

THE EFFECT OF NERVE GROWTH FACTOR ADMINISTRATION ON GUT MICROBIOTA HOMEOSTASIS IN AN OBESE, TYPE 2 DIABETES MELLITUS, AND ALZHEIMER'S DISEASE MOUSE MODEL

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Introduction

- High-Fat High-Sugar Western Diet
 - *Obesity*
 - Body Mass Index (BMI)
- Type II Diabetes Mellitus (T2DM)
 - *Sustained high blood sugar levels*
 - *Pancreatic beta cell dysfunction*
- Alzheimer's Disease (AD)
 - *Neurodegenerative disorder*
 - *Progressively greater cognitive decline*
 - ***Nerve Growth Factor (NGF)***

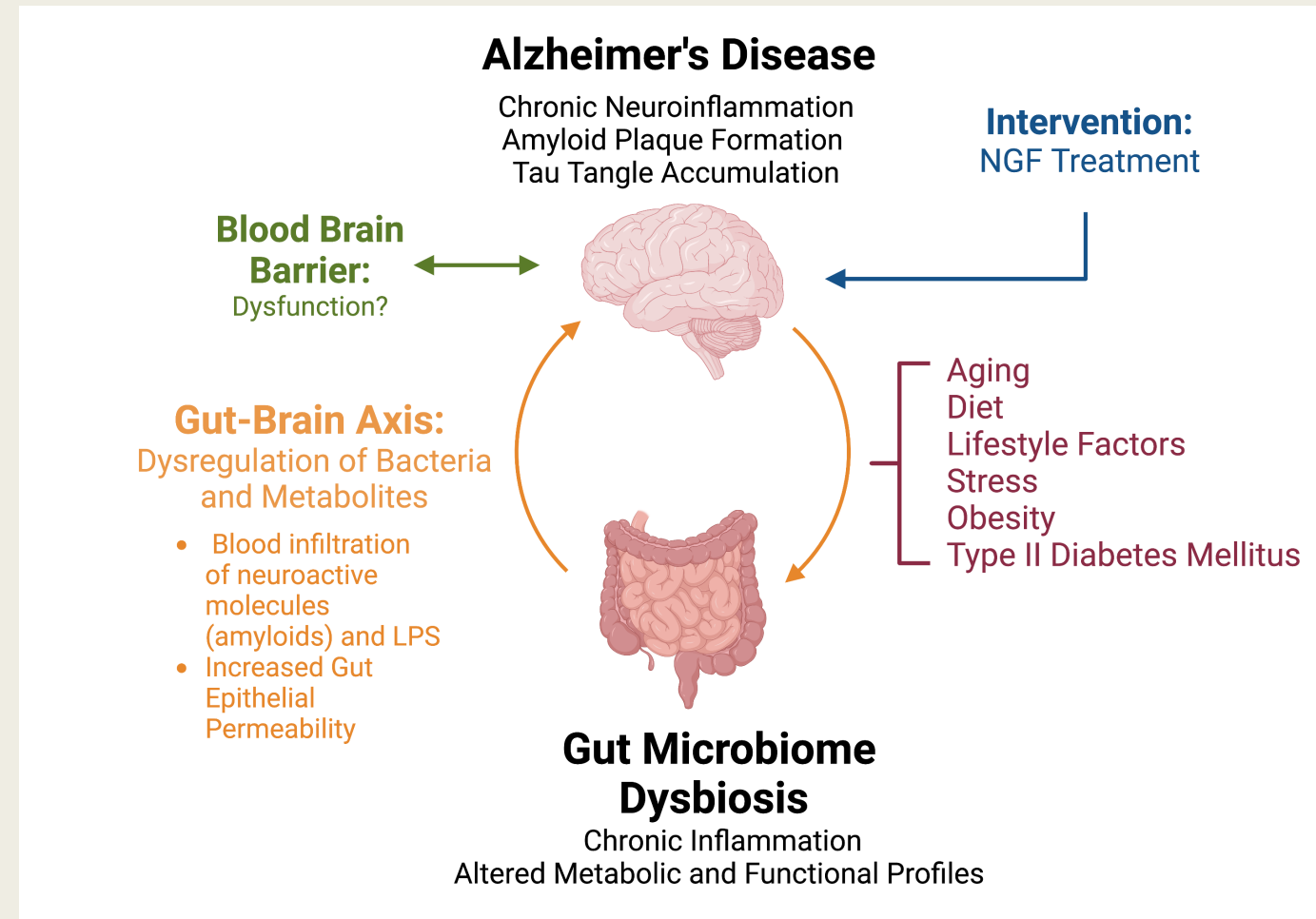


<https://www.obesityaction.org/get-educated/understanding-your-weight-and-health/classifications-of-obesity/>

➔ **Microbiome**

Microbiome

- **Microbiome:** Diverse gene collection of 10-100 trillion microbial cells with majority in GI tract
 - *Protective barrier*
 - *Regulator of metabolism*
 - *Inflammation*
- Dysbiosis leads to chronic diseases
 - *Diet-induced obesity*
 - *Associations with impaired NGF signaling*



Central Question

- Does NGF administration restore microbiota homeostasis in an obese, T2DM, and AD mouse model via reducing pro-inflammatory and increasing anti-inflammatory microbial taxa and altering their proportions?

