



Impact of the Total Western Diet for rodents on colon mucosal gene expression in a multi-generational murine model of colitis-associated colorectal cancer

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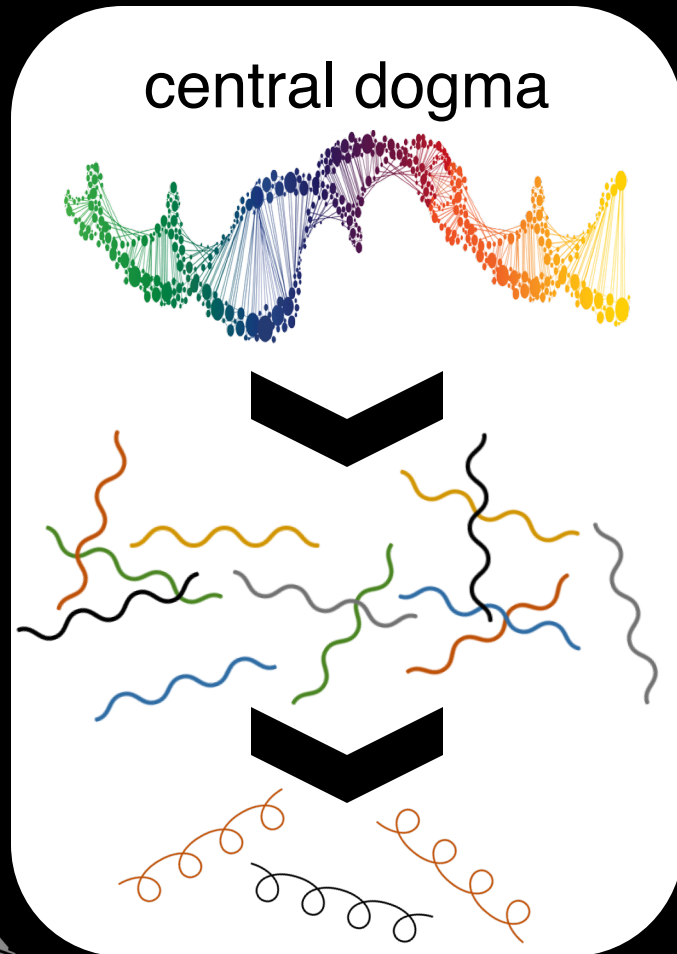
Abby Benninghoff

Colorectal cancer (CRC)

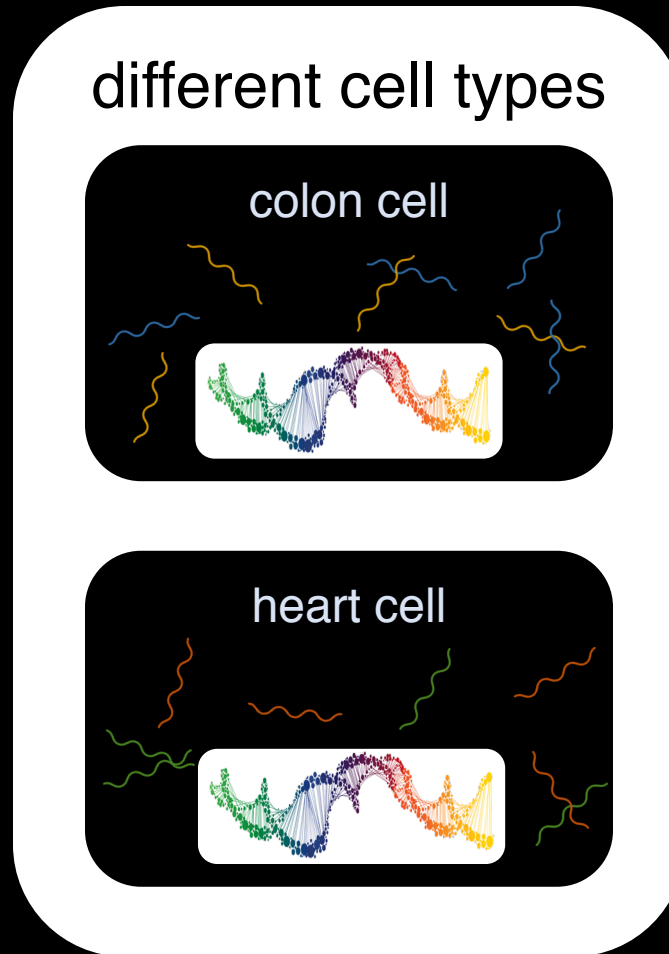
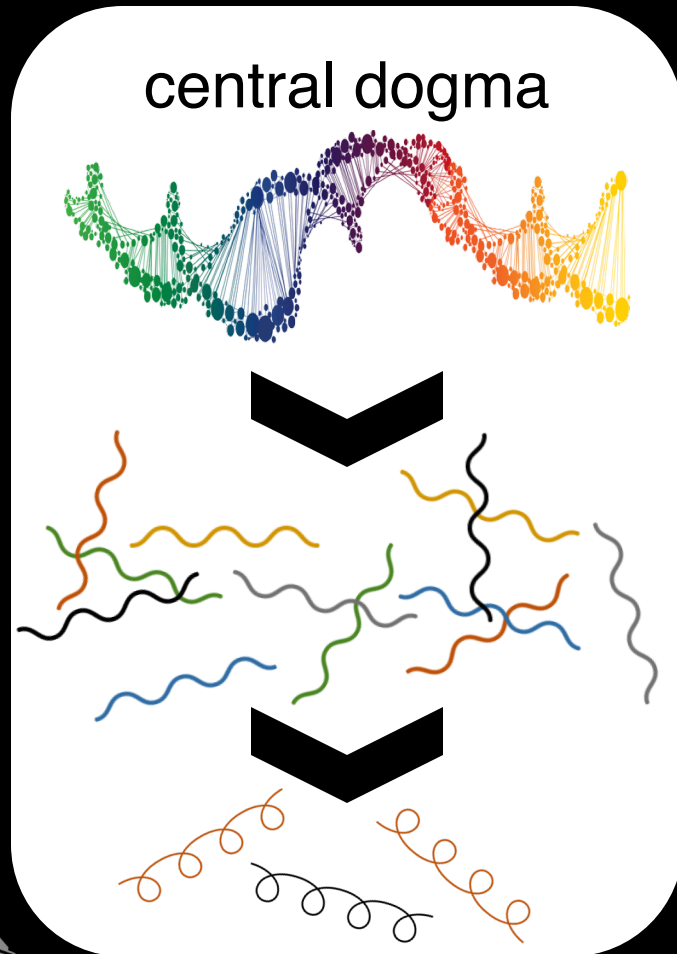
- CRC is the 2nd leading cause of cancer-related death in the US.
- Majority of CRC incidence is attributed to diet.



