

Peter Kharchenko

☎ +1 (617) 320-0520

✉ 19 Eames Ln., Upton, MA, USA

📍 peter.kharchenko@gmail.com

Education

- | | |
|-------------|--|
| 1998 - 2005 | Ph.D. Biophysics
Harvard University
Advisor: George M. Church
Thesis: <i>Local properties of metabolic networks</i> |
| 1994 - 1998 | B.S. Physics
University of California, Santa Barbara |
| 1994 - 1998 | B.S. Computer Science
University of California, Santa Barbara |

Postdoctoral training

- | | |
|-----------|---|
| 2005-2006 | Genetics
Harvard Medical School
Advisor: George M. Church |
| 2006-2010 | Epigenetics
Harvard Medical School
Advisor: Peter J. Park |

Academic appointments and positions

- | | |
|-----------|---|
| 2026- | Group Leader
Institute for Molecular Biotechnology (IMBA)
Austrian Academy of Sciences, Vienna, Austria |
| 2025-2026 | Visiting Professor
Institute of Science and Technology Austria (ISTA),
Institute for Molecular Biotechnology (IMBA)
Austria |
| 2022-2025 | Principal Investigator
Altos Labs
San Diego Institute of Science, Founding member |
| 2018-2022 | Associate Professor
Harvard Medical School
Department of Biomedical Informatics |

2015-2018	Assistant Professor Harvard Medical School Department of Biomedical Informatics, Founding member
2012-2015	Assistant Professor Children's Hospital Boston Boston, MA, USA
2010-2012	Instructor Harvard Medical School Center for Biomedical Informatics

Honors and prizes

2018	Endowed Chair <i>Gilbert S. Omenn Associate Professor of Biomedical Informatics</i>
2015	Career Award <i>National Science Foundation</i>
2012	New Scholar in Aging <i>Ellison Medical Foundation</i>

Research Interests

I am a computational biologist. My group has developed methods for genomic analysis of single cells, enabling statistical separation of distinct cellular states, detection of genomic aberrations in transcriptional data, and inference of cellular dynamics from snapshots of cellular state. We have collaborated closely with many experimental groups to apply these approaches to study development and maintenance of different tissues and the impact of diseases ranging from cancer to schizophrenia. My current aims are to understand how cells coordinate their activity within biological tissues, how these mechanisms break down in the context of aging or disease, and to investigate potential interventions that may improve tissue function. Much of the effort is focused on development and collaborative application of novel computational methods for understanding tissue function, including analysis of multi-omics and spatial assays.

Teaching and Mentorship

Teaching of Students in Courses

Harvard University

2012-2015	Introduction to Bioinformatics (BMI 714)	Harvard Medical School
	Graduate students	Instructor
2014-2018	Single-Cell Workshop	Harvard Medical School
	Graduate students, postdocs, researchers	Organizer, Instructor
2016	Bootcamp in Quantitative Methods (BMI650.0)	Harvard Medical School
	Graduate students	Instructor

2017-	Computational Skills for Biomedical Sciences (BMI715/BMI713)	Harvard Medical School
	Graduate students	Instructor

Formally Supervised Trainees

Graduate Students: Jean Fan (2018; Assistant Professor, Johns Hopkins University), Teng Gao (2024), Jonathan Mitchel (2026). Co-supervised: Sizun Jiang (2017), Viktor Petukhov (University of Copenhagen, 2022).

2013-2018	Jean Fan (BIG), currently Assistant Professor at Johns Hopkins University
2012-2016	Sizun Jiang (HMS Virology), currently Assistant Professor at Harvard Medical School
2020-2024	Teng Gao (BIG), currently Damon Runyon Fellow at Harvard Medical School
2020-2025	Jonathan Mitchel (BIG)

Postdoctoral Fellows: Ruslan Soldatov (Assistant Professor, MSKCC), Xin Wang (Associate Professor, Chinese University of Hong Kong), Shenglin Mei (Assistant Professor, Virginia Tech), Joseph Herman, Marion Riggs, Tibor Pakozdi, Nikolas Barkas, Tim Hu, Qiwen Hu, Rachelly Normand, Yida Zhang, Hira Sarkar (Assistant Professor, Vanderbilt University), Jimin Guo, Marco Serra. Altos Labs: Valentine Svensson, Sergei Manakov, Ivan Imaz Rosshandler, Lance Hentges, Alejandro Mossi Albiach, Marianna Yusupova, Elijah Cole.

