Poster Program

Poster session I
13:15-15:00 Monday, June 27, 2016

[P1.01]	**MAP3K4 kinase activity regulates the epigenetic remodeler HDAC6 during transitions between epithelial and mesenchymal phenotypes** R.J. Mobley*[1], S.M. Gomez[2], L.D. Duke[1], K.N. Abell-Hart[1], K. Lutz[2], J.S. Zawistowski[2], G.L. Johnson[2], A.N. Abell[1], *[1]The University of Memphis, USA, [2]University of North Carolina School of Medicine, USA*
[P1.02]	**Genome-wide functional interactions of five major transcription factors in mouse epiblast stem cells** H. Kondoh*[1,2], K. Matsuda[2], T. Mikami[2], S. Oki[3], S. Shigenobu[4], *[1]Kyoto Sangyo University, Japan, [2]Osaka University, Japan, [3]Kyushu University, Japan, [4]NIBB, Japan*
[P1.03]	**Inverse relationship between progesterone receptor and Myc in endometrial cancer** T. Kavlashvili*[1], Y. Jia[1], D. Dai[1], X. Meng[1,2], K.W. Thiel[1], K.K. Leslie[1,2], S. Yang[1,2], *[1]University of Iowa, USA, [2]University of Iowa Holden Comprehensive Cancer Center, USA*
[P1.04]	**RNAs in regulation of transcription** T.S. Ro-Choi*, Y.C. Choi, *Dong-A University, Republic of Korea*
[P1.05]	**AP-1: An enhancer binding transcription factor complex critical for stimulus-responsive enhancer licensing and activation** T. Vierbuchen*, E. Ling, C.J. Cowley, D.A. Harmin, M.E. Greenberg, *Harvard Medical School, USA*
[P1.06]	**Mechanisms of divergent oncogenic functions of the highly homologous ETS factors, ETS1 and ETS2** J.P. Plotnik*, P.C. Hollenhorst, *Indiana University, USA*
[P1.07]	**Distinct co-regulator interactions mediate the differing oncogenic functions of homologous ETS family transcription factors** V. Kedage, J.P. Plotnik, N. Selvaraj, J.A. Budka, P.C. Hollenhorst*, *Indiana University, USA*
[P1.08]	**Targeting aberrant poly-(ADP)-ribosylation in breast cancer** M. Marques*[1,2], A. Kazanets[1], A. Lovato[1], T. Zhao[1], S. Chen[1], M.A. Alaoui-Jamali[1,2], M. Witcher[1,2], *[1]Lady Davis Institute, Canada, [2]McGill University, Canada*
[P1.09]	**Tissue-specific transcriptional cascades are established through the synergy of many upstream regulators in Arabidopsis roots** E.E. Sparks*[1], C. Drapek[1], P.N. Benfey[1,2], *[1]Duke University, USA, [2]Howard Hughes Medical Institute, USA*
[P1.10]	**Folate receptor alpha (FRα) transcriptionally regulates the pluripotency genes and miRNAs to establish a complex regulatory system in cranial neural crest cells** V. Mohanty*[1], A. Shah[1], E. Allender[1], M.R. Siddiqui[1], S. Monick[1], S. Ichi[1,2], B. Mania-Farnell[3], T. Tomita[1], C.S. Mayanil[1], *[1]Northwestern University Feinberg School of Medicine, USA, [2]Japanese Red Cross Medical Center, Japan, [3]Purdue University at Calumet, USA*
[P1.11]	**Novel glioblastoma pathways from *Drosophila*: FBP integrates RTK-activated MYC transcription to drive glial overproliferation and brain overgrowth** O. Zaytseva*[1], J.E.A. Lee[1], N.C. Mitchell[1], L. Guo[1], A.S. Chahal[1], R. Luwor[1], D.L. Levens[2], R.D. Hannan[3,4], L.M. Quinn[1], *[1]University of Melbourne, Australia, [2]National Cancer Institute, USA, [3]Peter MacCallum Cancer Centre, Australia, [4]John Curtin School of Medicine, Australia*
[P1.12]	**Determining tumor suppressive roles of ETS factors in prostate cancer** J.A. Budka*, P.C. Hollenhorst, *Indiana University, USA*
[P1.13]	**Identification of functional domains required for Kdm3b effects during late stages of reprogramming** K. Tran*, M. Diny, D. Devine, R. Sridharan, *University of Wisconsin - Madison, USA*
[P1.14]	**Gene regulation dynamics in developing drosophila larval somatic muscles** A. Carayon[1,2], L. Bataillé[1,2], L. Dubois[1,2], A. Vincent[1,2], J-L. Frendo*[1,2], *[1]CNRS, France, [2]Université Toulouse III, France*
[P1.15]	**Genome-wide core promoter activity maps reveal a wide range of sequence-intrinsic transcription initiation strengths** M.A. Zabidi*, C. Arnold, M. Pagani, M. Rath, A. Stark, *Research Institute of Molecular Pathology (IMP), Austria*
