R21: Conservation and functional-characterization of tumor methylation sites

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Goal: Detect conservation of methylation

**Specific Aim 1:** Statistical methods to detect conservation of DNA methylation status at CpG sites.

**Specific Aim 2:** Evolutionary modeling of tumor evolution, with the goal of classification of CpG sites as stable or unstable, and reconstructing the state of the first tumor cell.

**Specific Aim 3:** CpG-level → genes/pathway-level.

**Specific Aim 4:** Software development and distribution.
Multi-regional sampling from ~100 colon tumors

- For many tumors, we have matched ‘normal’ data.
- Our preliminary data are pooled, rather than cell-level. So, we will have sample-level methylation proportions at each site, rather than ‘yes’/’no’ [1/0] cell-level data.

Illumina Infinium MethylationEPIC BeadChip Kit (www.illumina.com)

- Measures methylation at ~850,000 CpG sites.
- Comprehensive Genome-Wide Coverage
Distribution of methylation frequencies for 8 tumor samples
Shiny Apps - e.g., visualization

Samples are selected by specifying plate, well and sample id. Data is specified globally in the application.

Plotting window: Dynamically changes with data selection and input.
END

[More details on poster]