

Supplementary Table 8. Full list of enriched GO terms.

**OA hip versus NOF**

**Term**

GO:0007389~pattern specification process  
GO:0048598~embryonic morphogenesis  
GO:0009952~anterior/posterior pattern formation  
GO:0001501~skeletal system development  
GO:0048705~skeletal system morphogenesis  
GO:0048706~embryonic skeletal system development  
GO:0008092~cytoskeletal protein binding  
GO:0030695~GTPase regulator activity  
GO:0003779~actin binding  
GO:0060589~nucleoside-triphosphatase regulator activity  
GO:0003002~regionalization  
GO:0048704~embryonic skeletal system morphogenesis  
GO:0048562~embryonic organ morphogenesis  
GO:0005578~proteinaceous extracellular matrix  
GO:0031012~extracellular matrix  
GO:0005509~calcium ion binding  
GO:0009792~embryonic development ending in birth or egg hatching  
GO:0015629~actin cytoskeleton  
GO:0043009~chordate embryonic development  
GO:0048568~embryonic organ development  
GO:0044459~plasma membrane part  
GO:0005096~GTPase activator activity  
GO:0005083~small GTPase regulator activity  
GO:0044420~extracellular matrix part  
GO:0005581~collagen  
GO:0009891~positive regulation of biosynthetic process  
GO:0045941~positive regulation of transcription  
GO:0031328~positive regulation of cellular biosynthetic process  
GO:0035113~embryonic appendage morphogenesis  
GO:0030326~embryonic limb morphogenesis  
GO:0010557~positive regulation of macromolecule biosynthetic process  
GO:0010628~positive regulation of gene expression  
GO:0044421~extracellular region part  
GO:0048736~appendage development  
GO:0060173~limb development  
GO:0000902~cell morphogenesis  
GO:0005088~Ras guanyl-nucleotide exchange factor activity  
GO:0042995~cell projection  
GO:0005912~adherens junction  
GO:0005089~Rho guanyl-nucleotide exchange factor activity  
GO:0035108~limb morphogenesis

GO:0035107~appendage morphogenesis  
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic p  
GO:0030182~neuron differentiation  
GO:0048732~gland development  
GO:0045893~positive regulation of transcription, DNA-dependent  
GO:0000904~cell morphogenesis involved in differentiation  
GO:0051173~positive regulation of nitrogen compound metabolic process  
GO:0051254~positive regulation of RNA metabolic process  
GO:0048812~neuron projection morphogenesis  
GO:0045165~cell fate commitment  
GO:0070161~anchoring junction  
GO:0008047~enzyme activator activity  
GO:0005886~plasma membrane  
GO:0010604~positive regulation of macromolecule metabolic process  
GO:0032989~cellular component morphogenesis  
GO:0048666~neuron development  
GO:0031175~neuron projection development  
GO:0048667~cell morphogenesis involved in neuron differentiation  
GO:0045944~positive regulation of transcription from RNA polymerase II promoter  
GO:0030900~forebrain development  
GO:0030030~cell projection organization  
GO:0007409~axonogenesis  
GO:0007155~cell adhesion  
GO:0022610~biological adhesion  
GO:0006357~regulation of transcription from RNA polymerase II promoter  
GO:0043005~neuron projection  
GO:0048858~cell projection morphogenesis  
GO:0005085~guanyl-nucleotide exchange factor activity  
GO:0035295~tube development  
GO:0051056~regulation of small GTPase mediated signal transduction  
GO:0035239~tube morphogenesis  
GO:0004672~protein kinase activity  
GO:0032990~cell part morphogenesis  
GO:0021517~ventral spinal cord development  
GO:0009954~proximal/distal pattern formation  
GO:0005856~cytoskeleton  
GO:0016323~basolateral plasma membrane  
GO:0004714~transmembrane receptor protein tyrosine kinase activity  
GO:0031226~intrinsic to plasma membrane  
GO:0005583~fibrillar collagen  
GO:0030054~cell junction  
GO:0021522~spinal cord motor neuron differentiation  
GO:0006355~regulation of transcription, DNA-dependent  
GO:0008305~integrin complex  
GO:0007439~ectodermal gut development  
GO:0048567~ectodermal gut morphogenesis

GO:0030055~cell-substrate junction  
GO:0005887~integral to plasma membrane  
GO:0048754~branching morphogenesis of a tube  
GO:0007517~muscle organ development  
GO:0060284~regulation of cell development  
GO:0051252~regulation of RNA metabolic process  
GO:0031982~vesicle  
GO:0030424~axon  
GO:0005604~basement membrane  
GO:0005924~cell-substrate adherens junction  
GO:0031988~membrane-bounded vesicle  
GO:0048729~tissue morphogenesis  
GO:0031410~cytoplasmic vesicle  
GO:0005201~extracellular matrix structural constituent  
GO:0005099~Ras GTPase activator activity  
GO:0046332~SMAD binding  
GO:0051216~cartilage development  
GO:0046578~regulation of Ras protein signal transduction  
GO:0045664~regulation of neuron differentiation  
GO:0010629~negative regulation of gene expression  
GO:0032332~positive regulation of chondrocyte differentiation  
GO:0001708~cell fate specification  
GO:0008134~transcription factor binding  
GO:0019838~growth factor binding  
GO:0043167~ion binding  
GO:0021675~nerve development  
GO:0021515~cell differentiation in spinal cord  
GO:0016481~negative regulation of transcription  
GO:0007242~intracellular signaling cascade  
GO:0016023~cytoplasmic membrane-bounded vesicle  
GO:0030016~myofibril  
GO:0007267~cell-cell signaling  
GO:0051017~actin filament bundle formation  
GO:0035137~hindlimb morphogenesis  
GO:0050767~regulation of neurogenesis  
GO:0044449~contractile fiber part  
GO:0030934~anchoring collagen  
GO:0019898~extrinsic to membrane  
GO:0010558~negative regulation of macromolecule biosynthetic process  
GO:0005925~focal adhesion

## **OA hip cluster 1 versus OA hip cluster 2**

### **Term**

GO:0044459~plasma membrane part

GO:0005886~plasma membrane  
GO:0007155~cell adhesion  
GO:0022610~biological adhesion  
GO:0005509~calcium ion binding  
GO:0060589~nucleoside-triphosphatase regulator activity  
GO:0030695~GTPase regulator activity  
GO:0008092~cytoskeletal protein binding  
GO:0031226~intrinsic to plasma membrane  
GO:0007242~intracellular signaling cascade  
GO:0051056~regulation of small GTPase mediated signal transduction  
GO:0005887~integral to plasma membrane  
GO:0045202~synapse  
GO:0005083~small GTPase regulator activity  
GO:0042995~cell projection  
GO:0003779~actin binding  
GO:0005088~Ras guanyl-nucleotide exchange factor activity  
GO:0030054~cell junction  
GO:0005089~Rho guanyl-nucleotide exchange factor activity  
GO:0001501~skeletal system development  
GO:0005085~guanyl-nucleotide exchange factor activity  
GO:0046578~regulation of Ras protein signal transduction  
GO:0007167~enzyme linked receptor protein signaling pathway  
GO:0035023~regulation of Rho protein signal transduction  
GO:0007507~heart development  
GO:0015629~actin cytoskeleton  
GO:0006928~cell motion  
GO:0043005~neuron projection  
GO:0030424~axon  
GO:0030030~cell projection organization  
GO:0005096~GTPase activator activity  
GO:0048598~embryonic morphogenesis  
GO:0005216~ion channel activity  
GO:0016337~cell-cell adhesion  
GO:0000902~cell morphogenesis  
GO:0004714~transmembrane receptor protein tyrosine kinase activity  
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway  
GO:0007626~locomotory behavior  
GO:0006468~protein amino acid phosphorylation  
GO:0007610~behavior  
GO:0031012~extracellular matrix  
GO:0022838~substrate specific channel activity  
GO:0030182~neuron differentiation  
GO:0044057~regulation of system process  
GO:0044420~extracellular matrix part  
GO:0007243~protein kinase cascade  
GO:0015267~channel activity

GO:0044456~synapse part  
GO:0016477~cell migration  
GO:0022803~passive transmembrane transporter activity  
GO:0051216~cartilage development  
GO:0040012~regulation of locomotion  
GO:0005578~proteinaceous extracellular matrix  
GO:0032989~cellular component morphogenesis  
GO:0048666~neuron development  
GO:0030036~actin cytoskeleton organization  
GO:0051094~positive regulation of developmental process  
GO:0031175~neuron projection development  
GO:0043067~regulation of programmed cell death  
GO:0010941~regulation of cell death  
GO:0010557~positive regulation of macromolecule biosynthetic process  
GO:0019899~enzyme binding  
GO:0051270~regulation of cell motion  
GO:0004713~protein tyrosine kinase activity  
GO:0000904~cell morphogenesis involved in differentiation  
GO:0006811~ion transport  
GO:0048812~neuron projection morphogenesis  
GO:0009792~embryonic development ending in birth or egg hatching  
GO:0045893~positive regulation of transcription, DNA-dependent  
GO:0043009~chordate embryonic development  
GO:0042981~regulation of apoptosis  
GO:0006357~regulation of transcription from RNA polymerase II promoter  
GO:0005604~basement membrane  
GO:0045944~positive regulation of transcription from RNA polymerase II promoter  
GO:0051254~positive regulation of RNA metabolic process  
GO:0001568~blood vessel development  
GO:0044421~extracellular region part  
GO:0045597~positive regulation of cell differentiation  
GO:0007389~pattern specification process  
GO:0048562~embryonic organ morphogenesis  
GO:0048705~skeletal system morphogenesis  
GO:0048858~cell projection morphogenesis  
GO:0022604~regulation of cell morphogenesis  
GO:0001944~vasculature development  
GO:0007267~cell-cell signaling  
GO:0006955~immune response  
GO:0048534~hemopoietic or lymphoid organ development  
GO:0007268~synaptic transmission  
GO:0051674~localization of cell  
GO:0048870~cell motility  
GO:0018212~peptidyl-tyrosine modification  
GO:0048706~embryonic skeletal system development  
GO:0030029~actin filament-based process

GO:0010628~positive regulation of gene expression  
GO:0018108~peptidyl-tyrosine phosphorylation  
GO:0016310~phosphorylation  
GO:0014069~postsynaptic density  
GO:0031328~positive regulation of cellular biosynthetic process  
GO:0009891~positive regulation of biosynthetic process  
GO:0030334~regulation of cell migration  
GO:0048667~cell morphogenesis involved in neuron differentiation  
GO:0031252~cell leading edge  
GO:0002520~immune system development  
GO:0045941~positive regulation of transcription  
GO:0050769~positive regulation of neurogenesis  
GO:0030097~hemopoiesis  
GO:0007409~axonogenesis  
GO:0006793~phosphorus metabolic process  
GO:0006796~phosphate metabolic process  
GO:0005856~cytoskeleton  
GO:0060284~regulation of cell development  
GO:0042330~taxis  
GO:0006935~chemotaxis  
GO:0001775~cell activation  
GO:0051960~regulation of nervous system development  
GO:0032990~cell part morphogenesis  
GO:0006816~calcium ion transport  
GO:0001932~regulation of protein amino acid phosphorylation  
GO:0060090~molecular adaptor activity  
GO:0006952~defense response  
GO:0004672~protein kinase activity  
GO:0042734~presynaptic membrane  
GO:0008047~enzyme activator activity  
GO:0007010~cytoskeleton organization  
GO:0019901~protein kinase binding  
GO:0010720~positive regulation of cell development  
GO:0035113~embryonic appendage morphogenesis  
GO:0030326~embryonic limb morphogenesis  
GO:0048568~embryonic organ development  
GO:0009611~response to wounding  
GO:0019226~transmission of nerve impulse  
GO:0007156~homophilic cell adhesion  
GO:0070161~anchoring junction  
GO:0010324~membrane invagination  
GO:0006897~endocytosis  
GO:0007411~axon guidance  
GO:0035107~appendage morphogenesis  
GO:0035108~limb morphogenesis  
GO:0010604~positive regulation of macromolecule metabolic process

GO:0050767~regulation of neurogenesis  
GO:0006954~inflammatory response  
GO:0010959~regulation of metal ion transport  
GO:0051017~actin filament bundle formation  
GO:0045321~leukocyte activation  
GO:0034702~ion channel complex  
GO:0009719~response to endogenous stimulus  
GO:0000165~MAPKKK cascade  
GO:0050804~regulation of synaptic transmission  
GO:0048736~appendage development  
GO:0060173~limb development  
GO:0005581~collagen  
GO:0045165~cell fate commitment  
GO:0046649~lymphocyte activation  
GO:0051347~positive regulation of transferase activity  
GO:0048514~blood vessel morphogenesis  
GO:0051050~positive regulation of transport  
GO:0003002~regionalization  
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic p  
GO:0034707~chloride channel complex  
GO:0048704~embryonic skeletal system morphogenesis  
GO:0019838~growth factor binding  
GO:0046983~protein dimerization activity  
GO:0007229~integrin-mediated signaling pathway  
GO:0033674~positive regulation of kinase activity  
GO:0005261~cation channel activity  
GO:0031644~regulation of neurological system process  
GO:0008284~positive regulation of cell proliferation  
GO:0035295~tube development  
GO:0051173~positive regulation of nitrogen compound metabolic process  
GO:0046982~protein heterodimerization activity  
GO:0043583~ear development  
GO:0002521~leukocyte differentiation  
GO:0005254~chloride channel activity  
GO:0048839~inner ear development  
GO:0040017~positive regulation of locomotion  
GO:0040007~growth  
GO:0060348~bone development  
GO:0005912~adherens junction  
GO:0009952~anterior/posterior pattern formation  
GO:0010942~positive regulation of cell death  
GO:0009725~response to hormone stimulus  
GO:0010629~negative regulation of gene expression  
GO:0001503~ossification  
GO:0043068~positive regulation of programmed cell death  
GO:0005253~anion channel activity

GO:0030027~lamellipodium  
GO:0043269~regulation of ion transport  
GO:0016323~basolateral plasma membrane  
GO:0042127~regulation of cell proliferation  
GO:0045860~positive regulation of protein kinase activity  
GO:0051969~regulation of transmission of nerve impulse  
GO:0012501~programmed cell death  
GO:0008360~regulation of cell shape  
GO:0006915~apoptosis  
GO:0019220~regulation of phosphate metabolic process  
GO:0051174~regulation of phosphorus metabolic process  
GO:0016265~death  
GO:0031327~negative regulation of cellular biosynthetic process  
GO:0010033~response to organic substance  
GO:0000267~cell fraction  
GO:0030534~adult behavior  
GO:0043168~anion binding  
GO:0019900~kinase binding  
GO:0031982~vesicle  
GO:0001525~angiogenesis  
GO:0045937~positive regulation of phosphate metabolic process  
GO:0010562~positive regulation of phosphorus metabolic process  
GO:0008219~cell death  
GO:0031346~positive regulation of cell projection organization  
GO:0043065~positive regulation of apoptosis  
GO:0045211~postsynaptic membrane  
GO:0009897~external side of plasma membrane  
GO:0032102~negative regulation of response to external stimulus  
GO:0030879~mammary gland development  
GO:0007517~muscle organ development  
GO:0051046~regulation of secretion  
GO:0008289~lipid binding  
GO:0007423~sensory organ development  
GO:0042592~homeostatic process  
GO:0015674~di-, tri-valent inorganic cation transport  
GO:0008283~cell proliferation  
GO:0000122~negative regulation of transcription from RNA polymerase II promoter  
GO:0035137~hindlimb morphogenesis  
GO:0060341~regulation of cellular localization  
GO:0009890~negative regulation of biosynthetic process  
GO:0008016~regulation of heart contraction  
GO:0044093~positive regulation of molecular function  
GO:0051924~regulation of calcium ion transport  
GO:0008509~anion transmembrane transporter activity  
GO:0022836~gated channel activity  
GO:0033267~axon part



GO:0007265~Ras protein signal transduction  
GO:0009986~cell surface  
GO:0043062~extracellular structure organization  
GO:0042327~positive regulation of phosphorylation  
GO:0030155~regulation of cell adhesion  
GO:0042490~mechanoreceptor differentiation  
GO:0031344~regulation of cell projection organization  
GO:0001934~positive regulation of protein amino acid phosphorylation  
GO:0051384~response to glucocorticoid stimulus  
GO:0030278~regulation of ossification  
GO:0030001~metal ion transport  
GO:0016481~negative regulation of transcription  
GO:0019992~diacylglycerol binding  
GO:0005624~membrane fraction  
GO:0046873~metal ion transmembrane transporter activity  
GO:0043679~nerve terminal  
GO:0051253~negative regulation of RNA metabolic process  
GO:0043069~negative regulation of programmed cell death  
GO:0045892~negative regulation of transcription, DNA-dependent  
GO:0005626~insoluble fraction  
GO:0042325~regulation of phosphorylation  
GO:0005262~calcium channel activity  
GO:0031589~cell-substrate adhesion  
GO:0032403~protein complex binding  
GO:0045785~positive regulation of cell adhesion  
GO:0006936~muscle contraction  
GO:0030198~extracellular matrix organization  
GO:0060548~negative regulation of cell death  
GO:0043066~negative regulation of apoptosis  
GO:0035116~embryonic hindlimb morphogenesis  
GO:0030425~dendrite  
GO:0003012~muscle system process  
GO:0017124~SH3 domain binding  
GO:0031404~chloride ion binding  
GO:0032414~positive regulation of ion transmembrane transporter activity  
GO:0001649~osteoblast differentiation  
GO:0031532~actin cytoskeleton reorganization  
GO:0031960~response to corticosteroid stimulus  
GO:0048871~multicellular organismal homeostasis  
GO:0001763~morphogenesis of a branching structure  
GO:0012502~induction of programmed cell death  
GO:0051336~regulation of hydrolase activity  
GO:0032411~positive regulation of transporter activity  
GO:0022832~voltage-gated channel activity  
GO:0005244~voltage-gated ion channel activity  
GO:0031102~neuron projection regeneration

GO:0030554~adenyl nucleotide binding  
GO:0007584~response to nutrient  
GO:0022037~metencephalon development  
GO:0010558~negative regulation of macromolecule biosynthetic process  
GO:0060078~regulation of postsynaptic membrane potential  
GO:0045444~fat cell differentiation  
GO:0016563~transcription activator activity  
GO:0005070~SH3/SH2 adaptor activity  
GO:0048585~negative regulation of response to stimulus  
GO:0051172~negative regulation of nitrogen compound metabolic process  
GO:0042110~T cell activation  
GO:0006917~induction of apoptosis  
GO:0005524~ATP binding  
GO:0001883~purine nucleoside binding  
GO:0019956~chemokine binding  
GO:0030335~positive regulation of cell migration  
GO:0051899~membrane depolarization  
GO:0035051~cardiac cell differentiation  
GO:0010811~positive regulation of cell-substrate adhesion  
GO:0008134~transcription factor binding  
GO:0043408~regulation of MAPKKK cascade  
GO:0051047~positive regulation of secretion  
GO:0019904~protein domain specific binding  
GO:0031267~small GTPase binding  
GO:0032409~regulation of transporter activity  
GO:0032559~adenyl ribonucleotide binding  
GO:0004950~chemokine receptor activity  
GO:0006812~cation transport  
GO:0051272~positive regulation of cell motion  
GO:0010810~regulation of cell-substrate adhesion  
GO:0035239~tube morphogenesis  
GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic |  
GO:0008344~adult locomotory behavior  
GO:0032870~cellular response to hormone stimulus  
GO:0060079~regulation of excitatory postsynaptic membrane potential  
GO:0050679~positive regulation of epithelial cell proliferation  
GO:0030955~potassium ion binding  
GO:0050770~regulation of axonogenesis  
GO:0001882~nucleoside binding  
GO:0060537~muscle tissue development  
GO:0005516~calmodulin binding  
GO:0030902~hindbrain development  
GO:0032012~regulation of ARF protein signal transduction