Funding

K25AG037596 (Kharchenko, P.) PI NIH/NHLBI	09/01/2010 – 08/30/2015 TC \$623,515
--	---

Age-associated chromatin changes in hematopoiesis

Young Scholar Award (Kharchenko, P.) PI Ellison Medical Foundation :	06/01/2012 – 05/30/2017 TC \$361,520
---	---

Epigenetic maintenance of repetitive elements in aging

NSF-14-532 (Kharchenko, P.) PI NSF	05/01/2015 – 04/30/2021 TC \$623,515
---------------------------------------	---

CAREER: Statistical Modeling of Single Cell States Informative

R01HL131768 (Kharchenko, P.) PI NIH/NHLBI	08/15/2015 – 05/31/2021 TC \$2,438,664
--	---

Statistical Methods for analysis of Single Cell variability

R21 CA220147 (Kharchenko, P.) PI NIH/NCI	8/1/17 – 7/31/21 TC \$423,766
---	----------------------------------

Single-Cell analysis of tumor-microenvironment interactions in follicular lymphoma

R01DK107784 (MPI: Kharchenko; Scadden) NIH/NHLBI	01/01/2016 – 12/31/2019 TC \$2,056,250
---	---

Deconvoluting the hematopoietic niche under stress

U01 MH114828 (MPI: Kharchenko, Zhang) NIH	9/1/18 – 5/31/23 TC \$1,422,093
--	------------------------------------

Toward a human adult brain cell atlas with single-cell technologies

2019-202743 (Kharchenko, P.) Chang Zuckerberg Foundation	7/1/19 – 6/30/22 TC \$1,750,000
---	------------------------------------

Inferring cell interactions: spatial organization of human lymph nodes (Seed Networks)

Synergy 85629 (Kharchenko, P., MPI)	10/1/20 – 9/31/26
-------------------------------------	-------------------

European Research Council

TC \$2,305,156

Kill or differentiate: Using cell-cell interactions to unlock new cancer treatments: Forcing neural crest tumors back onto the developmental path

CAP (Kharchenko, P.)
Schmidt Futures Foundation
Cell Annotation Platform

12/1/20 – 11/31/23

TC \$2,805,434

Note: I transitioned to internal funding when joining Altos Labs in 2022, relinquishing or handing over all external grants.

KAW recruitment grant (Kharchenko, P.) PI 1/1/27 – 12/31/35

Knut and Alice Wallenberg Foundation TC SEK 50,000,000

Professorial recruitment grant, awarded on nomination by Karolinska Institutet; with SEK 3,000,000 matching from Karolinska Institutet

Publications

(Note: a complete list of my publications follows, with select publications **highlighted in color**)