Timeline and Treatment Groups



Dysregulation of gut microbiome = increased inflammation

NGF → regulation? = decreased inflammation

Timeline and Treatment Groups

Group #	Group Name	Treatment	Day	Week															
			0	1	2	3	4	5	6	7	8	9	10	11	12	13			
1	Lean Control + PBS	Chow Diet	Groups Separated base on Diet (chow or HFWD)																
2	Lean Control + NGF	Chow Diet and Treatment																	
3	HFWD	High Fat/High Sugar (Western) Diet																	
4	HFWD + NGF	High Fat/High Sugar (Western) Diet and Treatment																	
5	HFWD + STZ + PBS	Diabetes Model: High Fat/High Sugar (Western) Diet and STZ																	
6	HFWD + STZ + NGF	Diabetes Model with Treatment: High Fat/High Sugar (Western) Diet, STZ, + NGF																	
				Metabolic Cages															

Results: Body Weight

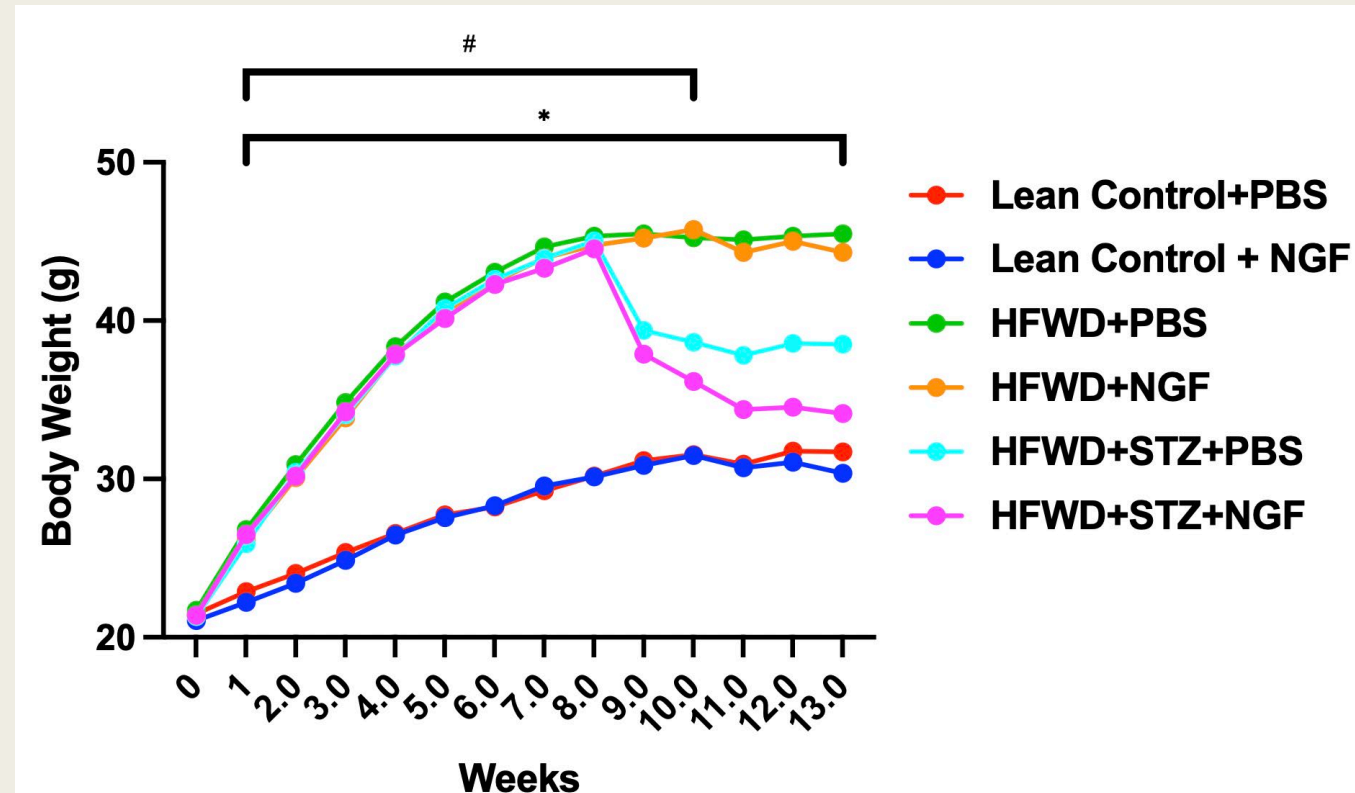
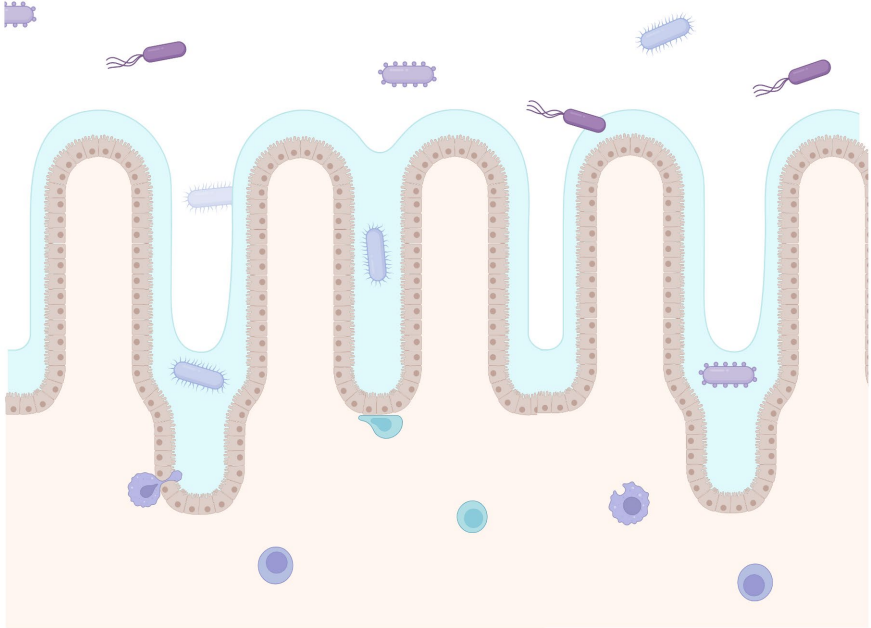


