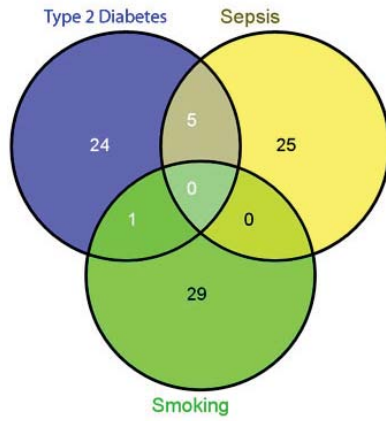
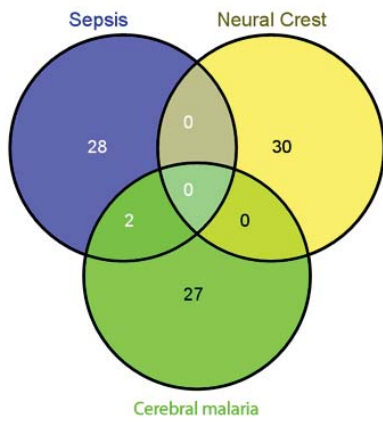


Supplemental Figure 1.

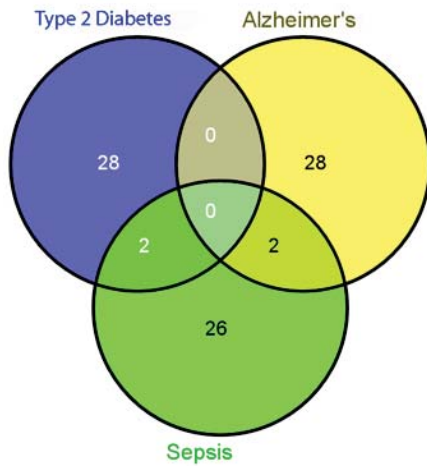
A. Overlap of top 30 Human gene sets in three independent Human gene expression studies .



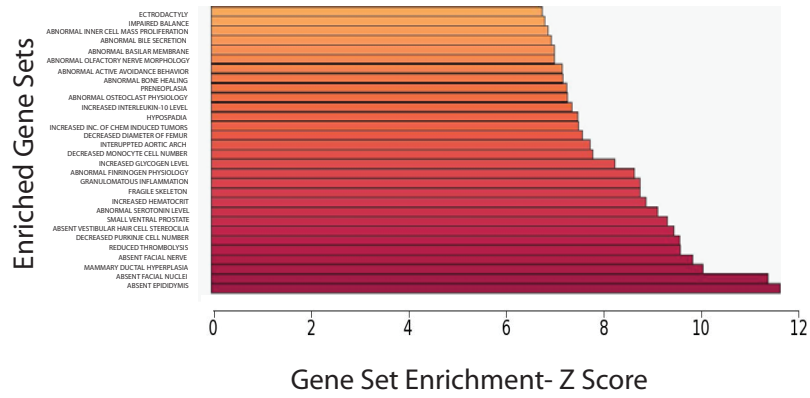
B. Overlap of top 30 Mouse gene sets in three independent Mouse gene expression studies .



C. Overlap of top 30 Mouse gene sets in three independent Human gene expression studies .



Alpha - Synuclein Knockout

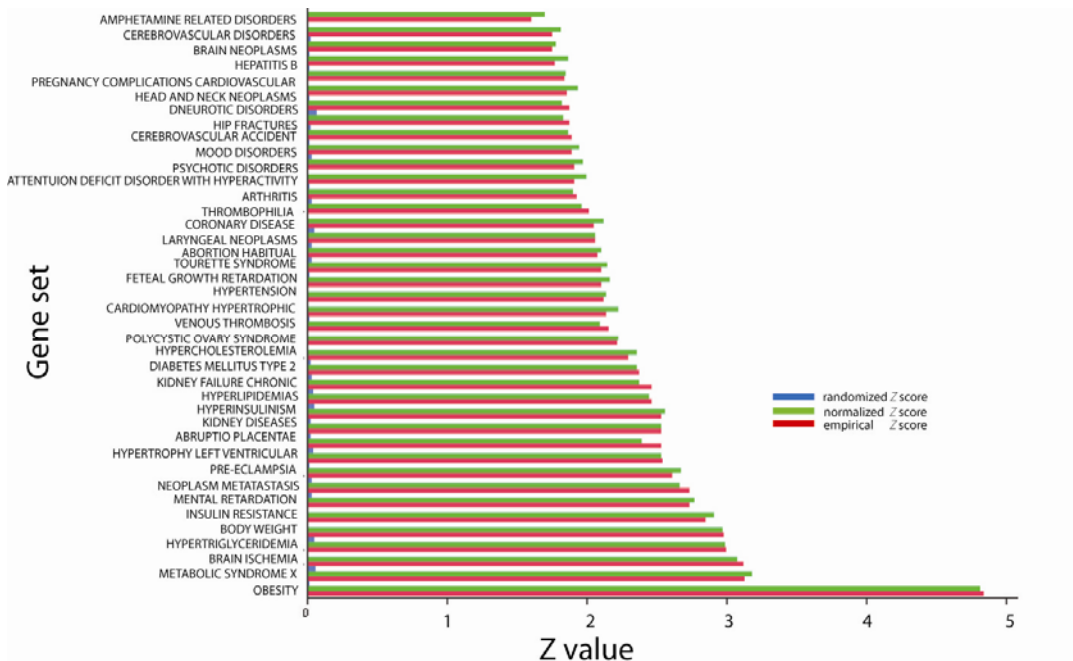


1 a)