1. **Kharchenko P**, Babb JF, Dalgarno A. Long-range interactions of sodium atoms. *Phys. Rev. A* 1997 55.5:3566-72
2. Segre D, Zucker J, Katz J, Lin X, D'haeseleer P, Rindone W, **Kharchenko P**, Nguyen D, Wright M, and Church GM. From annotated genomes to metabolic flux models and kinetic parameter fitting. *Omics* (2003) 7:301-16.
3. **Kharchenko P**, Vitkup D, Church GM. Filling gaps in a metabolic network using expression information. *Bioinformatics* (2004) Aug 4;20 Suppl 1:I178-I185
4. **Kharchenko P**, Church GM & Vitkup D. Expression dynamics of a cellular metabolic network. *Molecular Systems Biology* (2005)
5. **Kharchenko P**, Chen L, Freund Y, Vitkup D, Church GM. Identifying metabolic enzymes with multiple types of association evidence. *BMC Bioinformatics* 2006 Mar 29;7:177.
6. Vitkup D, **Kharchenko P**, Wagner A. Influence of metabolic network structure and function on enzyme evolution. *Genome Biology*. 2006;7(5):R39.
7. Wright MA, **Kharchenko P**, Church GM, Segrè D. Chromosomal periodicity of evolutionarily conserved gene pairs. *Proc Natl Acad Sci U S A*. 2007 Jun 19;104(25):10559-64.
8. Orford K*, **Kharchenko P***, Lai W, Dao MC, Worhunsky DJ, Ferro A, Janzen V, Park PJ, Scadden DT. Differential H3K4 methylation identifies developmentally poised hematopoietic genes. *Dev Cell*. 2008 May;14(5):798-809.
9. **Kharchenko P***, Woo CJ*, Tolstorukov MY, Kingston RE, Park PJ. Nucleosome positioning in human HOX gene clusters. *Genome Res*. 2008 Oct;18(10):1554-61
10. Alekseyenko AA, Peng S, Larschan E, Gorchakov AA, Lee OK, **Kharchenko P**, McGrath SD, Wang CI, Mardis ER, Park PJ, Kuroda MI. A sequence motif within chromatin entry sites directs MSL establishment on the Drosophila X chromosome. *Cell*. 2008 Aug 22;134(4):599-609
11. **Kharchenko PV**, Tolstorukov MY, Park PJ. Design and analysis of ChIP-seq experiments for DNA-binding proteins. *Nat Biotechnol*. 2008 Dec;26(12):1351-9
12. Tolstorukov MY*, **Kharchenko PV***, Goldman JA, Kingston RE, Park PJ. Comparative analysis of H2A.Z nucleosome organization in the human and yeast genomes. *Genome Res*. 2009 Jun;19(6):967-77
13. Goncharov A.A, Alekseyenko AA, **Kharchenko PV**, Park PJ, Kuroda MI. Long-range dosage compensation in Drosophila captures transcribed autosomal genes inserted on X. *Genes & Dev*. 2009; 23 (19).
14. Woo CJ, **Kharchenko PV**, Daheron L, Park PJ, Kingston RE. A region of human HoxD that confers Polycomb-group responsiveness. *Cell*. 2010 Jan 8;140(1):99-110
15. Day DS, Luquette LJ, Park PJ, **Kharchenko PV**. Estimating enrichment of repetitive elements from high-throughput sequence data. *Genome Biol*. 2010;11(6):R69.

