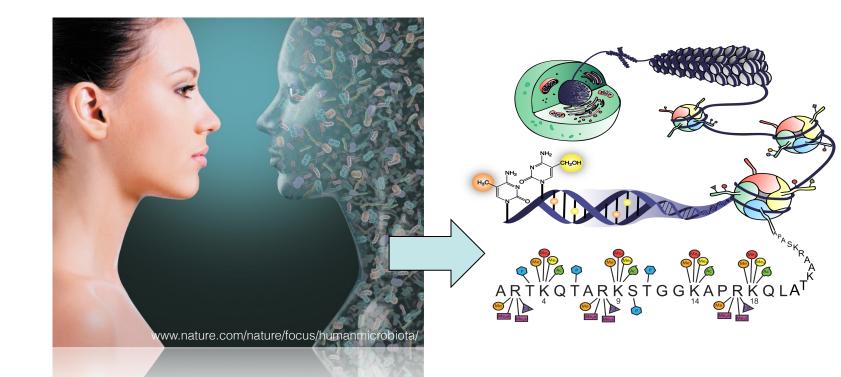
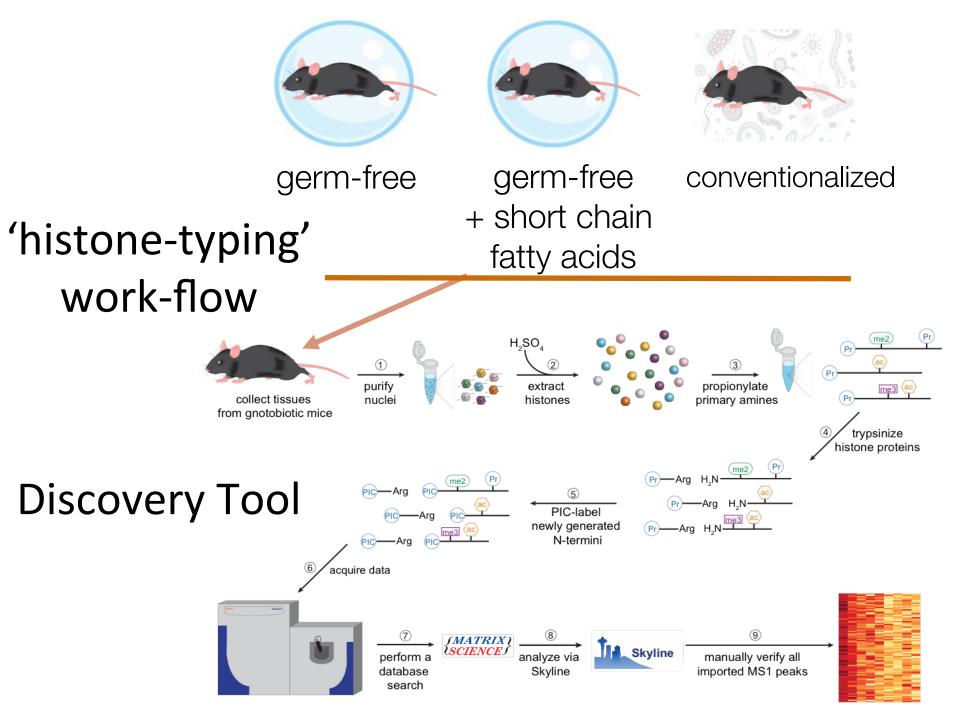
Environment, Metabolism and the Epigenome



Gut microbiota & the host epigenome

Collaboration with Federico Rey (UW)



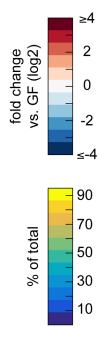
Gut microbiota regulate host histone **PTM** states

