**Supplemental Information for: Chromatin Architecture Around Stroke Haplotypes Provides Evidence that Genetic Risk is Conferred Through Vascular Cells**

***Running Head – Epigenetic Landscapes of Stroke Genetic Risk Loci***

**Supplemental Table 1. Cistrome datasets for histone mark analysis.\***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Year** | **1st Author** | **Journal** | **Source** | **Factors** | **GEO/ENCODE ID** |
| 2014 | Andersson, R.  | Nature | Natural Killer Cell; Blood   | H3K27ac | GSM999008 |
| H3K4me1 | GSM999007 |
| 2010 | Bernstein, B.E.  | Nat. Biotechnol.  | T Lymphocyte; Blood; CD4+  | H3K27ac | GSM1220560 |
| H3K4me1 | GSM1220567 |
| H3K9ac | GSM543004 |
| H3K4me3 | GSM1847952 |
| T Lymphocyte; Blood; CD8+  | H3K27ac | GSM1102781 |
| H3K4me1 | GSM1220569 |
| H3K9ac | GSM613813 |
| H3K4me3 | GSM1847967 |
| 2018 | Davis, C.A.  | Nucleic Acids Res.  | Smooth Muscle Cell  | H3K27ac | ENCSR210ZPC\_2 |
| H3K4me1 | ENCSR130IMV\_2 |
| H3K9ac | ENCSR540UZV\_2 |
| H3K4me3 | ENCSR515PKY\_2 |
| 2012 | ENCODE Project Consortium  | Nature | GM12878; B Lymphocyte; Blood  | H3K27ac | GSM733771 |
| H3K4me1 | GSM733772 |
| H3K9ac | GSM733677 |
| H3K4me3 | GSM1233906 |
| Endothelial Cell; Umbilical Vein  | H3K27ac | GSM733691 |
| H3K4me1 | GSM733690 |
| H3K9ac | GSM733735 |
| H3K4me3 | GSM1305207 |
| Fibroblast; Lung  | H3K27ac | GSM733646 |
| H3K4me1 | GSM733649 |
| H3K9ac | GSM733652 |
| H3K4me3 | GSM1418959 |
| Fibroblast; Skin  | H3K27ac | GSM733662 |
| H3K4me1 | GSM1003526 |
| H3K9ac | GSM733709 |
| H3K4me3 | GSM1615881 |
| Monocyte; Blood  | H3K27ac | GSM1003559 |
| H3K4me1 | GSM1003535 |
| H3K9ac | GSM1003515 |
| H3K4me3 | GSM2262927 |
| Neutrophil; Blood | H3K27ac | GSM2527660 |
| H3K4me1 | GSM2534489 |
| H3K4me3 | GSM2533981 |
| 2017 | Hogan, N.T. | Elife | Endothelial Cell; HAEC | H3K27ac | GSM2394402 |
| 2012 | Pham, T.H.  | Blood | Macrophage | H3K27ac | GSM785500 |
| H3K4me1 | GSM785498 |
| H3K4me3 | GSM1146441 |

\* Abbreviations: Biotechnol.=biotechnology, ENCODE=Encyclopedia of DNA Elements, GEO=Gene Expression Omnibus, Nat.=nature, Res.=research.