Epigenetic gene expression signatures

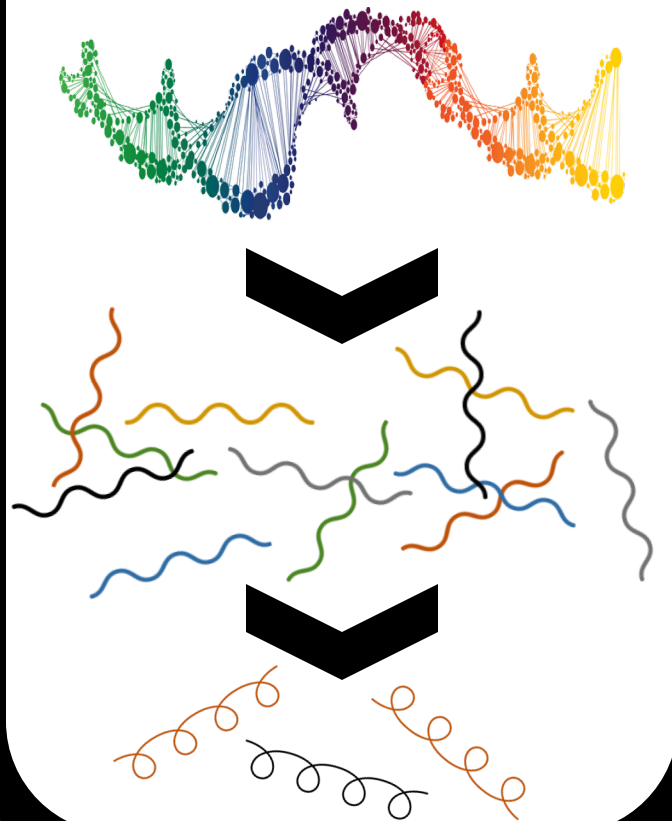


Epigenetic gene expression signatures



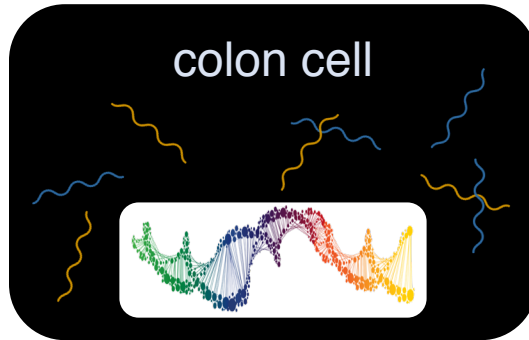
Epigenetic gene expression signatures

central dogma

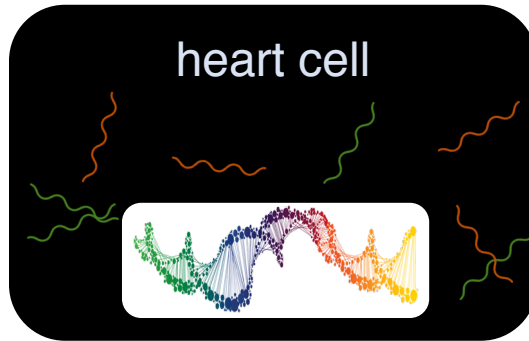


different cell types

colon cell

