lncRNA Literature Review

Jing He

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Projects update

- **AML WXS analysis**
- PAN cancer methylation
  - data downloading and preprocessing
  - STAD ($n = 479$), $PRAD(n = 304)$

Reminder

- What we have?
  - 16 patients with matched normal, tumor and relapse sample, whole exome sequencing
- What's our hypothesis?
  - are there exist MRs that can predict relapse?
- What's been done?
  - potential MRs (from Yishai); Somatic mutations and CNVs of the 16 patients

Methods

Stochastic of finding mutations...

- Probability of at least 2 patients have the same mutation:
  - M = #Mutations; N= # of patients
  - $1 - \frac{N! * {}^{M}_{N}}{M^N}$
- Given the number of raw variants, p-value of at least 2 patients have 1 common mutation is $3.85 * 10^{-05}$

MRs associate with CNVs and Mutations

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MRs' association with Mutations using PrePPI

Mutated Genes with Minor Allele Frequency

Mutated Genes with Minor Allele Frequency (cont. . .)