Krautkramer et al Mol Cell 2016 **Posters: James Dowell & Spencer Haws**

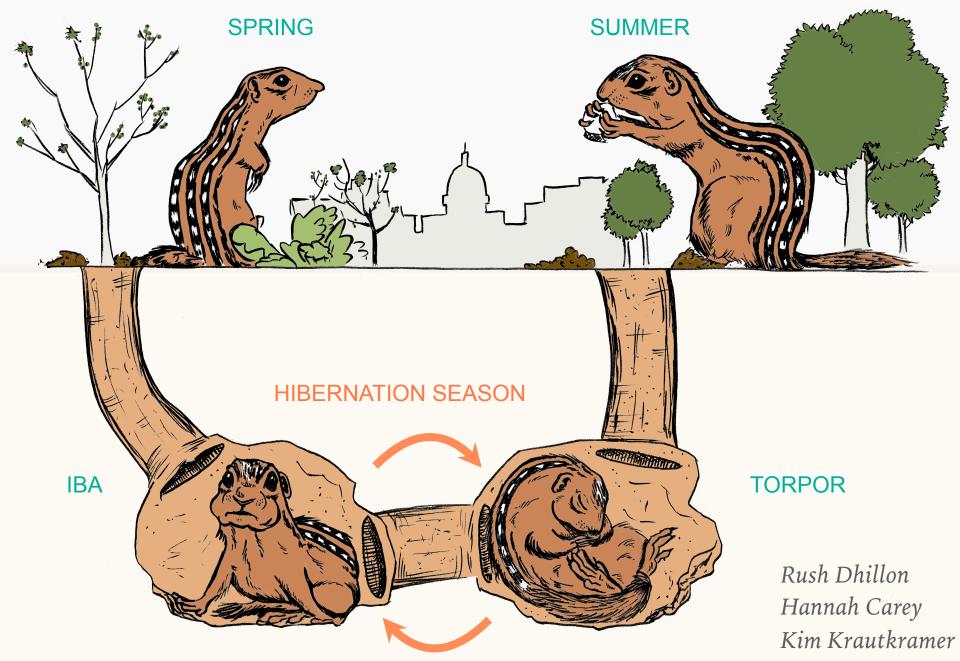


H3: K18ac+K23ac, ~4-fold H4: tetra-acetylation, 12-fold H3: K27me3+K36me2, ~4-fold H3: K18me1+K23un, ~8-fold