[P1.16]	**Combinatorial transcription factor requirements of hormone-responsive enhancers** F. Reiter*, G. Stampfel, A. Stark, *Research Institute of Molecular Pathology (IMP), Austria*
[P1.17]	**Tissue-specific cis-regulatory interactions in early Drosophila development** S. Krueger*, D. Vasiljevic, M. Selbach, R.P. Zinzen, *Max Delbrueck Center for Molecular Medicine (MDC), Germany*

[P1.18]	**MYS-1/TIP60 mediated X-upregulation in *C. elegans* males** A. Lau*, K. Zhu, E. Brouhard, G. Csankovszki, *University of Michigan, USA*
[P1.19]	**Hox proteins regulate the expression of Ret and Gfra during motor neuron subtype development** C. Catela*[1], M.M. Shin[1], D.H. Lee[1], J.P. Liu[2], J.S. Dasen[1], *[1]NYU School of Medicine, USA, [2]University of Virginia School of Medicine, USA*
[P1.20]	**The broadly expressed transcription factor GTF2IRD1 plays a specific role in regulating the topology and function of photoreceptors by modulating photoreceptor gene expression across the retina** T. Masuda*, D. Zack, *Johns Hopkins Univeristy, USA*
[P1.21]	**Longitudinal monitoring of in vitro cardiomyocyte differentiation at single-cell resolution elucidates lineage branching principles** R. Bargaje*[1], K. Trachana[1], C. McGinnis[1], J. Zhou[1], M. Shelton[1], C. Chadick[1], S. Cook[2], C. Cavanaugh[2], S. Huang[1,3], L. Hood[1], *[1]Institute for Systems Biology, USA, [2]UW Medicine Research, USA, [3]University of Calgary, Canada*
[P1.22]	**Elucidating mechanisms of TCF/LEF-independent ß-catenin regulated transcription** S. Abdulla*, S. Moreira, V. Gordon, E. Polena, B. Doble, *McMaster University, Canada*
[P1.23]	**Intronic regulation of human GLI1 DNA by cis DNA elements and epigenetic marks** J. Long[1], R. Taylor[2], J. Yoon[2], R. Childs[2], K. Sylvestersen[3], M.L. Nielsen[3], D.O. Walterhouse[2], D. Robbins[1], P. Iannaccone*[2], *[1]Miami University, USA, [2]Northwestern University Feinberg School of Medicine, Denmark, [3]University of Copenhagen, USA*
[P1.24]	**Downregulation of transcription factor forkhead box P3 sensitizes thyroid cancer cells to chemotherapies by inhibiting p65** G.G. Chen*, S.S. Wang, S. Yang, A.C. Vlantis, S.Y.W. Liu, E.K.W. Ng, S.K. Ng, M.C.F. Tong, C.A. van Hasselt, *The Chinese University of Hong Kong, China*
[P1.25]	**Identification of a YAP/TAZ/TEAD transcriptional program driving oncogenic growth** F. Zanconato*[1], M. Forcato[2], G. Battilana[1], L. Azzolin[1], E. Quaranta[1], S. Bicciato[2], M. Cordenonsi[1], S. Piccolo[1], *[1]University of Padova, Italy, [2]University of Modena and Reggio Emilia, Italy*
[P1.26]	**Hijacking the general transcription machinery by sequence specific transcription factors going awry** M. Seoane*[1], J. Strauss[1], A.C. Puller[1], P. Iglesias[1], M. Noshiravani[1], S. Feldhaus[1], M. Alawi[1,2], M.G. Kaul[1], J.M. Brandner[1], J. Du[3,8], *[1]University Medical Center Hamburg, Germany, [2]Heinrich Pette Institute, Germany, [3]Harvard Medical School Boston, USA, [4]University Duisburg-Essen, Germany, [5]University Hospital Zürich, Switzerland, [6]Medical School Hannover, Germany, [7]Massachusetts General Hospital, USA, [8]Merrymack Pharmaceuticals, USA*
[P1.27]	**Anchoring of heterochromatin to the nuclear lamina stabilizes condensin-mediated gene repression** M.J. Snyder, A.C. Lau, E.A. Brouhard, J. Jiang, M. Sifuentes, G. Csankovszki*, *University of Michigan, USA*
[P1.28]	**A combinatorial repression mechanism sets anterior pair-rule stripes in *Drosophila*** L.P. Andrioli*, G. Gueller, F. Clava, W. dos Santos, J. Paciência, A. Ferrão-Neto, A. Machado-Lima, L. Digiampietri, *Universidade de São Paulo, Brazil*
[P1.29]	**Nkx6.1 regulates notch1 expression in neural stem/progenitor cells during spinal cord development** Y. Li*, E. Tzatzalos, K.Y. Kwan, M. Grumet, L. Cai, *Rutgers University, USA*