16. modENCODE Consortium, Roy S*, Ernst J*, **Kharchenko PV***, Kheradpour P*, Nicolas Negre*, Matthew L Eaton*, et al., Kellis M. Identification of functional elements and regulatory circuits in Drosophila by large-scale data integration. *Science*. 2010;330(6012):1787-97
17. Tolstorukov MY, **Kharchenko PV**, Park PJ. Analysis of primary structure of chromatin with next-generation sequencing. *Epigenomics*. 2010;2(2):187-197. doi: 10.2217/epi.09.48. PMID: 22022339.
18. Egelhofer TA*, Minoda A*, Klugman S*, Kolasinska-Zwierz P, Alekseyenko AA, Cheung M, Day DS, Gadel S, Gorchakov AA, Gu T, **Kharchenko PV**, Kuan S, Latorre I, Linder-Basso D, Luu Y, Ngo Q, Perry M, Rechtsteiner A, Riddle NC, Schwartz YB, Shanower GA, Vielle A, Ahringer J, Elgin SC, Kuroda MI, Pirrotta V, Ren B, Strome S, Park PJ, Karpen GH, Hawkins RD, and Lieb JD. An assessment of histone-modification antibody quality. *Nat Struct Mol Biol*. 2011 Jan;18(1):91-3
19. Riddle NC*, Minoda A*, **Kharchenko PV***, Alekseyenko AA, Schwartz YB, Tolstorukov MY, Gorchakov AA, Kennedy C, Linder-Basso D, Jaffe JD, Shanower G, Kuroda MI, Pirrotta V, Park PJ, Elgin SC, Karpen GH. Plasticity in patterns of histone modifications and chromosomal proteins in the Drosophila heterochromatin. *Genome Research*. 2011 Feb;21(2):147-63
20. Eaton ML, Prinz JA, MacAlpine HK, Tretyakov G, **Kharchenko PV** and MacAlpine DM. Chromatin signatures of the Drosophila replication program. *Genome Research*. 2011 Feb;21(2):164-74
21. Ho JW, Bishop EP, **Kharchenko PV**, Nègre N, White KP, Park PJ. ChIP-chip versus ChIP-seq: A systematic comparison of two technologies. *BMC Genomics*, 2011, 12:134
22. Larschan E, Bishop EP, **Kharchenko PV**, Core L, Lis JT, Park PJ, Kuroda MI. X chromosome dosage compensation via enhanced transcriptional elongation in Drosophila males. *Nature*, 2011 Mar 3;471(7336):115-8.
23. **Kharchenko PV**, Alekseyenko AA, Schwartz YB, Minoda A, Riddle NC, Ernst J, Sabo PJ, Larschan E, Gorchakov AA, Gu T, Linder-Basso D, Plachetka A, Shanower G, Tolstorukov MY, Bishop EP, Canfield TP, Sandstrom R, Thurman RE, Stamatoyannopoulos JA, Kellis M, Elgin SC, Kuroda MI, Pirrotta V, Karpen GH*, Park PJ*. Comprehensive analysis of the chromatin landscape in Drosophila melanogaster. *Nature*, 2011 Mar 24;471(7339):480-5
 - Mentions in the press: Furlong E. “Molecular biology: A fly in the face of genomics”, *Nature* 2012
24. **Kharchenko PV**, Xi R, Park PJ. Evidence for dosage compensation between X and autosomes in mammals. *Nature Genetics*, 2011 Nov 28;43(12):1167-9
25. Simon MD, Wang CI, **Kharchenko PV**, West JA, Chapman BA, Alekseyenko AA, Borowsky ML, Kuroda MI, Kingston RE. The genomic binding sites of a noncoding RNA. *Proc Natl Acad Sci USA*. 2011 Dec 20;108(51):20497-502
26. Septyarskiy VB, **Kharchenko P**, Kondrashov AS, Bazykin GA. Heterogeneity of the transition/transversion ratio in Drosophila and Hominidae genomes. *Mol Biol Evol*. 2012 Aug;29(8):1943-55.
27. Alekseyenko AA, Ho JW, Peng S, Gelbart M, Tolstorukov MY, Plachetka A, **Kharchenko PV**, Jung YL, Gorchakov AA, Larschan E, Gu T, Minoda A, Riddle NC, Schwartz YB, Elgin SC, Karpen GH, Pirrotta V, Kuroda MI, Park PJ. Sequence-specific targeting of dosage compensation in Drosophila favors an active chromatin context. *PLoS Genet*. 2012 Apr;8(4):e1002646.
28. Lee A, Iskow R, Yang L, Gokcumen O, Haseley P, Luquette III JL, Lohr JG, Harris CC, Ding L, Wilson RK, Wheeler DA, Gibbs RA, Kucherlapati R, Lee C, **Kharchenko PV***, Park PJ*, and The Cancer Genome Atlas Research Network. Landscape of somatic retrotransposition in human cancers. *Science*. 2012 Aug 24;337(6097):967-71
 - Mentions in the press: Williams R. “Jumping genes a cause of cancer?”, *The Scientist* 2012
29. Schwartz YB*, Linder-Basso D*, **Kharchenko PV***, Tolstorukov MY, Kim M, Li HB, Gorchakov AA, Minoda A, Shanower G, Alekseyenko AA, Riddle NC, Jung YL, Gu T, Plachetka A, Elgin SC, Kuroda MI, Park PJ, Savitsky M, Karpen GH, Pirrotta V. Nature and function of insulator protein binding sites in the Drosophila genome. *Genome Research*. 2012 Nov;22(11):2188-98. doi: 10.1101/gr.138156.112.
30. Landt SG, Marinov GK, Kundaje A, Kheradpour P, Pauli F, Batzoglou S, Bernstein BE, Bickel P, Brown JB, Cayting P, Chen Y, Desalvo G, Epstein C, Fisher-Aylor KI, Euskirchen G, Gerstein M, Gertz J, Hartemink AJ, Hoffman MM, Iyer VR, Jung YL, Karmakar S, Kellis M, **Kharchenko PV**, Li Q, Liu T, Liu XS, Ma L, Milosavljevic A, Myers RM, Park PJ, Pazin MJ, Perry MD, Raha D, Reddy TE, Rozowsky J, Shores N, Sidow A, Slattery M, Stamatoyannopoulos JA, Tolstorukov MY, White KP, Xi S, Farnham PJ, Lieb JD, Wold BJ, Snyder M. ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. *Genome Research*. 2012 Sep;22(9):1813-31