**Supplemental Table 2. The 178 TAD transcripts.\***

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene ID** | **Entrez Gene Name** | **Location** | **Type(s)** |
| *ABCC10* | ATP binding cassette subfamily C member 10 | Plasma Membrane | transporter |
| *AC000065.1* | / | / | / |
| *AC000065.2* | / | / | / |
| *AC003986.2* | / | / | / |
| *AC003986.3* | / | / | / |
| *AC010082.1* | / | / | / |
| *AC010255.1* | / | / | / |
| *AC010255.2* | / | / | / |
| *AC010683.1* | / | / | / |
| *AC010896.1* | / | / | / |
| *AC013472.1* | / | / | / |
| *AC015977.1* | / | / | / |
| *AC018946.1* | / | / | / |
| *AC021422.1* | / | / | / |
| *AC073522.1* | / | / | / |
| *AC091167.6* | / | / | / |
| *AC092979.1* | / | / | / |
| *AC092979.2* | / | / | / |
| *AC093001.1* | / | / | / |
| *AC093001.2* | / | / | / |
| *AC093908.1* | / | / | / |
| *AC097450.1* | uncharacterized LOC105377476 | Other | other |
| *AC103739.1* | / | / | / |
| *AC103739.2* | / | / | / |
| *AC103739.3* | / | / | / |
| *AC108751.1* | / | / | / |
| *AC108751.2* | / | / | / |
| *AC108751.3* | / | / | / |
| *AC108751.4* | / | / | / |
| *AC113349.1* | synuclein alpha interacting protein | Cytoplasm | transcription regulator |
| *AC113349.2* | synuclein alpha interacting protein | Cytoplasm | transcription regulator |
| *AC119150.1* | / | / | / |
| *AC119150.2* | / | / | / |
| *AC124248.1* | / | / | / |
| *AC124248.2* | / | / | / |
| *ADGRF3* | adhesion G protein-coupled receptor F3 | Plasma Membrane | G-protein coupled receptor |
| *AL035587.1* | / | / | / |
| *AL035587.2* | / | / | / |
| *AL035587.3* | / | / | / |
| *AL121929.2* | / | / | / |
| *AL133355.1* | / | / | / |
| *AL133375.1* | / | / | / |
| *AL136304.1* | / | / | / |
| *AL157937.1* | / | / | / |
| *AL354709.1* | / | / | / |
| *AL354709.2* | / | / | / |
| *AL354760.1* | / | / | / |
| *AL355385.1* | / | / | / |
| *AL355385.2* | / | / | / |
| *AL359813.1* | / | / | / |
| *AL359813.2* | / | / | / |
| *AL359922.1* | / | / | / |
| *AL359922.2* | / | / | / |
| *AL359922.3* | / | / | / |
| *AL449423.1* | / | / | / |
| *AL583834.1* | / | / | / |
| *AL590383.1* | / | / | / |
| *AL591521.1* | / | / | / |
| *AL603832.1* | / | / | / |
| *AL603832.2* | / | / | / |
| *AL603832.3* | / | / | / |
| *BLM* | BLM RecQ like helicase | Nucleus | enzyme |
| *C6orf226* | chromosome 6 open reading frame 226 | Other | other |
| *CAPZA1* | capping actin protein of muscle Z-line subunit alpha 1 | Cytoplasm | other |
| *CDK6* | cyclin dependent kinase 6 | Nucleus | kinase |
| *CDK6-AS1* | CDK6 antisense RNA 1 | Other | other |
| *CDKN2A* | cyclin dependent kinase inhibitor 2A | Nucleus | transcription regulator |
| *CDKN2A-DT* | CDKN2A divergent transcript | Other | other |
| *CDKN2AIPNLP2* | CDKN2A interacting protein N-terminal like pseudogene 2 | Other | other |
| *CDKN2B* | cyclin dependent kinase inhibitor 2B | Nucleus | transcription regulator |
| *CDKN2B-AS1* | CDKN2B antisense RNA 1 | Other | other |
| *CENPA* | centromere protein A | Nucleus | other |
| *CIB4* | calcium and integrin binding family member 4 | Other | other |
| *CNPY3* | canopy FGF signaling regulator 3 | Cytoplasm | other |
| *CP* | ceruloplasmin | Extracellular Space | enzyme |
| *CPHL1P* | ceruloplasmin and hephaestin like 1, pseudogene | Other | other |
| *CRIP3* | cysteine rich protein 3 | Cytoplasm | other |
| *CRTC3* | CREB regulated transcription coactivator 3 | Nucleus | other |