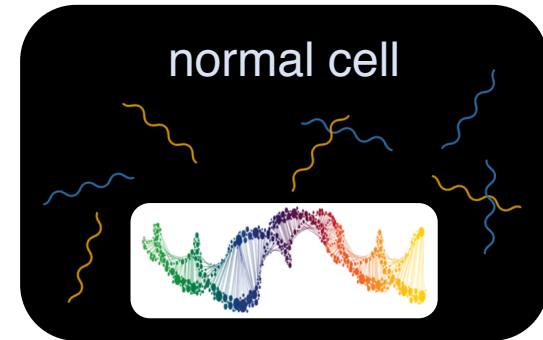


heart cell

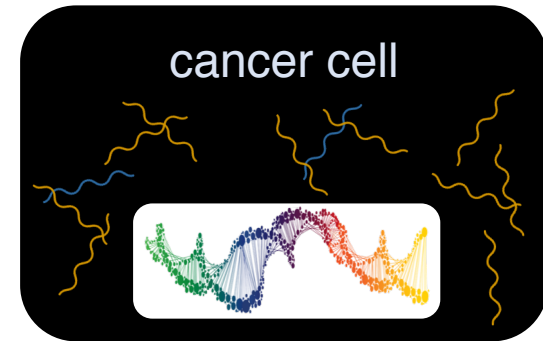


normal vs. cancer

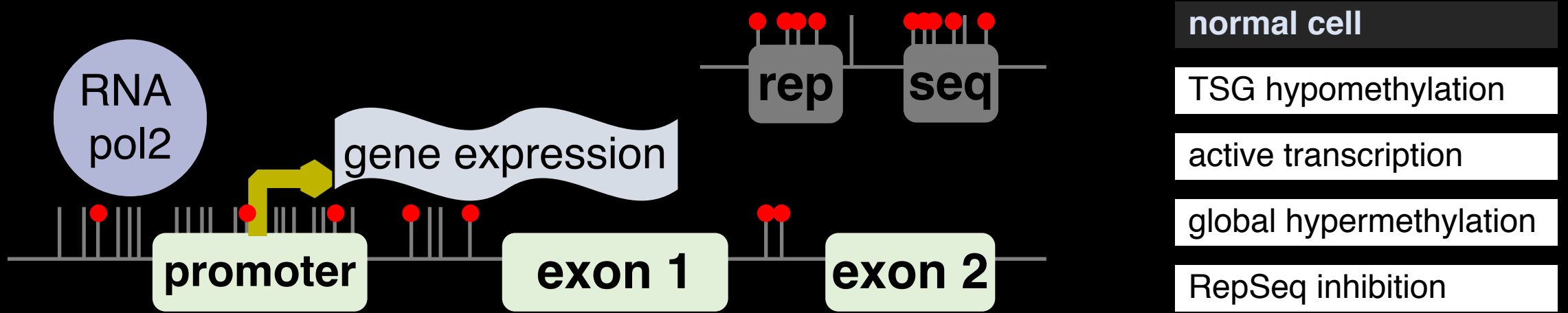
normal cell



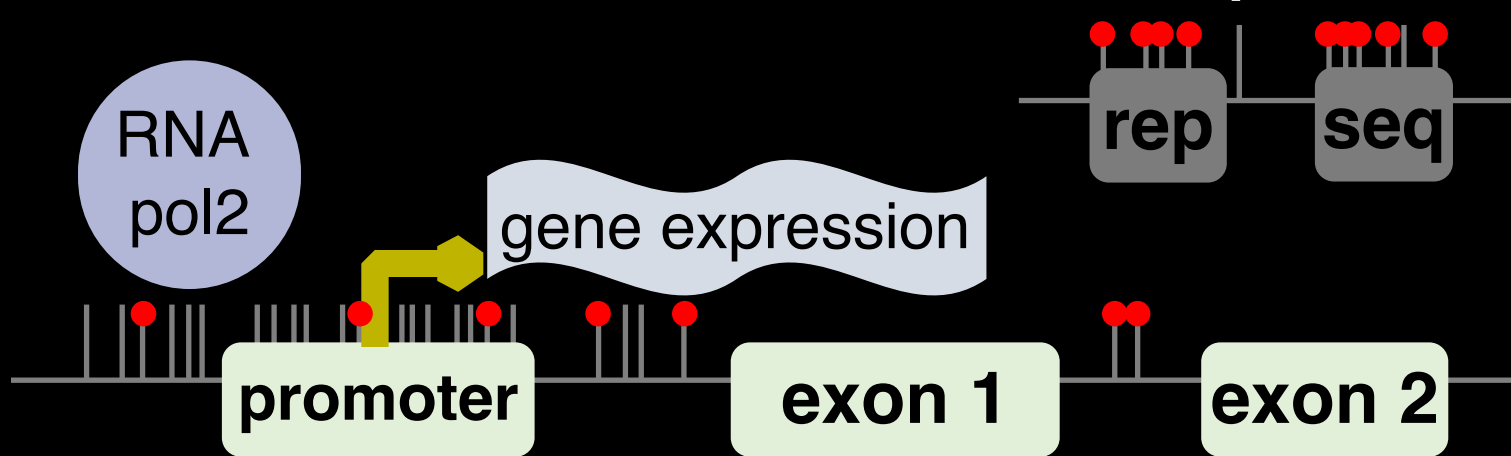
cancer cell



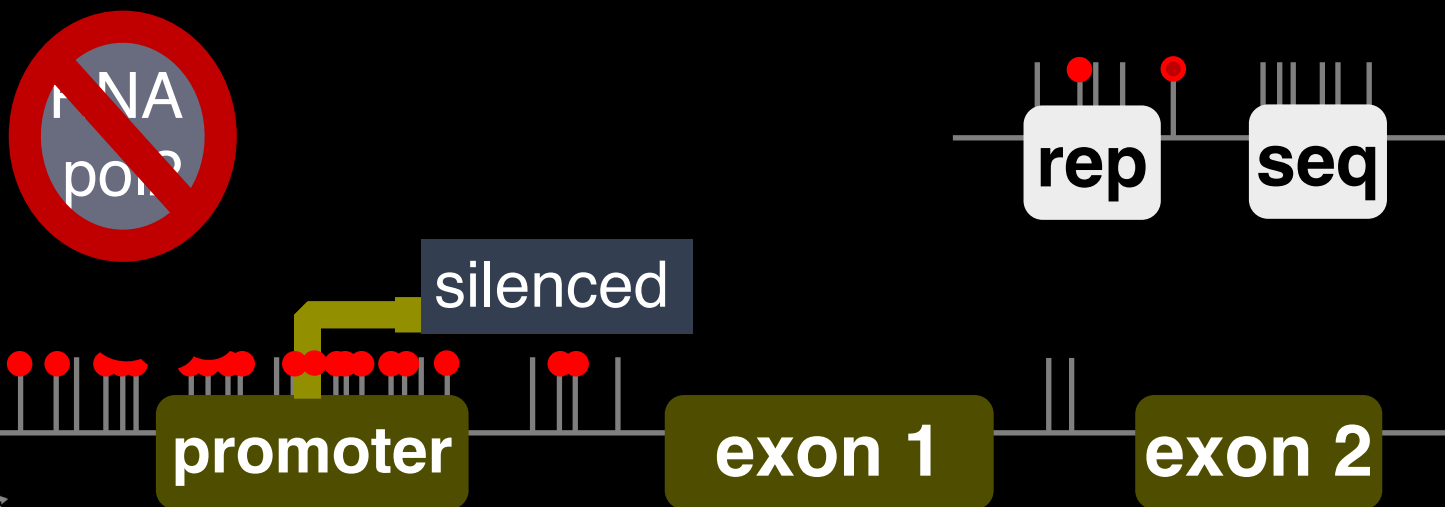
Heritable DNA methylation



Heritable DNA methylation