[P1.30]	**P63-mediated regulation of miR-29s** A. Schwendimann[1], A. Bachmann[1,2], J. Windhager[1], A. Voicu[1], C. Missero[3], S. Werner[1], S. Kurinna*[1], *[1]Institute of Molecular Health Sciences ETHZ, Switzerland, [2]Institute of Chemical Sciences and Engineering EPFL, Switzerland, [3]University of Naples Federico II, Italy*
[P1.31]	**The UMLILO long ncRNA exploits pre-formed 3D chromatin folding to coordinate rapid chemokine gene activation** S. Fanucchi*[1], E. Fok[1], E. Dalla[2], Y. Shibayana[1], M. Imakeav[3], K. Sung[4], M.M. Mhlanga[1], *[1]CSIR, South Africa, [2]LNCIB, Italy, [3]MIT, USA, [4]NUS, Singapore*
[P1.32]	**Sex-specific silencing of X-linked genes by Xist RNA** S. Gayen*, E. Maclary, M. Hinten, S. Kalantry, *University of Michigan, USA*
[P1.33]	**The evolution of morphology, one base pair at a time** E. Preger-Ben Noon*, D.L. Stern, *HHMI Janelia Research Campus, USA*
[P1.34]	**The effect of small molecule ligands on DNA structure: A dictionary and a wiki** Z. Leifer, *New York College of Podiatric Medicine, USA*
[P1.35]	**Global dynamics of Pol II pausing during transcriptional responses in human breast cancer cells** A. Abbas, A. Samarakkody, N. Koney, S. Nechaev*, *University of North Dakota, USA*
[P1.36]	**Repression of basally transcribed inactive x-linked genes by PRC2 and Xist RNA** E. Maclary*, M. Hinten, S. Sethuraman, C. Harris, S. Kalantry, *University of Michigan, USA*

[P1.37]	**Gene expression regulation by ALKBH1-mediated tRNA demethylation** K.L. Liu*, Y.F. Fu, C.H. He, *The University of Chicago, USA*
[P1.38]	**Nkx2.5 has a role in landscaping the DNA methylation of the zebrafish heart, in particular cis-regulatory elements regulating cardiac and epigenetic function** B. Gorsi*, T. Mosbruger, M. Smith, H.J. Yost, *University of Utah, USA*
[P1.39]	**Nipbl interacts with Zfp609 and the Integrator complex to regulate cortical neuron migration** D.L.C. van den Berg*[1], R. Azzarelli[1], B. Martynoga[1], D.H.W. Dekkers[2], J.A. Demmers[2], F. Guillemot[1], *[1]The Francis Crick Institute, UK, [2]Erasmus Medical Centre, The Netherlands*
[P1.40]	**Control of sexual cell fate identity by the conserved testis regulator DMRT1** M.W. Murphy*, M.D. Gearhart, R.E. Lindeman, D. Zarkower, V.J. Bardwell, *University of Minnesota, USA*
[P1.41]	**Massive increase of retrotransposition specifically in meiotic germ cells of piRNA knockout mice** S.J. Newkirk, F.C. Grandi, S. Lee, N. Vanden Berg, W. An*, *South Dakota State University, USA*
[P1.42]	**Single base pair differences in a shared regulatory motif determine differential expression of color-sensing Rhodopsins in Drosophila** J. Rister*, C. Desplan, *New York University, USA*
[P1.43]	**Kat2a loss of function increases transcriptional variability and promotes differentiation of pluripotent and leukaemic cells** N. Moris[1], S.J. Ridden[2], A.F. Domingues[1], S. Edri[1], S. Teichmann[3], B.J. Huntly[1], B.D. Macarthur[2], A.M. Arias[1], C. Pina*[1], *[1]University of Cambridge, UK, [2]University of Southampton, UK, [3]EMBL- European Bioinformatics Institute, UK*
[P1.46]	**A pioneer role of p63 in gene regulation during epidermal commitment and differentiation** E.N. Kouwenhoven[1,2], M. Oti[1], J. Qu[1], H. Niehues[2], S.J. van Heeringen[1], J. Schalkwijk[2], H.G. Stunnenberg[1], H. van Bokhoven[2], H. Zhou*[1,2], *[1]Radboud University, The Netherlands, [2]Radboud University Medical Centre, The Netherlands*
[P1.47]	**Identification of Xist mediated trans-chromosomal X repression outside of early human development further differentiates female from male nuclei** A.I. Laskowski*, E.L. Rice, J. He, J.M. Mathews, J.R. Leventhal, S.T. Kosak, *Northwestern University, USA*
[P1.48]	**Zelda promotes chromatin accessibility to activate the drosophila genome** K. Schulz*[1], E. Bondra[1], D. McKay[2], T. Kaplan[3], M. Harrison[1], *[1]University of Wisconsin Madison, USA, [2]University of North Carolina, USA, [3]The Hebrew University of Jerusalem, Israel*
[P1.49]	**Pitx2 is required for postnatal myofiber maintenance** C-N. Chang*, A.J. Singh, H-Y. Ma, K.A. Lytle, D.B. Jump, J.F. Stevens, M.K. Gross, C. Kioussi, *Oregon State University, USA*