Figure. Significant differences between groups 1 and 3 as well as groups 1 and 5 from weeks 1 to end of week 13 ($P < 0.05$) as marked by “*”. Significant differences between groups 1 and 6 from weeks one through week 10 ($P < 0.05$) as marked by “#”.

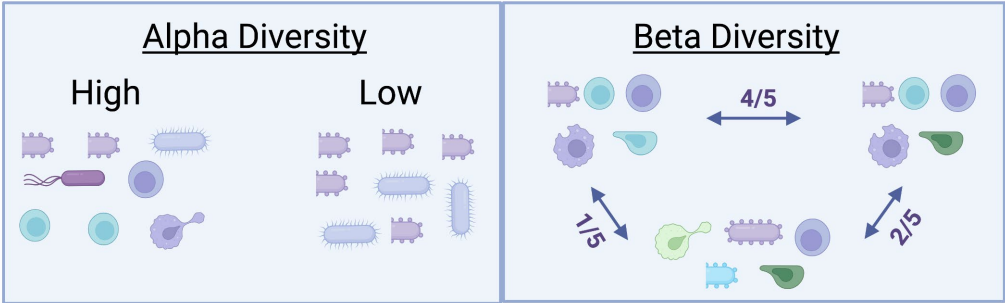
Methods: 16s rRNA Analysis

α -diversity & β -diversity

α -diversity:
the mean diversity of species within a sample

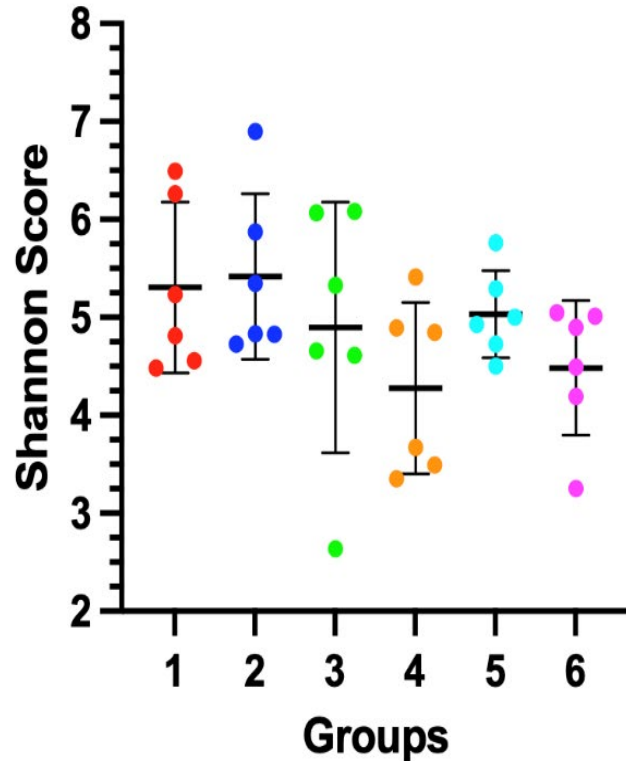


β -diversity:
Diversity similarity (or distance) between groups



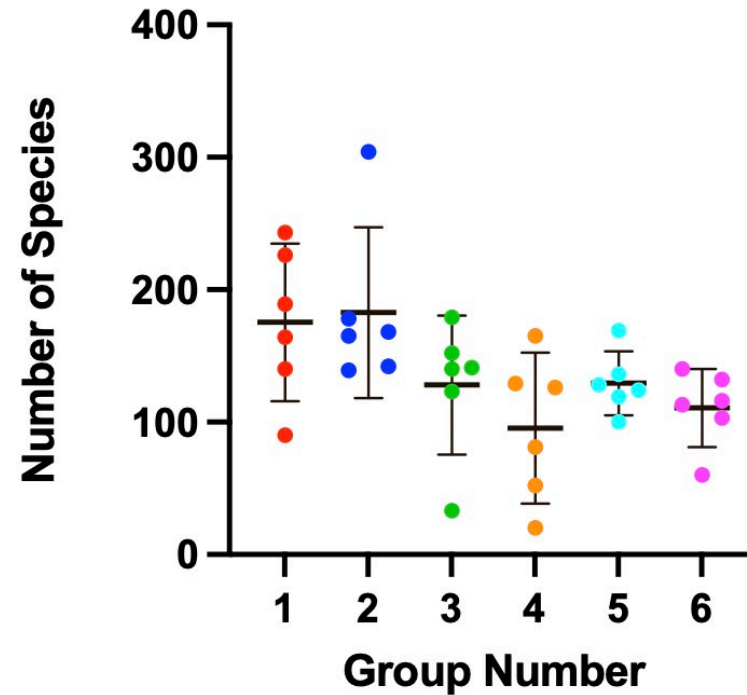
Results: α -diversity

Mean and Standard Deviation of Shannon Index



