidetes	Bacteroidia	Bacteroidales	Tannerellaceae	Parabacteroides	
OTU171	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae		
OTU175	Firmicutes	Bacilli	Lactobacillales	Streptococcaceae	Streptococcus	
OTU219	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae		
OTU228	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Butyrivibrio	
OTU229	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Butyrivibrio	
OTU255	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	
OTU256	Firmicutes	Clostridia	Clostridiales	Lachnospiraceae	Roseburia	Roseburia faecis
OTU335	Firmicutes	Negativicutes	Acidaminococcales			
OTU348	Firmicutes	Negativicutes	Veillonellales	Veillonellaceae	Dialister	
OTU350	Firmicutes	Negativicutes	Veillonellales	Veillonellaceae	Dialister	Dialister CAG 357



**Figure S1.** Heatmap of weighted UniFrac metrics (left) and unweighted UniFrac metrics (right) where the values represented in different color.



**Figure S2.** The functional characteristics of the gut microbiome in CRC patients' metabolic pathways where the different pathway names on the left and the abundance of each pathway in each patient are shown in color and are proportional to color intensity.