[P1.50]	**Differentiation of the invasive phenotype requires cell cycle arrest** D.Q. Matus, *Stony Brook University, USA*
[P1.51]	**Characterization of the maternal-to-zygotic transition in haplodiploid embryos** D. Arsala*, J.A. Lynch, *University of Illinois at Chicago, USA*
[P1.52]	**A fully synthetic transcriptional enhancer platform for study of regulatory protein function in a multicellular eukaryote** J. Crocker*, D. Stern, *Janelia Research Campus HHMI, USA*
[P1.53]	**Tethering Set1 to RNA polymerase II disrupts the H3K4 methylation gradient** C. He*, H. Suh, L.M. Soares, Y. Chun, S. Buratowski, *Harvard Medical School, USA*
[P1.54]	**Regulatory mechanisms of gene dosage sensitivity** K.R. McEwen, *Imperial College London, UK*
[P1.55]	**SEX-1 role play in Caenorhabditis elegans anchor cell fate specification and acquisition of invasive behavior** R.A. Herrera*, T.N. Medwig, D.Q. Matus, *Stony Brook University, USA*
[P1.56]	**Targeting an oncogenic chromatin cross-talk in pediatric leukemia** P. Ntziachristos*[1], K. Arcipowski[1], S. Kumar[2], C. Martinez[1], P. Thomas[1], N. Kelleher[1], Y. Zhu[1], R. Prinjha[3], S.A. Marshall[1], P. Van Vlierberghe[1], *[1]Northwestern University, USA, [2]Progenra Inc, USA, [3]GlaxoSmithKline, UK*
[P1.57]	**Mapping the chromatin state dynamics in myoblasts** A.J. Singh*, M.K. Gross, T.M. Filtz, C. Kioussi, *Oregon State University, USA*
[P1.58]	**Role of ultraconserved elements in *Iroquoix* gene regulation** L. Montefiori*, D. Sobreira, N. Sakabe, M. Nobrega, *University of Chicago, USA*
[P1.59]	**Hypothalamic IRX3 overexpression leads to obesity in mice** D.R. Sobreira*[1], I. Aneas[1], S. Smemo[1,2], M. Nobrega[1], *[1]University of Chicago, USA, [2]Columbia University, USA*

[P1.60]	**Pancreatic β cell enhancers regulate rhythmic transcription of genes controlling insulin secretion** M. Perelis*[1], B. Marcheva[1], K.M. Ramsey[1], M.J. Schipma[1], A.L. Hutchison[2], A. Taguchi[1], C.B. Peek[1], H. Hong[1], W. Huang[1], C. Omura[1], *[1]Northwestern University Feinberg School of Medicine, USA, [2]University of Chicago, USA*
[P1.61]	**The dual function of H4K20me1 in cell cycle progression and dosage compensation** J. Jiang*, E. Brouhard, L. Custer, G. Csankovszki, *University of Michigan, USA*
[P1.62]	**Novel insights into PXR isoforms and their relevance in cellular functions** Priyanka*, N. Puri, R.K. Tyagi, *Jawaharlal Nehru University, India*
[ST06]	**Transcription elongation factors represent in vivo cancer dependencies in glioblastoma** T.E. Miller*[1,2], B.B. Liau[3], L.C. Wallace[2], A.R. Morton[1], J.J. Morrow[1], J. Zuber[4], P.C. Scacheri[1], B.E. Bernstein[3,5], P.J. Tesar[1], J.N. Rich[2] et al, *[1]Case Western Reserve University Medical School, USA, [2]Cleveland Clinic Lerner Research Institute, USA, [3]Harvard Medical School, USA, [4]Research Institute of Molecular Pathology, Austria, [5]Broad Institute, USA*

Poster session II
13:15-15:15 Tuesday, June 28, 2016

[P2.01]	**Analysis of posterior HOX paralogue binding sites and target recognition** I. Jerkovic*[1,3], D.M. Ibrahim[1,2], P. Hansen[2], M. Orgeur[1], G. Andrey[1], P.N. Robinson[2], S. Mundlos[1,2], J. Hecht[4], *[1]Max Planck Institute for Molecular Genetics, Germany, [2]Universitätsmedizin Berlin, Germany, [3]Berlin-Brandenburg School for Regenerative Therapies, Germany, [4]Centre for Genomic Regulation, Spain*
[P2.02]	**Deployment of a new enhancer repertoire through Pax7 pioneer action** A. Mayran*[1,2], Y. Gauthier[1], K. Khetchoumian[1], A. Balsalobre[1], F. Hariri[2], T. Pastinen[2], J. Drouin[1], *[1]IRCM Institut de Recherches Cliniques de Montreal, Canada, [2]McGill University, Canada*
[P2.03]	**The identification of new KLF3 partner proteins by co-immunoprecipitation coupled with mass spectrometry** T. Chavalit*, W.F. Lim, K.G. Quinlan, M. Crossley, *University of New South Wales, Australia*