| *CRTC3-AS1* | CRTC3 antisense RNA 1 | Other | other |
| *CTTNBP2NL* | CTTNBP2 N-terminal like | Cytoplasm | other |
| *CUL7* | cullin 7 | Cytoplasm | enzyme |
| *CUL9* | cullin 9 | Cytoplasm | other |
| *DLK2* | delta like non-canonical Notch ligand 2 | Extracellular Space | other |
| *DMRTA1* | DMRT like family A1 | Nucleus | transcription regulator |
| *DNPH1* | 2'-deoxynucleoside 5'-phosphate N-hydrolase 1 | Nucleus | enzyme |
| *DPYSL5* | dihydropyrimidinase like 5 | Cytoplasm | enzyme |
| *DRC1* | dynein regulatory complex subunit 1 | Extracellular Space | other |
| *EDNRA* | endothelin receptor type A | Plasma Membrane | transmembrane receptor |
| *ERVFRD-3* | endogenous retrovirus group FRD member 3 | Other | other |
| *FAM166C* | family with sequence similarity 166 member C | Nucleus | other |
| *FES* | FES proto-oncogene, tyrosine kinase | Cytoplasm | kinase |
| *FKBP1AP4* | FKBP prolyl isomerase 1A pseudogene 4 | Other | other |
| *FURIN* | furin, paired basic amino acid cleaving enzyme | Cytoplasm | peptidase |
| *GABARAPL3* | GABA type A receptor associated protein like 3 pseudogene | Other | other |
| *GAREM2* | GRB2 associated regulator of MAPK1 subtype 2 | Cytoplasm | other |
| *GNMT* | glycine N-methyltransferase | Cytoplasm | enzyme |
| *GTF2F2P1* | general transcription factor IIF subunit 2 pseudogene 1 | Other | other |
| *GYG1* | glycogenin 1 | Cytoplasm | enzyme |
| *HADHA* | hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit alpha | Cytoplasm | enzyme |
| *HADHB* | hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta | Cytoplasm | enzyme |
| *HDAC9* | histone deacetylase 9 | Nucleus | transcription regulator |
| *HDAC9-AS1* | / | Other | other |
| *HLTF* | helicase like transcription factor | Nucleus | transcription regulator |
| *HLTF-AS1* | HLTF antisense RNA 1 | Other | other |
| *HPS3* | HPS3 biogenesis of lysosomal organelles complex 2 subunit 1 | Cytoplasm | other |
| *HSPE1P3* | heat shock protein family E (Hsp10) member 1 pseudogene 3 | Other | other |
| *IQGAP1* | IQ motif containing GTPase activating protein 1 | Cytoplasm | other |
| *KCNK3* | potassium two pore domain channel subfamily K member 3 | Plasma Membrane | ion channel |
| *KLC4* | kinesin light chain 4 | Other | other |
| *KLHDC3* | kelch domain containing 3 | Cytoplasm | other |
| *LINC01585* | long intergenic non-protein coding RNA 1585 | Other | other |
| *LINC02507* | / | Other | other |
| *LOX* | lysyl oxidase | Extracellular Space | enzyme |
| *LRRC73* | leucine rich repeat containing 73 | Other | other |
| *MAPRE3* | microtubule associated protein RP/EB family member 3 | Cytoplasm | enzyme |
| *MAPRE3-AS1* | MAPRE3 antisense RNA 1 | Other | other |
| *MEA1* | male-enhanced antigen 1 | Cytoplasm | other |
| *MED28P2* | mediator complex subunit 28 pseudogene 2 | Other | other |
| *MGC32805* | uncharacterized LOC153163 | Other | other |
| *MIR4256* | microRNA 4256 | Cytoplasm | microRNA |
| *MIR548G* | microRNA 579 | Cytoplasm | microRNA |
| *MIR6780B* | microRNA 6780b | Other | microRNA |
| *MOV10* | Mov10 RISC complex RNA helicase | Nucleus | enzyme |
| *MRPL2* | mitochondrial ribosomal protein L2 | Extracellular Space | other |
| *MRPL53P1* | mitochondrial ribosomal protein L53 pseudogene 1 | Other | other |
| *MTAP* | methylthioadenosine phosphorylase | Nucleus | enzyme |