**OA knee cluster 1 versus OA knee cluster 2**

## Term

GO:0030695~GTPase regulator activity  
GO:0060589~nucleoside-triphosphatase regulator activity  
GO:0044459~plasma membrane part  
GO:0007242~intracellular signaling cascade  
GO:0005886~plasma membrane  
GO:0007155~cell adhesion  
GO:0001501~skeletal system development  
GO:0022610~biological adhesion  
GO:0051056~regulation of small GTPase mediated signal transduction  
GO:0010557~positive regulation of macromolecule biosynthetic process  
GO:0005096~GTPase activator activity  
GO:0019899~enzyme binding  
GO:0009891~positive regulation of biosynthetic process  
GO:0048534~hemopoietic or lymphoid organ development  
GO:0031328~positive regulation of cellular biosynthetic process  
GO:0030097~hemopoiesis  
GO:0006468~protein amino acid phosphorylation  
GO:0045893~positive regulation of transcription, DNA-dependent  
GO:0005509~calcium ion binding  
GO:0002520~immune system development  
GO:0051254~positive regulation of RNA metabolic process  
GO:0007167~enzyme linked receptor protein signaling pathway  
GO:0048598~embryonic morphogenesis  
GO:0010604~positive regulation of macromolecule metabolic process  
GO:0010628~positive regulation of gene expression  
GO:0000904~cell morphogenesis involved in differentiation  
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic p  
GO:0043068~positive regulation of programmed cell death  
GO:0042981~regulation of apoptosis  
GO:0045941~positive regulation of transcription  
GO:0010942~positive regulation of cell death  
GO:0043065~positive regulation of apoptosis  
GO:0007243~protein kinase cascade  
GO:0051173~positive regulation of nitrogen compound metabolic process  
GO:0042127~regulation of cell proliferation  
GO:0000902~cell morphogenesis  
GO:0043067~regulation of programmed cell death  
GO:0008047~enzyme activator activity  
GO:0005083~small GTPase regulator activity  
GO:0010941~regulation of cell death  
GO:0045944~positive regulation of transcription from RNA polymerase II promoter  
GO:0008092~cytoskeletal protein binding  
GO:0001568~blood vessel development  
GO:0046578~regulation of Ras protein signal transduction

GO:0005085~guanyl-nucleotide exchange factor activity  
GO:0031012~extracellular matrix  
GO:0003779~actin binding  
GO:0048705~skeletal system morphogenesis  
GO:0001944~vasculature development  
GO:0032989~cellular component morphogenesis  
GO:0009611~response to wounding  
GO:0051094~positive regulation of developmental process  
GO:0007507~heart development  
GO:0002521~leukocyte differentiation  
GO:0035023~regulation of Rho protein signal transduction  
GO:0016310~phosphorylation  
GO:0045597~positive regulation of cell differentiation  
GO:0048562~embryonic organ morphogenesis  
GO:0048667~cell morphogenesis involved in neuron differentiation  
GO:0009792~embryonic development ending in birth or egg hatching  
GO:0019838~growth factor binding  
GO:0007409~axonogenesis  
GO:0030030~cell projection organization  
GO:0044420~extracellular matrix part  
GO:0005088~Ras guanyl-nucleotide exchange factor activity  
GO:0005578~proteinaceous extracellular matrix  
GO:0006357~regulation of transcription from RNA polymerase II promoter  
GO:0043009~chordate embryonic development  
GO:0012502~induction of programmed cell death  
GO:0006793~phosphorus metabolic process  
GO:0006796~phosphate metabolic process  
GO:0008284~positive regulation of cell proliferation  
GO:0048568~embryonic organ development  
GO:0051270~regulation of cell motion  
GO:0006928~cell motion  
GO:0006917~induction of apoptosis  
GO:0009968~negative regulation of signal transduction  
GO:0044421~extracellular region part  
GO:0051174~regulation of phosphorus metabolic process  
GO:0019220~regulation of phosphate metabolic process  
GO:0004672~protein kinase activity  
GO:0048812~neuron projection morphogenesis  
GO:0018212~peptidyl-tyrosine modification  
GO:0042995~cell projection  
GO:0051216~cartilage development  
GO:0031226~intrinsic to plasma membrane  
GO:0008285~negative regulation of cell proliferation  
GO:0030036~actin cytoskeleton organization  
GO:0010648~negative regulation of cell communication  
GO:0060173~limb development

GO:0048736~appendage development  
GO:0005887~integral to plasma membrane  
GO:0035108~limb morphogenesis  
GO:0035107~appendage morphogenesis  
GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway  
GO:0018108~peptidyl-tyrosine phosphorylation  
GO:0040012~regulation of locomotion  
GO:0001503~ossification  
GO:0048706~embryonic skeletal system development  
GO:0016337~cell-cell adhesion  
GO:0030326~embryonic limb morphogenesis  
GO:0035113~embryonic appendage morphogenesis  
GO:0001932~regulation of protein amino acid phosphorylation  
GO:0048514~blood vessel morphogenesis  
GO:0031175~neuron projection development  
GO:0042325~regulation of phosphorylation  
GO:0048858~cell projection morphogenesis  
GO:0030098~lymphocyte differentiation  
GO:0060348~bone development  
GO:0030029~actin filament-based process  
GO:0030198~extracellular matrix organization  
GO:0016477~cell migration  
GO:0016265~death  
GO:0008219~cell death  
GO:0030054~cell junction  
GO:0046324~regulation of glucose import  
GO:0007156~homophilic cell adhesion  
GO:0006954~inflammatory response  
GO:0002697~regulation of immune effector process  
GO:0017124~SH3 domain binding  
GO:0010827~regulation of glucose transport  
GO:0005089~Rho guanyl-nucleotide exchange factor activity  
GO:0005604~basement membrane  
GO:0032844~regulation of homeostatic process  
GO:0007389~pattern specification process  
GO:0001558~regulation of cell growth  
GO:0032990~cell part morphogenesis  
GO:0005581~collagen  
GO:0045202~synapse  
GO:0048704~embryonic skeletal system morphogenesis  
GO:0001775~cell activation  
GO:0051046~regulation of secretion  
GO:0004714~transmembrane receptor protein tyrosine kinase activity  
GO:0060021~palate development  
GO:0035295~tube development  
GO:0048870~cell motility

GO:0051674~localization of cell  
GO:0008624~induction of apoptosis by extracellular signals  
GO:0042326~negative regulation of phosphorylation  
GO:0042476~odontogenesis  
GO:0051017~actin filament bundle formation  
GO:0006915~apoptosis  
GO:0048666~neuron development  
GO:0009890~negative regulation of biosynthetic process  
GO:0012501~programmed cell death  
GO:0035116~embryonic hindlimb morphogenesis  
GO:0015629~actin cytoskeleton  
GO:0001649~osteoblast differentiation  
GO:0045321~leukocyte activation  
GO:0043062~extracellular structure organization  
GO:0030334~regulation of cell migration  
GO:0045937~positive regulation of phosphate metabolic process  
GO:0010562~positive regulation of phosphorus metabolic process  
GO:0045930~negative regulation of mitotic cell cycle  
GO:0030155~regulation of cell adhesion  
GO:0043467~regulation of generation of precursor metabolites and energy  
GO:0004713~protein tyrosine kinase activity  
GO:0007010~cytoskeleton organization  
GO:0004674~protein serine/threonine kinase activity  
GO:0005160~transforming growth factor beta receptor binding  
GO:0060389~pathway-restricted SMAD protein phosphorylation  
GO:0045749~negative regulation of S phase of mitotic cell cycle  
GO:0051347~positive regulation of transferase activity  
GO:0040007~growth  
GO:0010563~negative regulation of phosphorus metabolic process  
GO:0045936~negative regulation of phosphate metabolic process  
GO:0042327~positive regulation of phosphorylation  
GO:0032583~regulation of gene-specific transcription  
GO:0016481~negative regulation of transcription  
GO:0031982~vesicle  
GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway  
GO:0010558~negative regulation of macromolecule biosynthetic process  
GO:0043005~neuron projection  
GO:0016563~transcription activator activity  
GO:0040017~positive regulation of locomotion  
GO:0030879~mammary gland development  
GO:0010629~negative regulation of gene expression  
GO:0019992~diacylglycerol binding  
GO:0005626~insoluble fraction  
GO:0030099~myeloid cell differentiation  
GO:0031327~negative regulation of cellular biosynthetic process  
GO:0030182~neuron differentiation

GO:0001934~positive regulation of protein amino acid phosphorylation  
GO:0009897~external side of plasma membrane  
GO:0035051~cardiac cell differentiation  
GO:0040008~regulation of growth  
GO:0000267~cell fraction  
GO:0046983~protein dimerization activity  
GO:0043583~ear development  
GO:0019900~kinase binding  
GO:0008134~transcription factor binding  
GO:0008361~regulation of cell size  
GO:0045637~regulation of myeloid cell differentiation  
GO:0010810~regulation of cell-substrate adhesion  
GO:0001816~cytokine production  
GO:0032535~regulation of cellular component size  
GO:0008289~lipid binding  
GO:0019904~protein domain specific binding  
GO:0005201~extracellular matrix structural constituent  
GO:0033674~positive regulation of kinase activity  
GO:0042113~B cell activation  
GO:0006952~defense response  
GO:0007610~behavior  
GO:0007584~response to nutrient  
GO:0005099~Ras GTPase activator activity  
GO:0006897~endocytosis  
GO:0010324~membrane invagination  
GO:0007626~locomotory behavior  
GO:0019207~kinase regulator activity  
GO:0031625~ubiquitin protein ligase binding  
GO:0042803~protein homodimerization activity  
GO:0000060~protein import into nucleus, translocation  
GO:0051272~positive regulation of cell motion  
GO:0051020~GTPase binding  
GO:0005539~glycosaminoglycan binding  
GO:0046649~lymphocyte activation  
GO:0019901~protein kinase binding  
GO:0007423~sensory organ development  
GO:0001525~angiogenesis  
GO:0002683~negative regulation of immune system process  
GO:0017015~regulation of transforming growth factor beta receptor signaling pathway  
GO:0030510~regulation of BMP signaling pathway  
GO:0045892~negative regulation of transcription, DNA-dependent  
GO:0045444~fat cell differentiation  
GO:0016044~membrane organization  
GO:0042592~homeostatic process  
GO:0051253~negative regulation of RNA metabolic process  
GO:0009986~cell surface

GO:0045646~regulation of erythrocyte differentiation  
 GO:0001837~epithelial to mesenchymal transition  
 GO:0046326~positive regulation of glucose import  
 GO:0010828~positive regulation of glucose transport  
 GO:0060341~regulation of cellular localization  
 GO:0010033~response to organic substance  
 GO:0048585~negative regulation of response to stimulus  
 GO:0048839~inner ear development  
 GO:0044093~positive regulation of molecular function  
 GO:0019898~extrinsic to membrane  
 GO:0002706~regulation of lymphocyte mediated immunity  
 GO:0006955~immune response  
 GO:0009306~protein secretion  
 GO:0030528~transcription regulator activity  
 GO:0031267~small GTPase binding  
 GO:0017016~Ras GTPase binding  
 GO:0043167~ion binding  
 GO:0009725~response to hormone stimulus  
 GO:0001952~regulation of cell-matrix adhesion  
 GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic |  
 GO:0009719~response to endogenous stimulus  
 GO:0007411~axon guidance  
 GO:0051172~negative regulation of nitrogen compound metabolic process

## OA hip versus OA knee

### Term

GO:0007389~pattern specification process  
 GO:0048598~embryonic morphogenesis  
 GO:0009952~anterior/posterior pattern formation  
 GO:0043565~sequence-specific DNA binding  
 GO:0001501~skeletal system development  
 GO:0048705~skeletal system morphogenesis  
 GO:0048706~embryonic skeletal system development  
 GO:0003002~regionalization  
 GO:0048704~embryonic skeletal system morphogenesis  
 GO:0048562~embryonic organ morphogenesis  
 GO:0009792~embryonic development ending in birth or egg hatching  
 GO:0043009~chordate embryonic development  
 GO:0048568~embryonic organ development  
 GO:0015629~actin cytoskeleton  
 GO:0003700~transcription factor activity  
 GO:0030528~transcription regulator activity  
 GO:0009891~positive regulation of biosynthetic process  
 GO:0045941~positive regulation of transcription



GO:0031328~positive regulation of cellular biosynthetic process  
GO:0030326~embryonic limb morphogenesis  
GO:0035113~embryonic appendage morphogenesis  
GO:0010557~positive regulation of macromolecule biosynthetic process  
GO:0010628~positive regulation of gene expression  
GO:0048736~appendage development  
GO:0060173~limb development  
GO:0060589~nucleoside-triphosphatase regulator activity  
GO:0000902~cell morphogenesis  
GO:0030695~GTPase regulator activity  
GO:0035108~limb morphogenesis  
GO:0035107~appendage morphogenesis  
GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic p  
GO:0030182~neuron differentiation  
GO:0048732~gland development  
GO:0045893~positive regulation of transcription, DNA-dependent  
GO:0000904~cell morphogenesis involved in differentiation  
GO:0051173~positive regulation of nitrogen compound metabolic process  
GO:0051254~positive regulation of RNA metabolic process  
GO:0048812~neuron projection morphogenesis  
GO:0045165~cell fate commitment  
GO:0010604~positive regulation of macromolecule metabolic process  
GO:0032989~cellular component morphogenesis  
GO:0048666~neuron development  
GO:0031175~neuron projection development  
GO:0048667~cell morphogenesis involved in neuron differentiation  
GO:0045944~positive regulation of transcription from RNA polymerase II promoter  
GO:0030900~forebrain development  
GO:0030030~cell projection organization  
GO:0007409~axonogenesis  
GO:0007155~cell adhesion  
GO:0022610~biological adhesion  
GO:0005856~cytoskeleton  
GO:0006357~regulation of transcription from RNA polymerase II promoter  
GO:0048858~cell projection morphogenesis  
GO:0035295~tube development  
GO:0044459~plasma membrane part  
GO:0044456~synapse part  
GO:0042995~cell projection  
GO:0051056~regulation of small GTPase mediated signal transduction  
GO:0003779~actin binding  
GO:0035239~tube morphogenesis  
GO:0032990~cell part morphogenesis  
GO:0021517~ventral spinal cord development  
GO:0009954~proximal/distal pattern formation  
GO:0005886~plasma membrane

GO:0045202~synapse  
GO:0030054~cell junction  
GO:0019898~extrinsic to membrane  
GO:0021522~spinal cord motor neuron differentiation  
GO:0014069~postsynaptic density  
GO:0006355~regulation of transcription, DNA-dependent  
GO:0044430~cytoskeletal part  
GO:0005083~small GTPase regulator activity  
GO:0048567~ectodermal gut morphogenesis  
GO:0007439~ectodermal gut development  
GO:0008092~cytoskeletal protein binding  
GO:0048754~branching morphogenesis of a tube  
GO:0007517~muscle organ development  
GO:0060284~regulation of cell development  
GO:0051252~regulation of RNA metabolic process  
GO:0005096~GTPase activator activity  
GO:0048729~tissue morphogenesis  
GO:0051216~cartilage development  
GO:0046578~regulation of Ras protein signal transduction  
GO:0045664~regulation of neuron differentiation  
GO:0010629~negative regulation of gene expression  
GO:0032332~positive regulation of chondrocyte differentiation  
GO:0001708~cell fate specification  
GO:0016459~myosin complex  
GO:0021675~nerve development  
GO:0021515~cell differentiation in spinal cord  
GO:0043005~neuron projection  
GO:0016481~negative regulation of transcription  
GO:0007242~intracellular signaling cascade  
GO:0031012~extracellular matrix  
GO:0007267~cell-cell signaling  
GO:0051017~actin filament bundle formation  
GO:0035137~hindlimb morphogenesis  
GO:0050767~regulation of neurogenesis  
GO:0010558~negative regulation of macromolecule biosynthetic process

| Count | %          | PValue   | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichment |
|-------|------------|----------|---------------|------------|----------|-----------|-----------------|
| 72    | 3.567889   | 3.68E-14 | GNA13, EVX1   | 1406       | 267      | 13528     | 2.594594595     |
| 79    | 3.9147671  | 2.90E-14 | DLC1, NDST1   | 1406       | 307      | 13528     | 2.475922176     |
| 49    | 2.42814668 | 1.83E-14 | ZEB2, GLI3, P | 1406       | 140      | 13528     | 3.367567568     |
| 77    | 3.81565907 | 2.14E-12 | CYP24A1, NC   | 1406       | 319      | 13528     | 2.322460391     |
| 40    | 1.98216056 | 2.98E-12 | NDST1, HOXA   | 1406       | 112      | 13528     | 3.436293436     |
| 32    | 1.58572844 | 6.52E-12 | NDST1, HOXA   | 1406       | 77       | 13528     | 3.998595999     |
| 120   | 5.03144654 | 3.17E-12 | MTSS1, MAE    | 1639       | 504      | 12983     | 1.886022255     |
| 101   | 4.23480084 | 1.02E-11 | DLC1, IQGAP   | 1639       | 404      | 12983     | 1.980323368     |
| 86    | 3.60587002 | 2.14E-11 | MTSS1, LIMA   | 1639       | 326      | 12983     | 2.089666376     |
| 101   | 4.23480084 | 4.01E-11 | DLC1, IQGAP   | 1639       | 413      | 12983     | 1.937168621     |
| 54    | 2.67591675 | 4.11E-11 | EVX1, ZEB2, C | 1406       | 197      | 13528     | 2.63739882      |
| 26    | 1.28840436 | 7.75E-11 | NDST1, GLI3,  | 1406       | 57       | 13528     | 4.388809862     |
| 42    | 2.08126858 | 7.00E-11 | NDST1, PAX2   | 1406       | 133      | 13528     | 3.038406828     |
| 81    | 3.39622642 | 2.03E-10 | LTBP2, COL2A  | 1571       | 320      | 12782     | 2.059480426     |
| 86    | 3.60587002 | 1.20E-10 | LTBP2, COL2A  | 1571       | 345      | 12782     | 2.028158931     |
| 181   | 7.58909853 | 3.34E-10 | S100A4, S100  | 1639       | 919      | 12983     | 1.560124177     |
| 74    | 3.66699703 | 4.19E-10 | DLC1, GNA13   | 1406       | 334      | 13528     | 2.131736527     |
| 70    | 2.93501048 | 1.12E-09 | MTSS1, LIMA   | 1571       | 269      | 12782     | 2.117231702     |
| 73    | 3.61744301 | 6.91E-10 | DLC1, GNA13   | 1406       | 331      | 13528     | 2.121989059     |
| 47    | 2.32903865 | 9.81E-10 | NDST1, EGLN   | 1406       | 172      | 13528     | 2.629164048     |
| 356   | 14.9266247 | 3.20E-09 | DLC1, ATP1B   | 1571       | 2203     | 12782     | 1.314795258     |
| 61    | 2.55765199 | 3.12E-09 | DLC1, PREX1,  | 1639       | 220      | 12983     | 2.196358644     |
| 70    | 2.93501048 | 8.06E-09 | DLC1, MLPH,   | 1639       | 274      | 12983     | 2.023688113     |
| 37    | 1.55136268 | 8.96E-08 | LUM, COL2A1   | 1571       | 117      | 12782     | 2.572992323     |
| 18    | 0.75471698 | 1.55E-07 | COL18A1, CC   | 1571       | 35       | 12782     | 4.184341184     |
| 118   | 5.84737364 | 6.24E-08 | THRB, GDF7,   | 1406       | 695      | 13528     | 1.633599067     |
| 100   | 4.95540139 | 8.79E-08 | THRB, GDF7,   | 1406       | 564      | 13528     | 1.70596128      |
| 116   | 5.74826561 | 9.52E-08 | THRB, GDF7,   | 1406       | 685      | 13528     | 1.629354902     |
| 28    | 1.38751239 | 1.05E-07 | WNT5A, HOXA   | 1406       | 87       | 13528     | 3.096613855     |
| 28    | 1.38751239 | 1.05E-07 | WNT5A, HOXA   | 1406       | 87       | 13528     | 3.096613855     |
| 111   | 5.50049554 | 1.66E-07 | THRB, GDF7,   | 1406       | 654      | 13528     | 1.633027523     |
| 101   | 5.0049554  | 2.03E-07 | THRB, GDF7,   | 1406       | 581      | 13528     | 1.67260548      |
| 169   | 7.08595388 | 6.35E-07 | UTS2, CHIA, I | 1571       | 960      | 12782     | 1.432313548     |
| 30    | 1.48662042 | 3.71E-07 | WNT5A, HOXA   | 1406       | 103      | 13528     | 2.802414065     |
| 30    | 1.48662042 | 3.71E-07 | WNT5A, HOXA   | 1406       | 103      | 13528     | 2.802414065     |
| 69    | 3.41922696 | 4.38E-07 | NRP2, CCKAF   | 1406       | 356      | 13528     | 1.864864865     |
| 30    | 1.25786164 | 5.57E-07 | PREX1, AKAP   | 1639       | 88       | 12983     | 2.700440956     |
| 129   | 5.40880503 | 1.22E-06 | S100A4, MTS   | 1571       | 697      | 12782     | 1.505842535     |
| 42    | 1.76100629 | 1.12E-06 | DLC1, KCNJ1!  | 1571       | 155      | 12782     | 2.204652882     |
| 27    | 1.13207547 | 5.23E-07 | PREX1, AKAP   | 1639       | 74       | 12983     | 2.890201672     |
| 29    | 1.4370664  | 5.30E-07 | WNT5A, HOXA   | 1406       | 99       | 13528     | 2.818454818     |

