

**Supplementary Table 1:** QC Analysis results; RIN (RNA Integrity Number) for NBC, mPIA, and sPIA samples

<b>Animal</b>	<b>RIN value</b>
NBC Male 1	9.9
NBC Male 2	9.9
NBC Male 3	9.7
NBC Male 4	9.9
NBC Female 1	9.4
NBC Female 2	9.6
NBC Female 3	9.4
NBC Female 4	9.4
mPIA Male 1	9.5
mPIA Male 2	9.5
mPIA Male 3	9.4
mPIA Male 4	9.4
mPIA Female 1	9.5
mPIA Female 2	9.5
mPIA Female 3	9.6
mPIA Female 4	9.6
sPIA Male 1	9.6
sPIA Male 2	9.4
sPIA Male 3	9.7
sPIA Male 4	9.2
sPIA Female 1	9.5
sPIA Female 2	9.7
sPIA Female 3	9.5
sPIA Female 4	9.6

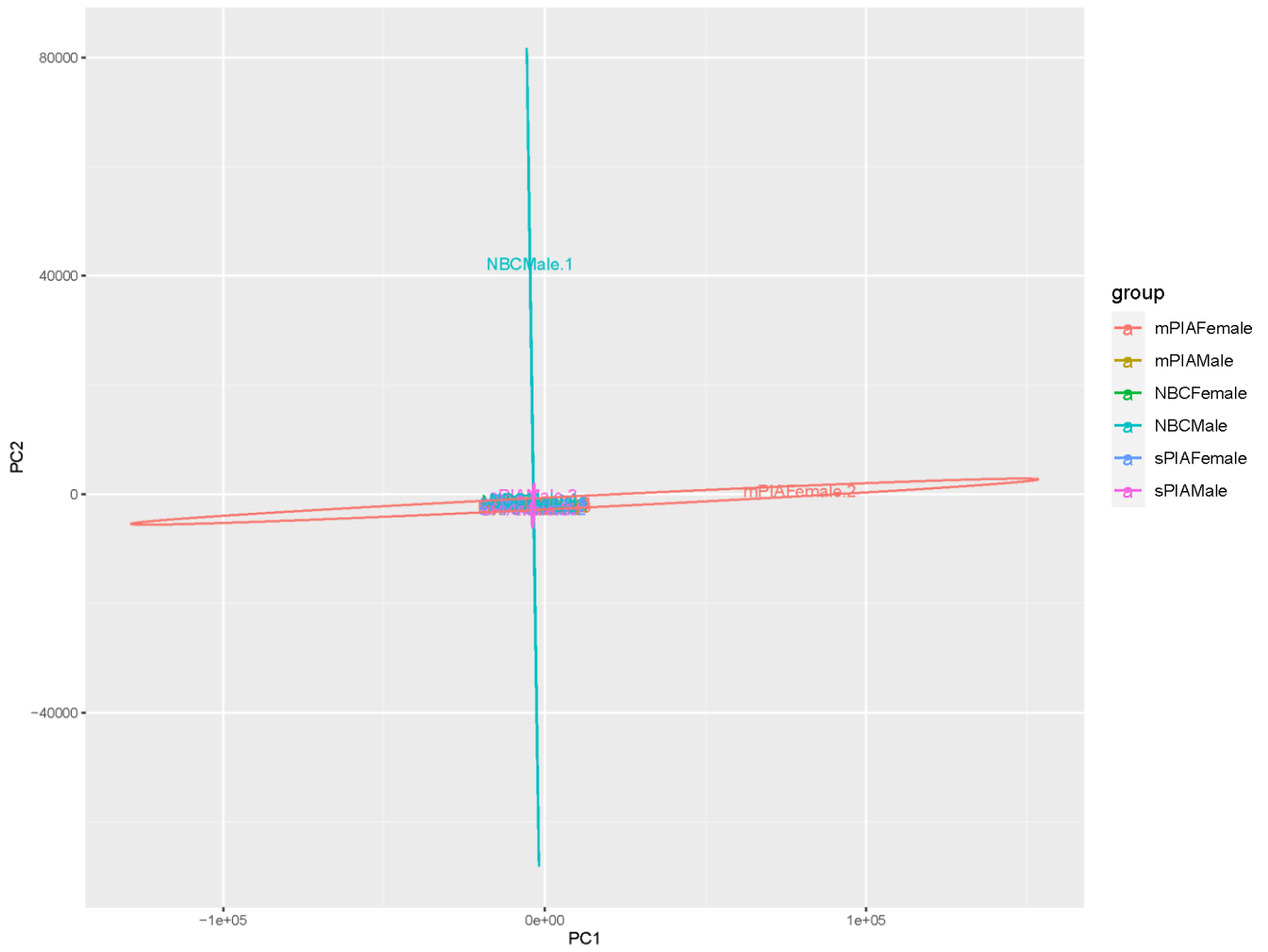
**Supplementary Table 2:** TaqMan probe IDs used for qPCR