| *NDUFA3P4* | / | Other | other |
| *NPM1P13* | nucleophosmin 1 pseudogene 13 | Other | other |
| *OTOF* | otoferlin | Plasma Membrane | other |
| *PEX6* | peroxisomal biogenesis factor 6 | Cytoplasm | enzyme |
| *POLR1C* | RNA polymerase I and III subunit C | Nucleus | enzyme |
| *PPM1J* | protein phosphatase, Mg2+/Mn2+ dependent 1J | Other | phosphatase |
| *PPP2R5D* | protein phosphatase 2 regulatory subunit B'delta | Nucleus | phosphatase |
| *PRMT5P1* | protein arginine methyltransferase 5 pseudogene 1 | Other | other |
| *PTCRA* | pre T cell antigen receptor alpha | Plasma Membrane | other |
| *PTK7* | protein tyrosine kinase 7 (inactive) | Plasma Membrane | kinase |
| *RHOC* | ras homolog family member C | Plasma Membrane | enzyme |
| *RN7SKP266* | / | Other | other |
| *RN7SL363P* | / | Other | other |
| *RN7SL403P* | / | Other | other |
| *RN7SL7P* | RNA, 7SL, cytoplasmic 7, pseudogene | Other | other |
| *RNU6-10P* | RNA, U6 small nuclear 10, pseudogene | Other | other |
| *RNU6-1113P* | RNA, U6 small nuclear 1113, pseudogene | Other | other |
| *RNU7-70P* | RNA, U7 small nuclear 70 pseudogene | Other | other |
| *RPL12P47* |  - | Other | other |
| *RPL24P4* | ribosomal protein L24 pseudogene 4 | Other | other |
| *RPL37P11* | ribosomal protein L37 pseudogene 11 | Other | other |
| *RPL7L1* | ribosomal protein L7 like 1 | Cytoplasm | transcription regulator |
| *RPS2P28* | ribosomal protein S2 pseudogene 28 | Other | other |
| *RRP36* | ribosomal RNA processing 36 | Nucleus | other |
| *SELENOI* | selenoprotein I | Cytoplasm | enzyme |
| *SH3PXD2A* | SH3 and PX domains 2A | Cytoplasm | other |
| *SH3PXD2A-AS1* | SH3PXD2A antisense RNA 1 | Other | other |
| *SLC22A7* | solute carrier family 22 member 7 | Plasma Membrane | transporter |
| *SLC35F6* | solute carrier family 35 member F6 | Cytoplasm | other |
| *SNCAIP* | synuclein alpha interacting protein | Cytoplasm | transcription regulator |
| *SNORD18* | / | / | / |
| *SRF* | serum response factor | Nucleus | transcription regulator |
| *SRFBP1* | serum response factor binding protein 1 | Nucleus | other |
| *ST7L* | suppression of tumorigenicity 7 like | Other | other |
| *STN1* | STN1 subunit of CST complex | Nucleus | other |
| *TJAP1* | tight junction associated protein 1 | Plasma Membrane | other |
| *TM4SF1* | transmembrane 4 L six family member 1 | Plasma Membrane | other |
| *TM4SF18* | transmembrane 4 L six family member 18 | Other | other |
| *TM4SF1-AS1* | TM4SF1 antisense RNA 1 | Other | other |
| *TM4SF4* | transmembrane 4 L six family member 4 | Plasma Membrane | other |
| *TTBK1* | tau tubulin kinase 1 | Other | kinase |
| *TUBB8P1* | tubulin beta 8 class VIII pseudogene 1 | Other | other |
| *TWIST1* | twist family bHLH transcription factor 1 | Nucleus | transcription regulator |
| *UBA52P6* | ubiquitin A-52 residue ribosomal protein fusion product 1 pseudogene 6 | Other | other |
| *UBQLN4P1* | ubiquilin 4 pseudogene 1 | Other | other |
| *WNT2B* | Wnt family member 2B | Extracellular Space | other |
| *Y\_RNA* | / | / | / |
| *YIPF3* | Yip1 domain family member 3 | Cytoplasm | other |
| *ZNF318* | zinc finger protein 318 | Nucleus | other |
| *ZNF474* | zinc finger protein 474 | Other | other |
| *ZNF474-AS1* | uncharacterized LOC107986445 | Other | other |
| *ZNF774* | zinc finger protein 774 | Other | other |

\* “/” = none.