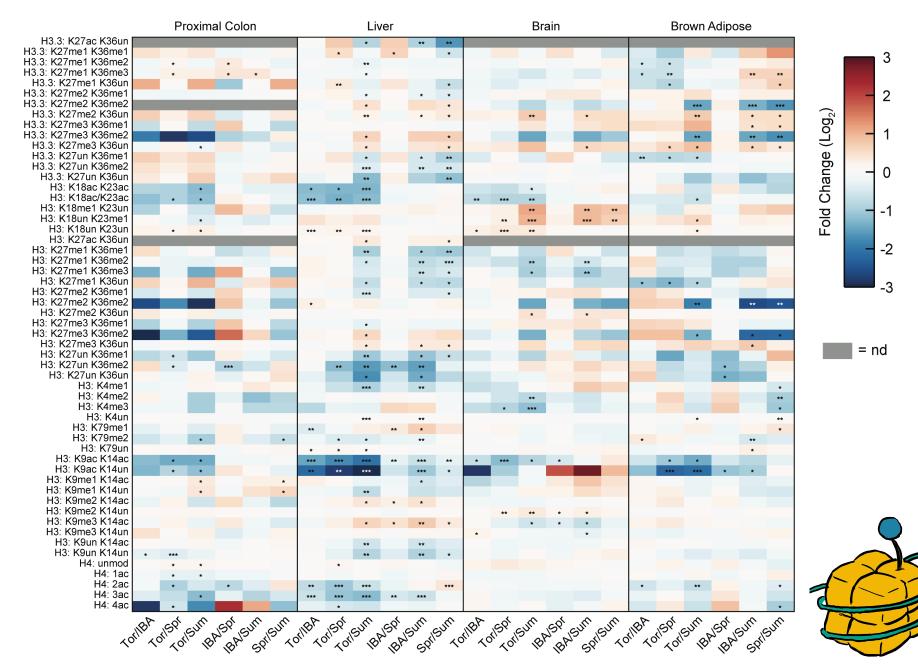
			,							
H3.3: K27ac K36un		0.000				0.038		0.000	0.047	
H3.3: K27me1 K36me1					0.022		0.037	0.002		
H3.3: K27me1 K36me2	0.050	0.001		0.004				0.030		
H3.3: K27me1 K36me3	0.027	0.001		0.000						
H3.3: K27me1 K36un			0.035					0.000		
H3.3: K27me2 K36me1		0.005		0.014	0.003			0.000		
H3.3: K27me2 K36me2		0.014							0.109	
H3.3: K27me2 K36un	[0.012	0.049			0.035	0.008		
H3.3: K27me3 K36me1		0.023			0.009			0.001		
H3.3: K27me3 K36me2		0.031			0.017			0.028		
H3.3: K27me3 K36un		0.000		0.000					0.006	
H3.3: K27un K36me1		0.071	0.008				[
H3.3: K27un K36me2				0.033	0.013					
H3.3: K27un K36un		0.012	0.024	0.039	0.002			0.004		
H3: K18ac K23ac		0.005	0.024	0.000	0.002	0.022		0.004		
		0.005	0.012		0.025	0.022	0.050	0.010		
H3: K18ac/K23ac	0.007		0.012		0.035		0.050	0.010	0.012	
H3: K18me1 K23un	0.007	0.000			0.012			0.002	0.012	
H3: K18un K23me1	0.043	0.001			0.008			0.002		
H3: K18un K23un			0.011			0.047	0.039	0.008		
H3: K27ac K36un	0.033		0.017		0.001			0.000		
H3: K27me1 K36me1		0.069			0.003					
H3: K27me1 K36me2			0.027	0.010				0.001		
H3: K27me1 K36me3	0.009	0.013		0.021				0.023		
H3: K27me1 K36un			0.008	0.049	0.048	0.036		0.000		
H3: K27me2 K36me1		0.002			0.002			0.002		
H3: K27me2 K36me2		0.037				:	0.039			
H3: K27me2 K36un			0.011		0.002			0.000	0.020	
H3: K27me3 K36me1					0.009			0.000	0.035	
H3: K27me3 K36me2	0.043	0.011								
H3: K27me3 K36un		0.002			0.005	0.040		0.000		
H3: K27un K36me1			0.009		0.003				0.040	
H3: K27un K36me2										
H3: K27un K36un			0.047		0.007			0.005	0.007	
H3: K4me1					0.000			0.018		
H3: K4me2		 ,	0.038		0.001			0.015	0.002	
H3: K4me3		(0.001				0.002	
H3: K4un		0.036			0.000			0.007		
		0.030			0.000			0.007	0.017	
H3: K79me1								0.022	0.017	
H3: K79me2										
H3: K79un					0.049					
H3: K9ac K14ac		0.006				0.015				
H3: K9ac K14un		0.048			0.008					
H3: K9me1 K14ac				0.001	0.001					
H3: K9me1 K14un					0.003		0.027	0.045		
H3: K9me2 K14ac		0.027								
H3: K9me2 K14un						0.001		0.012	0.040	
H3: K9me3 K14ac									0.016	
H3: K9me3 K14un					0.006			0.042		
H3: K9un K14ac	[0.050			0.023		0.012	0.005	0.025	
H3: K9un K14un	[0.028			0.000			0.000		
unmod		0.000			0.012	0.002		0.000		
1 ac		0.000			0.007	0.009		0.000		
2ac		0.001				0.000		0.004	0.005	
3ac	0.002	0.005			0.034	0.007		0.002		
3ac 4ac	0.002	0.048			0.034	0.006		0.002		
Tissue:	Liv	Liv	Liv	Col	Col	Col	Adi	Adi	Adi	
Diet:	ch	ch	Н	ch	ch	Н	ch	ch	н	
Condition:	R	D	R	R	D	R	R	D	R	



CIRCANNUAL CYCLE OF THE 13-LINED GROUND SQUIRREL



HISTONE PTM STATES VARY THROUGHOUT THE YEAR



Efforts at WID

Building a pipeline for multi-omics integration that includes epigenomics, histone typing, metabolomics and metagenomics

Showcase these efforts as GRAND Challenges within the Healthy People multi-disciplinary team at WID and throughout campus