|     |            |          |               |      |      |       |             |
|-----|------------|----------|---------------|------|------|-------|-------------|
| 29  | 1.4370664  | 5.30E-07 | WNT5A, HOX    | 1406 | 99   | 13528 | 2.818454818 |
| 105 | 5.20317146 | 5.75E-07 | THRB, GDF7,   | 1406 | 624  | 13528 | 1.619022869 |
| 80  | 3.96432111 | 6.02E-07 | NRP2, CCKAF   | 1406 | 438  | 13528 | 1.757373812 |
| 35  | 1.73439049 | 6.91E-07 | CGA, NRG3, I  | 1406 | 135  | 13528 | 2.494494494 |
| 85  | 4.21209118 | 7.40E-07 | EVX1, THRB,   | 1406 | 477  | 13528 | 1.714544733 |
| 52  | 2.57680872 | 7.81E-07 | NRP2, CCKAF   | 1406 | 244  | 13528 | 2.050509526 |
| 107 | 5.30227948 | 8.22E-07 | THRB, GDF7,   | 1406 | 644  | 13528 | 1.598623468 |
| 85  | 4.21209118 | 1.06E-06 | EVX1, THRB,   | 1406 | 481  | 13528 | 1.700286565 |
| 47  | 2.32903865 | 1.04E-06 | NRP2, CCKAF   | 1406 | 213  | 13528 | 2.123080827 |
| 35  | 1.73439049 | 1.42E-06 | ERBB4, EVX1   | 1406 | 139  | 13528 | 2.42271048  |
| 44  | 1.84486373 | 3.14E-06 | DLC1, KCNJ1!  | 1571 | 172  | 12782 | 2.081358341 |
| 74  | 3.10272537 | 1.49E-06 | DLC1, NRG3,   | 1639 | 335  | 12983 | 1.749778259 |
| 541 | 22.6834382 | 5.07E-06 | DLC1, FHIT, F | 1571 | 3777 | 12782 | 1.165394351 |
| 132 | 6.54112983 | 2.60E-06 | DLC1, THRB,   | 1406 | 857  | 13528 | 1.481976726 |
| 72  | 3.567889   | 3.06E-06 | NRP2, CCKAF   | 1406 | 397  | 13528 | 1.744979236 |
| 64  | 3.17145689 | 3.04E-06 | NRP2, CCKAF   | 1406 | 339  | 13528 | 1.816471339 |
| 52  | 2.57680872 | 3.45E-06 | NRP2, CCKAF   | 1406 | 256  | 13528 | 1.954391892 |
| 45  | 2.22993062 | 3.60E-06 | NRP2, CCKAF   | 1406 | 209  | 13528 | 2.071641019 |
| 68  | 3.36967294 | 4.11E-06 | EVX1, THRB,   | 1406 | 371  | 13528 | 1.763531726 |
| 36  | 1.7839445  | 4.42E-06 | DLC1, CCKAR   | 1406 | 152  | 13528 | 2.278805121 |
| 67  | 3.32011893 | 6.18E-06 | NRP2, CCKAF   | 1406 | 368  | 13528 | 1.751762632 |
| 42  | 2.08126858 | 6.07E-06 | NRP2, CCKAF   | 1406 | 193  | 13528 | 2.093824394 |
| 110 | 5.45094153 | 8.01E-06 | DLC1, CADM    | 1406 | 700  | 13528 | 1.511969112 |
| 110 | 5.45094153 | 8.63E-06 | DLC1, CADM    | 1406 | 701  | 13528 | 1.509812237 |
| 113 | 5.59960357 | 1.00E-05 | THRB, ARNT2   | 1406 | 727  | 13528 | 1.49552028  |
| 70  | 2.93501048 | 1.77E-05 | NRP2, S100A   | 1571 | 342  | 12782 | 1.665307976 |
| 49  | 2.42814668 | 1.06E-05 | NRP2, CCKAF   | 1406 | 245  | 13528 | 1.924324324 |
| 40  | 1.67714885 | 8.70E-06 | PREX1, AKAP   | 1639 | 152  | 12983 | 2.084550914 |
| 45  | 2.22993062 | 1.43E-05 | DLC1, GNA1E   | 1406 | 220  | 13528 | 1.968058968 |
| 49  | 2.42814668 | 2.30E-05 | DLC1, ITPKB,  | 1406 | 252  | 13528 | 1.870870871 |
| 30  | 1.48662042 | 3.35E-05 | DLC1, GNA1E   | 1406 | 127  | 13528 | 2.272824005 |
| 112 | 4.69601677 | 2.48E-05 | FGFRL1, PRK   | 1639 | 606  | 12983 | 1.464001434 |
| 49  | 2.42814668 | 3.51E-05 | NRP2, CCKAF   | 1406 | 256  | 13528 | 1.841638514 |
| 9   | 0.44598612 | 4.37E-05 | HOXC10, ISL2  | 1406 | 15   | 13528 | 5.772972973 |
| 11  | 0.54509415 | 4.54E-05 | HOXD9, HOX    | 1406 | 23   | 13528 | 4.601645123 |
| 216 | 9.05660377 | 7.52E-05 | PDLIM7, TUB   | 1571 | 1381 | 12782 | 1.272572989 |
| 45  | 1.88679245 | 1.06E-04 | DLC1, KCNJ1!  | 1571 | 203  | 12782 | 1.803595338 |
| 22  | 0.92243187 | 4.64E-05 | EGFR, FGFR2   | 1639 | 67   | 12983 | 2.601021737 |
| 192 | 8.05031447 | 1.18E-04 | ATP1B1, ADC   | 1571 | 1215 | 12782 | 1.285723491 |
| 8   | 0.33542977 | 1.88E-04 | TNXB, COL27   | 1571 | 12   | 12782 | 5.424145979 |
| 92  | 3.85744235 | 2.24E-04 | DLC1, KCNJ1!  | 1571 | 518  | 12782 | 1.445042751 |
| 8   | 0.39643211 | 1.25E-04 | HOXC10, ISL2  | 1406 | 13   | 13528 | 5.920997921 |
| 230 | 11.3974232 | 1.56E-04 | HOXD12, HO    | 1406 | 1773 | 13528 | 1.248151705 |
| 12  | 0.50314465 | 3.87E-04 | ITGA9, ITGB8  | 1571 | 29   | 12782 | 3.366711297 |
| 7   | 0.3468781  | 1.80E-04 | NOTCH1, FO    | 1406 | 10   | 13528 | 6.735135135 |
| 7   | 0.3468781  | 1.80E-04 | NOTCH1, FO    | 1406 | 10   | 13528 | 6.735135135 |

|     |            |          |               |      |      |       |             |
|-----|------------|----------|---------------|------|------|-------|-------------|
| 28  | 1.17400419 | 3.85E-04 | DLC1, KCNJ1!  | 1571 | 112  | 12782 | 2.034054742 |
| 184 | 7.7148847  | 4.51E-04 | ATP1B1, ADC   | 1571 | 1188 | 12782 | 1.260155126 |
| 18  | 0.89197225 | 2.53E-04 | GNA13, FLT1   | 1406 | 65   | 13528 | 2.664449064 |
| 40  | 1.98216056 | 2.50E-04 | FOXK1, UTRN   | 1406 | 211  | 13528 | 1.824004099 |
| 39  | 1.93260654 | 2.81E-04 | IRX3, NBN, H  | 1406 | 205  | 13528 | 1.830454845 |
| 232 | 11.4965312 | 3.26E-04 | HOXD12, HO    | 1406 | 1813 | 13528 | 1.231227918 |
| 111 | 4.65408805 | 7.51E-04 | MTSS1, CADF   | 1571 | 670  | 12782 | 1.347940755 |
| 35  | 1.46750524 | 7.96E-04 | NRP2, KIAA1!  | 1571 | 159  | 12782 | 1.790991597 |
| 21  | 0.88050314 | 9.29E-04 | COL18A1, CC   | 1571 | 78   | 12782 | 2.190520492 |
| 26  | 1.09014675 | 8.78E-04 | DLC1, KCNJ1!  | 1571 | 106  | 12782 | 1.995676351 |
| 96  | 4.02515723 | 9.16E-04 | MTSS1, CADF   | 1571 | 568  | 12782 | 1.3751356   |
| 35  | 1.73439049 | 4.01E-04 | DLC1, SHROC   | 1406 | 180  | 13528 | 1.870870871 |
| 106 | 4.44444444 | 0.00112  | MTSS1, CADF   | 1571 | 642  | 12782 | 1.343363257 |
| 24  | 1.00628931 | 3.04E-04 | COL18A1, CC   | 1639 | 86   | 12983 | 2.210593527 |
| 25  | 1.04821803 | 2.86E-04 | DLC1, TBC1D   | 1639 | 91   | 12983 | 2.176179525 |
| 16  | 0.67085954 | 3.41E-04 | SMAD6, CREI   | 1639 | 46   | 12983 | 2.755232512 |
| 19  | 0.94152626 | 4.44E-04 | PRKCA, WNT    | 1406 | 74   | 13528 | 2.470416362 |
| 39  | 1.93260654 | 4.60E-04 | DLC1, ASAP2   | 1406 | 210  | 13528 | 1.786872587 |
| 28  | 1.38751239 | 4.82E-04 | IRX3, NBN, S  | 1406 | 133  | 13528 | 2.025604552 |
| 77  | 3.81565907 | 5.14E-04 | EIF2C2, RSF1  | 1406 | 504  | 13528 | 1.46996997  |
| 6   | 0.29732408 | 5.13E-04 | THRB, HOXA!   | 1406 | 8    | 13528 | 7.216216216 |
| 15  | 0.74331021 | 5.11E-04 | EVX1, HOXA!   | 1406 | 51   | 13528 | 2.829888712 |
| 92  | 3.85744235 | 4.14E-04 | E2F2, ELF3, T | 1639 | 513  | 12983 | 1.420582845 |
| 27  | 1.13207547 | 4.77E-04 | LTBP2, LTBP!  | 1639 | 105  | 12983 | 2.036904036 |
| 596 | 24.9895178 | 4.66E-04 | SLC9A9, FHIT  | 1639 | 4241 | 12983 | 1.113202289 |
| 10  | 0.49554014 | 5.97E-04 | HOXB3, HOX    | 1406 | 25   | 13528 | 3.848648649 |
| 10  | 0.49554014 | 5.97E-04 | HOXC10, ISL!  | 1406 | 25   | 13528 | 3.848648649 |
| 71  | 3.51833499 | 6.18E-04 | RSF1, FOXK1,  | 1406 | 459  | 13528 | 1.488311841 |
| 166 | 8.2259663  | 6.50E-04 | GNA13, CYP2   | 1406 | 1256 | 13528 | 1.271647444 |
| 92  | 3.85744235 | 0.00163  | MTSS1, CADF   | 1571 | 550  | 12782 | 1.360967537 |
| 26  | 1.09014675 | 0.00176  | ALDOA, ABLI   | 1571 | 111  | 12782 | 1.90578102  |
| 88  | 4.36075322 | 7.66E-04 | CGA, UTS2, C  | 1406 | 600  | 13528 | 1.411171171 |
| 9   | 0.44598612 | 7.81E-04 | SHROOM1, S    | 1406 | 21   | 13528 | 4.123552124 |
| 10  | 0.49554014 | 8.30E-04 | HOXD9, NOT    | 1406 | 26   | 13528 | 3.700623701 |
| 32  | 1.58572844 | 8.63E-04 | IRX3, NBN, S  | 1406 | 166  | 13528 | 1.854770433 |
| 26  | 1.09014675 | 0.00229  | ALDOA, MYL!   | 1571 | 113  | 12782 | 1.872050382 |
| 6   | 0.25157233 | 0.00228  | COL9A1, COL   | 1571 | 9    | 12782 | 5.424145979 |
| 83  | 3.48008386 | 0.00247  | CHMP4C, PTO   | 1571 | 494  | 12782 | 1.367016547 |
| 81  | 4.01387512 | 9.45E-04 | EIF2C2, RSF1  | 1406 | 547  | 13528 | 1.424773951 |
| 24  | 1.00628931 | 0.00259  | DLC1, DIXDC!  | 1571 | 102  | 12782 | 1.914404463 |

| Count | %          | PValue   | Genes      | List Total | Pop Hits | Pop Total | Fold Enrichment |
|-------|------------|----------|------------|------------|----------|-----------|-----------------|
| 841   | 14.9857448 | 7.46E-27 | HRAS, OSMR | 3661       | 2203     | 12782     | 1.332847872     |

|      |            |          |              |      |      |       |             |
|------|------------|----------|--------------|------|------|-------|-------------|
| 1301 | 23.1824661 | 3.45E-21 | HRAS, CDIPT, | 3661 | 3777 | 12782 | 1.202622697 |
| 315  | 5.6129722  | 8.54E-22 | DLC1, PVR, C | 3848 | 700  | 13528 | 1.582016632 |
| 316  | 5.63079116 | 5.23E-22 | DLC1, PVR, C | 3848 | 701  | 13528 | 1.584774943 |
| 373  | 6.64647185 | 7.71E-16 | S100A4, LTBF | 3715 | 919  | 12983 | 1.418435393 |
| 193  | 3.43905916 | 3.77E-15 | DLC1, RAB3G  | 3715 | 413  | 12983 | 1.633140302 |
| 190  | 3.38560228 | 2.85E-15 | DLC1, RAB3G  | 3715 | 404  | 12983 | 1.643571019 |
| 223  | 3.97362794 | 3.71E-14 | CROCC, PDLII | 3715 | 504  | 12983 | 1.546288641 |
| 459  | 8.17890235 | 4.53E-13 | OSMR, SHKB   | 3661 | 1215 | 12782 | 1.318971744 |
| 473  | 8.42836778 | 1.16E-13 | HRAS, PLEKH  | 3848 | 1256 | 13528 | 1.323945271 |
| 127  | 2.26300784 | 2.62E-13 | DLC1, HRAS,  | 3848 | 252  | 13528 | 1.771747022 |
| 446  | 7.94725588 | 3.14E-12 | OSMR, SHKB   | 3661 | 1188 | 12782 | 1.310742865 |
| 162  | 2.88667142 | 8.71E-12 | SEPT5, SEPT3 | 3661 | 355  | 12782 | 1.593256672 |
| 133  | 2.3699216  | 3.60E-12 | DLC1, RGL3,  | 3715 | 274  | 12983 | 1.696357242 |
| 279  | 4.97148967 | 3.48E-11 | S100A4, SNC  | 3661 | 697  | 12782 | 1.397560153 |
| 150  | 2.67284391 | 2.41E-11 | MTSS1, ENAF  | 3715 | 326  | 12983 | 1.608014268 |
| 56   | 0.99786172 | 3.51E-11 | RGL3, ITSN2, | 3715 | 88   | 12983 | 2.223932461 |
| 215  | 3.83107627 | 1.93E-10 | DLC1, CADM   | 3661 | 518  | 12782 | 1.449131459 |
| 49   | 0.87312901 | 9.32E-11 | ITSN2, PLEKH | 3715 | 74   | 12983 | 2.314091885 |
| 147  | 2.61938703 | 2.15E-11 | CASR, THRA,  | 3848 | 319  | 13528 | 1.62003793  |
| 81   | 1.44333571 | 3.42E-10 | RGL3, RASGE  | 3715 | 152  | 12983 | 1.862334419 |
| 104  | 1.85317177 | 1.65E-10 | DLC1, HRAS,  | 3848 | 210  | 13528 | 1.741055341 |
| 152  | 2.70848182 | 2.60E-10 | MTSS1, LTBP  | 3848 | 342  | 13528 | 1.562485562 |
| 59   | 1.0513186  | 3.24E-10 | DLC1, PLEKH  | 3848 | 99   | 13528 | 2.095151095 |
| 105  | 1.87099073 | 3.69E-10 | DLC1, TNNC1  | 3848 | 215  | 13528 | 1.716917275 |
| 123  | 2.191732   | 2.94E-09 | MTSS1, MAE   | 3661 | 269  | 12782 | 1.596437482 |
| 197  | 3.510335   | 7.25E-10 | PVR, CTHRC1  | 3848 | 475  | 13528 | 1.458045738 |
| 148  | 2.63720599 | 6.75E-09 | S100A4, SNC  | 3661 | 342  | 12782 | 1.510896425 |
| 80   | 1.42551675 | 1.45E-08 | NRP2, SNCG,  | 3661 | 159  | 12782 | 1.756677129 |
| 157  | 2.79757662 | 4.55E-09 | MTSS1, GDF7  | 3848 | 368  | 13528 | 1.499858763 |
| 103  | 1.83535282 | 1.35E-08 | DLC1, RAB3G  | 3715 | 220  | 12983 | 1.636178882 |
| 135  | 2.40555952 | 6.41E-09 | DLC1, GDF5,  | 3848 | 307  | 13528 | 1.545944592 |
| 162  | 2.88667142 | 1.55E-08 | GABRB3, GRI  | 3715 | 386  | 12983 | 1.466708973 |
| 124  | 2.20955096 | 6.03E-09 | PVR, THRA, C | 3848 | 276  | 13528 | 1.579469101 |
| 152  | 2.70848182 | 7.67E-09 | S100A4, GDF  | 3848 | 356  | 13528 | 1.501039501 |
| 42   | 0.74839629 | 2.66E-08 | NRP2, FGFR2  | 3715 | 67   | 12983 | 2.190739439 |
| 104  | 1.85317177 | 1.42E-08 | MTSS1, GRIK  | 3848 | 224  | 13528 | 1.632239382 |
| 122  | 2.17391304 | 1.53E-08 | SNCG, HRAS,  | 3848 | 274  | 13528 | 1.565336814 |
| 256  | 4.5616536  | 1.36E-08 | GDF7, GDF6,  | 3848 | 667  | 13528 | 1.34931287  |
| 190  | 3.38560228 | 1.30E-08 | SNCG, HRAS,  | 3848 | 469  | 13528 | 1.424227245 |
| 145  | 2.58374911 | 8.94E-08 | CTHRC1, LTB  | 3661 | 345  | 12782 | 1.467398232 |
| 164  | 2.92230934 | 5.56E-08 | GABRB3, GRI  | 3715 | 398  | 12983 | 1.440048155 |
| 178  | 3.17177477 | 3.00E-08 | TUBB2B, GDF  | 3848 | 438  | 13528 | 1.428711114 |
| 133  | 2.3699216  | 4.03E-08 | SNCG, HRAS,  | 3848 | 309  | 13528 | 1.513183834 |
| 61   | 1.08695652 | 1.88E-07 | FGF9, MMRN   | 3661 | 117  | 12782 | 1.820300371 |
| 154  | 2.74411974 | 4.60E-08 | THOP1, STAT  | 3848 | 370  | 13528 | 1.463246615 |
| 168  | 2.99358517 | 8.77E-08 | GABRB3, GRI  | 3715 | 412  | 12983 | 1.425044101 |