**Supplemental Table 3. IPA disease and biological functions of genes within stroke associated, histone-marked TADs.**

|  |  |  |
| --- | --- | --- |
| **Categories** | **Diseases or Functions Annotation** | **q-value** |
| Cancer, Organismal Injury and Abnormalities | Malignant solid tumor | 2.88E-07 |
| Cancer, Organismal Injury and Abnormalities | Nonhematologic malignant neoplasm | 1.17E-06 |
| Cancer, Organismal Injury and Abnormalities | Extracranial solid tumor | 3.98E-06 |
| Cancer, Organismal Injury and Abnormalities | Non-melanoma solid tumor | 9.28E-06 |
| Cancer, Organismal Injury and Abnormalities | Carcinoma | 0.000023 |
| Cancer, Organismal Injury and Abnormalities | Abdominal neoplasm | 0.000153 |
| Cancer, Organismal Injury and Abnormalities | Abdominal cancer | 0.000299 |
| Cancer, Organismal Injury and Abnormalities | Abdominal carcinoma | 0.000218 |
| Cancer, Organismal Injury and Abnormalities | Intraabdominal organ tumor | 0.000716 |
| Cancer, Organismal Injury and Abnormalities | Head and neck tumor | 0.000119 |
| Cancer, Organismal Injury and Abnormalities | Adenocarcinoma | 0.000985 |
| Cancer, Organismal Injury and Abnormalities | Formation of solid tumor | 0.00108 |
| Cancer, Organismal Injury and Abnormalities | Abdominal adenocarcinoma | 0.00108 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Digestive organ tumor | 0.00588 |
| Cancer, Organismal Injury and Abnormalities | Cancer of secretory structure | 0.000627 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Digestive system cancer | 0.00704 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities | Endocrine gland tumor | 0.000235 |
| Cancer, Organismal Injury and Abnormalities | Head and neck cancer | 0.00106 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities | Endocrine carcinoma | 0.000333 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Gastrointestinal tract cancer | 0.00211 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities | Nonpituitary endocrine tumor | 0.00034 |
| Cancer, Organismal Injury and Abnormalities | Head and neck carcinoma | 0.00149 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities | Thyroid carcinoma | 0.000454 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Malignant neoplasm of large intestine | 0.000966 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Gastrointestinal carcinoma | 0.00285 |
| Cancer, Organismal Injury and Abnormalities | Incidence of tumor | 0.00201 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Large intestine carcinoma | 0.00108 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Gastrointestinal adenocarcinoma | 0.00271 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Large intestine adenocarcinoma | 0.00189 |
| Cancer, Organismal Injury and Abnormalities | Tumorigenesis of epithelial neoplasm | 0.00336 |
| Cancer, Organismal Injury and Abnormalities | Frequency of tumor | 0.00461 |
| Cancer, Organismal Injury and Abnormalities | Development of carcinoma | 0.00519 |
| Cancer, Organismal Injury and Abnormalities | Breast or colorectal cancer | 0.00504 |
| Cancer, Neurological Disease, Organismal Injury and Abnormalities | Grade 3-4 glioma cancer | 0.00959 |
| Cancer, Neurological Disease, Organismal Injury and Abnormalities | Grade 4 high grade glioma | 0.00153 |
| Cancer, Neurological Disease, Organismal Injury and Abnormalities | Grade 4 malignant glioma | 0.00153 |
