

1^o Knockout Phenotypes: Physiologic and Pathologic Analyses

The Texas Institute of Genomic Medicine (TIGM) offers a full line of anatomical and physiological characterizations for knockout and transgenic mice. Mice are characterized by *in vivo* physiology and pathology screening: gross anatomy examination, histological examination of tissues, and blood collection for hematology and clinical chemistry.

Clinical & Pathology Assay Summary

Clinical Chemistry		Hematology	
Acid phosphatase		Hemoglobin	
Albumin	Ferritin	Homocysteine	
Alkaline phosphatase	Gamma Glutamyltransferase	Packed cell volume (PCV)	
Alanine aminotransferase	Glucose	White blood count (WBC)	
Ammonia	Iron	Plasma volume	
Amylase	Iron binding capacity (total)	Platelet count	
Aspartate aminotransferase	Lactate	Serum B12	
Bilirubin	Lactate dehydrogenase	Serum folate	
Calcium	Lipase	Red cell folate	
Cholinesterase	β 2-microglobulin	Red cell mass	
Cholesterol	Osmolality	Reticulocyte count	
Creatine kinase (CPK)	Protein (total)		
Creatinine	Uric Acid		
C-Reactive Protein (CRP)			
Carbon Dioxide			
Electrolytes (Na, K, Cl, Mg)			
Pathology/Histology Tissues			
Adrenal Gland	Mammary Gland (Female)	Esophagus	Spinal Cord
Aorta	Muscle (Quadriceps)	Eye	Spleen
Bone Marrow (Femoral)	Nasal Cavity	Fat (Brown)	Stomach
Bulbourethral Gland (Male)	Nerve (Sciatic)	Femur/Stifle	Teeth
Cecum	Ovaries (Female)	Gall Bladder	Testes (Male)
Cerebellum	Pancreas	Harderian Gland	Thymus
Cerebrum	Parathyroid	Heart	Thyroid
Clitoral Gland (Female)	Placenta (Female)	Ileum	Tongue
Colon (Proximal and Distal)	Pituitary	Inner Ear	Trachea
Costrochondral Junction	Preputial Gland (Male)	Jejunum	Urethra (Penile, Male)
Diaphragm	Prostate (Male)	Kidneys	Urinary Bladder
Duodenum	Salivary Glands	Lacrimal Gland (Exorbital)	Uterus (Female)
Epididymis (Male)	Skin (Dorsal)	Liver	Vagina/Cervix (Female)
Lymph Node		Lung	Vesicular Glands (Male)

2^o Knockout Phenotype Etiology: Genomic and Proteomic Analyses

The Texas Institute of Genomic Medicine (TIGM) also offers a full line of genomic and proteomic characterizations for knockout mice. These analyses include whole genome microarrays 2-Dimensional Gel Electrophoresis (2DE) protein analyses of the embryonic or fetal tissues that contribute to anatomical malformations in adult structures and organs. Mice having human disease phenotypes (*e.g.* altered physiology or blood chemistry), as characterized by clinical and pathology screens, are subjected to genomic and proteomic profiling.

Genomic and Proteomic Assays

Gene Expression Platform

GE CodeLink Microarray Scanner (Open System) AND/OR Affymetrix GeneChip Array Scanner & Workstation
Illumina Platform

Protein Expression Platform

2-Dimensional Gel Electrophoresis (2DE)

Data obtained from the genetically modified mice is analyzed based on the rationale that genes/proteins that share common biochemical or developmental signaling pathways will result in phenotypes that share common features. Phenotypic data is associated with gene and protein expression data in both a top-down and bottoms-up approach. Briefly, a genetic relationship (network) learning tool incorporates the data into our existing Biosystem Analysis Framework (BAF). Our BAF is comprised of a suite of integrated genomic/proteomic analysis and mathematical modeling tools and databases. The BAF core tools are based on Dynamic Bayesian Networks (DBNs). DBNs allow us to combine prior knowledge (*e.g.* metabolic pathways or gene ontologies) with empirical time-course expression data for modeling, pattern recognition, and genetic network inference. These profiles can then be used for in silico prediction of gene and protein targets that can be expected to result in or mitigate disease phenotypes. Ultimately, these profiles may provide disease protein footprints, biomarkers, and pharmaceutical targets