Gene set	(emperical_p)	(p1000)
	Diabetes vs. Control	Diabetes vs. Control
OBSESITY	3.0068E-07	7.4076E-07
METABOLIC_SYNDROME_X	0.0055784	0.00073253
BRAIN_ISCHEMIA	0.000063102	0.001035
HYPERTRIGLYCERIDEMIA	0.0045224	0.0013847
BODY_WEIGHT	0.0088178	0.0014522
INSULIN_RESISTANCE	0.0040196	0.0018119
MENTAL_RETARDATION	0.00100062	0.00281
NEOPLASM_METASTASIS	0.0048278	0.0038426
PRE-ECLAMPSIA	0.020742	0.0037546
HYPERTROPHY_LEFT_VENTRICULAR	0.02835	0.0055632
ABRUPTIO_PLACENTAE	0.0031176	0.0082935
KIDNEY_DISEASES	0.032776	0.0056388
HYPERINSULINISM	0.0175314	0.0051668
HYPERLIPIDEMIAS	0.02364	0.0071137
KIDNEY_FAILURE_CHRONIC	0.0071476	0.0086369
DIABETES_MELLITUS_TYPE_2	0.0133476	0.0092131
HYPERCHOLESTEROLEMIA	0.022926	0.0091805
POLYCYSTIC_OVARY_SYNDROME	0.026574	0.012877
VENOUS_THROMBOSIS	0.0097108	0.018037
CARDIOMYOPATHY_HYPERTROPHIC	0.0108394	0.012881
HYPERTENSION	0.027906	0.01611
FETAL_GROWTH_RETARDATION	0.029482	0.015034
TOURETTE_SYNDROME	0.0112824	0.015809
ABORTION_HABITUAL	0.0103886	0.017744
LARYNGEAL_NEOPLASMS	0.025996	0.01978
CORONARY_DISEASE	0.029984	0.016794
CARDIOVASCULAR_DISEASES	0.055996	0.022346
ARTHRITIS	0.025966	0.0285
ATTENTION_DEFICIT_DISORDER_WITH_HYPERACTIVITY	0.032798	0.022831
PSYCHOTIC_DISORDERS	0.0068932	0.024131
MOOD_DISORDERS	0.042728	0.02561
CEREBROVASCULAR_ACCIDENT	0.02442	0.031062
HIP_FRACTURES	0.0150896	0.033106
NEUROTIC_DISORDERS	0.034202	0.034203
HEAD_AND_NECK_NEOPLASMS	0.04242	0.02629
PREGNANCY_COMPLICATIONS_CARDIOVASCULAR	0.046064	0.032019
HEPATITIS_B	0.020334	0.030973
BRAIN_NEOPLASMS	0.03358	0.03745
CEREBROVASCULAR_DISORDERS	0.046322	0.034598
AMPHETAMINE-RELATED_DISORDERS	0.035314	0.04473

2
3
4
5

b)



6

Supplementary Figure 1. Gene set overlap

A. Overlap of human gene sets vs human gene expression

Overlap in the top 30 gene sets between Human Type 2 Diabetes -ArrayExpress # E-CBIL-30, Sepsis-GEO #GSE8182, and Smoking – GEO # GSE994, using the human GAD disease gene sets. The R^2 value of all human GAD gene sets between all three analyses are: Type 2 diabetes vs. Sepsis: $R^2= 0.0005$; Sepsis vs. Smoking: $R^2= 0.0094$; Smoking vs. Type 2 Diabetes: $R^2= 0.0021$

B. Overlap of mouse gene sets vs mouse gene expression

Overlap in the top 30 gene sets between mouse Sepsis –GEO # GSE4479, Neural crest/development-GEO #GSE11356, and Cerebral Malaria – GEO # GSE7814, using the mouse MP gene sets. The R^2 value of all mouse MP gene sets between all three analyses are: Sepsis vs. Neural crest/ development: $R^2= 0.0051$; Neural crest/ development vs. Cerebral Malaria: $R^2= 0.015$; Cerebral Malaria vs. Sepsis: $R^2= 0.00002$

C. Overlap of mouse gene sets vs human gene expression

Overlap in the top 30 gene sets between Human Type 2 Diabetes -ArrayExpress # E-CBIL-30, Alzheimer's GEO# GSE2197, and human Sepsis-GEO #GSE8182, using the mouse MP gene sets. The R^2 values of all mouse MP gene sets between all three analyses are: Type 2 Diabetes vs. Alzheimer's: $R^2= 0.0037$; Alzheimer's vs. Sepsis: $R^2= 0.0017$; Sepsis vs. Type 2 Diabetes: $R^2= 0.0014$

Supplemental Figure 2. Mouse Alpha-Synuclein Knockout-Brain versus Mouse gene sets. Ribbon graphs of the top 30 highest Z-scores of the statistically significant ($p < 0.05$) PAGE results in a mouse Alpha-Synuclein Knockout mouse model. Alpha-Synuclein GEO # GSE4758, using the mouse MP gene sets. These results are not biased toward brain physiology as reflective of the ubiquitous nature of alpha-synuclein expression.

Supplementary Figure 3.

Empirically determined p values versus permutation determined p values

- A.** Comparison of empirical p values versus permuted p values of the top 40 gene sets.
- B.** Comparison of empirical Z value (red), randomized (blue), and normalized (green) enrichment scores. The empirical Z score is calculated using our Z score formula directly from our D/P webPAGE utility using the gene expression change ratios. The randomized Z score is the mean value of the Z score that produced by 1000 permutations of the gene expression change ratios and also 400 permutation of the gene set labels at the same time. The normalized Z score is obtained by adopting the empirical Z score and normalizing it by the mean of 1000 times the Z score of the gene set.