| Cancer, Neurological Disease, Organismal Injury and Abnormalities | Grade 4 astrocytoma | 0.00153 |
| Cancer, Neurological Disease, Organismal Injury and Abnormalities | Brain astrocytoma | 0.00159 |
| Cancer, Organismal Injury and Abnormalities | Breast or pancreatic cancer | 0.00407 |
| Cancer, Gastrointestinal Disease, Hepatic System Disease, Organismal Injury and Abnormalities | Liver tumor | 0.00855 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Hepatobiliary carcinoma | 0.00698 |
| Cancer, Gastrointestinal Disease, Hepatic System Disease, Organismal Injury and Abnormalities | Liver carcinoma | 0.00475 |
| Cancer, Organismal Injury and Abnormalities, Reproductive System Disease | Breast or ovarian cancer | 0.00219 |
| Cancer, Organismal Injury and Abnormalities, Reproductive System Disease | Breast or ovarian carcinoma | 0.000631 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities, Reproductive System Disease | Ovarian tumor | 0.000107 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities, Reproductive System Disease | Ovarian cancer | 0.000214 |
| Gene Expression | Expression of RNA | 0.00509 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities, Reproductive System Disease | Ovarian carcinoma | 0.000152 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities, Reproductive System Disease | Development of ovarian tumor | 0.000231 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities, Reproductive System Disease | Ovarian adenocarcinoma | 0.000654 |
| Cellular Assembly and Organization, Cellular Function and Maintenance | Organization of cytoplasm | 0.00847 |
| Cancer, Organismal Injury and Abnormalities | Serous adenocarcinoma | 0.000247 |
| Cardiovascular System Development and Function, Organismal Development | Angiogenesis | 0.000758 |
| Embryonic Development, Organismal Development | Development of body trunk | 0.00401 |
| Cardiovascular System Development and Function, Organismal Development | Vasculogenesis | 0.000334 |
| Cancer, Organismal Injury and Abnormalities | Clear-cell adenocarcinoma | 0.00115 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities, Reproductive System Disease | Ovarian serous tumor | 0.000427 |
| Cancer, Organismal Injury and Abnormalities, Renal and Urological Disease | Renal clear cell adenocarcinoma | 0.00241 |
| Cardiovascular System Development and Function, Embryonic Development, Organ Development, Organismal Development, Tissue Development | Cardiogenesis | 0.000071 |
| Cellular Assembly and Organization | Development of cytoplasm | 0.000214 |
| Cellular Assembly and Organization | Organization of organelle | 0.00119 |
| Hereditary Disorder, Neurological Disease, Organismal Injury and Abnormalities | Autosomal recessive neurological disorder | 0.00366 |
| Lymphoid Tissue Structure and Development, Tissue Morphology | Quantity of lymphatic system cells | 0.00777 |
| Cellular Development, Cellular Growth and Proliferation, Hematological System Development and Function, Hematopoiesis, Lymphoid Tissue Structure and Development, Tissue Development | Leukopoiesis | 0.0087 |
| Cancer, Organismal Injury and Abnormalities | Anaplastic carcinoma | 8.62E-05 |
| Post-Translational Modification | Phosphorylation of protein | 0.00572 |