[P2.04]	**Transcriptionally paused genes distinguish quiescence from irreversible arrest and are critical for cell cycle reentry** H. Gala*, D. Saha, J. Dhawan, *Center for Cellular and Molecular Biology, India*
[P2.05]	**A specific co-activator interaction defines the oncogenic mechanism of ETS factors rearranged in prostate cancer** V. Kedage*[1], N. Selvaraj[2], J. Budka[2], T. Jerde[2], P. Hollenhorst[2], *[1]Indiana University, USA, [2]Indiana University School of Medicine, USA*
[P2.06]	**Histone H3 Threonine phosphorylation regulates asymmetric histone inheritance in the drosophila male germline** J. Xie*[1], M. Wooten[1], V. Tran[1,4], B.C. Chen[3,2], C. Pozmanter[1], C. Simbolon[1], E. Betzig[2], X. Chen[1], *[1]Johns Hopkins University, USA, [2]HHMI, USA, [3]Academia Sinica, Taiwan, [4]Fred Hutchinson Cancer Research Center, USA*
[P2.07]	**Direct quantification of transcriptional regulation at an endogenous gene locus** H. Xu*[1,2], A. Sokac[1], I. Golding[1,2], *[1]Baylor College of Medicine, USA, [2]Center for Theoretical Biological Physics, Rice University, USA*
[P2.08]	**Loss of hfp generates an ectopic niche to drive stem cell tumour formation** M. Tran[1], N.C. Mitchell[1], A. Chahal[1], R.D. Hannan[2], D.L. Levens[3], L.M. Quinn*[1], *[1]University of Melbourne, Australia, [2]Australian National University, Australia, [3]National Institutes of Health, USA*
[P2.09]	**Pro-survival p53 target genes have evolved clusters of interacting polymorphic response elements that can affect cancer risk** P. Zhang*[1], G. Stracquadanio[1], X. Wang[1,2], J. Zeron-Medina[1,3], S. Nornes[1], S. Moore[1], Y. Bi[1], M. Wallace[1], N. Sacilotto[1], G. Bond[1], *[1]University of Oxford, UK, [2]National Institute of Environmental Health Sciences-National Institutes of Health, USA, [3]Vall d'Hebron University Hospital, Spain*
[P2.10]	**Understanding the role of non-coding variation in human disease** M.C. Suciu*, M. Kassouf, R. Schwessinger, J. Telenius, J.R. Hughes, D.R. Higgs, *Weatherall Institute for Molecular Medicine, University of Oxford, UK*
[P2.11]	**Defining the essential function of FBP/KSRP proteins: Drosophila Psi interacts with the mediator complex to modulate MYC transcription and tissue growth** L. Guo*[1], O. Zaytseva[1], Z. Nie[2], N.C. Mitchell[1], J.E.A. Lee[1], L. Parsons[1], R.D. Hannan[3,4], D.L. Levens[2], L.M. Quinn[1], *[1]University of Melbourne, Australia, [2]National Cancer Institute, USA, [3]The John Curtin School of Medical Research, Australia, [4]Peter MacCallum Cancer Centre, Australia*

[P2.12]	**Zebrafish ezh2 affects the maintenance of cellular identity during development through effects on both maternal and zygotic gene expression** B. San[2], N.D. Chrispijn*[1], N. Wittkopp[3,4], S. van Heeringen[1], A. Lagendijk[3], M. Aben[2], J. Bakkers[3], R.F. Ketting[3,4], L.M. Kamminga[1,2], *[1]Radboud University, The Netherlands, [2]Radboud University Medical Center, The Netherlands, [3]Hubrecht Institute-KNAW, The Netherlands, [4]Institute of Molecular Biology, Germany*
[P2.13]	**Catalytic-dependent and independent activities of Polycomb repressive complex 1 differentially regulate skin stem cell specification** I. Cohen*[1], V. Valdes[1], K. Dauber[1], D. Zhao[1,4], D. Zheng[1,4], W. Bickmore[1,3], H. Koseki[1,2], E. Ezhkova[1], *[1]Icahn School of Medicine at Mount Sinai, USA, [2]RIKEN Center for Integrative Medical Sciences, Japan, [3]University of Edinburgh, UK, [4]Albert Einstein College of Medicine, USA*
[P2.14]	**Genome-wide quantitative assessment of enhancer activities in human cells by STARR-seq** L. Boryn, A.R. Woodfin*, M.A. Zabidi, C.D. Arnold, M. Pagani, A. Stark, *Institute of Molecular Pathology, Austria*
[P2.15]	**Genomic heritability of variants in gene regulatory regions for quantitative traits in mice** H. Ohmiya*, G. Morota, *University of Nebraska-Lincoln, USA*