Descriptive statistics for calculated Shannon values. Mean and standard deviations.

Observed Number of Species



Means with 95% confidence intervals of Observed Number of Species

Results: Relative Abundances

Relative Abundances (Family Level) Groups 1, 2, and 6						
Family	Identification	1	2	6	P	FDR P
L5	Lachnospiraceae	0.048	0.049	0.012	0.052	0.256
L5	Clostridiaceae	0.001	0.001	0.000	0.054	0.256
L5	Peptococcaceae	0.000	0.000	0.000	0.059	0.267

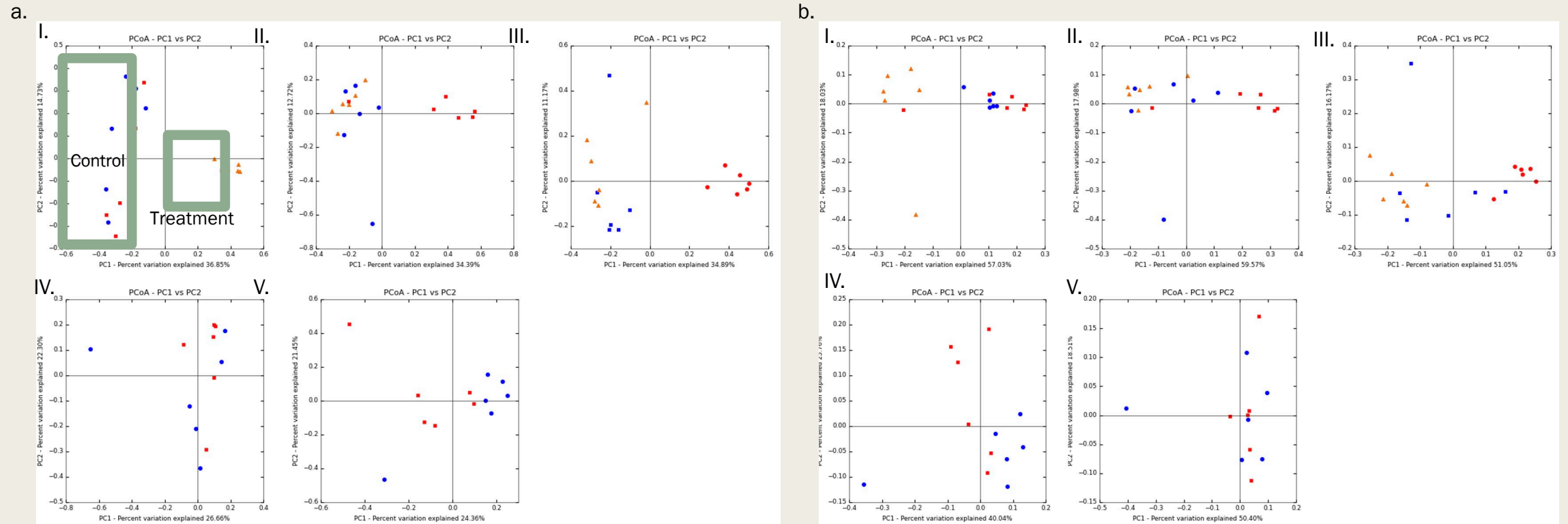
Treatment groups (3-6) contained significantly more pro-inflammatory and less anti-inflammatory bacteria compared to control groups (1-2)