|     |            |          |              |      |     |       |             |
|-----|------------|----------|--------------|------|-----|-------|-------------|
| 109 | 1.94226657 | 1.87E-07 | SEPT5, SNCA  | 3661 | 246 | 12782 | 1.547000575 |
| 121 | 2.15609408 | 5.13E-08 | PVR, CTHRC1  | 3848 | 276 | 13528 | 1.541256139 |
| 168 | 2.99358517 | 1.06E-07 | GABRB3, GRI  | 3715 | 413 | 12983 | 1.421593631 |
| 44  | 0.78403421 | 8.66E-08 | WNT5A, THR   | 3848 | 74  | 13528 | 2.090352307 |
| 90  | 1.60370634 | 8.48E-08 | DLC1, RTN4,  | 3848 | 192 | 13528 | 1.647933992 |
| 134 | 2.38774056 | 3.68E-07 | CTHRC1, LTB  | 3661 | 320 | 12782 | 1.462021989 |
| 162 | 2.88667142 | 9.62E-08 | S100A4, GDF  | 3848 | 397 | 13528 | 1.434574276 |
| 141 | 2.51247327 | 1.87E-07 | GDF7, CNP, C | 3848 | 339 | 13528 | 1.462237595 |
| 101 | 1.7997149  | 2.38E-07 | DLC1, MTSS1  | 3848 | 226 | 13528 | 1.571127629 |
| 119 | 2.12045617 | 3.14E-07 | XRCC5, XRCC  | 3848 | 278 | 13528 | 1.504875933 |
| 111 | 1.97790449 | 3.77E-07 | GDF7, CNP, C | 3848 | 256 | 13528 | 1.524338942 |
| 295 | 5.25659301 | 4.38E-07 | DLC1, XRCC5  | 3848 | 812 | 13528 | 1.277216493 |
| 296 | 5.27441197 | 4.32E-07 | DLC1, XRCC5  | 3848 | 815 | 13528 | 1.276828693 |
| 244 | 4.34782609 | 4.67E-07 | HRAS, CDX1,  | 3848 | 654 | 13528 | 1.311627789 |
| 201 | 3.58161083 | 7.84E-07 | A2M, PDLIM1  | 3715 | 523 | 12983 | 1.343106985 |
| 88  | 1.56806842 | 5.38E-07 | DLC1, RTN4,  | 3848 | 193 | 13528 | 1.602964463 |
| 78  | 1.38987883 | 7.66E-07 | NRP2, NRP1,  | 3715 | 166 | 12983 | 1.642111192 |
| 106 | 1.88880969 | 6.31E-07 | S100A4, GDF  | 3848 | 244 | 13528 | 1.527265601 |
| 280 | 4.98930862 | 6.31E-07 | SLC9A9, ATP1 | 3848 | 768 | 13528 | 1.281726438 |
| 95  | 1.69280114 | 6.25E-07 | NRP2, NRP1,  | 3848 | 213 | 13528 | 1.567987272 |
| 137 | 2.44119743 | 7.22E-07 | DLC1, XRCC2  | 3848 | 334 | 13528 | 1.442024475 |
| 185 | 3.29650748 | 7.47E-07 | CDX1, THRA,  | 3848 | 477 | 13528 | 1.36348976  |
| 136 | 2.42337847 | 7.11E-07 | DLC1, XRCC2  | 3848 | 331 | 13528 | 1.444473058 |
| 291 | 5.18531718 | 7.72E-07 | DLC1, XRCC5  | 3848 | 804 | 13528 | 1.272434605 |
| 266 | 4.73984319 | 8.87E-07 | CDX1, STAT5  | 3848 | 727 | 13528 | 1.286310329 |
| 43  | 0.76621525 | 2.46E-06 | FRAS1, FGF9, | 3661 | 78  | 12782 | 1.924743835 |
| 149 | 2.65502495 | 9.94E-07 | CDX1, THRA,  | 3848 | 371 | 13528 | 1.411922601 |
| 185 | 3.29650748 | 1.42E-06 | CDX1, THRA,  | 3848 | 481 | 13528 | 1.352150968 |
| 105 | 1.87099073 | 1.54E-06 | LMO2, CSPG4  | 3848 | 245 | 13528 | 1.506682507 |
| 337 | 6.00498931 | 4.81E-06 | PVR, GDF3, C | 3661 | 960 | 12782 | 1.225625398 |
| 99  | 1.76407698 | 1.99E-06 | XRCC5, XRCC  | 3848 | 229 | 13528 | 1.519841306 |
| 112 | 1.99572345 | 2.33E-06 | CDX1, HOXD1  | 3848 | 267 | 13528 | 1.474705475 |
| 64  | 1.1404134  | 2.57E-06 | NDST1, FGF9  | 3848 | 133 | 13528 | 1.691713692 |
| 56  | 0.99786172 | 2.76E-06 | THRA, NDST1  | 3848 | 112 | 13528 | 1.757796258 |
| 104 | 1.85317177 | 2.93E-06 | GDF7, CNP, M | 3848 | 245 | 13528 | 1.492333149 |
| 63  | 1.12259444 | 3.19E-06 | DLC1, RTN4,  | 3848 | 131 | 13528 | 1.690704798 |
| 106 | 1.88880969 | 3.10E-06 | LMO2, CSPG4  | 3848 | 251 | 13528 | 1.484672536 |
| 222 | 3.95580898 | 3.17E-06 | UTS2, LTBP4, | 3848 | 600 | 13528 | 1.300769231 |
| 251 | 4.4725588  | 3.08E-06 | CADM1, MAE1  | 3848 | 690 | 13528 | 1.278860466 |
| 109 | 1.94226657 | 3.33E-06 | XRCC5, MAE1  | 3848 | 260 | 13528 | 1.473844555 |
| 122 | 2.17391304 | 3.44E-06 | SEPT5, UTS2, | 3848 | 298 | 13528 | 1.439269419 |
| 125 | 2.22736992 | 3.57E-06 | PVR, CTHRC1  | 3848 | 307 | 13528 | 1.431430177 |
| 125 | 2.22736992 | 3.57E-06 | PVR, CTHRC1  | 3848 | 307 | 13528 | 1.431430177 |
| 30  | 0.53456878 | 3.70E-06 | TPST2, ERBB4 | 3848 | 48  | 13528 | 2.197245322 |
| 42  | 0.74839629 | 3.91E-06 | NDST1, FGF9  | 3848 | 77  | 13528 | 1.917595918 |
| 102 | 1.81753386 | 4.31E-06 | DLC1, MTSS1  | 3848 | 241 | 13528 | 1.487927123 |

|     |            |          |               |      |      |       |             |
|-----|------------|----------|---------------|------|------|-------|-------------|
| 215 | 3.83107627 | 4.56E-06 | CDX1, GDF7,   | 3848 | 581  | 13528 | 1.300950759 |
| 29  | 0.51674982 | 4.42E-06 | ERBB4, STAT5  | 3848 | 46   | 13528 | 2.216351803 |
| 285 | 5.07840342 | 4.52E-06 | GDF7, STAT5   | 3848 | 800  | 13528 | 1.252429834 |
| 39  | 0.69493942 | 8.87E-06 | ERBB4, CNNE   | 3661 | 71   | 12782 | 1.917808957 |
| 248 | 4.41910192 | 5.34E-06 | HRAS, CDX1,   | 3848 | 685  | 13528 | 1.272798458 |
| 251 | 4.4725588  | 5.75E-06 | HRAS, CDX1,   | 3848 | 695  | 13528 | 1.269660031 |
| 76  | 1.35424091 | 6.43E-06 | DLC1, RTN4,   | 3848 | 169  | 13528 | 1.580976516 |
| 90  | 1.60370634 | 7.33E-06 | NRP2, NRP1,   | 3848 | 209  | 13528 | 1.513891514 |
| 64  | 1.1404134  | 1.46E-05 | MTSS1, SH3P   | 3661 | 138  | 12782 | 1.619198049 |
| 113 | 2.01354241 | 8.09E-06 | XRCC5, MAE/   | 3848 | 276  | 13528 | 1.439354907 |
| 208 | 3.70634355 | 8.61E-06 | CDX1, GDF7,   | 3848 | 564  | 13528 | 1.296530573 |
| 34  | 0.60584462 | 8.51E-06 | XRCC5, XRCC   | 3848 | 59   | 13528 | 2.02593467  |
| 99  | 1.76407698 | 9.45E-06 | XRCC5, MAE/   | 3848 | 236  | 13528 | 1.474761267 |
| 84  | 1.49679259 | 9.39E-06 | NRP2, NRP1,   | 3848 | 193  | 13528 | 1.530102442 |
| 337 | 6.00498931 | 9.73E-06 | GDF7, STAT5   | 3848 | 973  | 13528 | 1.217630707 |
| 337 | 6.00498931 | 9.73E-06 | GDF7, STAT5   | 3848 | 973  | 13528 | 1.217630707 |
| 463 | 8.25017819 | 1.94E-05 | KIFC1, TUBB2  | 3661 | 1381 | 12782 | 1.170540371 |
| 88  | 1.56806842 | 1.08E-05 | XRCC5, RTN4   | 3848 | 205  | 13528 | 1.509132397 |
| 72  | 1.28296507 | 1.13E-05 | NRP2, HRAS,   | 3848 | 160  | 13528 | 1.582016632 |
| 72  | 1.28296507 | 1.13E-05 | NRP2, HRAS,   | 3848 | 160  | 13528 | 1.582016632 |
| 116 | 2.06699929 | 1.23E-05 | MICB, MICA,   | 3848 | 287  | 13528 | 1.420936348 |
| 83  | 1.47897363 | 1.45E-05 | XRCC5, RTN4   | 3848 | 192  | 13528 | 1.519761348 |
| 105 | 1.87099073 | 1.59E-05 | GDF7, CNP, N  | 3848 | 256  | 13528 | 1.441942243 |
| 65  | 1.15823236 | 1.64E-05 | JPH4, JPH3, C | 3848 | 142  | 13528 | 1.609250095 |
| 76  | 1.35424091 | 1.77E-05 | INS-IGF2, GD  | 3848 | 173  | 13528 | 1.544422146 |
| 37  | 0.6593015  | 1.32E-05 | MTSS1, GRAF   | 3715 | 67   | 12983 | 1.929937125 |
| 222 | 3.95580898 | 2.16E-05 | A2M, MASP1    | 3848 | 615  | 13528 | 1.269043152 |
| 221 | 3.93799002 | 1.53E-05 | LTBP1, LTBP4  | 3715 | 606  | 12983 | 1.274488404 |
| 20  | 0.35637919 | 4.00E-05 | KCNMA1, SN    | 3661 | 29   | 12782 | 2.407859168 |
| 132 | 2.35210264 | 1.80E-05 | DLC1, RAB3G   | 3715 | 335  | 12983 | 1.377036219 |
| 164 | 2.92230934 | 2.49E-05 | DLC1, MTSS1   | 3848 | 436  | 13528 | 1.322378836 |
| 67  | 1.19387028 | 1.75E-05 | NELL1, PDLIM  | 3715 | 147  | 12983 | 1.592845698 |
| 37  | 0.6593015  | 2.70E-05 | XRCC5, XRCC   | 3848 | 69   | 13528 | 1.885172798 |
| 44  | 0.78403421 | 2.68E-05 | WNT5A, HOX    | 3848 | 87   | 13528 | 1.778000812 |
| 44  | 0.78403421 | 2.68E-05 | WNT5A, HOX    | 3848 | 87   | 13528 | 1.778000812 |
| 75  | 1.33642195 | 2.75E-05 | NDST1, LMO    | 3848 | 172  | 13528 | 1.532961853 |
| 194 | 3.45687812 | 2.96E-05 | A2M, MASP1    | 3848 | 530  | 13528 | 1.286839525 |
| 135 | 2.40555952 | 3.56E-05 | SEPT5, UTS2,  | 3848 | 350  | 13528 | 1.356014256 |
| 60  | 1.06913756 | 3.55E-05 | PCDHA6, PCI   | 3848 | 131  | 13528 | 1.610195045 |
| 74  | 1.31860299 | 6.78E-05 | DLC1, ENAH,   | 3661 | 172  | 12782 | 1.502112144 |
| 91  | 1.6215253  | 4.23E-05 | HRAS, PDLIM   | 3848 | 220  | 13528 | 1.454176904 |
| 91  | 1.6215253  | 4.23E-05 | HRAS, PDLIM   | 3848 | 220  | 13528 | 1.454176904 |
| 51  | 0.90876693 | 4.22E-05 | NRP2, NRP1,   | 3848 | 107  | 13528 | 1.675656246 |
| 48  | 0.85531005 | 4.31E-05 | WNT5A, HOX    | 3848 | 99   | 13528 | 1.704529705 |
| 48  | 0.85531005 | 4.31E-05 | WNT5A, HOX    | 3848 | 99   | 13528 | 1.704529705 |
| 296 | 5.27441197 | 4.67E-05 | DLC1, HRAS,   | 3848 | 857  | 13528 | 1.214253658 |



|     |            |          |               |      |     |       |             |
|-----|------------|----------|---------------|------|-----|-------|-------------|
| 72  | 1.28296507 | 4.99E-05 | XRCC5, RTN4   | 3848 | 166 | 13528 | 1.524835308 |
| 126 | 2.24518888 | 5.06E-05 | A2M, MASP1    | 3848 | 325 | 13528 | 1.362968175 |
| 41  | 0.73057733 | 5.18E-05 | HCRT, JPH4, I | 3848 | 81  | 13528 | 1.779497446 |
| 16  | 0.28510335 | 5.40E-05 | ACTN4, FSCN   | 3848 | 21  | 13528 | 2.678546679 |
| 98  | 1.74625802 | 5.62E-05 | MICB, MICA,   | 3848 | 242 | 13528 | 1.423669696 |
| 85  | 1.51461155 | 9.03E-05 | GABRB3, GLF   | 3661 | 205 | 12782 | 1.447651914 |
| 152 | 2.70848182 | 5.71E-05 | ADCY3, A2M,   | 3848 | 405 | 13528 | 1.319432253 |
| 78  | 1.38987883 | 6.01E-05 | NDST1, INS-1  | 3848 | 184 | 13528 | 1.490305523 |
| 61  | 1.08695652 | 6.41E-05 | SNCG, HRAS,   | 3848 | 136 | 13528 | 1.576846643 |
| 49  | 0.87312901 | 6.49E-05 | FGF9, GNA12   | 3848 | 103 | 13528 | 1.672466342 |
| 49  | 0.87312901 | 6.49E-05 | FGF9, GNA12   | 3848 | 103 | 13528 | 1.672466342 |
| 22  | 0.39201711 | 1.05E-04 | COL4A4, COL   | 3661 | 35  | 12782 | 2.194591642 |
| 62  | 1.10477548 | 6.75E-05 | EVX1, GDF7,   | 3848 | 139 | 13528 | 1.568106014 |
| 83  | 1.47897363 | 6.74E-05 | MICB, MICA,   | 3848 | 199 | 13528 | 1.466302406 |
| 97  | 1.72843906 | 6.72E-05 | ADCY3, ADCY   | 3848 | 240 | 13528 | 1.420885308 |
| 87  | 1.55024947 | 7.24E-05 | RTN4, NRP2,   | 3848 | 211 | 13528 | 1.449557104 |
| 91  | 1.6215253  | 7.64E-05 | SEPT5, MCHF   | 3848 | 223 | 13528 | 1.434613986 |
| 82  | 1.46115467 | 8.13E-05 | BMI1, CDX1,   | 3848 | 197 | 13528 | 1.463343078 |
| 221 | 3.93799002 | 8.77E-05 | CDX1, HRAS,   | 3848 | 624 | 13528 | 1.245105683 |
| 30  | 0.53456878 | 1.43E-04 | FXYD1, FXYD   | 3661 | 55  | 12782 | 1.904397706 |
| 31  | 0.55238774 | 1.01E-04 | NDST1, PRRX   | 3848 | 57  | 13528 | 1.911988912 |
| 50  | 0.89094797 | 6.16E-05 | A2M, LTBP1,   | 3715 | 105 | 12983 | 1.664167147 |
| 197 | 3.510335   | 5.93E-05 | RAB3GAP2, N   | 3715 | 542 | 12983 | 1.270232378 |
| 36  | 0.64148254 | 1.09E-04 | ITGAL, BCAR:  | 3848 | 70  | 13528 | 1.808019008 |
| 93  | 1.65716322 | 1.14E-04 | ADCY3, ADCY   | 3848 | 231 | 13528 | 1.415368415 |
| 109 | 1.94226657 | 7.76E-05 | KCNU1, SHKE   | 3715 | 275 | 12983 | 1.385192218 |
| 66  | 1.17605132 | 1.29E-04 | SNCG, HRAS,   | 3848 | 153 | 13528 | 1.516530105 |
| 153 | 2.72630078 | 1.29E-04 | HRAS, OSMR    | 3848 | 414 | 13528 | 1.299240712 |
| 89  | 1.58588738 | 1.32E-04 | DLC1, NRP1,   | 3848 | 220 | 13528 | 1.422216972 |
| 226 | 4.02708482 | 1.37E-04 | CDX1, HRAS,   | 3848 | 644 | 13528 | 1.233732777 |
| 86  | 1.53243051 | 8.89E-05 | RAB3GAP2, J   | 3715 | 208 | 12983 | 1.444945129 |
| 45  | 0.80185317 | 1.53E-04 | FGF9, USH1C   | 3848 | 95  | 13528 | 1.665280665 |
| 58  | 1.03349964 | 1.52E-04 | TM7SF4, LRR   | 3848 | 131 | 13528 | 1.556521877 |
| 37  | 0.6593015  | 9.94E-05 | FXYD1, FXYD   | 3715 | 72  | 12983 | 1.795913713 |
| 39  | 0.69493942 | 1.60E-04 | FGF9, USH1C   | 3848 | 79  | 13528 | 1.735545672 |
| 46  | 0.81967213 | 1.66E-04 | ERBB4, IL16,  | 3848 | 98  | 13528 | 1.650176079 |
| 76  | 1.35424091 | 1.65E-04 | ATP6V0E1, G   | 3848 | 183 | 13528 | 1.460027493 |
| 55  | 0.98004277 | 1.70E-04 | CASR, THRA,   | 3848 | 123 | 13528 | 1.572012913 |
| 66  | 1.17605132 | 2.50E-04 | DLC1, ENAH,   | 3661 | 155 | 12782 | 1.486658854 |
| 61  | 1.08695652 | 1.72E-04 | HNF1B, CDX1   | 3848 | 140 | 13528 | 1.531793882 |
| 159 | 2.83321454 | 1.75E-04 | DLC1, CADM    | 3848 | 435 | 13528 | 1.285009678 |
| 137 | 2.44119743 | 1.79E-04 | ADCY3, A2M,   | 3848 | 367 | 13528 | 1.312360149 |
| 181 | 3.22523165 | 1.79E-04 | JDP2, EIF2C2  | 3848 | 504 | 13528 | 1.262544138 |
| 52  | 0.92658589 | 1.88E-04 | CASR, THRA,   | 3848 | 115 | 13528 | 1.589659224 |
| 158 | 2.81539558 | 2.02E-04 | DLC1, CADM    | 3848 | 433 | 13528 | 1.282825906 |
| 39  | 0.69493942 | 1.31E-04 | FXYD1, FXYD   | 3715 | 78  | 12983 | 1.747375505 |