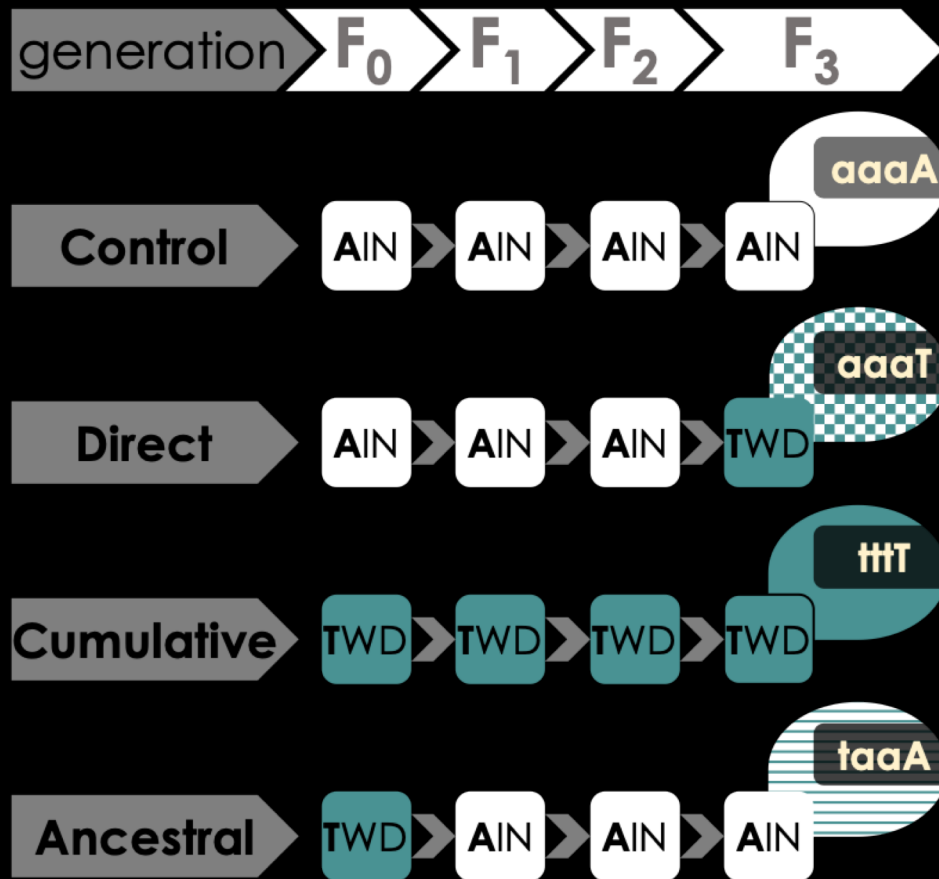
- normal cell
- TSG hypomethylation
- active transcription
- global hypermethylation
- RepSeq inhibition



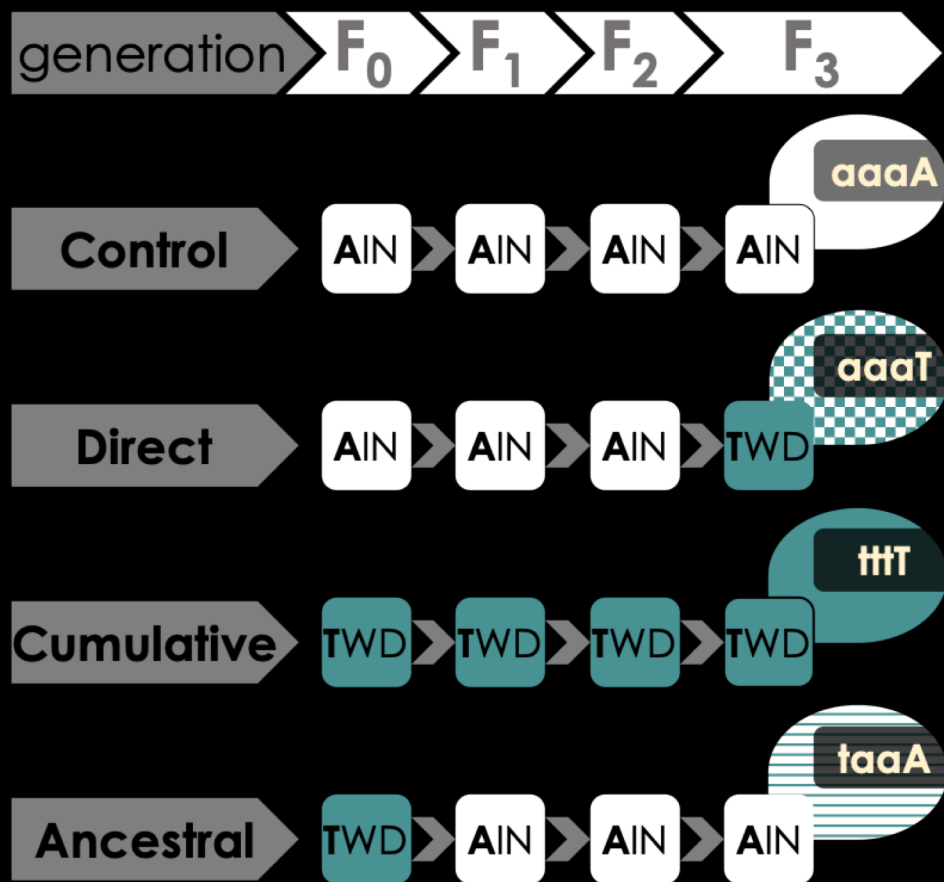
- tumor cell
- TSG hypermethylation
- silenced transcription
- global hypomethylation
- genome instability