| Cellular Development, Cellular Growth and Proliferation, Hematological System Development and Function, Hematopoiesis, Lymphoid Tissue Structure and Development, Tissue Development | Hematopoiesis of mononuclear leukocytes | 0.00913 |
| Cellular Development, Cellular Growth and Proliferation, Connective Tissue Development and Function | Proliferation of fibroblast cell lines | 0.000742 |
| Cell Death and Survival | Cell death of fibroblast cell lines | 0.00075 |
| Endocrine System Disorders, Gastrointestinal Disease, Metabolic Disease, Organismal Injury and Abnormalities, Renal and Urological Disease | Diabetic nephropathy | 0.000855 |
| Tissue Morphology | Quantity of stem cells | 0.00288 |
| Developmental Disorder | Hypoplasia | 0.00586 |
| Developmental Disorder | Growth Failure | 0.00934 |
| Cell Death and Survival | Apoptosis of fibroblast cell lines | 0.000592 |
| Cellular Response to Therapeutics | Sensitivity of cells | 0.000651 |
| Cell Cycle | Senescence of cells | 0.000651 |
| Cancer, Organismal Injury and Abnormalities, Reproductive System Disease | Female genital tract serous carcinoma | 0.00247 |
| Cancer, Organismal Injury and Abnormalities | Pelvic serous carcinoma | 0.00247 |
| Cellular Assembly and Organization | Formation of cytoskeleton | 0.00324 |
| Cell Morphology | Morphology of blood cells | 0.00507 |
| Cellular Assembly and Organization, Tissue Development | Formation of filaments | 0.0052 |
| Hematological System Development and Function, Hematopoiesis, Tissue Morphology | Quantity of hematopoietic progenitor cells | 0.0067 |
| Developmental Disorder | Hypoplasia of organ | 0.00976 |
| Developmental Disorder | Thoracic hypoplasia | 0.00011 |
| Cancer, Organismal Injury and Abnormalities, Respiratory Disease | Undifferentiated lung carcinoma | 0.000411 |
| Cancer | Transformation of fibroblast cell lines | 0.000973 |
| Cell Death and Survival | Apoptosis of stem cells | 0.00105 |
| Cell Morphology | Morphology of tumor cell lines | 0.0011 |
| Cell Death and Survival, Neurological Disease, Organismal Injury and Abnormalities | Cell death of brain cells | 0.00148 |
| Lymphoid Tissue Structure and Development, Organ Morphology, Tissue Morphology | Quantity of lymphoid organ | 0.00187 |
| Cardiovascular Disease, Developmental Disorder, Organismal Injury and Abnormalities | Congenital heart disease | 0.00202 |
| Cellular Movement | Invasion of carcinoma cell lines | 0.00232 |
| Cellular Movement | Invasion of breast cancer cell lines | 0.00633 |
| Cellular Development, Cellular Growth and Proliferation, Tissue Development | Development of stem cells | 0.00645 |
| Cellular Development, Cellular Growth and Proliferation | Colony formation of tumor cell lines | 0.00762 |
| Metabolic Disease, Organismal Injury and Abnormalities | Abnormal metabolism | 0.00908 |
| Developmental Disorder, Immunological Disease, Organismal Injury and Abnormalities | Hypoplasia of thymus gland | 3.77E-05 |
| Cancer, Organismal Injury and Abnormalities | Recurrent malignant solid tumor | 0.00117 |
| Cell Morphology | Morphology of stem cells | 0.00137 |
| Energy Production, Lipid Metabolism, Small Molecule Biochemistry | Oxidation of fatty acid | 0.00142 |
| Cancer, Cardiovascular Disease, Organismal Injury and Abnormalities | Hemangioma | 0.00203 |
| Cell Death and Survival | Apoptosis of hematopoietic progenitor cells | 0.00253 |
