Meeting with Pat, Kim and Kaitlin – 1/13/16, updated w meeting notes

**KWS Analysis plan**

Samples: (n = 20 patients)

* 2 luminal samples from right and left sides
* 3 mucosa/biopsy samples from right and left sides
* Several grams of home collected stool in or not in preservative (RNA later)
* 2 FIT tests – 1 analyzed and cartridge saved, one unanalyzed
  + Most at 0ng, 4 samples ~100ng, 1 sample is 573ng
  + Interesting that 25% of patients have a detectable FIT. Can look at as a subgroup
* Basic metadata—height, weight, age, gender, race (not racially diverse group)
* Photos of places where biopsies taken and depths (furthest point reached). Might need the latter data to compare variation in location between patients.

Research questions:

1. Right vs. left
   1. Right feces vs left luminal
   2. Right mucosa vs left mucosa
   3. lumen vs mucosa
   4. R/L feces vs spontaneously evacuated stool
2. Metagenomics of right vs left
   1. Does metagenomic content explain any similarities/differences observed?
   2. Does metagenomic content track with known differences in gut biogeography at these sites? pH, oxygen gradients…
3. Human transcriptomics
   1. What does human transcriptome look like in right vs left colon mucosa?
   2. Do any transcriptomic observations track with observed species or microbial processes at each site?
4. Can FIT and microbiome be analyzed on one sample?
   1. Yes, Niel in Schloss lab has found that (using different samples)
   2. Is there another interesting question to be asked with FIT?
   3. Could look at home collected vs analyzed/unanalyzed
5. Compare to R vs L cancer datasets? These probably are unprepped….
6. \*\* make sure to thank the Rose and Sara P foundation \*\*

What I propose doing (in what order):

1. 16S and metagenomics of R vs L samples, spontaneous stool, FIT preservative extract?
   1. Isolate DNA from 1 sample per site per patient (5 samples per pt)
   2. Can do 16S and metagenomics on same sample on MiSeq
   3. Leaves 2 samples/site/pt in freezer
2. Human transcriptomics
   1. Isolate RNA from 1 sample per site per pt (2 per pt)
   2. RNA isolation and RNA-seq run separately from 16S on HiSeq + core instruments
   3. Leaves 1 mucosal sample/site/pt in freezer
3. FIT tests- what to do with these?

Timeline:

* DNA isolation takes 1 day, library prep and 16S runs take ~2 weeks. We are backed up for the MiSeq currently so this could probably be done in ~ 1 month or so
* Can do RNA isolation concurrently, or one at a time
* Analysis

**PTSP plans** Kaitlin will talk to PTSP people first to see if or how will need to adjust plan.

If we do need to adjust it, can use this data as preliminary data for the grant, propose new aims. Either could do bacterial transcriptomics (difficult) on this patient set or:

Fish oil, asprin affects on microbiome (known to affect colon cancer) Nadeem or Verani potential PIs to collab with.

Setting up a new study would give more training in IRB and patient recruitment, etc.

If we wanted to do more patient collection, we would not be able to get more bucket stool kits, due to cost and availability. Would need to design follow-up questions not using buckets. Could be another option to use cdiff home collected kits that have been used in the Schloss lab in the past, follow-up on these if we are really interested in home collected stools