[P2.16]	**Specific functions of an autism-associated chromatin remodeling factor Brg1/SMARCA4 in neuron development** Z. Zhang[1], Y. Luo[1], M. Cao[1], J. Gu[2], C.W. Chang[1], X. Shi[1], X. Zhan[1], K.M. Huber[1], Z. Xuan[2], J.I. Wu*[1], *[1]Unuversity of Texas Southwestern Medical Center, USA, [2]University of Texas at Dallas, USA*
[P2.17]	**Regulation of transcriptional bursting in the Drosophila embryo** T. Fukaya*, B. Lim, M. Levine, *Princeton University, USA*
[P2.18]	**The HSF-1 developmental program is linked to E2F and distinct from the heat shock response** J. Li*, L. Chauve, G. Phelps, R.M. Brielmann, R.I. Morimoto, *Northwestern University, USA*
[P2.19]	**Cold-temperature induced transcriptional regulation of thermogenic gene programs in human white adipocytes** M.L. Rexius-Hall*, D.T. Eddington, J. Rehman, *University of Illinois at Chicago, USA*
[P2.20]	**Lineage conversion of human fibroblasts to bipotential CD34$^+$ progenitors generates functional endothelial cells and erythroblasts via Sox17/Sox18** L. Zhang*[1], A. Jambusaria[1], S. Kim[1], B. Herbert[2], A.B. Malik[1], J. Rehman[1], *[1]The University of Illinois College of Medicine, USA, [2]Indiana University School of Medicine, USA*
[P2.21]	**Identification of proteins interacting with gypsy-associated RNAs by affinity pull down** I. Bag*, K. D'Orazio, P. Lopez, R. Dale, E.P. Lei, *National Institutes of Health, USA*
[P2.22]	**Roles for chromosome neighborhoods in development and cancer** D.S. Day*[1], D. Hnisz[1], A.S. Weintraub[1,2], X. Ji[1], D.B. Dadon[1,2], Z.P. Fan[1], D. Borges-Rivera[1], C.H. Li[1,2], R.A. Young[1,2], *[1]Whitehead Institute, USA, [2]Massachusetts Institute of Technology, USA*
[P2.23]	**Transcriptome profiling central regulators for endothelial angiogenesis** K.H. Liao*[1], S.J. Chang[2], T.S. Hwang[1], H.C. Chang[1], C.L. Chien[1], S.H. Yang[1], C.H. Lin[1], W.L. Hwang[1], O.K. Lee[1,3], H.W. Wang[1], *[1]National Yang-Ming University, Taiwan, [2]Hsinchu Mackay Memorial Hospital, Taiwan, [3]Taipei City Hospital, Taiwan*
[P2.24]	**Regulation of RUNX2 expression in cancer requires the complex interplay between intergenic and intragenic regulatory elements** V. Sancisi*, G. Manzotti, T. Rossi, G. Gobbi, M. Gugnoni, G. Gandolfi, A. Ciarrocchi, *Arcispedale Santa Maria Nuova - IRCCS, Italy*
[P2.25]	**YAP/TAZ/TEAD cooperate with AP-1 for growth control and tumorigenesis** F. Zanconato[1], G. Battilana*[1], M. Forcato[2], E. Quaranta[1], L. Azzolin[1], A. Rosato[1], S. Bicciato[2], M. Cordenonsi[1], S. Piccolo[1], *[1]University of Padova, Italy, [2]University of Modena and Reggio Emilia, Italy*
[P2.26]	**Endogenous retroviruses and the control of gene regulatory networks in the brain** P.L. Brattås, M. Jönsson, L. Fasching, M. Parmar, J. Jakobsson*, *Lund University, Sweden*
[P2.27]	**Long-range rDNA-genomic interactions regulate RNA polymerase II gene programs during malignant transformation** J. Diesch[1], M. Bywater[1], E. Sanij[1,2], A. Ganley[3], D. Cameron[5,2], R. Pearson[1,2], G. McArthur[1,2], J. O'Sullivan[4], R. Hannan[5,1], G. Poortinga*[1,2], *[1]Peter MacCallum Cancer Centre, Australia, [2]University of Melbourne, Australia, [3]Massey University, New Zealand, [4]University of Auckland, New Zealand, [5]Australian National University, Australia*
[P2.28]	**Molecular characterization of the role of RNA-mediated chromatin remodeling inhibition in Coffin Siris Syndrome, an intellectual disability disorder** I. Cajigas*, M. Bastidas, J.D. Kohtz, *Northwestern University, USA*

[P2.29]	**Research funding for studies of aging biology** J. Velazquez, *National Institute on Aging, USA*
[P2.30]	**Role of long noncoding RNAs in normal murine hematopoiesis and malignant transformation** M.J. Delas*[1,2], L.R. Sabin[1], E. Dolzhenko[3], M. Zhou[3], S.R.V. Knott[1,2], S.A. Wild[2,5], D.R. Kelley[4], J.L. Rinn[4], A.D. Smith[3], G.J. Hannon[1,2], *[1]Cold Spring Harbor Laboratory, USA, [2]University of Cambridge, UK, [3]University of Southern California, USA, [4]Harvard University, USA, [5]German Cancer Research Center, Germany*