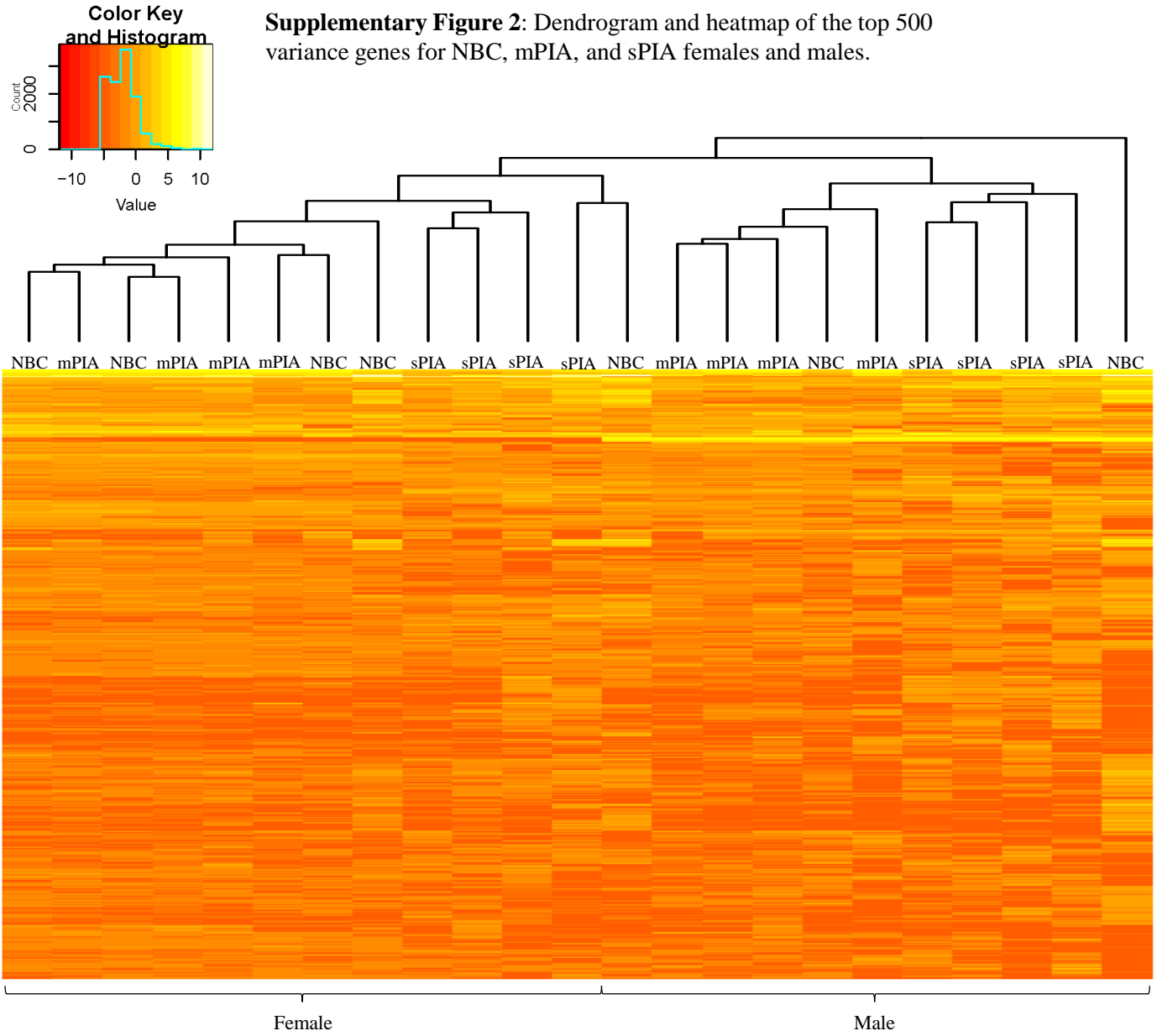
<b>Gene Name</b>	<b>Gene Symbol</b>	<b>TaqMan ID</b>
CXCL10	<i>CXCL10</i>	Mm00445235_m1
EDN1	<i>EDN1</i>	Mm00441242_m1
IL-6	<i>IL-6</i>	Mm00446190_m1
CCL2	<i>CCL2</i>	Mm00441242_m1
IL-1 $\beta$	<i>IL-1<math>\beta</math></i>	Mm00434228_m1
MHC II	<i>H2-Ab1</i>	Mm00439216_m1
TLR4	<i>TLR4</i>	Mm00445273_m1
Tnf- $\alpha$	<i>Tnf-<math>\alpha</math></i>	Mm00443258_m1
CREB1	<i>CREB1</i>	Mm00501607_m1
KCNC4	<i>KCNC4</i>	Mm00521443_m1
SLC2A4	<i>SLC2A4</i>	Mm00436615_m1
TH	<i>TH</i>	Mm00447557_m1