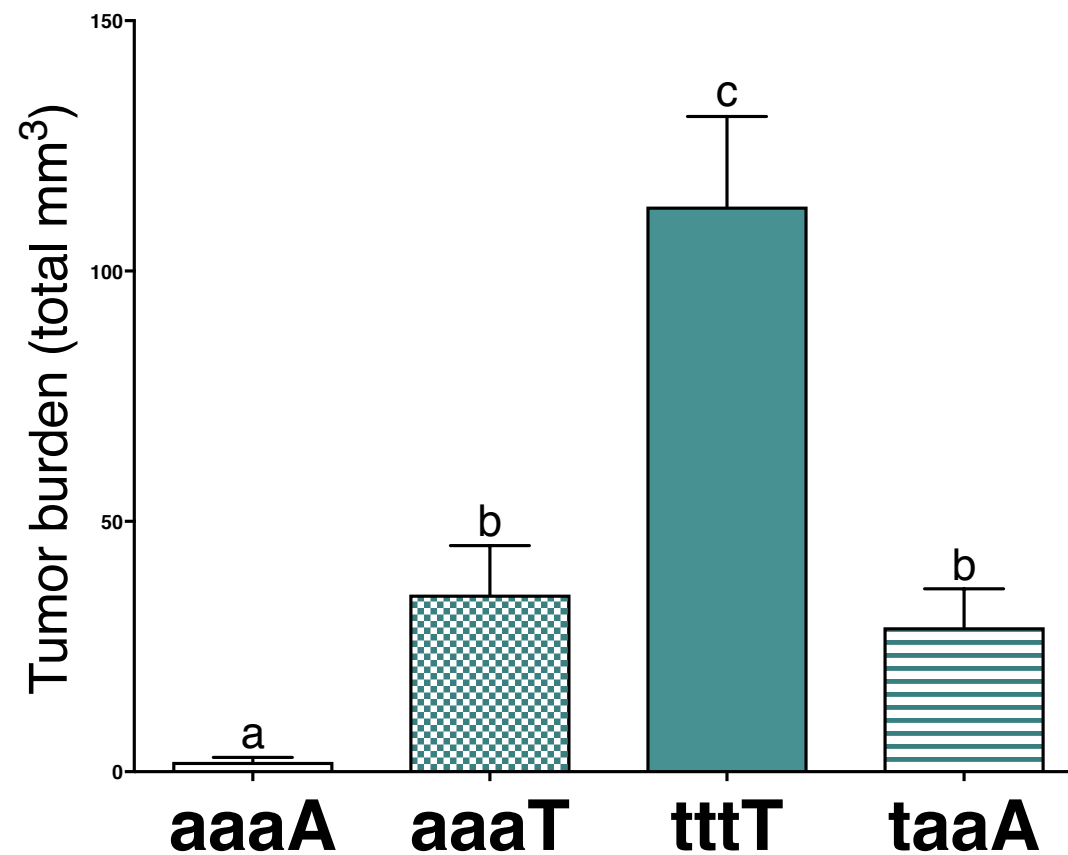
Study design



Study design



CRC outcome





Knowledge gap

Objective:

evaluate differentially expressed genes (DEGs) of colonic mucosal cells from 3rd generation offspring.

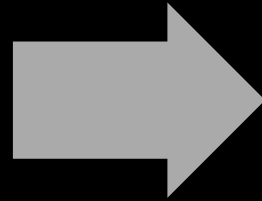




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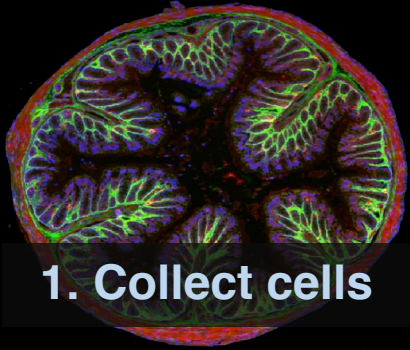
Hypothesis:

Total Western Diet (TWD) exposure will upregulate or downregulate genes that play a role in CRC.





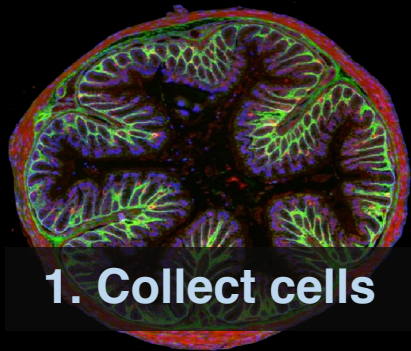
Methods



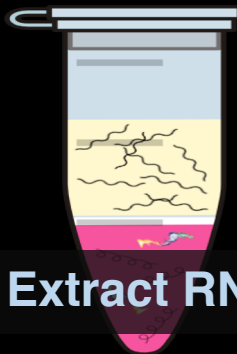
1. Collect cells



Methods

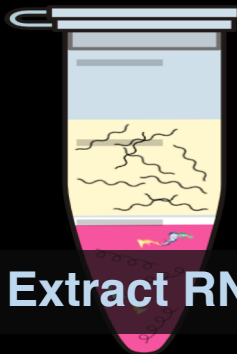
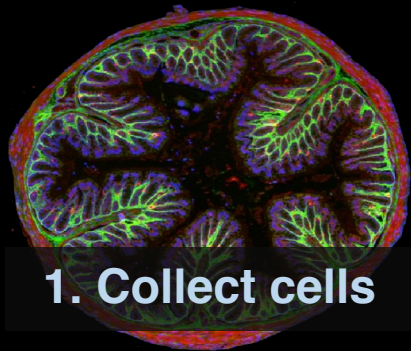


1. Collect cells

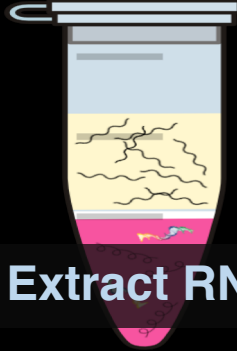
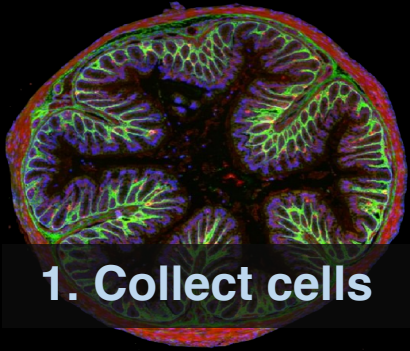


2. Extract RNA

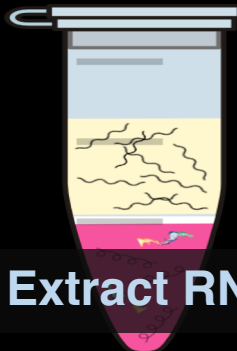
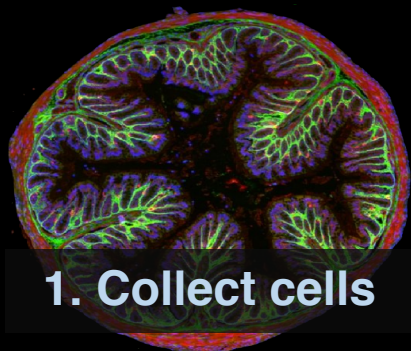
Methods