31. Riddle NC, Jung YL, Gu T, Alekseyenko AA, Asker D, Gui H, **Kharchenko PV**, Minoda A, Plachetka A, Schwartz YB, Tolstorukov MY, Kuroda MI, Pirrotta V, Karpen GH, Park PJ, Elgin SC. Enrichment of HP1a on Drosophila Chromosome 4 Genes Creates an Alternate Chromatin Structure Critical for Regulation in this Heterochromatic Domain. *PLoS Genet*. 2012 Sep;8(9):e1002954
32. ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome. *Nature*. 2012 Sep 6;489(7414):57-74
33. Wang CI, Alekseyenko AA, Leroy G, Elia AE, Gorchakov AA, Britton LM, Elledge SJ, **Kharchenko PV**, Garcia BA, Kuroda MI. Chromatin proteins captured by ChIP-mass spectrometry are linked to dosage compensation in Drosophila. *Nat Struct Mol Biol*. 2013 Feb;20(2):202-9
34. Ferrari F, Jung YL, **Kharchenko PV**, Plachetka A, Alekseyenko AA, Kuroda MI, Park PJ. Comment on "Drosophila dosage compensation involves enhanced Pol II recruitment to male X-linked promoters". *Science*. 2013 Apr 19;340(6130):273.
35. Apostolou E, Ferrari F, Walsh RM, Bar-Nur O, Stadtfeld M, Cheloufi S, Stuart HT, Polo JM, Ohsumi TK, Borowsky ML, **Kharchenko PV**, Park PJ, Hochedlinger K. Genome-wide Chromatin Interactions of the Nanog Locus in Pluripotency, Differentiation, and Reprogramming. *Cell Stem Cell*. 2013 Jun 6;12(6):699-712.
36. Woo CJ, **Kharchenko PV**, Daheron L, Park PJ, Kingston RE. Variable requirements for DNA-binding proteins at Polycomb-dependent repressive regions in the human HOX clusters. *Mol Cell Biol*. 2013 Jun 17.
37. Portal D, Zhou H, Zhao B, **Kharchenko PV**, Lowry E, Wong L, Quackenbush J, Holloway D, Jiang S, Lu Y, Kieff E. Epstein-Barr virus nuclear antigen leader protein localizes to promoters and enhancers with cell transcription factors and EBNA2. *Proc Natl Acad Sci U S A*. 2013 Nov 12;110(46):18537-42.
38. Ferrari F, Plachetka A, Alekseyenko AA, Jung YL, Ozsolak F, **Kharchenko PV**, Park PJ, Kuroda MI. "Jump start and gain" model for dosage compensation in Drosophila based on direct sequencing of nascent transcripts. *Cell Rep*. 2013 Nov 14;5(3):629-36. doi: 10.1016/j.celrep.2013.09.037.
39. Jiang S, