

Table S1. Significantly dysregulated genes in GOrilla analysis and common to all comparisons

Abcg2	Chkb	Eme2	Haghl	Mapkapk5	Nudcd2	Polr3b
Ahr	Chrd	Exosc4	Hfe	Mboat1	Nup85	Prpsap2
Alkbh7	Csgalnact2	Fancg	Id1	Mcm7	Parp9	Psmg2
Amn1	Dcxr	Fcgr1	Ifi203	Moap1	Pedh20	Ptpre
Ap5z1	Dhodh	Fdx1	Igtp	Mospd3	Pcdha2	Ptprr
Arhgap25	Dhps	Fn3k	Kcns1	Myd88	Pex10	Rad18
Arhgap27	Dock2	Fuz	Kif11	Ncf2	Pigh	Rbm11
B4galt1	Dock8	Gp1bb	Lamtor4	Ndufaf2	Pigx	Sardh
Cbr3	Dph2	Gstm4	Lbp	Nostrin	Plcd3	
Ccnf	Ehbp111	Hacl1	Lsm7	Nphp1	Plk5	

Table S2. Significant dysregulated biological process in Figure 3 (18Aβ vs. 3Vh).

Yellow box 10-3 < p < 10-5	Detoxification*
	Locomotion*
	Primary metabolic process
	Secondary metabolic process
	Cellular metabolic process
	Extracellular structure organization*
	Response to xenobiotic stimulus*
	Cell motility*
	Taxis*
	Drinking behavior*
	Regulation of cell adhesion
	Regulation of blood pressure
	Regulation of catalytic activity
	Lipid metabolic process
	Small molecule catabolic process
	Cell-matrix adhesion*
	Chemotaxis*
	Cell migration*
	Mitotic cell cycle phase transition*
	Regulation of systemic arterial blood pressure
	Carbohydrate derivative metabolic process
	Purine-containing compound metabolic process
	Thioester metabolic process
	Organic acid catabolic process
	Leukocyte migration*
	Cell chemotaxis*
	Positive regulation of hydrolase activity
	Regulation of systemic arterial blood pressure mediated by a chemical signal
	Endocrine process
	Proteolysis
	Positive regulation of amine transport
	Regulation of tube size
	Vascular process in circulatory system
	Regulation of systemic arterial blood pressure by hormone
	Organonitrogen compound biosynthetic process
	Carboxylic acid catabolic process
	Intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress*
	G protein-coupled purinergic receptor signaling pathway*
	Regulation of tube diameter
	Regulation of blood vessel size
	Regulation of systemic arterial blood pressure by renin-angiotensin
	Nucleoside bisphosphate metabolic process
Monocarboxylic acid catabolic process	
Adenosine receptor signaling pathway*	
Regulation of norepinephrine secretion	
Regulation of kinase activity	
Regulation of blood vessel diameter	

	Regulation of systemic arterial blood pressure by circulatory renin-angiotensin
	Regulation of blood volume by renin-angiotensin
	Purine nucleoside bisphosphate metabolic process
	Dopamine biosynthetic process
	Fatty acid catabolic process
	Regulation of protein kinase activity
	Positive regulation of blood vessel diameter
	Brain renin-angiotensin system
	Ribonucleoside bisphosphate metabolic process
	Regulation of mineralocorticoid secretion
	Regulation of cyclin-dependent protein kinase activity
	Regulation of protein serine/threonine kinase activity
	Vasodilation
	Acyl-CoA metabolic process
	Lysine biosynthetic process
	Regulation of aldosterone secretion
	Regulation of cyclin-dependent protein serine/threonine kinase activity
	Renal system process involved in regulation of systemic arterial blood pressure
	Lysine biosynthetic process via aminoadipic acid
	Renin-angiotensin regulation of aldosterone production
Orange box 10-5 < p < 10-7	Metabolic process
	Organic substance metabolic process
	Small molecule metabolic process
	Organic acid metabolic process
	Extracellular matrix organization*
	Cellular lipid metabolic process
	Oxoacid metabolic process
	Carboxylic acid metabolic process
	Monocarboxylic acid metabolic process
	Fatty acid metabolic process

*biological processes highlighted in the green box

Table S3. Significant dysregulated biological process in Figure 4a (18Aβ vs. 3Aβ).

Yellow box 10-3 < p < 10-5	Detoxification
	Locomotion
	Metabolic process
	Biological adhesion
	Movement of cell or subcellular component
	Biosynthetic process
	Organic substance metabolic process*
	Primary metabolic process*
	Glycosylation*
	Extracellular matrix organization
	Cellular biosynthetic process
	Small molecule catabolic process
	Organic acid metabolic process
	Organic substance biosynthetic process*
	Extracellular matrix organization
	Mitotic cell cycle phase transition
	Organic acid catabolic process
	Cellular lipid metabolic process
	Oxoacid metabolic process
	Carbohydrate biosynthetic process*
	Organonitrogen compound biosynthetic process*
	Cellular carbohydrate biosynthetic process
	Carboxylic acid metabolic process
	Proteolysis *
	Macromolecule glycosylation*
	Monocarboxylic acid metabolic process
	Carboxylic acid catabolic process
	Fatty acid metabolic process
	Monocarboxylic acid catabolic process
	Protein glycosylation*
	Fatty acid catabolic process
	Aspartate family amino acid catabolic process*
	Lysine metabolic process*
Regulation of protein kinase activity*	
L-lysine metabolic process	
Lysine catabolic process*	
Lysine biosynthetic process*	
Regulation of cyclin-dependent protein kinase activity*	
L-lysine catabolic process	
Lysine biosynthetic process via aminoadipic acid*	
Regulation of cyclin-dependent protein serine/threonine kinase activity*	
Orange box 10-5 < p < 10-7	Cellular process
	Small molecule metabolic process

*biological processes highlighted in the green box

Table S4. Significant dysregulated biological process in Figure 4b (18A β vs. 18Vh).

Yellow box $10^{-3} < p < 10^{-5}$	Regulation of localization
	Regulation of system process
	Negative regulation of transport
	Proteolysis