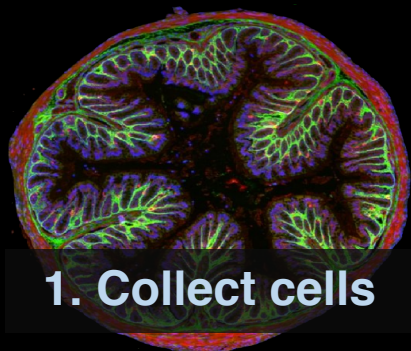
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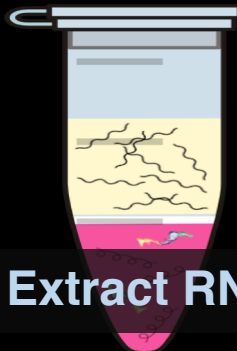
Methods



Methods



1. Collect cells



2. Extract RNA



3. Sorting



4. Sequencing



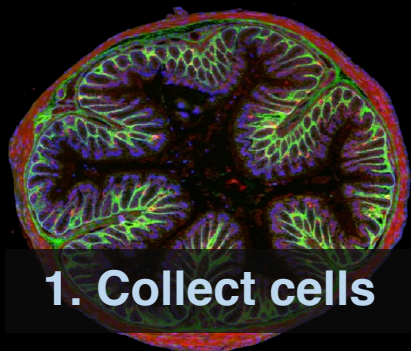
5. Quality control



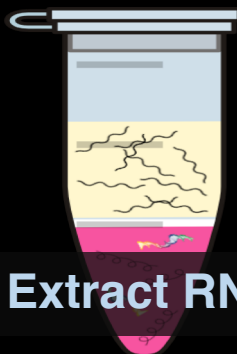
6. Trimming



Methods



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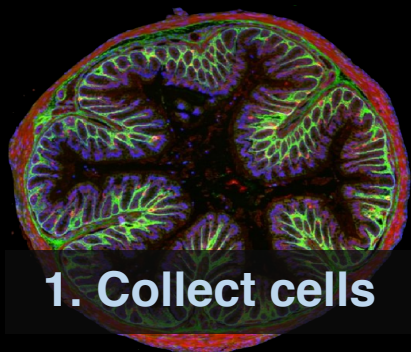


6. Trimming

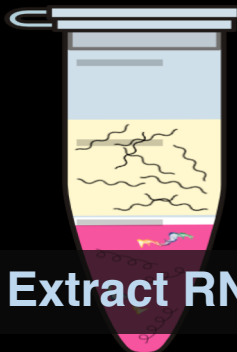


7. Alignment

Methods



1. Collect cells



2. Extract RNA



3. Sorting



4. Sequencing



5. Quality control



6. Trimming

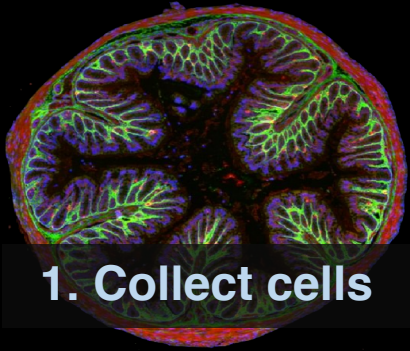


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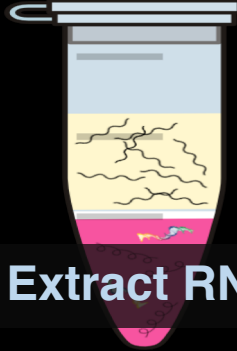


8. Quantification

Methods



1. Collect cells



2. Extract RNA



3. Sorting



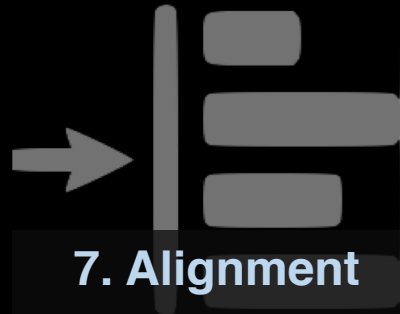
4. Sequencing



5. Quality control



6. Trimming



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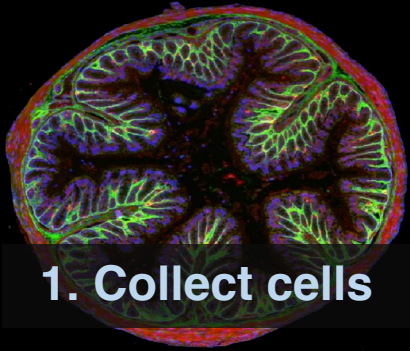


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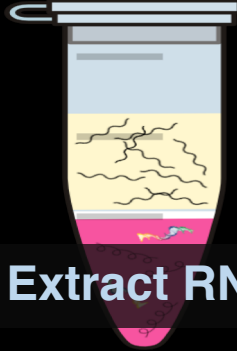


9. Filtering

Methods



1. Collect cells



2. Extract RNA



3. Sorting



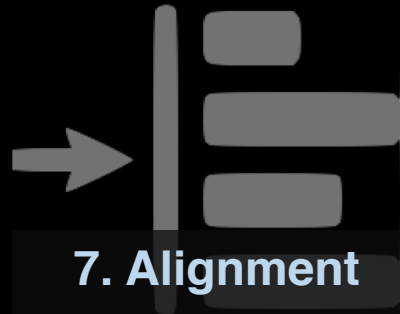
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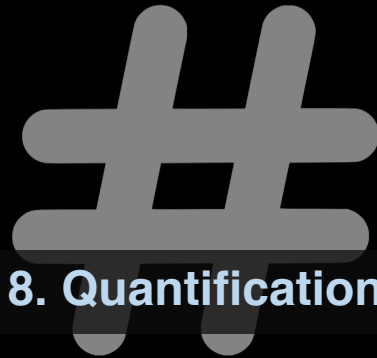
5. Quality control