| Hematological System Development and Function, Hematopoiesis, Lymphoid Tissue Structure and Development, Organ Morphology, Tissue Morphology | Quantity of thymocytes | 0.00312 |
| Cell Death and Survival, Neurological Disease, Organismal Injury and Abnormalities | Cell death of cerebral cortex cells | 0.00354 |
| Cancer, Endocrine System Disorders, Organismal Injury and Abnormalities, Reproductive System Disease | Serous ovarian adenocarcinoma | 0.00369 |
| Hematological System Development and Function, Organismal Development, Tissue Morphology | Quantity of blood | 0.00433 |
| Cardiovascular System Development and Function | Morphogenesis of cardiovascular system | 0.00493 |
| Cellular Development, Cellular Growth and Proliferation, Embryonic Development, Organismal Development | Proliferation of embryonic cells | 0.00506 |
| Cellular Development, Connective Tissue Development and Function, Skeletal and Muscular System Development and Function, Tissue Development | Differentiation of osteoblasts | 0.006 |
| Cardiovascular Disease, Hereditary Disorder, Organismal Injury and Abnormalities | Familial vascular disease | 0.00675 |
| Embryonic Development, Hematological System Development and Function, Lymphoid Tissue Structure and Development, Organ Development, Organismal Development, Tissue Development | Formation of lymphoid organ | 0.00773 |
| Metabolic Disease, Organismal Injury and Abnormalities | Disorder of lipid metabolism | 0.00825 |
| Cancer, Gastrointestinal Disease, Organismal Injury and Abnormalities | Metastatic colorectal cancer | 0.00948 |

**Supplemental Table 4. Networks of genes within stroke associated, histone-marked TADs.\***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Network**  | **Molecules in Network** | **P-Score** | **Focus Mol.** | **Top Diseases and Functions** |
| 1 | ABCC10, ADGRF3, AF366264, C6orf226, CRTC3, CUL7, CUL9, EMD, GABARAPL1, GFY, Gm2694, GPR62, GYG1, HADHA, HADHB, HNF4A, HNRNPD, HNRNPK, HPS3, KLHDC3, MDM2, Mdm2-Tp53-Mdm4, Mdm2-Tp53-ubiquitin, MEA1, mir-548, miR-548c-3p (miRNAs w/seed AAAAAUC), MIR194-2HG, MOV10, MRPL2, PEX6, PTEN, RPL7L1, SIRT6, TP53, ZNF774 | 39 | 18 | Developmental Disorder, Hereditary Disorder, Organismal Injury and Abnormalities |
| 2 | 26s Proteasome, BCR (complex), Cdk, CDK4/6, CDK4/6-Cyclin D1, CDK6, CDKN2A, CDKN2B, CDKN2B-AS1, CENPA, CP, CTTNBP2NL, Cyclin D, DNA-methyltransferase, DPYSL5, ERK1/2, FES, FURIN, GNMT, Hif1, INK4, LOX, Mek, P glycoprotein, p70 S6k, Pdgf (complex), PDGF BB, PP2A, Ppp2c, Rb, RHOC, RRP36, STN1, Tgf beta, TWIST1 | 33 | 16 | Cancer, Cellular Response to Therapeutics, Organismal Injury and Abnormalities |
| 3 | Actin, Akt, Alpha catenin, Alpha tubulin, BLM, CAPZA1, CD3, CG, Ck2, ERK, estrogen receptor, F Actin, FSH, GAREM2, Hsp90, Igm, IQGAP1, KCNK3, MAP2K1/2, MAPRE3, mediator, Notch, PARP, PI3K (complex), Pkc(s), PTK7, Rnr, SH3PXD2A, SNCAIP, SRC (family), SRF, SRFBP1, TM4SF1, tubulin, ZNF318 | 26 | 13 | Cardiovascular Disease, Cell Cycle, Cellular Movement |
| 4 | 1-palmitoyl-2-arachidonoyl-phosphatidylcholine, 2'-fucosyllactose, AKT2, BAX, Ca2, CAV3, CFHR3, CIB4, COQ10B, Ctf2, DLK2, DRC1, ELAVL1, FUT6, GDPGP1, GRTP1, HNF1A, L-triiodothyronine, MTAP, MTCP1, OTOF, PARM1, PPM1J, PPP2R5D, S100PBP, SELENOI, SLC22A7, STAT3, TM4SF4, TRPM5, TTBK1, UBB, Ybx1-ps3, YIPF3, ZBED3 | 23 | 12 | Cellular Compromise, Neurological Disease, Organismal Injury and Abnormalities |

\* Abbreviations: mol.=molecules.