**Supplementary Table 3: Top 5 physiological system and functions affected by mPIA and sPIA in males and females**

mPIA Males			sPIA Males		
Name	P-value range	Genes affected	Name	Activation z-score	Genes affected
Tissue Development	2.05E-.04 - 2.81E-011	304	Cancer	1.08E-03 - 5.54E-09	171
Connective Tissue Development and Function	2.45E-.04 - 7.31E-09	184	Organ Development	1.09E-03 - 5.54E-09	131
Skeletal and Muscular System Development and Function	2.84E-.04 - 7.31E-09	134	Organismal Development	6.99E-04 – 1.55E-08	259
Immune Cell Trafficking	2.79E-.04 - 8.22E-09	158	Tissue Development	1.06E-03 – 1.26E-07	250
Digestive System Development and Function	2.32E-.04 - 8.66E-09	132	Tissue Morphology	1.09E-03 – 1.26E-07	218
mPIA Females			sPIA Females		
Name	P-value range	Genes affected	Name	P-value range	Genes affected
Cardiovascular System Development and Function	8.85E-.03 - 2.22E-06	19	Cardiovascular System Development and Function	9.81E-04 - 1.72E-07	320
Organ Morphology	8.93E-.03 - 2.22E-06	17	Organismal Development	1.07E-03 – 1.72E-07	542
Organismal Development	8.93E-.03 - 2.22E-06	29	Nervous System Development and Function	1.07E-03 – 2.94E-07	387
Embryonic Development	8.93E-.03 – 1.30E-05	10	Behavior	1.01E-03 – 6.55E-07	157
Hematological System Development and Function	8.93E-.03 – 1.30E-05	21	Tissue Development	9.81E-04 – 6.68E-07	500

**Supplementary Figure 1:** Principle component analysis of NBC, mPIA, and sPIA females and males.





**Supplementary Figure 3:** Interaction between STAT1 and upstream regulators belonging to the IRF family with  $z$  value  $\geq 2$  (Table 2) a) Direct interaction between IRF1, IRF3, IRF5, IRF7, and STAT1. All genes influence each other and themselves in an upregulatory manner. b) There is approximately a 60% overlap between genes affected by STAT1 and genes affected by the IRF family. CXCL10, RSAD2, TNFSF10 (Tnf superfamily 10) are among genes upregulated by all 5 genes. IL-6 is upregulated by members of the IRF family and although affected by STAT1, lacks predicted directionality.