6. Trimming



7. Alignment



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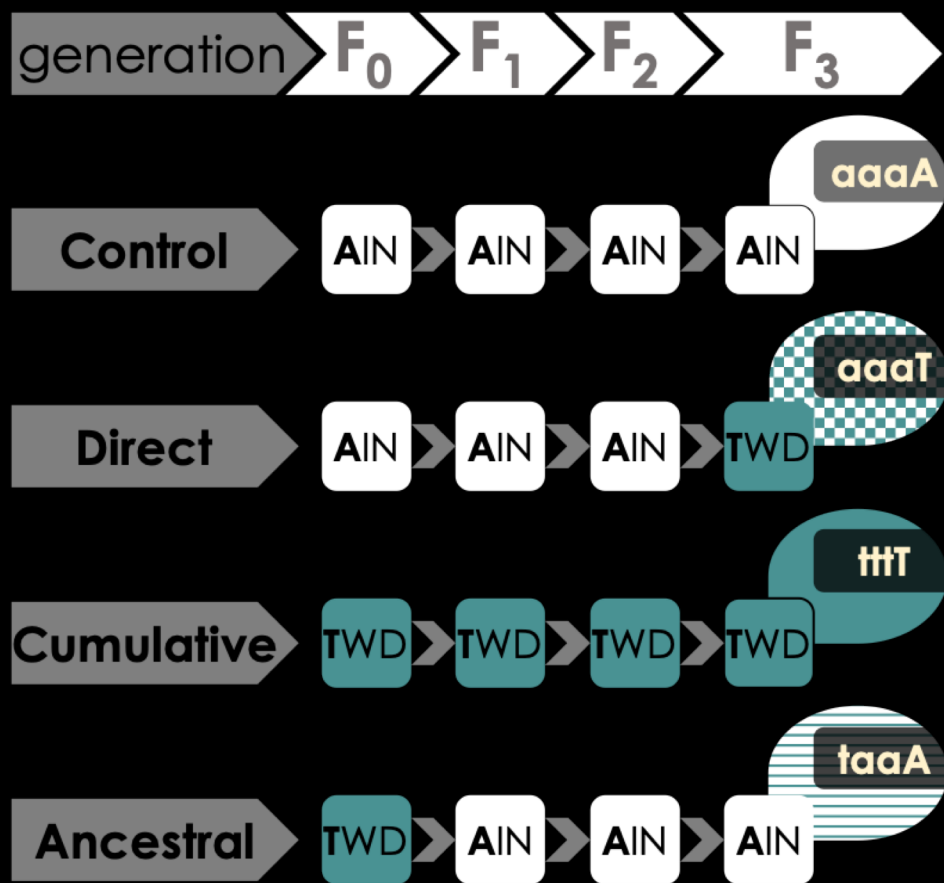