Relative Abundances (Family Level) Groups 1, 3, and 5						
Family	Identification	1	3	5	P	FDR_P
L5	Family XIII	0.002	0.000	0.000	0.004	0.114
L5	Muribaculaceae	0.126	0.026	0.016	0.006	0.114
L5	Prevotellaceae	0.031	0.000	0.000	0.008	0.114
L5	Marinifilaceae	0.004	0.000	0.000	0.012	0.114
L5	Burkholderiaceae	0.001	0.002	0.000	0.012	0.114
L5	Streptococcaceae	0.011	0.043	0.065	0.020	0.156
L5	Desulfovibrionaceae	0.009	0.020	0.020	0.023	0.156
L5	Rikenellaceae	0.011	0.003	0.003	0.030	0.173
L5	Bifidobacteriaceae	0.014	0.067	0.111	0.033	0.173
L5	Erysipelotrichaceae	0.042	0.201	0.178	0.041	0.192

Relative Abundances (Family Level) Groups 2, 3, and 4						
Family	Identification	2	3	4	P	FDR_P
L5	Prevotellaceae	0.025	0.000	0.000	0.001	0.021
L5	Rikenellaceae	0.010	0.003	0.001	0.001	0.021
L5	Muribaculaceae	0.120	0.026	0.011	0.002	0.026
L5	Streptococcaceae	0.000	0.043	0.044	0.003	0.026
L5	Erysipelotrichaceae	0.002	0.201	0.273	0.003	0.026
L5	Marinifilaceae	0.003	0.000	0.000	0.004	0.031
L5	Burkholderiaceae	0.001	0.002	0.000	0.005	0.031
L5	Bifidobacteriaceae	0.000	0.067	0.071	0.005	0.031
L5	Tannerellaceae	0.000	0.028	0.001	0.013	0.066
L5	Family XIII	0.001	0.000	0.000	0.017	0.079
L5	Clostridiaceae 1	0.001	0.000	0.000	0.022	0.093
L5	Enterococcaceae	0.002	0.007	0.014	0.026	0.100
L5	Desulfovibrionaceae	0.008	0.020	0.013	0.028	0.100
L5	Bacteroidaceae	0.020	0.029	0.007	0.036	0.122
L5	Lachnospiraceae	0.460	0.270	0.185	0.046	0.145

Results: β -diversity

Group Comparison	BC	W	UW
I. <u>1 2 6</u>	0.001**	0.002**	0.001**
II. <u>1 3 5</u>	0.001**	0.003**	0.002**
III. <u>2 3 4</u>	0.001**	0.001**	0.001**
IV. <u>4 6</u>	0.042*	0.07	0.29
V. <u>5 6</u>	0.092	0.028*	0.609



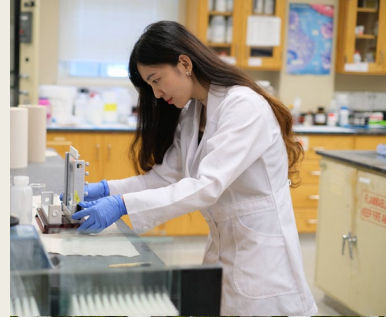
Kruskal-Wallis values 2D visualization for (a) Bray-Curtis Dissimilarities comparisons between groups. (b) Weighted Uni-Frac.