|     |            |          |               |      |      |       |             |
|-----|------------|----------|---------------|------|------|-------|-------------|
| 35  | 0.62366358 | 3.18E-04 | FGD2, SH3RF   | 3661 | 70   | 12782 | 1.745697897 |
| 46  | 0.81967213 | 2.22E-04 | HCRT, MCHR    | 3848 | 99   | 13528 | 1.633507634 |
| 82  | 1.46115467 | 3.32E-04 | DLC1, ATP1B   | 3661 | 203  | 12782 | 1.410317513 |
| 269 | 4.79330007 | 2.27E-04 | DLC1, HRAS,   | 3848 | 787  | 13528 | 1.20164471  |
| 89  | 1.58588738 | 2.29E-04 | ADCY3, ADCY   | 3848 | 223  | 13528 | 1.403084008 |
| 63  | 1.12259444 | 2.32E-04 | SNCG, HRAS,   | 3848 | 147  | 13528 | 1.506682507 |
| 214 | 3.81325731 | 2.35E-04 | DLC1, HRAS,   | 3848 | 611  | 13528 | 1.231320456 |
| 29  | 0.51674982 | 2.37E-04 | DLC1, FGD2,   | 3848 | 54   | 13528 | 1.888003388 |
| 211 | 3.75980043 | 2.50E-04 | DLC1, HRAS,   | 3848 | 602  | 13528 | 1.232209337 |
| 174 | 3.10049893 | 2.54E-04 | ADCY3, DLC1   | 3848 | 485  | 13528 | 1.261264119 |
| 174 | 3.10049893 | 2.54E-04 | ADCY3, DLC1   | 3848 | 485  | 13528 | 1.261264119 |
| 249 | 4.43692088 | 2.60E-04 | DLC1, HRAS,   | 3848 | 724  | 13528 | 1.209091901 |
| 198 | 3.52815396 | 2.60E-04 | EIF2C2, FOXF  | 3848 | 561  | 13528 | 1.240797358 |
| 248 | 4.41910192 | 2.65E-04 | ADCY3, EIF2C  | 3848 | 721  | 13528 | 1.209246801 |
| 360 | 6.41482537 | 3.81E-04 | RAB3GAP2, L   | 3661 | 1083 | 12782 | 1.160574779 |
| 41  | 0.73057733 | 2.69E-04 | SNCG, GRIK1   | 3848 | 86   | 13528 | 1.676038292 |
| 44  | 0.78403421 | 1.62E-04 | FXYD1, FXYD   | 3715 | 92   | 12983 | 1.671402657 |
| 75  | 1.33642195 | 1.61E-04 | NELL1, PDLIM  | 3715 | 179  | 12983 | 1.464281149 |
| 232 | 4.13399857 | 4.18E-04 | A2M, CADM1    | 3661 | 670  | 12782 | 1.208960931 |
| 63  | 1.12259444 | 2.90E-04 | NRP2, RTN4,   | 3848 | 148  | 13528 | 1.496502219 |
| 46  | 0.81967213 | 2.93E-04 | DLC1, CSF2, T | 3848 | 100  | 13528 | 1.617172557 |
| 46  | 0.81967213 | 2.93E-04 | DLC1, CSF2, T | 3848 | 100  | 13528 | 1.617172557 |
| 247 | 4.40128297 | 2.99E-04 | DLC1, HRAS,   | 3848 | 719  | 13528 | 1.207720934 |
| 26  | 0.46329294 | 3.03E-04 | KIT, CDH4, A  | 3848 | 47   | 13528 | 1.94479586  |
| 156 | 2.77975766 | 3.02E-04 | DLC1, CADM    | 3848 | 430  | 13528 | 1.275424261 |
| 58  | 1.03349964 | 4.74E-04 | GABRB3, GRI   | 3661 | 135  | 12782 | 1.500007082 |
| 70  | 1.24732716 | 5.06E-04 | GPR125, CSP   | 3661 | 170  | 12782 | 1.437633562 |
| 27  | 0.48111119 | 3.70E-04 | DRD2, INS-IG  | 3848 | 50   | 13528 | 1.898419958 |
| 32  | 0.5702067  | 3.80E-04 | NEURL, NRG1   | 3848 | 63   | 13528 | 1.785697786 |
| 84  | 1.49679259 | 3.83E-04 | FOXK1, TNNC   | 3848 | 211  | 13528 | 1.399572376 |
| 81  | 1.44333571 | 3.78E-04 | SEPT5, SNCG   | 3848 | 202  | 13528 | 1.409717791 |
| 164 | 2.92230934 | 2.21E-04 | CDIPT, TSPO,  | 3715 | 450  | 12983 | 1.27364259  |
| 90  | 1.60370634 | 3.87E-04 | FGF9, USH1C   | 3848 | 229  | 13528 | 1.381673914 |
| 256 | 4.5616536  | 3.90E-04 | SLC9A9, XRC   | 3848 | 751  | 13528 | 1.198391057 |
| 72  | 1.28296507 | 4.22E-04 | STEAP4, JPH4  | 3848 | 176  | 13528 | 1.438196938 |
| 157 | 2.79757662 | 4.27E-04 | XRCC5, TSPO   | 3848 | 436  | 13528 | 1.265935837 |
| 102 | 1.81753386 | 4.37E-04 | JDP2, MAEL,   | 3848 | 266  | 13528 | 1.348084348 |
| 17  | 0.30292231 | 4.36E-04 | RARG, DICER   | 3848 | 26   | 13528 | 2.298656645 |
| 96  | 1.7106201  | 4.50E-04 | SEPT5, SNCG   | 3848 | 248  | 13528 | 1.360874522 |
| 200 | 3.56379187 | 4.67E-04 | EIF2C2, FOXF  | 3848 | 573  | 13528 | 1.227082902 |
| 37  | 0.6593015  | 4.72E-04 | THRA, IRX5, T | 3848 | 77   | 13528 | 1.689310689 |
| 204 | 3.63506771 | 4.79E-04 | ADCY3, DLC1   | 3848 | 586  | 13528 | 1.223858145 |
| 34  | 0.60584462 | 4.82E-04 | HCRT, JPH4, I | 3848 | 69   | 13528 | 1.73232095  |
| 63  | 1.12259444 | 2.77E-04 | GABRB3, GLF   | 3715 | 147  | 12983 | 1.497750433 |
| 118 | 2.10263721 | 2.75E-04 | GRIK1, GABR   | 3715 | 310  | 12983 | 1.330260062 |
| 28  | 0.49893086 | 7.25E-04 | GABRB3, GRI   | 3661 | 54   | 12782 | 1.810353374 |

|     |            |          |               |      |     |       |             |
|-----|------------|----------|---------------|------|-----|-------|-------------|
| 47  | 0.83749109 | 5.28E-04 | ARHGDIG, HF   | 3848 | 105 | 13528 | 1.573646174 |
| 128 | 2.2808268  | 7.80E-04 | PVR, MICA, C  | 3661 | 348 | 12782 | 1.284191556 |
| 67  | 1.19387028 | 5.86E-04 | ELF3, CADM1   | 3848 | 163 | 13528 | 1.4450595   |
| 44  | 0.78403421 | 5.85E-04 | CSF2, TNF, G  | 3848 | 97  | 13528 | 1.59470176  |
| 58  | 1.03349964 | 6.12E-04 | STAT5A, JAG:  | 3848 | 137 | 13528 | 1.488353036 |
| 18  | 0.32074127 | 6.44E-04 | KCNMA1, DF    | 3848 | 29  | 13528 | 2.182091906 |
| 41  | 0.73057733 | 6.41E-04 | RTN4, NRP1,   | 3848 | 89  | 13528 | 1.61954262  |
| 41  | 0.73057733 | 6.41E-04 | CSF2, TNF, G  | 3848 | 89  | 13528 | 1.61954262  |
| 37  | 0.6593015  | 6.39E-04 | ALPL, A2M, T  | 3848 | 78  | 13528 | 1.66765286  |
| 37  | 0.6593015  | 6.39E-04 | PDLIM7, ENP   | 3848 | 78  | 13528 | 1.66765286  |
| 165 | 2.9401283  | 6.60E-04 | SLC9A9, ATP:  | 3848 | 465 | 13528 | 1.247468312 |
| 163 | 2.90449038 | 6.84E-04 | JDP2, THRA, ' | 3848 | 459 | 13528 | 1.248456601 |
| 34  | 0.60584462 | 3.88E-04 | PRKCZ, CDIP1  | 3715 | 68  | 12983 | 1.747375505 |
| 272 | 4.84675695 | 0.00102  | HRAS, CADM    | 3661 | 809 | 12782 | 1.173868549 |
| 123 | 2.191732   | 4.07E-04 | SNCA, KCNU:   | 3715 | 328 | 12983 | 1.310531629 |
| 21  | 0.37419815 | 0.00101  | KCNMA1, UC    | 3661 | 37  | 12782 | 1.981603018 |
| 132 | 2.35210264 | 7.16E-04 | JDP2, MAEL,   | 3848 | 362 | 13528 | 1.281928763 |
| 131 | 2.33428368 | 7.26E-04 | XRCC5, HRAS   | 3848 | 359 | 13528 | 1.282848522 |
| 130 | 2.31646472 | 7.37E-04 | JDP2, MAEL,   | 3848 | 356 | 13528 | 1.283783784 |
| 281 | 5.00712758 | 0.00109  | HRAS, CADM    | 3661 | 839 | 12782 | 1.169347101 |
| 165 | 2.9401283  | 7.37E-04 | ADCY3, ADCY   | 3848 | 466 | 13528 | 1.244791341 |
| 38  | 0.67712046 | 4.30E-04 | TRPV1, TRPV   | 3715 | 79  | 12983 | 1.681019473 |
| 44  | 0.78403421 | 7.59E-04 | DLC1, LIMS1,  | 3848 | 98  | 13528 | 1.578429293 |
| 79  | 1.40769779 | 4.52E-04 | INS-IGF2, GN  | 3715 | 196 | 12983 | 1.408598621 |
| 30  | 0.53456878 | 8.39E-04 | PRKCZ, TNF,   | 3848 | 60  | 13528 | 1.757796258 |
| 63  | 1.12259444 | 8.25E-04 | UTS2, TNNC1   | 3848 | 153 | 13528 | 1.447596918 |
| 46  | 0.81967213 | 8.32E-04 | ADAMTS14, I   | 3848 | 104 | 13528 | 1.554973613 |
| 131 | 2.33428368 | 8.23E-04 | XRCC5, HRAS   | 3848 | 360 | 13528 | 1.279285054 |
| 129 | 2.29864576 | 8.48E-04 | XRCC5, HRAS   | 3848 | 354 | 13528 | 1.281105747 |
| 13  | 0.23164647 | 8.39E-04 | RARG, DICER   | 3848 | 18  | 13528 | 2.539039039 |
| 66  | 1.17605132 | 0.00125  | ADCY2, CADM   | 3661 | 163 | 12782 | 1.413694002 |
| 68  | 1.21168924 | 8.69E-04 | UTS2, TACR2   | 3848 | 168 | 13528 | 1.422977923 |
| 44  | 0.78403421 | 5.12E-04 | MTSS1, ENAF   | 3715 | 96  | 12983 | 1.601760879 |
| 37  | 0.6593015  | 5.33E-04 | FXYP1, FXYP   | 3715 | 77  | 12983 | 1.67929594  |
| 8   | 0.14255167 | 9.01E-04 | ACTN4, PLCG   | 3848 | 8   | 13528 | 3.515592516 |
| 23  | 0.40983607 | 9.06E-04 | BMP4, SATB2   | 3848 | 42  | 13528 | 1.925205425 |
| 12  | 0.21382751 | 9.51E-04 | PRKCZ, CDC4   | 3848 | 16  | 13528 | 2.636694387 |
| 39  | 0.69493942 | 9.78E-04 | ALPL, A2M, T  | 3848 | 85  | 13528 | 1.613036566 |
| 39  | 0.69493942 | 9.78E-04 | ERBB4, TRPV   | 3848 | 85  | 13528 | 1.613036566 |
| 35  | 0.62366358 | 9.86E-04 | NRP1, DRD2,   | 3848 | 74  | 13528 | 1.662780244 |
| 118 | 2.10263721 | 9.94E-04 | DLC1, CADM    | 3848 | 321 | 13528 | 1.29233619  |
| 123 | 2.191732   | 0.00105  | DLC1, RAB3G   | 3848 | 337 | 13528 | 1.283139108 |
| 9   | 0.16037063 | 0.00107  | ACTN4, PLCG   | 3848 | 10  | 13528 | 3.164033264 |
| 78  | 1.38987883 | 6.44E-04 | KCNK17, KCN   | 3715 | 195 | 12983 | 1.397900404 |
| 78  | 1.38987883 | 6.44E-04 | KCNK17, KCN   | 3715 | 195 | 12983 | 1.397900404 |
| 10  | 0.17818959 | 0.0011   | SMO, RTN4R    | 3848 | 12  | 13528 | 2.92966043  |

|     |            |          |               |      |      |       |             |
|-----|------------|----------|---------------|------|------|-------|-------------|
| 507 | 9.0342124  | 6.76E-04 | XRCC5, KIFC1  | 3715 | 1577 | 12983 | 1.123550261 |
| 58  | 1.03349964 | 0.00115  | ARSB, MICB,   | 3848 | 140  | 13528 | 1.456459756 |
| 20  | 0.35637919 | 0.00114  | PHOX2A, LM    | 3848 | 35   | 13528 | 2.008910009 |
| 189 | 3.36778332 | 0.00117  | JDP2, EIF2C2  | 3848 | 547  | 13528 | 1.214711125 |
| 15  | 0.26728439 | 0.00117  | HCRT, GRIK1,  | 3848 | 23   | 13528 | 2.292777728 |
| 27  | 0.4811119  | 0.00116  | STEAP4, BBS   | 3848 | 53   | 13528 | 1.790962225 |
| 148 | 2.63720599 | 7.29E-04 | THRA, RBM4,   | 3715 | 410  | 12983 | 1.261519877 |
| 26  | 0.46329294 | 7.61E-04 | GRAP, GRB2,   | 3715 | 49   | 12983 | 1.854357678 |
| 44  | 0.78403421 | 0.00125  | PRKCZ, MICB   | 3848 | 100  | 13528 | 1.546860707 |
| 180 | 3.20741269 | 0.00127  | JDP2, THRA,   | 3848 | 519  | 13528 | 1.219280641 |
| 53  | 0.94440485 | 0.00129  | MICB, MICA,   | 3848 | 126  | 13528 | 1.478780979 |
| 117 | 2.08481825 | 0.0013   | DLC1, CADM    | 3848 | 320  | 13528 | 1.285388514 |
| 476 | 8.48182466 | 8.08E-04 | XRCC5, KIFC1  | 3715 | 1477 | 12983 | 1.126270467 |
| 513 | 9.14112616 | 8.48E-04 | XRCC5, KIFC1  | 3715 | 1601 | 12983 | 1.119804664 |
| 17  | 0.30292231 | 8.46E-04 | A2M, CXCR1,   | 3715 | 27   | 12983 | 2.200398784 |
| 40  | 0.71275837 | 0.00135  | ERBB4, INS-IG | 3848 | 89   | 13528 | 1.58004158  |
| 23  | 0.40983607 | 0.00136  | HCRT, PRKCZ   | 3848 | 43   | 13528 | 1.880433206 |
| 17  | 0.30292231 | 0.00136  | ACTC1, BMP2,  | 3848 | 28   | 13528 | 2.134466884 |
| 17  | 0.30292231 | 0.00136  | PRKCZ, CCDC   | 3848 | 28   | 13528 | 2.134466884 |
| 180 | 3.20741269 | 9.27E-04 | HMGN3, THF    | 3715 | 513  | 12983 | 1.226228424 |
| 47  | 0.83749109 | 0.00138  | SH3RF1, TNF   | 3848 | 109  | 13528 | 1.51589769  |
| 47  | 0.83749109 | 0.00138  | SEPT5, TNF, C | 3848 | 109  | 13528 | 1.51589769  |
| 122 | 2.17391304 | 9.19E-04 | DLC1, MTSS1   | 3715 | 331  | 12983 | 1.288095538 |
| 45  | 0.80185317 | 9.09E-04 | FGD2, DIAPH   | 3715 | 101  | 12983 | 1.557067281 |
| 19  | 0.33856023 | 0.00143  | JPH4, JPH3, C | 3848 | 33   | 13528 | 2.024129024 |
| 481 | 8.57091946 | 9.83E-04 | XRCC5, KIFC1  | 3715 | 1497 | 12983 | 1.122895949 |
| 16  | 0.28510335 | 0.00103  | CXCR1, CXCR   | 3715 | 25   | 12983 | 2.236640646 |
| 190 | 3.38560228 | 0.00153  | SLC9A9, ATP   | 3848 | 553  | 13528 | 1.207888929 |
| 43  | 0.76621525 | 0.00153  | ERBB4, INS-IG | 3848 | 98   | 13528 | 1.5425559   |
| 24  | 0.42765502 | 0.00159  | PRKCZ, NF2,   | 3848 | 46   | 13528 | 1.834222182 |
| 53  | 0.94440485 | 0.00159  | DLC1, NRP1,   | 3848 | 127  | 13528 | 1.467137034 |
| 177 | 3.15395581 | 0.00164  | JDP2, THRA,   | 3848 | 512  | 13528 | 1.215351319 |
| 27  | 0.4811119  | 0.00164  | SNCG, DRD2,   | 3848 | 54   | 13528 | 1.757796258 |
| 55  | 0.98004277 | 0.00164  | ADCY3, ADCY   | 3848 | 133  | 13528 | 1.453816454 |
| 13  | 0.23164647 | 0.00169  | HCRT, GRIK1,  | 3848 | 19   | 13528 | 2.405405405 |
| 22  | 0.39201711 | 0.00171  | EGFR, B4GAL   | 3848 | 41   | 13528 | 1.886415496 |
| 54  | 0.96222381 | 0.00123  | KCNK17, KCN   | 3715 | 128  | 12983 | 1.474348082 |
| 28  | 0.49893086 | 0.00183  | RTN4, NRP1,   | 3848 | 57   | 13528 | 1.726957727 |
| 514 | 9.15894512 | 0.00135  | XRCC5, KIFC1  | 3715 | 1612 | 12983 | 1.114331277 |
| 52  | 0.92658589 | 0.00192  | TNNC1, UTRN   | 3848 | 125  | 13528 | 1.462486486 |
| 58  | 1.03349964 | 0.00133  | ADCY3, ADCY   | 3715 | 140  | 12983 | 1.447825418 |
| 29  | 0.51674982 | 0.002    | DLC1, HNF1B   | 3848 | 60   | 13528 | 1.699203049 |
| 23  | 0.40983607 | 0.002    | ARFGAP1, CY   | 3848 | 44   | 13528 | 1.837696088 |