[P2.31]	**A cell autonomous mechanism determines disparate actions of retinoic acid signal in development and cancer** S. Rossetti, N. Sacchi*, *Roswell Park Cancer Institute, USA*
[P2.32]	**Genetic deletion of a recently evolved 2.4 Mb tandem zinc finger gene cluster causes retrotransposon activation in mice** G. Wolf*, M. Tinkham, D. Hoang, T.S. Macfarlan, *The National Institutes of Health, USA*
[P2.33]	**Computational characterization of tissue-specific endothelial cell populations via transcriptional networks derived from heterogeneous signaling pathways** A. Jambusaria*, J. Klomp, A.B. Malik, J. Rehman, *University of Illinois at Chicago, USA*
[P2.34]	**Orchestration of X-chromosome inactivation by the X-inactivation escapee Smcx/Kdm5c** S. Gayen, E. Maclary, C. Vallianatos, S. Iwase, S. Kalantry*, *University of Michigan, USA*
[P2.35]	**ASXL3 in neural fate commitment and autism spectrum disorder** Y-C. Tsan, R. KC, A. Srivastava, S.L. Bielas*, *University of Michigan School of Medicine, USA*
[P2.36]	**The dosage compensation complex regulates brain development in drosophila melanogaster** M.A. Tsiarli*, L. Xu, E. Larschan, *Brown University, USA*
[P2.37]	**Phosphorylation of the Brg1 chromatin remodeling enzyme by casein kinase 2 regulates myoblast proliferation and viability** T. Padilla-Benavides, B.T. Nasipak, A.L. Paskavitz, J.M. Schnabl, A.N. Imbalzano*, *UMass Medical School, USA*
[P2.38]	**Mechanisms underlying enhancer switching at the Nodal locus in differentiating ESCs** A. Benhaddou*, F. Furfaro, M. Vieira, P. Hersen, B. Sorre, J. Collignon, *Université Paris 7, France*
[P2.39]	**Biotin tagging MeCP2 in vivo reveals contextual insights into the Rett syndrome transcriptome** B.S. Johnson*[1], Y. Zhao[1], M.D. Fasolino[1], J.M. Lamonica[1], Y.J. Kim[2], K.H. Wood[1], Y. Cui[1], D. Goffin[1], T.H. Kim[2], Z. Zhou[1], *[1]University of Pennsylvania, USA, [2]University of Texas Dallas, USA*
[P2.40]	**The differential interactome of HP1 family of proteins in pluripotent cells** N.Z. Zaidan*, M. Scalf, L. Smith, R. Sridharan, *University of Wisconsin-Madison, USA*
[P2.41]	**Poised epigenetic states in the transition of somatic cells to pluripotency** R. Sridharan*, S. Roy, *University of Wisconsin-Madison, USA*
[P2.42]	**The pause-inducing factor Spt5 is globally required for coding and non-coding RNA synthesis by RNA Polymerase II** T. Henriques[1], B.S. Scruggs*[1], R.A. Flynn[1,2], G.W. Muse[1], M. Inouye[1], A. Burkholder[1], H.Y. Chang[1,2], D.C. Fargo[1], K. Adelman[1], *[1]National Institute of Environmental Health Sciences, USA, [2]Stanford University, USA*
[P2.43]	**Hedgehog signaling modulates a differentiation clock for cardiac development** M. Rowton*, S. Lazaravic, K. Ikegami, A. Hoffman, J. Steimle, C. Kim, A. Guzzetta, S. Yu, E. Hanson, I.P. Moskowitz, *University of Chicago, USA*
[P2.44]	**Genomic analysis of lipid effects on the macrophage inflammatory response** N. Gokey*, T. Henriques, G. Muse, A. Burkholder, D. Fargo, K. Adelman, *National Institute of Environmental Health Science, USA*
[P2.45]	**Molecular mechanisms of Asxl3 in neurodevelopmental disorders** A. Srivastava*, R. KC, A. Moccia, S.L. Bielas, *University of Michigan School of Medicine, USA*
[P2.46]	**An intronic enhancer complex regulates skeletal development by modulating Ihh expression** A.J. Will*[1,2], D.G. Lupiáñez[1,2], G. Cova[2], G. Andrey[2], M. Osterwalder[3], A. Visel[3], M. Spielmann[1,2], E. Klopocki[4], S. Mundlos[1,2], *[1]Charité - Universitätsmedizin Berlin, Germany, [2]Max Planck Institute for Molecular Genetics, Germany, [3]Lawrence Berkeley National Laboratory, Canada, [4]Biozentrum Universität Würzburg, Germany*
[P2.47]	**7SK-BAF axis controls pervasive transcription at enhancers** R. Flynn, B. Do*, A. Rubin, E. Calo, B. Lee, H. Kuchelmeister, E. Kool, J. Wysocka, P. Khavari, H. Chang, *Stanford University, USA*