Conclusion + Discussion

- Diet significantly impacted gut microbiome composition
- Obese and T2D Groups more similar to one another than to the lean control groups
- Limitations:
 - *Only male mice*
 - *Study length*
 - *More frequent sampling needed at key timepoints in the study*
- Future Work
 - *Analysis of selected genes to investigate potential disturbances to the intestinal barrier, potentially correlating with dysbiosis of gut-brain axis*

Acknowledgements

- Dr. Jeganathan
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 - *My brother, Dr. Andrew Moeller*
 - *Ramsay & Julia*



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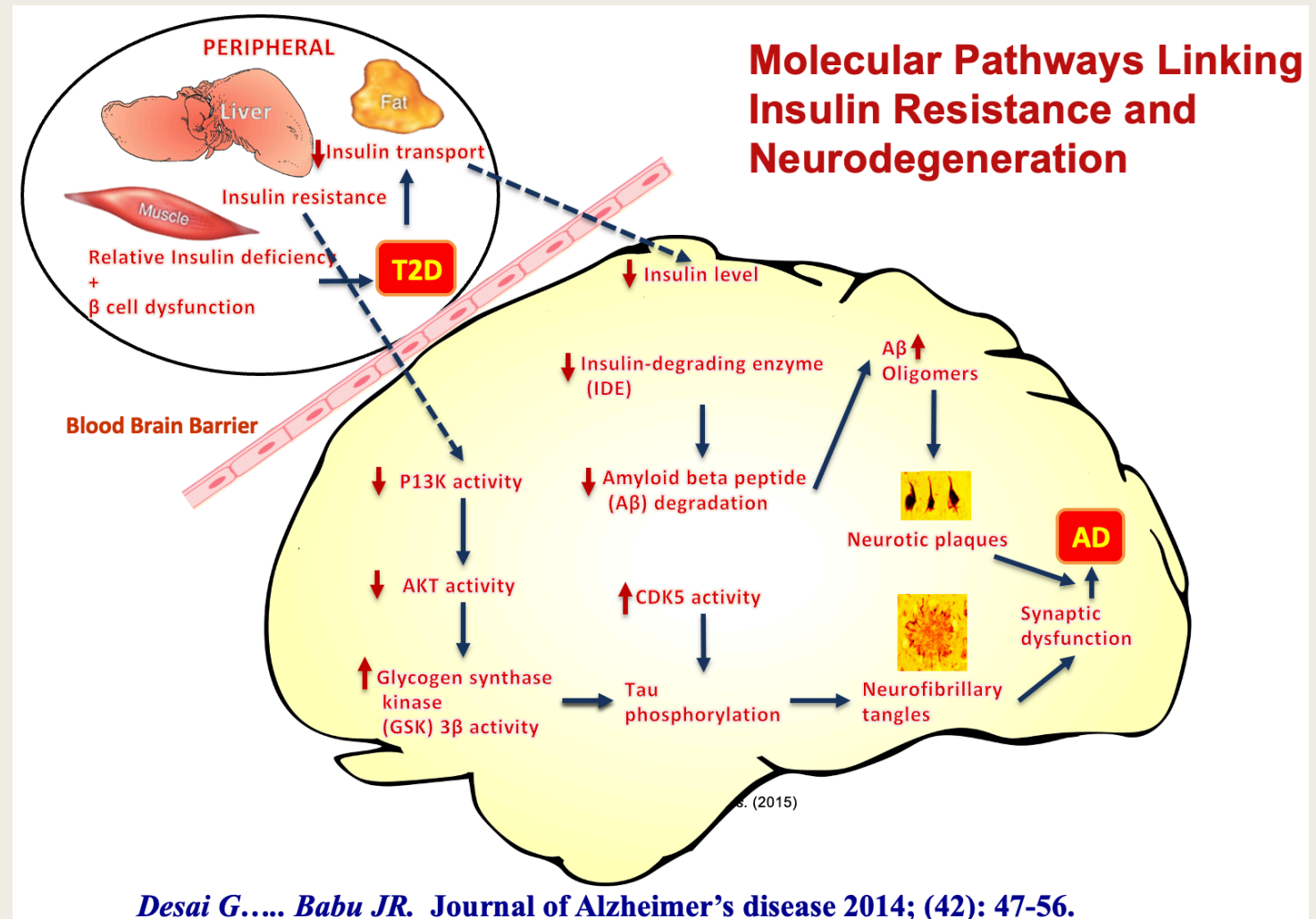




QUESTIONS?

AD + Nerve Growth Factor (NGF)

- NGF: growth, survival, apoptosis of neurons within mammals
 - *Regulator of synthesis and secretion of insulin*
- In pre-clinical AD, Impaired signaling associated
- In AD, proNGF malfunctions, dysregulation of cortical cholinergic synapses and basal forebrain cholinergic cell bodies