| Count | %          | PValue   | Genes         | List Total | Pop Hits | Pop Total | Fold Enrichment |
|-------|------------|----------|---------------|------------|----------|-----------|-----------------|
| 116   | 4.39393939 | 8.93E-15 | ALS2, DLC1, F | 1813       | 404      | 12983     | 2.056145659     |
| 117   | 4.43181818 | 1.92E-14 | ALS2, DLC1, F | 1813       | 413      | 12983     | 2.028677736     |
| 411   | 15.5681818 | 3.40E-13 | DLC1, STRN, F | 1745       | 2203     | 12782     | 1.3665663       |
| 263   | 9.96212121 | 7.83E-14 | ADCY3, ADCY   | 1845       | 1256     | 13528     | 1.535335646     |
| 640   | 24.2424242 | 4.04E-12 | DLC1, FHIT, S | 1745       | 3777     | 12782     | 1.241184579     |
| 163   | 6.17424242 | 1.77E-12 | DLC1, MTSS1   | 1845       | 700      | 13528     | 1.707366628     |
| 92    | 3.48484848 | 1.41E-12 | CASR, NDST1   | 1845       | 319      | 13528     | 2.114629899     |
| 164   | 6.21212121 | 9.81E-13 | DLC1, MTSS1   | 1845       | 701      | 13528     | 1.715390712     |
| 77    | 2.91666667 | 5.17E-12 | DLC1, ALS2, F | 1845       | 252      | 13528     | 2.240409515     |
| 149   | 5.64393939 | 9.78E-11 | THRB, GDF6,   | 1845       | 654      | 13528     | 1.67049717      |
| 68    | 2.57575758 | 1.64E-10 | DLC1, RAB3G   | 1813       | 220      | 12983     | 2.213418242     |
| 126   | 4.77272727 | 3.51E-10 | ALS2, A2M, S  | 1813       | 523      | 12983     | 1.725226456     |
| 154   | 5.83333333 | 3.95E-10 | THRB, GDF6,   | 1845       | 695      | 13528     | 1.62469985      |
| 74    | 2.8030303  | 5.22E-10 | XRCC4, TM7S   | 1845       | 260      | 13528     | 2.086870961     |
| 152   | 5.75757576 | 4.68E-10 | THRB, GDF6,   | 1845       | 685      | 13528     | 1.627010069     |
| 69    | 2.61363636 | 6.14E-10 | XRCC4, TM7S   | 1845       | 236      | 13528     | 2.143750861     |
| 148   | 5.60606061 | 8.29E-10 | GDF6, STAT5   | 1845       | 667      | 13528     | 1.626945877     |
| 114   | 4.31818182 | 1.14E-09 | THRB, STAT5   | 1845       | 477      | 13528     | 1.752361473     |
| 193   | 7.31060606 | 1.53E-09 | S100A4, S100  | 1813       | 919      | 12983     | 1.503900316     |
| 76    | 2.87878788 | 1.53E-09 | XRCC4, TM7S   | 1845       | 276      | 13528     | 2.019025176     |
| 114   | 4.31818182 | 1.92E-09 | THRB, STAT5   | 1845       | 481      | 13528     | 1.737788821     |
| 88    | 3.33333333 | 2.71E-09 | MTSS1, NRP1   | 1845       | 342      | 13528     | 1.886660644     |
| 81    | 3.06818182 | 3.65E-09 | DLC1, NDST1   | 1845       | 307      | 13528     | 1.934567411     |
| 177   | 6.70454545 | 5.31E-09 | DLC1, THRB,   | 1845       | 857      | 13528     | 1.514361879     |
| 130   | 4.92424242 | 5.87E-09 | THRB, GDF6,   | 1845       | 581      | 13528     | 1.640606561     |
| 68    | 2.57575758 | 7.22E-09 | ALS2, S100A4  | 1845       | 244      | 13528     | 2.043413746     |
| 137   | 5.18939394 | 7.70E-09 | THRB, GDF6,   | 1845       | 624      | 13528     | 1.609804739     |
| 103   | 3.90151515 | 1.01E-08 | DLC1, CADM    | 1845       | 433      | 13528     | 1.744160924     |
| 167   | 6.32575758 | 1.01E-08 | DLC1, XRCC4   | 1845       | 804      | 13528     | 1.522992086     |
| 126   | 4.77272727 | 1.14E-08 | THRB, GDF6,   | 1845       | 564      | 13528     | 1.6380557       |
| 103   | 3.90151515 | 1.31E-08 | DLC1, CADM    | 1845       | 435      | 13528     | 1.736141794     |
| 102   | 3.86363636 | 1.41E-08 | DLC1, CADM    | 1845       | 430      | 13528     | 1.739277746     |
| 91    | 3.4469697  | 1.52E-08 | NDST1, INS-1  | 1845       | 370      | 13528     | 1.803336996     |
| 139   | 5.26515152 | 1.82E-08 | THRB, GDF6,   | 1845       | 644      | 13528     | 1.582581764     |
| 163   | 6.17424242 | 1.95E-08 | DLC1, XRCC4   | 1845       | 787      | 13528     | 1.51862343      |
| 88    | 3.33333333 | 2.10E-08 | ALS2, S100A4  | 1845       | 356      | 13528     | 1.812466125     |
| 167   | 6.32575758 | 2.07E-08 | DLC1, XRCC4   | 1845       | 812      | 13528     | 1.507987238     |
| 86    | 3.25757576 | 1.42E-08 | DLC1, ALS2, F | 1813       | 335      | 12983     | 1.83836142      |
| 74    | 2.8030303  | 1.73E-08 | DLC1, ALS2, F | 1813       | 274      | 12983     | 1.93400864      |
| 167   | 6.32575758 | 2.76E-08 | DLC1, XRCC4   | 1845       | 815      | 13528     | 1.502436364     |
| 90    | 3.40909091 | 3.67E-08 | ELF1, EVX1, T | 1845       | 371      | 13528     | 1.778712774     |
| 116   | 4.39393939 | 3.00E-08 | MTSS1, UTRN   | 1813       | 504      | 12983     | 1.64818025      |
| 66    | 2.5        | 5.10E-08 | NRP1, LMO2,   | 1845       | 245      | 13528     | 1.975218185     |
| 59    | 2.23484848 | 5.86E-08 | DLC1, ALS2, F | 1845       | 210      | 13528     | 2.060012905     |

|     |            |          |               |      |      |       |             |
|-----|------------|----------|---------------|------|------|-------|-------------|
| 48  | 1.81818182 | 5.19E-08 | ALS2, RALGP   | 1813 | 152  | 12983 | 2.261387058 |
| 85  | 3.21969697 | 4.48E-08 | CTHRC1, LTB   | 1745 | 345  | 12782 | 1.804692496 |
| 82  | 3.10606061 | 8.29E-08 | MTSS1, TLN1   | 1813 | 326  | 12983 | 1.801247974 |
| 38  | 1.43939394 | 1.15E-07 | NDST1, TIPAI  | 1845 | 112  | 13528 | 2.487727449 |
| 66  | 2.5        | 1.36E-07 | NRP1, LMO2,   | 1845 | 251  | 13528 | 1.928001814 |
| 92  | 3.48484848 | 2.43E-07 | ALS2, S100A4  | 1845 | 397  | 13528 | 1.699161052 |
| 115 | 4.35606061 | 2.69E-07 | A2M, MASP1    | 1845 | 530  | 13528 | 1.590959759 |
| 70  | 2.65151515 | 3.26E-07 | XRCC4, THRB   | 1845 | 278  | 13528 | 1.846249829 |
| 58  | 2.1969697  | 3.44E-07 | DLC1, NRP1,   | 1845 | 215  | 13528 | 1.978002143 |
| 41  | 1.5530303  | 3.91E-07 | CSF2, GPR18   | 1845 | 131  | 13528 | 2.294826124 |
| 34  | 1.28787879 | 4.35E-07 | DLC1, ALS2, F | 1845 | 99   | 13528 | 2.518146232 |
| 159 | 6.02272727 | 4.69E-07 | GDF6, STAT5   | 1845 | 800  | 13528 | 1.457284553 |
| 60  | 2.27272727 | 6.14E-07 | XRCC4, THRB   | 1845 | 229  | 13528 | 1.92111336  |
| 41  | 1.5530303  | 6.07E-07 | NDST1, PRRX   | 1845 | 133  | 13528 | 2.26031746  |
| 56  | 2.12121212 | 7.10E-07 | ALS2, NRP1, C | 1845 | 209  | 13528 | 1.964621828 |
| 79  | 2.99242424 | 8.07E-07 | DLC1, ALS2, D | 1845 | 334  | 13528 | 1.73427454  |
| 35  | 1.32575758 | 1.10E-06 | A2M, LTBP1,   | 1813 | 105  | 12983 | 2.387019673 |
| 52  | 1.96969697 | 1.56E-06 | ALS2, NRP1, C | 1845 | 193  | 13528 | 1.975528315 |
| 84  | 3.18181818 | 1.64E-06 | ALS2, MTSS1   | 1845 | 368  | 13528 | 1.673665606 |
| 37  | 1.40151515 | 1.22E-06 | AMTN, DAG1    | 1745 | 117  | 12782 | 2.316430338 |
| 31  | 1.17424242 | 1.38E-06 | ALS2, PREX1,  | 1813 | 88   | 12983 | 2.522645791 |
| 76  | 2.87878788 | 1.15E-06 | CTHRC1, LTB   | 1745 | 320  | 12782 | 1.739670487 |
| 144 | 5.45454545 | 2.15E-06 | THRB, STAT5   | 1845 | 727  | 13528 | 1.45232999  |
| 77  | 2.91666667 | 2.21E-06 | DLC1, ALS2, D | 1845 | 331  | 13528 | 1.705689419 |
| 75  | 2.84090909 | 2.56E-06 | DLC1, CADM    | 1845 | 321  | 13528 | 1.713142365 |
| 183 | 6.93181818 | 2.65E-06 | GDF6, STAT5   | 1845 | 973  | 13528 | 1.379035587 |
| 183 | 6.93181818 | 2.65E-06 | GDF6, STAT5   | 1845 | 973  | 13528 | 1.379035587 |
| 91  | 3.4469697  | 3.11E-06 | XRCC4, NRP1   | 1845 | 414  | 13528 | 1.611677991 |
| 47  | 1.78030303 | 3.52E-06 | NDST1, LMO2   | 1845 | 172  | 13528 | 2.003579757 |
| 51  | 1.93181818 | 3.65E-06 | DLC1, NRP1,   | 1845 | 193  | 13528 | 1.937537386 |
| 101 | 3.82575758 | 4.03E-06 | MTSS1, CTHRC  | 1845 | 475  | 13528 | 1.559067751 |
| 74  | 2.8030303  | 4.47E-06 | DLC1, CADM    | 1845 | 320  | 13528 | 1.695582656 |
| 56  | 2.12121212 | 4.58E-06 | DLC1, ELF1, F | 1845 | 221  | 13528 | 1.85794553  |
| 180 | 6.81818182 | 3.91E-06 | CTHRC1, A2M   | 1745 | 960  | 12782 | 1.373424069 |
| 102 | 3.86363636 | 5.86E-06 | ADCY3, DLC1   | 1845 | 485  | 13528 | 1.542040064 |
| 102 | 3.86363636 | 5.86E-06 | ADCY3, DLC1   | 1845 | 485  | 13528 | 1.542040064 |
| 125 | 4.73484848 | 4.26E-06 | LTBP1, EFNA2  | 1813 | 606  | 12983 | 1.477116134 |
| 54  | 2.04545455 | 6.81E-06 | ALS2, NRP1, C | 1845 | 213  | 13528 | 1.85888011  |
| 20  | 0.75757576 | 7.29E-06 | TPST2, LYN, F | 1845 | 48   | 13528 | 3.055103884 |
| 137 | 5.18939394 | 5.98E-06 | ALS2, S100A4  | 1745 | 697  | 12782 | 1.439763538 |
| 26  | 0.98484848 | 8.11E-06 | PTH1R, PRRX   | 1845 | 74   | 13528 | 2.576195708 |
| 218 | 8.25757576 | 8.01E-06 | ADCY3, ATP1   | 1745 | 1215 | 12782 | 1.314266983 |
| 80  | 3.03030303 | 9.56E-06 | DLC1, DLEC1,  | 1845 | 361  | 13528 | 1.624875196 |
| 56  | 2.12121212 | 9.32E-06 | DLC1, MTSS1   | 1845 | 226  | 13528 | 1.81684054  |
| 60  | 2.27272727 | 9.48E-06 | DLC1, ELF1, C | 1845 | 248  | 13528 | 1.773931288 |
| 32  | 1.21212121 | 1.07E-05 | HOXA13, GN    | 1845 | 103  | 13528 | 2.277980372 |

|     |            |          |               |      |      |       |             |
|-----|------------|----------|---------------|------|------|-------|-------------|
| 32  | 1.21212121 | 1.07E-05 | HOXA13, GN    | 1845 | 103  | 13528 | 2.277980372 |
| 213 | 8.06818182 | 1.11E-05 | ADCY3, ATP1   | 1745 | 1188 | 12782 | 1.313307864 |
| 31  | 1.17424242 | 1.27E-05 | HOXA13, GN    | 1845 | 99   | 13528 | 2.295956859 |
| 31  | 1.17424242 | 1.27E-05 | HOXA13, GN    | 1845 | 99   | 13528 | 2.295956859 |
| 55  | 2.08333333 | 1.50E-05 | MTSS1, NRP1   | 1845 | 224  | 13528 | 1.800329075 |
| 19  | 0.71969697 | 1.53E-05 | LYN, ERBB3, I | 1845 | 46   | 13528 | 3.028537764 |
| 49  | 1.85606061 | 1.59E-05 | DLC1, IL16, I | 1845 | 192  | 13528 | 1.871251129 |
| 34  | 1.28787879 | 1.71E-05 | CASR, INS-IG  | 1845 | 115  | 13528 | 2.167795452 |
| 26  | 0.98484848 | 1.78E-05 | NDST1, PRRX   | 1845 | 77   | 13528 | 2.475824447 |
| 64  | 2.42424242 | 1.94E-05 | CADM1, CLS1   | 1845 | 276  | 13528 | 1.700231727 |
| 28  | 1.06060606 | 2.11E-05 | HOXA13, GN    | 1845 | 87   | 13528 | 2.35980438  |
| 28  | 1.06060606 | 2.11E-05 | HOXA13, GN    | 1845 | 87   | 13528 | 2.35980438  |
| 45  | 1.70454545 | 2.25E-05 | CSF2, PRKCZ,  | 1845 | 173  | 13528 | 1.907232483 |
| 52  | 1.96969697 | 2.37E-05 | NRP1, IL18, L | 1845 | 211  | 13528 | 1.806999833 |
| 60  | 2.27272727 | 2.61E-05 | ALS2, NRP1, I | 1845 | 256  | 13528 | 1.718495935 |
| 96  | 3.63636364 | 2.68E-05 | ADCY3, ALS2,  | 1845 | 466  | 13528 | 1.510506298 |
| 58  | 2.1969697  | 2.67E-05 | ALS2, NRP1, I | 1845 | 245  | 13528 | 1.735797799 |
| 31  | 1.17424242 | 2.97E-05 | GPR183, XRC   | 1845 | 103  | 13528 | 2.206793485 |
| 35  | 1.32575758 | 3.03E-05 | CASR, INS-IG  | 1845 | 123  | 13528 | 2.086412409 |
| 57  | 2.15909091 | 3.25E-05 | DLC1, MTSS1   | 1845 | 241  | 13528 | 1.73418345  |
| 31  | 1.17424242 | 3.64E-05 | ELF3, ELN, CC | 1845 | 104  | 13528 | 2.185574317 |
| 63  | 2.38636364 | 3.75E-05 | CTHRC1, NRF   | 1845 | 276  | 13528 | 1.673665606 |
| 137 | 5.18939394 | 4.16E-05 | ALS2, DLC1, T | 1845 | 724  | 13528 | 1.387456018 |
| 136 | 5.15151515 | 4.55E-05 | ALS2, DLC1, T | 1845 | 719  | 13528 | 1.386906687 |
| 104 | 3.93939394 | 3.67E-05 | DLC1, GABRE   | 1745 | 518  | 12782 | 1.470641989 |
| 15  | 0.56818182 | 4.68E-05 | PRKCA, PRKC   | 1845 | 33   | 13528 | 3.332840601 |
| 36  | 1.36363636 | 5.08E-05 | CADM1, CLS1   | 1845 | 131  | 13528 | 2.014969279 |
| 71  | 2.68939394 | 5.18E-05 | A2M, ELF3, M  | 1845 | 325  | 13528 | 1.601814467 |
| 30  | 1.13636364 | 5.36E-05 | A2M, TNF, C   | 1845 | 101  | 13528 | 2.177895838 |
| 30  | 1.13636364 | 2.94E-05 | MTSS1, BCAF   | 1813 | 96   | 12983 | 2.237830943 |
| 15  | 0.56818182 | 6.96E-05 | PRKCA, PRKC   | 1845 | 34   | 13528 | 3.234815878 |
| 25  | 0.9469697  | 3.93E-05 | ALS2, PREX1,  | 1813 | 74   | 12983 | 2.419276695 |
| 25  | 0.9469697  | 7.03E-05 | AMTN, DAG1    | 1745 | 78   | 12782 | 2.347733451 |
| 32  | 1.21212121 | 9.35E-05 | GCLC, LMO2,   | 1845 | 114  | 13528 | 2.058175248 |
| 60  | 2.27272727 | 9.34E-05 | NRP1, EVX1,   | 1845 | 267  | 13528 | 1.647696477 |
| 47  | 1.78030303 | 9.55E-05 | NRP1, INS-IG  | 1845 | 194  | 13528 | 1.776369681 |
| 58  | 2.1969697  | 9.81E-05 | ALS2, NRP1, I | 1845 | 256  | 13528 | 1.661212737 |
| 15  | 0.56818182 | 1.02E-04 | COL18A1, CC   | 1745 | 35   | 12782 | 3.139255014 |
| 75  | 2.84090909 | 9.91E-05 | ALS2, SEPT5,  | 1745 | 355  | 12782 | 1.547520077 |
| 20  | 0.75757576 | 1.19E-04 | SATB2, NDST   | 1845 | 57   | 13528 | 2.572719061 |
| 63  | 2.38636364 | 1.24E-04 | XRCC4, TOLL   | 1845 | 287  | 13528 | 1.609518144 |
| 48  | 1.81818182 | 1.31E-04 | SEPT5, SNCA   | 1845 | 202  | 13528 | 1.742316671 |
| 23  | 0.87121212 | 6.60E-05 | FGFR2, FGFR   | 1813 | 67   | 12983 | 2.458273991 |
| 14  | 0.53030303 | 1.49E-04 | SATB2, ARID   | 1845 | 32   | 13528 | 3.207859079 |
| 51  | 1.93181818 | 1.51E-04 | DLC1, NRP1,   | 1845 | 220  | 13528 | 1.699748707 |
| 66  | 2.5        | 1.60E-04 | CTHRC1, NRF   | 1845 | 307  | 13528 | 1.576314187 |

|     |            |          |               |      |     |       |             |
|-----|------------|----------|---------------|------|-----|-------|-------------|
| 66  | 2.5        | 1.60E-04 | CTHRC1, NRF   | 1845 | 307 | 13528 | 1.576314187 |
| 31  | 1.17424242 | 1.62E-04 | BID, TNF, PRI | 1845 | 112 | 13528 | 2.029461866 |
| 17  | 0.64393939 | 1.72E-04 | PRKCA, PTPR   | 1845 | 45  | 13528 | 2.769960855 |
| 19  | 0.71969697 | 1.78E-04 | BGLAP, BMP2   | 1845 | 54  | 13528 | 2.579865502 |
| 11  | 0.41666667 | 1.81E-04 | FSCN2, SORB   | 1845 | 21  | 13528 | 3.840702026 |
| 114 | 4.31818182 | 1.90E-04 | DLC1, TSPO, I | 1845 | 602 | 13528 | 1.388499041 |
| 71  | 2.68939394 | 2.01E-04 | ALS2, NRP1, I | 1845 | 339 | 13528 | 1.535662837 |
| 109 | 4.12878788 | 2.23E-04 | THRB, RBM9,   | 1845 | 573 | 13528 | 1.394790883 |
| 115 | 4.35606061 | 2.29E-04 | DLC1, TSPO, I | 1845 | 611 | 13528 | 1.380046926 |
| 10  | 0.37878788 | 2.42E-04 | NOTCH1, RAI   | 1845 | 18  | 13528 | 4.073471846 |
| 59  | 2.23484848 | 2.17E-04 | MTSS1, FERM   | 1745 | 269 | 12782 | 1.606582802 |
| 16  | 0.60606061 | 2.58E-04 | SATB2, BMP2   | 1845 | 42  | 13528 | 2.793237837 |
| 54  | 2.04545455 | 2.62E-04 | XRCC4, TOLL   | 1845 | 242 | 13528 | 1.63612175  |
| 40  | 1.51515152 | 2.58E-04 | ALS2, CADM1   | 1845 | 163 | 13528 | 1.799324987 |
| 41  | 1.5530303  | 2.75E-04 | DLC1, INS-IGF | 1845 | 169 | 13528 | 1.778829717 |
| 28  | 1.06060606 | 2.93E-04 | DLC1, CSF2, T | 1845 | 100 | 13528 | 2.05302981  |
| 28  | 1.06060606 | 2.93E-04 | DLC1, CSF2, T | 1845 | 100 | 13528 | 2.05302981  |
| 11  | 0.41666667 | 2.92E-04 | MYO16, PML    | 1845 | 22  | 13528 | 3.666124661 |
| 35  | 1.32575758 | 3.03E-04 | PRKCZ, TNF, I | 1845 | 137 | 13528 | 1.873202382 |
| 13  | 0.49242424 | 3.17E-04 | IRS2, INS-IGF | 1845 | 30  | 13528 | 3.17730804  |
| 42  | 1.59090909 | 1.45E-04 | FGFR2, FGFR   | 1813 | 166 | 12983 | 1.811834209 |
| 86  | 3.25757576 | 3.38E-04 | DLC1, MTSS1   | 1845 | 436 | 13528 | 1.446269362 |
| 88  | 3.33333333 | 1.74E-04 | CDK18, LTBP   | 1813 | 430 | 12983 | 1.465519055 |
| 10  | 0.37878788 | 1.66E-04 | SMAD7, SMA    | 1813 | 17  | 12983 | 4.212387658 |
| 8   | 0.3030303  | 3.65E-04 | BMP2, SMAD    | 1845 | 12  | 13528 | 4.888166215 |
| 7   | 0.26515152 | 3.69E-04 | MYO16, BCL6   | 1845 | 9   | 13528 | 5.702860584 |
| 53  | 2.00757576 | 3.91E-04 | ADCY3, ALS2   | 1845 | 240 | 13528 | 1.619205059 |
| 43  | 1.62878788 | 3.96E-04 | FGFR2, FGFR   | 1845 | 183 | 13528 | 1.722878256 |
| 17  | 0.64393939 | 4.02E-04 | PRKCA, PTPR   | 1845 | 48  | 13528 | 2.596838302 |
| 17  | 0.64393939 | 4.02E-04 | PRKCA, PTPR   | 1845 | 48  | 13528 | 2.596838302 |
| 27  | 1.02272727 | 4.25E-04 | CSF2, TNF, IN | 1845 | 97  | 13528 | 2.040935378 |
| 34  | 1.28787879 | 4.29E-04 | TNF, EVX1, IN | 1845 | 134 | 13528 | 1.86042147  |
| 89  | 3.37121212 | 4.72E-04 | THRB, FOXK1   | 1845 | 459 | 13528 | 1.421721546 |
| 123 | 4.65909091 | 3.88E-04 | SEPT5, MTSS   | 1745 | 670 | 12782 | 1.344725655 |
| 28  | 1.06060606 | 4.89E-04 | LTBP2, LTBP3  | 1845 | 103 | 13528 | 1.993232826 |
| 103 | 3.90151515 | 4.88E-04 | THRB, RBM9,   | 1845 | 547 | 13528 | 1.380661207 |
| 70  | 2.65151515 | 4.53E-04 | ALS2, S100A4  | 1745 | 342 | 12782 | 1.499254344 |
| 84  | 3.18181818 | 2.39E-04 | ELF1, ELF3, F | 1813 | 410 | 12983 | 1.467143799 |
| 27  | 1.02272727 | 5.05E-04 | IL16, INS-IGF | 1845 | 98  | 13528 | 2.020109507 |
| 20  | 0.75757576 | 5.09E-04 | B4GALT1, IRS  | 1845 | 63  | 13528 | 2.327698198 |
| 96  | 3.63636364 | 5.19E-04 | THRB, FOXK1   | 1845 | 504 | 13528 | 1.396618919 |
| 22  | 0.83333333 | 2.54E-04 | PRKCA, PRKC   | 1813 | 68  | 12983 | 2.316813212 |
| 149 | 5.64393939 | 4.36E-04 | ALS2, SEPT5,  | 1745 | 839 | 12782 | 1.300851402 |
| 26  | 0.98484848 | 5.19E-04 | CSF2, TM7SF   | 1845 | 93  | 13528 | 2.049876155 |
| 105 | 3.97727273 | 5.37E-04 | THRB, RBM9,   | 1845 | 561 | 13528 | 1.37234613  |
| 85  | 3.21969697 | 6.23E-04 | ALS2, NRP1,   | 1845 | 438 | 13528 | 1.422925097 |