[P2.48]	**Hox proteins generate neuronal diversity by regulating the transcriptional output of a single terminal selector gene** P. Kratsios*[1,2], S.Y. Kerk[1], O. Hobert[1], *[1]Columbia University, USA, [2]University of Chicago, USA*
[P2.49]	**Elucidating the mechanisms of Zelda-mediated transcriptional activation** D.C. Hamm*, E.R. Bondra, M.M. Harrison, *University of Wisconsin - Madison, USA*
[P2.50]	**Lack of Mecp2 interferes with mechanisms of cortical progenitors proliferation and differentiation** F. Bedogni*[1], C. Cobolli Gigli[1], L. Scaramuzza[1], D. Pozzi[2], M. Matteoli[2], N. Landsberger[1], *[1]San Raffaele Research Institute, Italy, [2]Humanitas Clinical and Research Center, Italy*
[P2.51]	**Topologically associated domains are ancient features that coincide with Metazoan clusters of extreme noncoding conservation** N. Harmston[1,2], E. Ing-Simmons*[1], G. Tan[1], M. Perry[1], M. Merkenschlager[1], B. Lenhard[1], *[1]MRC Clinical Sciences Centre, UK, [2]Duke-NUS Graduate Medical School, Singapore*
[P2.52]	**Coordination of repressive and patterning inputs at the even-skipped locus: Unexpected role for the ETS transcription factor Pointed** J.L. Webber*, J. Zhang, I. Rebay, *University of Chicago, USA*
[P2.53]	**The essential function of E2F is to control skeletal muscle growth** M.P. Zappia*[1], A.B.M.M.K. Islam[2], M.V. Frolov[1], *[1]University of Illinois at Chicago, USA, [2]University of Dhaka, Bangladesh*
[P2.54]	**Histone H3 lysine 9 methylation states have distinct functions in heterochromatin establishment and inheritance** G. Jih*, M. Currie, N. Iglesias, D. Moazed, *Harvard Medical School, USA*
[P2.55]	**Differential impacts of the E protein/Id protein axis on innate lymphoid cell development** R.F. de Pooter*, E.C. Zook, B.L. Kee, *University of Chicago, USA*
[P2.56]	**The circadian system regulates age-onset rhythmic expression of stress response genes** R. Kuintzle, E. Chow, T. Bonar, B. Gvakharia, J. Giebultowicz, D.A. Hendrix*, *Oregon State University, USA*
[P2.57]	**miR-216 suppression allows Müller glia reprogramming during zebrafish retina regeneration** N. Kara*, K. Rajaram, A.H. Zhao, E.R. Summerbell, J.G. Patton, *Vanderbilt University, USA*
[P2.58]	**Understanding mechanisms of GLI-mediated transcription during craniofacial development and disease using the ciliopathic mutant, talpid2** Y.T. Chang*, C.F. Chang, P. Chaturvedi, S.A. Brugmann, Cincinnati Children's Hospital Medical Center, USA
[ST01]	**Blast from the past – how skeletal progenitor transcriptomes are shaped by embryonic origin** P. Tschopp*, C.J. Tabin, *Harvard Medical School, USA*
[ST05]	**Inhibition of cyclin-dependent kinases 12/13 in cancers marked by genomic instability** M. Krajewska*[1], D. Day[2], T. Zhang[1], N. Kwiatkowski[1], N. Moore[1], E. Chipumuro[1], A. Greenleaf[3], R. Young[2], N. Gray[1], R.E. George[1], *[1]Harvard Medical School, USA, [2]Massachusetts Institute of Technology, Cambridge, USA, [3]Duke University Medical Center, USA*
[ST07]	**The mysterious absence of plant enhancers: Complementary approaches for enhancer discovery** M.W. Dorrity*[1], J.C. Cuperus[1], S. Fields[1,2], C. Queitsch[1], *[1]University of Washington, USA, [2]Howard Hughes Medical Institute, USA*
[ST11]	**Competition between histones and transcription complex assembly regulates the onset of transcription in zebrafish embryos** S.R. Joseph[1], M. Palfy[1], L. Hilbert[1,2], M. Kumar[1], A. Shevchenko[1], V. Zaburdaev[2], N.L. Vastenhouw*[1] *[1]MPI-CBG, Germany, [2]MPI-PKS, Germany*
[ST13]	**The function of transposable elements during development of the early mouse embryo** J.W. Jachowicz*[1], M.E. Torres-Padilla[2], *[1]Helmholtz Zentrum München, Germany, [2]Institut de Génétique et de Biologie Moléculaire et Cellulaire, France*
[ST14]	**The TFIIA-L paralog Moonshiner drives transcription of heterochromatin to generate piRNA precursors in *Drosophila*** P.R. Andersen*, L. Tirian, J. Brennecke, *IMBA - Institute of Molecular Biotechnology, Austria*