Body Weight Averages

		Lean Control + PBS			Lean Control + NGF			HFWD + PBS			HFWD + NGF			HFWD + STZ + PBS			HFWD + STZ + NGF		
		Mean	SD	N	Mean	SD	N	Mean	SD	N	Mean	SD	N	Mean	SD	N	Mean	SD	N
Week	0	21.49	1.089	N = 10	21.05	1.141	N = 10	21.71	1.377	N = 11	21.33	0.833	N = 10	21.30	1.050	N = 11	21.40	0.636	N = 10
	1	22.9	1.208		22.21	1.289		26.81	1.876		26.15	1.806		25.91	2.073		26.49	1.315	
	2	24.04	1.406		23.42	1.433		30.92	1.950		30.08	2.192		30.42	2.899		30.19	1.947	
	3	25.36	1.592		24.87	1.514		34.85	1.822		33.87	2.800		34.05	2.967		34.23	2.055	
	4	26.56	1.677		26.47	1.651		38.36	1.442		37.83	2.617		37.77	2.795		37.85	2.087	
	5	27.73	1.991		27.56	1.287		41.19	1.402		40.57	2.596		40.76	2.775		40.15	2.330	
	6	28.24	2.111		28.31	1.567		43.07	1.434		42.45	2.626		42.62	2.756		42.28	2.257	
	7	29.26	2.095		29.57	1.413		44.65	1.519		43.95	2.269		43.94	2.279		43.32	2.478	
	8	30.18	2.283		30.15	1.571		45.33	1.160		44.77	2.335		45.04	2.538		44.54	2.213	
	9	31.16	2.531		30.85	1.497		45.49	1.559		45.22	1.677		39.38	2.791		37.88	2.246	
	10	31.53	2.653		31.49	1.574		45.23	4.079		45.75	1.697		38.64	3.262		36.16	3.612	
	11	30.93	2.552		30.71	1.490		45.10	1.847		44.32	2.509		37.81	3.397		34.38	4.247	
	12	31.76	2.576		31.07	1.402		45.34	2.614		45.02	1.937		38.57	3.953		34.55	4.997	
	13	31.72	2.756	30.37	1.835	45.48	3.012	44.31	2.164	38.50	4.449	34.14	5.319						

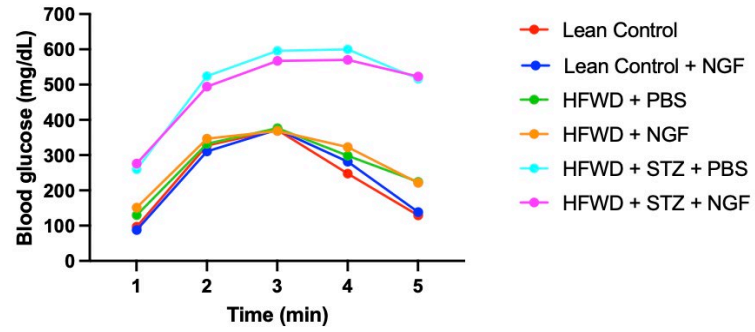
		1			3			Significance	
		Mean	SD	N	Mean	SD	N	P Value	ns
	0	21.49	1.089	N = 10	21.71	1.377	N = 11	0.9983	ns
	1	22.9	1.208		26.81	1.876		0.0003	***
	2	24.04	1.406		30.92	1.950		<0.0001	****
	3	25.36	1.592		34.85	1.822		<0.0001	****
	4	26.56	1.677		38.36	1.442		<0.0001	****
	5	27.73	1.991		41.19	1.402		<0.0001	****
	6	28.24	2.111		43.07	1.434		<0.0001	****
	7	29.26	2.095		44.65	1.519		<0.0001	****
	8	30.18	2.283		45.33	1.160		<0.0001	****
	9	31.16	2.531		45.49	1.559		<0.0001	****
	10	31.53	2.653		45.23	4.079		<0.0001	****
	11	30.93	2.552		45.10	1.847		<0.0001	****
	12	31.76	2.576		45.34	2.614		<0.0001	****
	13	31.72	2.756	45.48	3.012	<0.0001	****		

		1			5			Significance	
		Mean	SD	N	Mean	SD	N	P Value	ns
	0	21.49	1.089	N = 10	21.30	1.050	N = 11	0.9983	ns
	1	22.90	1.208		25.91	2.073		0.0086	**
	2	24.04	1.406		30.42	2.899		0.0001	****
	3	25.36	1.592		34.05	2.967		<0.0001	****
	4	26.56	1.677		37.77	2.795		<0.0001	****
	5	27.73	1.991		40.76	2.775		<0.0001	****
	6	28.24	2.111		42.62	2.756		<0.0001	****
	7	29.26	2.095		43.94	2.279		<0.0001	****
	8	30.18	2.283		45.04	2.538		<0.0001	****
	9	31.16	2.531		39.38	2.791		<0.0001	****
	10	31.53	2.653		38.64	3.262		0.0003	****
	11	30.93	2.552		37.81	3.397		0.0006	****
	12	31.76	2.576		38.57	3.953		0.0022	**
	13	31.72	2.756	38.50	4.449	0.0062	**		