9. Filtering



10. DEG analysis

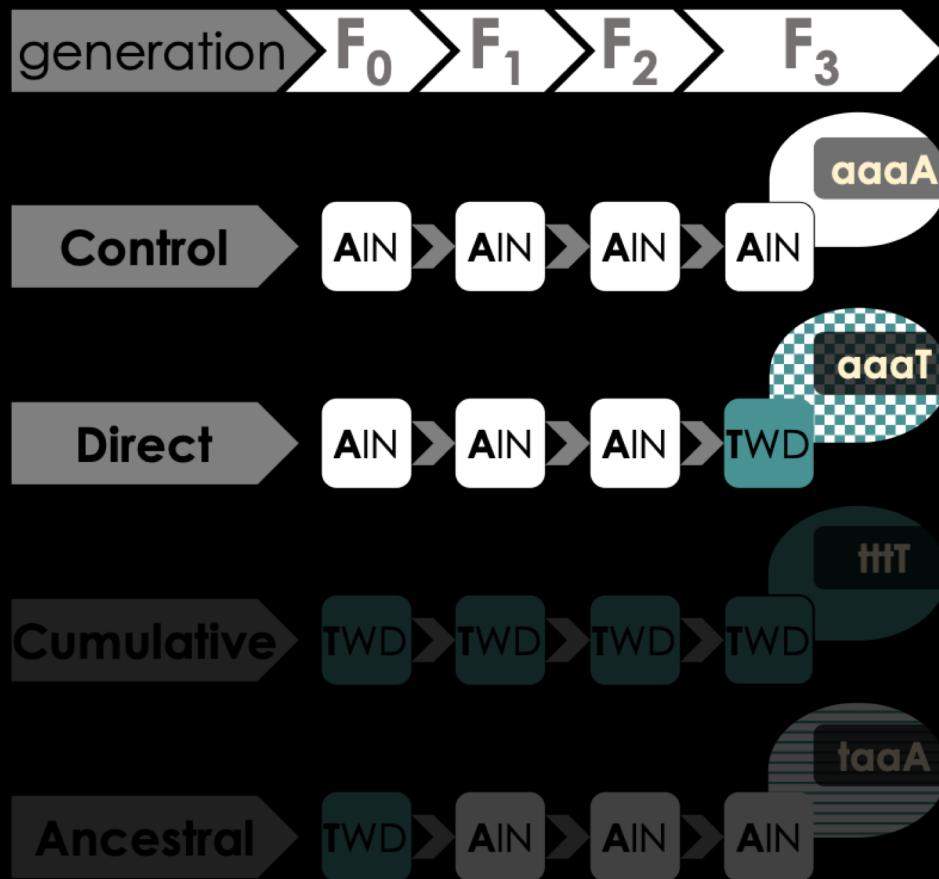
Study design



Preliminary results

- Cancer vs. controls
 - ~700-4500 DEGs

Study design

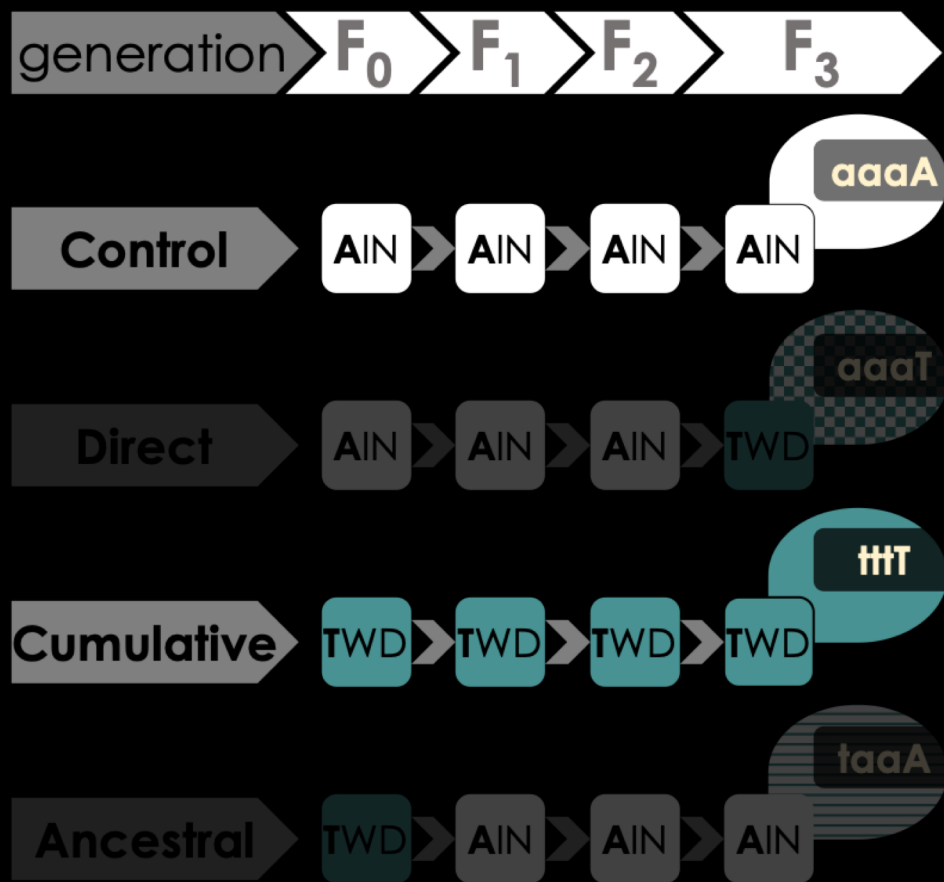


Preliminary results

- Cancer vs. controls
 - ~700-4500 DEGs
- Cancer cohorts
 - aaaA vs aaaT
 - 36 DEGs



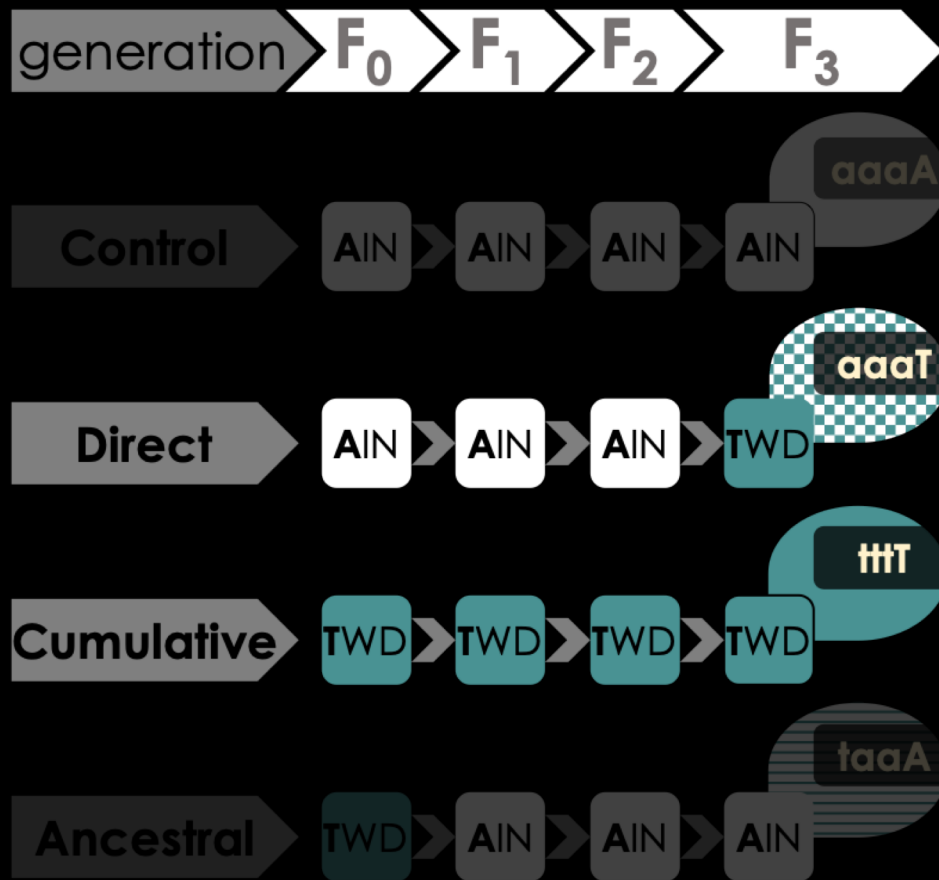
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36 DEGs
 - aaaA to tttT
119 DEGs

Study design



Preliminary results

- Cancer vs. controls
 - ~700-4500 DEGs
- Cancer cohorts
 - aaaA vs aaaT
36 DEGs
 - aaaA to tttT
119 DEGs
- Sham cohorts
 - aaaT vs. tttT
101 DEGs
 - defense response
 - immune response
 - response to interferon



Summary & conclusions

- Multigenerational exposure to the Western dietary pattern may alter gene expression and health outcome in offspring.



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- Metanalysis of clinical CRC gene expression signature reveals DEGs related to immune function.
- Many DEGs in human CRC are associated with aberrant DNA methylation.
- Ongoing analysis will include methylation status.



Acknowledgements

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