|     |            |          |               |      |      |       |             |
|-----|------------|----------|---------------|------|------|-------|-------------|
| 25  | 0.9469697  | 6.33E-04 | CSF2, TNF, IN | 1845 | 89   | 13528 | 2.059620596 |
| 40  | 1.51515152 | 6.41E-04 | PARD3, TNF,   | 1745 | 170  | 12782 | 1.723512557 |
| 12  | 0.45454545 | 6.75E-04 | BMP2, MYOC    | 1845 | 28   | 13528 | 3.142392567 |
| 69  | 2.61363636 | 6.81E-04 | NRP1, INS-IG  | 1845 | 341  | 13528 | 1.483651622 |
| 185 | 7.00757576 | 6.24E-04 | ALS2, SEPT5,  | 1745 | 1083 | 12782 | 1.251257385 |
| 105 | 3.97727273 | 3.48E-04 | ALS2, RAB3G   | 1813 | 542  | 12983 | 1.387290031 |
| 26  | 0.98484848 | 7.31E-04 | PRRX1, SOBP   | 1845 | 95   | 13528 | 2.006720867 |
| 43  | 1.62878788 | 3.97E-04 | PRKCZ, BCAR   | 1813 | 179  | 12983 | 1.720254401 |
| 100 | 3.78787879 | 3.89E-04 | THRB, ARNT2   | 1813 | 513  | 12983 | 1.395917937 |
| 46  | 1.74242424 | 7.79E-04 | FGFR2, FGFR   | 1845 | 206  | 13528 | 1.637298392 |
| 21  | 0.79545455 | 7.93E-04 | ZBTB7A, BGL   | 1845 | 70   | 13528 | 2.199674797 |
| 16  | 0.60606061 | 7.87E-04 | PRKCZ, NF1,   | 1845 | 46   | 13528 | 2.55034759  |
| 16  | 0.60606061 | 7.87E-04 | BCL10, NOX5   | 1845 | 46   | 13528 | 2.55034759  |
| 57  | 2.15909091 | 8.18E-04 | ALS2, NRP1,   | 1845 | 271  | 13528 | 1.542207422 |
| 89  | 3.37121212 | 5.26E-04 | TSPO, PLEKH   | 1813 | 450  | 12983 | 1.416298339 |
| 69  | 2.61363636 | 5.56E-04 | DLC1, MTSS1   | 1813 | 331  | 12983 | 1.492788738 |
| 25  | 0.9469697  | 5.20E-04 | ELN, ENAM, C  | 1813 | 86   | 12983 | 2.081703203 |
| 50  | 1.89393939 | 9.31E-04 | ADCY3, ALS2,  | 1845 | 231  | 13528 | 1.587066953 |
| 22  | 0.83333333 | 9.58E-04 | XRCC4, KLF6,  | 1845 | 76   | 13528 | 2.122493225 |
| 112 | 4.24242424 | 9.65E-04 | ALS2, A2M, M  | 1845 | 615  | 13528 | 1.335303942 |
| 89  | 3.37121212 | 9.54E-04 | ALS2, CASR, I | 1845 | 469  | 13528 | 1.391407654 |
| 34  | 1.28787879 | 9.76E-04 | ALPL, KYNU,   | 1845 | 140  | 13528 | 1.780689121 |
| 26  | 0.98484848 | 5.19E-04 | DLC1, PREX1,  | 1813 | 91   | 12983 | 2.046016862 |
| 48  | 1.81818182 | 9.99E-04 | STON2, SORL   | 1845 | 220  | 13528 | 1.599763489 |
| 48  | 1.81818182 | 9.99E-04 | STON2, SORL   | 1845 | 220  | 13528 | 1.599763489 |
| 57  | 2.15909091 | 0.00107  | ALS2, IL16, H | 1845 | 274  | 13528 | 1.525321939 |
| 26  | 0.98484848 | 7.38E-04 | ALS2, CDK5R   | 1813 | 93   | 12983 | 2.0020165   |
| 14  | 0.53030303 | 7.33E-04 | BCL10, SLC22  | 1813 | 36   | 12983 | 2.784856285 |
| 69  | 2.61363636 | 7.19E-04 | ALS2, KYNU,   | 1813 | 334  | 12983 | 1.479380456 |
| 13  | 0.49242424 | 0.00119  | TNF, PML, GL  | 1845 | 34   | 13528 | 2.803507094 |
| 26  | 0.98484848 | 0.00119  | INS-IGF2, BC  | 1845 | 98   | 13528 | 1.945290637 |
| 29  | 1.09848485 | 8.06E-04 | ALS2, DIAPH3  | 1813 | 109  | 12983 | 1.905235886 |
| 35  | 1.32575758 | 7.14E-04 | FGFR2, FGFR   | 1813 | 140  | 12983 | 1.790264755 |
| 44  | 1.66666667 | 0.00126  | GPR183, XRC   | 1845 | 199  | 13528 | 1.621200855 |
| 36  | 1.36363636 | 8.82E-04 | PRKCZ, BCAR   | 1813 | 147  | 12983 | 1.753728739 |
| 49  | 1.85606061 | 0.00136  | PRRX1, SOBP   | 1845 | 229  | 13528 | 1.568909244 |
| 35  | 1.32575758 | 0.00133  | NRP1, IL18, L | 1845 | 148  | 13528 | 1.73397788  |
| 23  | 0.87121212 | 0.00134  | PTPRC, A2M,   | 1845 | 83   | 13528 | 2.031828126 |
| 14  | 0.53030303 | 0.00138  | CIDEA, SMAD   | 1845 | 39   | 13528 | 2.6320895   |
| 12  | 0.45454545 | 0.00132  | RGMA, BMP1    | 1845 | 30   | 13528 | 2.932899729 |
| 70  | 2.65151515 | 0.00138  | FOXK1, SPI1,  | 1845 | 356  | 13528 | 1.441734417 |
| 17  | 0.64393939 | 0.00136  | CTBP2, BBS9,  | 1845 | 53   | 13528 | 2.351853556 |
| 74  | 2.8030303  | 0.00141  | SORL1, BNIP3  | 1845 | 381  | 13528 | 1.424111417 |
| 132 | 5          | 0.0014   | SLC9A9, CASI  | 1845 | 751  | 13528 | 1.288757537 |
| 71  | 2.68939394 | 0.00136  | FOXK1, SPI1,  | 1845 | 362  | 13528 | 1.438093099 |
| 69  | 2.61363636 | 0.00121  | TM7SF4, COF   | 1745 | 348  | 12782 | 1.452356487 |

|     |            |         |                 |      |      |       |             |
|-----|------------|---------|-----------------|------|------|-------|-------------|
| 9   | 0.34090909 | 0.00144 | INHBA, LMO4     | 1845 | 18   | 13528 | 3.666124661 |
| 9   | 0.34090909 | 0.00144 | S100A4, NOTCH1  | 1845 | 18   | 13528 | 3.666124661 |
| 10  | 0.37878788 | 0.00148 | AKT1, PRKCZ     | 1845 | 22   | 13528 | 3.332840601 |
| 10  | 0.37878788 | 0.00148 | AKT1, PRKCZ     | 1845 | 22   | 13528 | 3.332840601 |
| 52  | 1.96969697 | 0.00152 | SEPT5, SNCA     | 1845 | 248  | 13528 | 1.537407116 |
| 127 | 4.81060606 | 0.0016  | ADCY3, A2M      | 1845 | 721  | 13528 | 1.291533515 |
| 26  | 0.98484848 | 0.00162 | PRKCZ, A2M      | 1845 | 100  | 13528 | 1.906384824 |
| 22  | 0.83333333 | 0.00164 | KCNMA1, NCAM1   | 1845 | 79   | 13528 | 2.041892216 |
| 106 | 4.01515152 | 0.00167 | ALS2, ADCY3     | 1845 | 586  | 13528 | 1.326311311 |
| 92  | 3.48484848 | 0.00144 | STRN, NBEA      | 1745 | 494  | 12782 | 1.3641567   |
| 17  | 0.64393939 | 0.00169 | PTPRC, CRTA     | 1845 | 54   | 13528 | 2.308300713 |
| 122 | 4.62121212 | 0.00173 | XRCC4, MASF1    | 1845 | 690  | 13528 | 1.296426692 |
| 12  | 0.45454545 | 0.0018  | TRAF3IP2, NLRP1 | 1845 | 31   | 13528 | 2.83829006  |
| 252 | 9.54545455 | 0.00114 | STAT5A, MEIS1   | 1813 | 1512 | 12983 | 1.193509836 |
| 27  | 1.02272727 | 0.00118 | ALS2, DIAPH3    | 1813 | 101  | 12983 | 1.91434251  |
| 25  | 0.9469697  | 0.00125 | ALS2, DIAPH3    | 1813 | 91   | 12983 | 1.967323906 |
| 650 | 24.6212121 | 0.00124 | SLC9A9, FHIT    | 1813 | 4241 | 12983 | 1.097545004 |
| 71  | 2.68939394 | 0.00197 | ADCY3, A2M      | 1845 | 367  | 13528 | 1.41850055  |
| 11  | 0.41666667 | 0.002   | DDR1, PRKCZ     | 1845 | 27   | 13528 | 2.987212687 |
| 94  | 3.56060606 | 0.00201 | THRB, FOXK1     | 1845 | 512  | 13528 | 1.346155149 |
| 77  | 2.91666667 | 0.00205 | ADCY3, A2M      | 1845 | 405  | 13528 | 1.394032587 |
| 27  | 1.02272727 | 0.00204 | CDK5R1, NRF1    | 1845 | 107  | 13528 | 1.850193754 |
| 95  | 3.59848485 | 0.00206 | THRB, FOXK1     | 1845 | 519  | 13528 | 1.342126562 |

| Count | %          | PValue   | Genes          | List Total | Pop Hits | Pop Total | Fold Enrichment |
|-------|------------|----------|----------------|------------|----------|-----------|-----------------|
| 72    | 3.567889   | 3.68E-14 | GNA13, EVX1    | 1406       | 267      | 13528     | 2.594594595     |
| 79    | 3.9147671  | 2.90E-14 | DLC1, NDST1    | 1406       | 307      | 13528     | 2.475922176     |
| 49    | 2.42814668 | 1.83E-14 | ZEB2, GLI3, P  | 1406       | 140      | 13528     | 3.367567568     |
| 123   | 6.09514371 | 5.35E-13 | THRB, HOXD12   | 1364       | 607      | 12983     | 1.928755188     |
| 77    | 3.81565907 | 2.14E-12 | CYP24A1, NCAM1 | 1406       | 319      | 13528     | 2.322460391     |
| 40    | 1.98216056 | 2.98E-12 | NDST1, HOXD12  | 1406       | 112      | 13528     | 3.436293436     |
| 32    | 1.58572844 | 6.52E-12 | NDST1, HOXD12  | 1406       | 77       | 13528     | 3.998595999     |
| 54    | 2.67591675 | 4.11E-11 | EVX1, ZEB2, C  | 1406       | 197      | 13528     | 2.63739882      |
| 26    | 1.28840436 | 7.75E-11 | NDST1, GLI3,   | 1406       | 57       | 13528     | 4.388809862     |
| 42    | 2.08126858 | 7.00E-11 | NDST1, PAX2    | 1406       | 133      | 13528     | 3.038406828     |
| 74    | 3.66699703 | 4.19E-10 | DLC1, GNA13    | 1406       | 334      | 13528     | 2.131736527     |
| 73    | 3.61744301 | 6.91E-10 | DLC1, GNA13    | 1406       | 331      | 13528     | 2.121989059     |
| 47    | 2.32903865 | 9.81E-10 | NDST1, EGLN3   | 1406       | 172      | 13528     | 2.629164048     |
| 62    | 3.07234886 | 1.48E-09 | SRCIN1, MYC    | 1310       | 269      | 12782     | 2.248883339     |
| 161   | 7.97819623 | 2.65E-09 | THRB, LMO4,    | 1364       | 975      | 12983     | 1.571744492     |
| 224   | 11.1000991 | 2.48E-08 | HOXD12, PDI    | 1364       | 1512     | 12983     | 1.410122733     |
| 118   | 5.84737364 | 6.24E-08 | THRB, GDF7,    | 1406       | 695      | 13528     | 1.633599067     |
| 100   | 4.95540139 | 8.79E-08 | THRB, GDF7,    | 1406       | 564      | 13528     | 1.70596128      |

|     |            |          |               |      |      |       |             |
|-----|------------|----------|---------------|------|------|-------|-------------|
| 116 | 5.74826561 | 9.52E-08 | THRB, GDF7,   | 1406 | 685  | 13528 | 1.629354902 |
| 28  | 1.38751239 | 1.05E-07 | WNT5A, HOX    | 1406 | 87   | 13528 | 3.096613855 |
| 28  | 1.38751239 | 1.05E-07 | WNT5A, HOX    | 1406 | 87   | 13528 | 3.096613855 |
| 111 | 5.50049554 | 1.66E-07 | THRB, GDF7,   | 1406 | 654  | 13528 | 1.633027523 |
| 101 | 5.0049554  | 2.03E-07 | THRB, GDF7,   | 1406 | 581  | 13528 | 1.67260548  |
| 30  | 1.48662042 | 3.71E-07 | WNT5A, HOX    | 1406 | 103  | 13528 | 2.802414065 |
| 30  | 1.48662042 | 3.71E-07 | WNT5A, HOX    | 1406 | 103  | 13528 | 2.802414065 |
| 78  | 3.86521308 | 3.22E-07 | DLC1, RAB3G   | 1364 | 413  | 12983 | 1.797650409 |
| 69  | 3.41922696 | 4.38E-07 | NRP2, CCKAF   | 1406 | 356  | 13528 | 1.864864865 |
| 77  | 3.81565907 | 2.65E-07 | DLC1, RAB3G   | 1364 | 404  | 12983 | 1.814136857 |
| 29  | 1.4370664  | 5.30E-07 | WNT5A, HOX    | 1406 | 99   | 13528 | 2.818454818 |
| 29  | 1.4370664  | 5.30E-07 | WNT5A, HOX    | 1406 | 99   | 13528 | 2.818454818 |
| 105 | 5.20317146 | 5.75E-07 | THRB, GDF7,   | 1406 | 624  | 13528 | 1.619022869 |
| 80  | 3.96432111 | 6.02E-07 | NRP2, CCKAF   | 1406 | 438  | 13528 | 1.757373812 |
| 35  | 1.73439049 | 6.91E-07 | CGA, NRG3, I  | 1406 | 135  | 13528 | 2.494494494 |
| 85  | 4.21209118 | 7.40E-07 | EVX1, THRB,   | 1406 | 477  | 13528 | 1.714544733 |
| 52  | 2.57680872 | 7.81E-07 | NRP2, CCKAF   | 1406 | 244  | 13528 | 2.050509526 |
| 107 | 5.30227948 | 8.22E-07 | THRB, GDF7,   | 1406 | 644  | 13528 | 1.598623468 |
| 85  | 4.21209118 | 1.06E-06 | EVX1, THRB,   | 1406 | 481  | 13528 | 1.700286565 |
| 47  | 2.32903865 | 1.04E-06 | NRP2, CCKAF   | 1406 | 213  | 13528 | 2.123080827 |
| 35  | 1.73439049 | 1.42E-06 | ERBB4, EVX1   | 1406 | 139  | 13528 | 2.42271048  |
| 132 | 6.54112983 | 2.60E-06 | DLC1, THRB,   | 1406 | 857  | 13528 | 1.481976726 |
| 72  | 3.567889   | 3.06E-06 | NRP2, CCKAF   | 1406 | 397  | 13528 | 1.744979236 |
| 64  | 3.17145689 | 3.04E-06 | NRP2, CCKAF   | 1406 | 339  | 13528 | 1.816471339 |
| 52  | 2.57680872 | 3.45E-06 | NRP2, CCKAF   | 1406 | 256  | 13528 | 1.954391892 |
| 45  | 2.22993062 | 3.60E-06 | NRP2, CCKAF   | 1406 | 209  | 13528 | 2.071641019 |
| 68  | 3.36967294 | 4.11E-06 | EVX1, THRB,   | 1406 | 371  | 13528 | 1.763531726 |
| 36  | 1.7839445  | 4.42E-06 | DLC1, CCKAR   | 1406 | 152  | 13528 | 2.278805121 |
| 67  | 3.32011893 | 6.18E-06 | NRP2, CCKAF   | 1406 | 368  | 13528 | 1.751762632 |
| 42  | 2.08126858 | 6.07E-06 | NRP2, CCKAF   | 1406 | 193  | 13528 | 2.093824394 |
| 110 | 5.45094153 | 8.01E-06 | DLC1, CADM    | 1406 | 700  | 13528 | 1.511969112 |
| 110 | 5.45094153 | 8.63E-06 | DLC1, CADM    | 1406 | 701  | 13528 | 1.509812237 |
| 193 | 9.56392468 | 2.94E-06 | KIFC1, KRTAF  | 1310 | 1381 | 12782 | 1.363613047 |
| 113 | 5.59960357 | 1.00E-05 | THRB, ARNT2   | 1406 | 727  | 13528 | 1.49552028  |
| 49  | 2.42814668 | 1.06E-05 | NRP2, CCKAF   | 1406 | 245  | 13528 | 1.924324324 |
| 45  | 2.22993062 | 1.43E-05 | DLC1, GNA13   | 1406 | 220  | 13528 | 1.968058968 |
| 284 | 14.0733399 | 9.38E-06 | DLC1, SEC31/  | 1310 | 2203 | 12782 | 1.257857259 |
| 49  | 2.42814668 | 8.07E-06 | CADM1, GRII   | 1310 | 246  | 12782 | 1.943517657 |
| 107 | 5.30227948 | 1.62E-05 | GNA13, ENAI   | 1310 | 697  | 12782 | 1.497885157 |
| 49  | 2.42814668 | 2.30E-05 | DLC1, ITPKB,  | 1406 | 252  | 13528 | 1.870870871 |
| 61  | 3.02279485 | 9.76E-06 | ENAH, MYO7    | 1364 | 326  | 12983 | 1.781036918 |
| 30  | 1.48662042 | 3.35E-05 | DLC1, GNA13   | 1406 | 127  | 13528 | 2.272824005 |
| 49  | 2.42814668 | 3.51E-05 | NRP2, CCKAF   | 1406 | 256  | 13528 | 1.841638514 |
| 9   | 0.44598612 | 4.37E-05 | HOXC10, ISL2  | 1406 | 15   | 13528 | 5.772972973 |
| 11  | 0.54509415 | 4.54E-05 | HOXD9, HOX    | 1406 | 23   | 13528 | 4.601645123 |
| 451 | 22.3488603 | 3.81E-05 | DLC1, FHIT, S | 1310 | 3777 | 12782 | 1.165083561 |