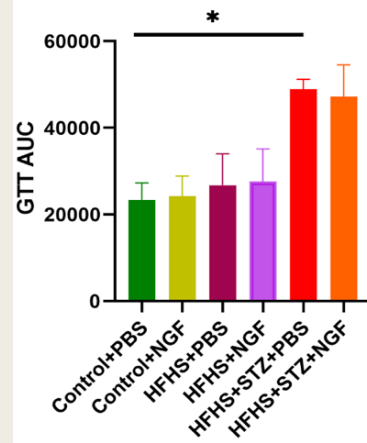
		1			6			Significance	
		Mean	SD	N	Mean	SD	N	P Value	ns
	0	21.49	1.089	N = 10	21.40	0.636	N = 10	0.9999	ns
	1	22.9	1.208		26.49	1.315		<0.0001	****
	2	24.04	1.406		30.19	1.947		<0.0001	****
	3	25.36	1.592		34.23	2.055		<0.0001	****
	4	26.56	1.677		37.85	2.087		<0.0001	****
	5	27.73	1.991		40.15	2.330		<0.0001	****
	6	28.24	2.111		42.28	2.257		<0.0001	****
	7	29.26	2.095		43.32	2.478		<0.0001	****
	8	30.18	2.283		44.54	2.213		<0.0001	****
	9	31.16	2.531		37.88	2.246		<0.0001	****
	10	31.53	2.653		36.16	3.612		0.0448	*
	11	30.93	2.552		34.38	4.247		0.2931	ns
	12	31.76	2.576		34.55	4.997		0.6298	ns
	13	31.72	2.756	34.14	5.319	0.7919	ns		

		5			6			Significance	
		Mean	SD	N	Mean	SD	N	P Value	ns
	0	21.30	1.050	N = 11	21.40	0.636	N = 10	0.9998	ns
	1	25.91	2.073		26.49	1.315		0.9684	
	2	30.42	2.899		30.19	1.947		>0.9999	
	3	34.05	2.967		34.23	2.055		>0.9999	
	4	37.77	2.795		37.85	2.087		>0.9999	
	5	40.76	2.775		40.15	2.330		0.9931	
	6	42.62	2.756		42.28	2.257		0.9996	
	7	43.94	2.279		43.32	2.478		0.9904	
	8	45.04	2.538		44.54	2.213		0.9964	
	9	39.38	2.791		37.88	2.246		0.7469	
	10	38.64	3.262		36.16	3.612		0.5828	
	11	37.81	3.397		34.38	4.247		0.3658	
	12	38.57	3.953		34.55	4.997		0.365	
	13	38.50	4.449	34.14	5.319	0.3669			

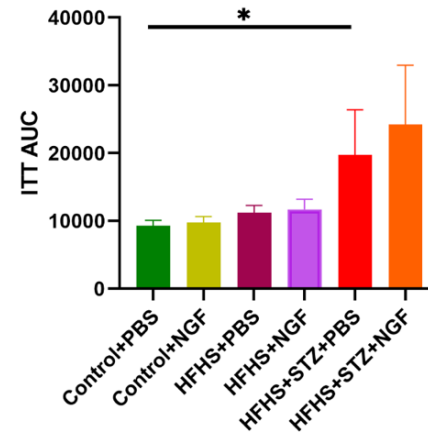
Glucose Tolerance Test



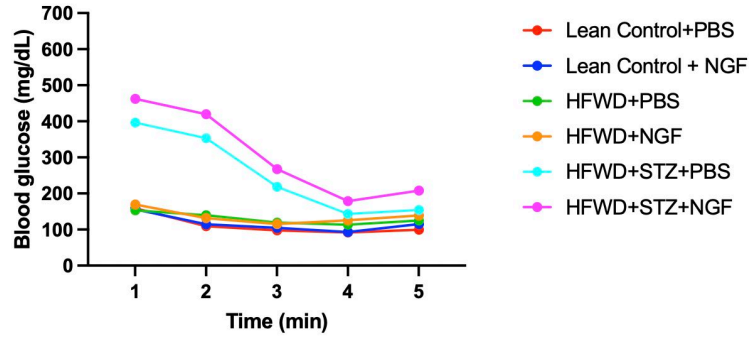
GTT Area Under the Curve



ITT Area Under the Curve



ITT



Relative Abundances (Family Level) Groups 4 and 6					
Family	Identification	4	6	P	FDR_P
L5	Burkholderiaceae	0.000	0.002	0.007	0.348
L5	Rikenellaceae	0.001	0.003	0.036	0.586
L5	Lactobacillaceae	0.218	0.105	0.037	0.586

Relative Abundances (Family Level) Groups 5 and 6					
Family	Identification	5	6	P	FDR_P
L5	Burkholderiaceae	5.17E-05	0.0019	0.0326	0.9475