|     |            |          |              |      |      |       |             |
|-----|------------|----------|--------------|------|------|-------|-------------|
| 61  | 3.02279485 | 6.38E-05 | ENAH, CADM   | 1310 | 355  | 12782 | 1.676598215 |
| 82  | 4.06342914 | 6.37E-05 | DLC1, ENAH,  | 1310 | 518  | 12782 | 1.544584279 |
| 78  | 3.86521308 | 1.06E-04 | GNA13, GNA   | 1310 | 494  | 12782 | 1.540618722 |
| 8   | 0.39643211 | 1.25E-04 | HOXC10, ISL2 | 1406 | 13   | 13528 | 5.920997921 |
| 19  | 0.94152626 | 2.15E-04 | DNM3, ANKS   | 1310 | 71   | 12782 | 2.611095581 |
| 230 | 11.3974232 | 1.56E-04 | HOXD12, HO   | 1406 | 1773 | 13528 | 1.248151705 |
| 132 | 6.54112983 | 2.05E-04 | KIFC1, KRTAF | 1310 | 952  | 12782 | 1.352896273 |
| 51  | 2.52725471 | 6.64E-05 | DLC1, MLPH,  | 1364 | 274  | 12983 | 1.771659674 |
| 7   | 0.3468781  | 1.80E-04 | NOTCH1, FO   | 1406 | 10   | 13528 | 6.735135135 |
| 7   | 0.3468781  | 1.80E-04 | NOTCH1, FO   | 1406 | 10   | 13528 | 6.735135135 |
| 81  | 4.01387512 | 9.65E-05 | ENAH, MYO7   | 1364 | 504  | 12983 | 1.529731357 |
| 18  | 0.89197225 | 2.53E-04 | GNA13, FLT1  | 1406 | 65   | 13528 | 2.664449064 |
| 40  | 1.98216056 | 2.50E-04 | FOXK1, UTRN  | 1406 | 211  | 13528 | 1.824004099 |
| 39  | 1.93260654 | 2.81E-04 | IRX3, NBN, H | 1406 | 205  | 13528 | 1.830454845 |
| 232 | 11.4965312 | 3.26E-04 | HOXD12, HO   | 1406 | 1813 | 13528 | 1.231227918 |
| 42  | 2.08126858 | 1.83E-04 | DLC1, RAB3G  | 1364 | 220  | 12983 | 1.817135431 |
| 35  | 1.73439049 | 4.01E-04 | DLC1, SHROC  | 1406 | 180  | 13528 | 1.870870871 |
| 19  | 0.94152626 | 4.44E-04 | PRKCA, WNT   | 1406 | 74   | 13528 | 2.470416362 |
| 39  | 1.93260654 | 4.60E-04 | DLC1, ASAP2  | 1406 | 210  | 13528 | 1.786872587 |
| 28  | 1.38751239 | 4.82E-04 | IRX3, NBN, S | 1406 | 133  | 13528 | 2.025604552 |
| 77  | 3.81565907 | 5.14E-04 | EIF2C2, RSF1 | 1406 | 504  | 13528 | 1.46996997  |
| 6   | 0.29732408 | 5.13E-04 | THRB, HOXA   | 1406 | 8    | 13528 | 7.216216216 |
| 15  | 0.74331021 | 5.11E-04 | EVX1, HOXA1  | 1406 | 51   | 13528 | 2.829888712 |
| 17  | 0.84241824 | 6.74E-04 | CGNL1, SHRC  | 1310 | 65   | 12782 | 2.551896653 |
| 10  | 0.49554014 | 5.97E-04 | HOXB3, HOX   | 1406 | 25   | 13528 | 3.848648649 |
| 10  | 0.49554014 | 5.97E-04 | HOXC10, ISL2 | 1406 | 25   | 13528 | 3.848648649 |
| 55  | 2.72547076 | 8.10E-04 | NRP2, KIAA1  | 1310 | 342  | 12782 | 1.569148699 |
| 71  | 3.51833499 | 6.18E-04 | RSF1, FOXK1, | 1406 | 459  | 13528 | 1.488311841 |
| 166 | 8.2259663  | 6.50E-04 | GNA13, CYP2  | 1406 | 1256 | 13528 | 1.271647444 |
| 55  | 2.72547076 | 9.99E-04 | LTBP2, TGFB  | 1310 | 345  | 12782 | 1.555503927 |
| 88  | 4.36075322 | 7.66E-04 | CGA, UTS2, C | 1406 | 600  | 13528 | 1.411171171 |
| 9   | 0.44598612 | 7.81E-04 | SHROOM1, S   | 1406 | 21   | 13528 | 4.123552124 |
| 10  | 0.49554014 | 8.30E-04 | HOXD9, NOT   | 1406 | 26   | 13528 | 3.700623701 |
| 32  | 1.58572844 | 8.63E-04 | IRX3, NBN, S | 1406 | 166  | 13528 | 1.854770433 |
| 81  | 4.01387512 | 9.45E-04 | EIF2C2, RSF1 | 1406 | 547  | 13528 | 1.424773951 |

## Benjamini

4.63E-11  
5.45E-11  
6.90E-11  
2.02E-09  
2.25E-09  
4.09E-09  
4.28E-09  
6.85E-09  
9.60E-09  
1.35E-08  
2.21E-08  
3.24E-08  
3.29E-08  
6.27E-08  
7.45E-08  
8.99E-08  
1.58E-07  
2.32E-07  
2.37E-07  
3.08E-07  
4.95E-07  
7.00E-07  
1.55E-06  
1.11E-05  
1.60E-05  
1.81E-05  
2.36E-05  
2.39E-05  
2.47E-05  
2.47E-05  
3.69E-05  
4.24E-05  
5.62E-05  
7.34E-05  
7.34E-05  
8.24E-05  
8.33E-05  
8.40E-05  
8.68E-05  
8.80E-05  
9.50E-05

9.50E-05  
9.83E-05  
9.85E-05  
1.08E-04  
1.11E-04  
1.13E-04  
1.15E-04  
1.38E-04  
1.39E-04  
1.79E-04  
1.94E-04  
2.01E-04  
2.85E-04  
3.16E-04  
3.49E-04  
3.57E-04  
3.82E-04  
3.88E-04  
4.30E-04  
4.49E-04  
5.96E-04  
6.01E-04  
7.54E-04  
7.92E-04  
8.97E-04  
9.11E-04  
9.30E-04  
0.001064641  
0.00122515  
0.001924609  
0.002742144  
0.002775898  
0.002807596  
0.003422605  
0.003483249  
0.003573841  
0.004690628  
0.004799229  
0.00484066  
0.007242045  
0.008123388  
0.009385793  
0.011418988  
0.012532619  
0.012967912  
0.012967912

0.013157384  
0.013870547  
0.017467684  
0.017580271  
0.019028141  
0.021667618  
0.021890237  
0.022152811  
0.022758543  
0.023361904  
0.023366833  
0.026176331  
0.026234257  
0.026967246  
0.027112423  
0.028298511  
0.028418128  
0.02893235  
0.029801693  
0.030278282  
0.030699819  
0.031039043  
0.032257373  
0.03325639  
0.034263977  
0.034526711  
0.034526711  
0.035148346  
0.036423298  
0.036618527  
0.038235396  
0.042127413  
0.042346194  
0.044288197  
0.045393322  
0.046127089  
0.047600423  
0.048237499  
0.048905488  
0.048998941

**Benjamini**  
5.85E-24

1.35E-18  
2.34E-18  
2.87E-18  
1.51E-12  
2.44E-12  
2.80E-12  
1.80E-11  
1.18E-10  
2.13E-10  
3.60E-10  
6.15E-10  
1.37E-09  
1.40E-09  
4.54E-09  
7.79E-09  
9.72E-09  
2.17E-08  
2.26E-08  
2.37E-08  
7.38E-08  
1.51E-07  
2.04E-07  
2.22E-07  
2.25E-07  
2.89E-07  
3.98E-07  
5.88E-07  
1.13E-06  
2.27E-06  
2.62E-06  
2.71E-06  
2.73E-06  
2.76E-06  
3.01E-06  
4.30E-06  
4.58E-06  
4.68E-06  
4.68E-06  
4.78E-06  
6.37E-06  
8.30E-06  
8.66E-06  
1.11E-05  
1.13E-05  
1.20E-05  
1.21E-05



1.22E-05  
1.28E-05  
1.37E-05  
1.98E-05  
2.02E-05  
2.06E-05  
2.11E-05  
3.95E-05  
4.83E-05  
6.16E-05  
7.13E-05  
7.76E-05  
7.91E-05  
8.01E-05  
8.95E-05  
8.95E-05  
9.29E-05  
9.63E-05  
9.89E-05  
1.01E-04  
1.04E-04  
1.05E-04  
1.06E-04  
1.06E-04  
1.19E-04  
1.29E-04  
1.30E-04  
1.81E-04  
1.93E-04  
2.36E-04  
2.43E-04  
2.79E-04  
3.00E-04  
3.16E-04  
3.29E-04  
3.30E-04  
3.33E-04  
3.35E-04  
3.39E-04  
3.39E-04  
3.43E-04  
3.50E-04  
3.50E-04  
3.56E-04  
3.70E-04  
4.01E-04

4.04E-04  
4.05E-04  
4.07E-04  
4.09E-04  
4.66E-04  
4.94E-04  
5.43E-04  
6.10E-04  
6.35E-04  
6.63E-04  
6.85E-04  
6.87E-04  
7.31E-04  
7.37E-04  
7.42E-04  
7.42E-04  
7.98E-04  
8.15E-04  
8.35E-04  
8.35E-04  
8.99E-04  
0.001045789  
0.001131526  
0.001155479  
0.001229017  
0.001424681  
0.001479003  
0.001562664  
0.001566491  
0.001665821  
0.001683905  
0.001692435  
0.001784619  
0.001791488  
0.001791488  
0.001796191  
0.001909037  
0.002243206  
0.002262032  
0.00252786  
0.002604443  
0.002604443  
0.002628758  
0.002629083  
0.002629083  
0.002815383

0.002972235  
0.002981325  
0.003020817  
0.003116975  
0.003212287  
0.003212847  
0.003229181  
0.003363929  
0.003550157  
0.00355547  
0.00355547  
0.003581029  
0.003592938  
0.003624532  
0.00364867  
0.003813742  
0.003989038  
0.004204773  
0.004493112  
0.004663035  
0.005105254  
0.005179097  
0.005219723  
0.00545929  
0.00565373  
0.006250844  
0.006310659  
0.006357875  
0.006413934  
0.006579105  
0.006873775  
0.007233465  
0.007251133  
0.007388786  
0.007497596  
0.007645831  
0.007670719  
0.007742781  
0.007796941  
0.007799418  
0.007864956  
0.007892103  
0.007955181  
0.008213051  
0.008765312  
0.00935255

0.009540776  
0.009545429  
0.009606743  
0.009695024  
0.009707026  
0.009770265  
0.009793455  
0.009819052  
0.010277794  
0.010370991  
0.010370991  
0.010457996  
0.010518624  
0.010576173  
0.010602221  
0.010644209  
0.01079718  
0.011087975  
0.011234173  
0.011407584  
0.011443681  
0.011443681  
0.011565298  
0.011567032  
0.011626253  
0.01231735  
0.012720195  
0.014018786  
0.014178409  
0.014199213  
0.014202402  
0.014204453  
0.014242918  
0.014288316  
0.0153339  
0.015426072  
0.015562363  
0.015619281  
0.015922974  
0.016426254  
0.016484043  
0.016609569  
0.016628239  
0.016632797  
0.017044653  
0.017623949

0.018062683  
0.018367486  
0.019801558  
0.019879456  
0.020555162  
0.021216542  
0.021230292  
0.021230292  
0.021315943  
0.021315943  
0.021609759  
0.022260397  
0.022544637  
0.022686347  
0.022933667  
0.022977205  
0.023128352  
0.02333341  
0.023402808  
0.023426147  
0.023537328  
0.023568557  
0.023948272  
0.024091608  
0.025709184  
0.025712337  
0.025775537  
0.025799725  
0.025844176  
0.02584515  
0.026082178  
0.026324372  
0.02650253  
0.026857189  
0.027116753  
0.027130638  
0.028302021  
0.028945452  
0.028945452  
0.029017884  
0.02910456  
0.030597168  
0.030996137  
0.031527033  
0.031527033  
0.031657778

0.032282653  
0.0325912  
0.032734967  
0.032837483  
0.032842545  
0.032882939  
0.033928712  
0.034541413  
0.034759463  
0.035213399  
0.035518361  
0.035725945  
0.035792148  
0.035921283  
0.036633031  
0.036652581  
0.036721615  
0.036750124  
0.036750124  
0.036780476  
0.037132751  
0.037132751  
0.037242574  
0.037632871  
0.038154793  
0.038193294  
0.039120551  
0.040393918  
0.040561962  
0.041605184  
0.041711297  
0.042279819  
0.042452071  
0.042590196  
0.043235403  
0.043537899  
0.045801335  
0.04622014  
0.048112365  
0.048314852  
0.048512237  
0.04996861  
0.050061174

## Benjamini

1.26E-11  
1.37E-11  
2.16E-10  
3.47E-10  
1.28E-09  
1.97E-09  
2.09E-09  
2.18E-09  
4.58E-09  
7.23E-08  
7.77E-08  
1.25E-07  
2.50E-07  
2.57E-07  
2.59E-07  
2.72E-07  
3.34E-07  
4.20E-07  
4.36E-07  
5.22E-07  
6.09E-07  
8.01E-07  
1.01E-06  
1.39E-06  
1.45E-06  
1.69E-06  
1.71E-06  
2.04E-06  
2.12E-06  
2.19E-06  
2.43E-06  
2.51E-06  
2.60E-06  
2.99E-06  
3.09E-06  
3.11E-06  
3.17E-06  
3.36E-06  
3.51E-06  
3.94E-06  
5.09E-06  
5.33E-06  
6.86E-06  
7.65E-06

8.20E-06  
9.48E-06  
1.18E-05  
1.46E-05  
1.68E-05  
2.91E-05  
3.14E-05  
3.71E-05  
3.81E-05  
4.23E-05  
4.60E-05  
4.84E-05  
6.05E-05  
6.12E-05  
6.85E-05  
7.62E-05  
1.42E-04  
1.44E-04  
1.48E-04  
1.55E-04  
1.64E-04  
1.83E-04  
1.91E-04  
1.92E-04  
2.19E-04  
2.21E-04  
2.21E-04  
2.55E-04  
2.84E-04  
2.89E-04  
3.14E-04  
3.42E-04  
3.44E-04  
4.14E-04  
4.33E-04  
4.33E-04  
4.66E-04  
4.95E-04  
5.21E-04  
5.43E-04  
5.71E-04  
6.36E-04  
6.42E-04  
6.46E-04  
6.47E-04  
7.07E-04



7.07E-04  
7.80E-04  
8.28E-04  
8.28E-04  
9.62E-04  
9.67E-04  
9.94E-04  
0.001052427  
0.001081512  
0.001162193  
0.001246148  
0.001246148  
0.00131164  
0.001363706  
0.001484668  
0.00148779  
0.001497781  
0.00162708  
0.001640761  
0.001734419  
0.001921244  
0.001957404  
0.002141929  
0.002316472  
0.002330546  
0.00235531  
0.002529193  
0.002550505  
0.002607868  
0.002984096  
0.003350521  
0.003716757  
0.004048682  
0.004405244  
0.004444536  
0.004449018  
0.0045232  
0.004992591  
0.005231791  
0.005420479  
0.005613886  
0.005846488  
0.00585164  
0.006576421  
0.006609688  
0.006920952

0.006920952  
0.00694381  
0.007327587  
0.007503767  
0.007565101  
0.007854214  
0.008224545  
0.009039178  
0.009187514  
0.009632544  
0.009808648  
0.010099383  
0.010146981  
0.010163967  
0.010573882  
0.011040057  
0.011040057  
0.011112431  
0.011332667  
0.011756149  
0.012079369  
0.012407553  
0.012949241  
0.013016346  
0.013305713  
0.013346147  
0.014022939  
0.014058518  
0.014186551  
0.014186551  
0.014863457  
0.01486464  
0.016233905  
0.01628348  
0.016547736  
0.016640633  
0.016786789  
0.016848632  
0.016961059  
0.016974166  
0.017053801  
0.01708494  
0.01714041  
0.017163005  
0.017488673  
0.020120281

0.020302053  
0.021196535  
0.021465015  
  0.02150561  
0.021768019  
0.022229065  
0.022899326  
  0.02327239  
0.023782474  
0.024209654  
0.024305022  
0.024312415  
0.024312415  
0.024908936  
0.027326693  
0.027860567  
  0.02802045  
0.028095653  
0.028520942  
0.028533738  
0.028594921  
  0.02866907  
0.029123612  
0.029132533  
0.029132533  
0.031092507  
0.032274632  
0.033095882  
0.033516107  
0.033949545  
  0.0341199  
0.034130794  
0.034420253  
0.035811806  
0.036222175  
0.037062192  
0.037080886  
0.037144197  
0.037156319  
0.037194392  
0.037254007  
0.037283326  
0.037370014  
0.037402158  
  0.0375004  
0.037858475

0.037943788  
0.037943788  
0.038911445  
0.038911445  
0.039691655  
0.0413457  
0.041575088  
0.041904431  
0.042542106  
0.042603683  
0.042766481  
0.043429803  
0.044937508  
0.045133319  
0.045453658  
0.045622844  
0.046419081  
0.048671883  
0.049172557  
0.04923844  
0.049504743  
0.049622851  
0.049669818

### **Benjamini**

4.63E-11  
5.45E-11  
6.90E-11  
6.73E-10  
2.02E-09  
2.25E-09  
4.09E-09  
2.21E-08  
3.24E-08  
3.29E-08  
1.58E-07  
2.37E-07  
3.08E-07  
8.42E-07  
1.67E-06  
1.04E-05  
1.81E-05  
2.36E-05

2.39E-05  
2.47E-05  
2.47E-05  
3.69E-05  
4.24E-05  
7.34E-05  
7.34E-05  
8.10E-05  
8.24E-05  
8.34E-05  
9.50E-05  
9.50E-05  
9.83E-05  
9.85E-05  
1.08E-04  
1.11E-04  
1.13E-04  
1.15E-04  
1.38E-04  
1.39E-04  
1.79E-04  
3.16E-04  
3.49E-04  
3.57E-04  
3.82E-04  
3.88E-04  
4.30E-04  
4.49E-04  
5.96E-04  
6.01E-04  
7.54E-04  
7.92E-04  
8.33E-04  
8.97E-04  
9.30E-04  
0.00122515  
0.001331252  
0.00152585  
0.001843766  
0.001924609  
0.002041853  
0.002742144  
0.002807596  
0.003422605  
0.003483249  
0.003603126

0.004522255  
0.005155859  
0.006687992  
0.009385793  
0.011028859  
0.011418988  
0.011574894  
0.011849594  
0.012967912  
0.012967912  
0.01505141  
0.017467684  
0.017580271  
0.019028141  
0.021667618  
0.025228539  
0.026176331  
0.028418128  
0.02893235  
0.029801693  
0.030278282  
0.030699819  
0.031039043  
0.031426862  
0.034526711  
0.034526711  
0.034786187  
0.035148346  
0.036423298  
0.039723146  
0.042127413  
0.042346194  
0.044288197  
0.045393322  
0.048905488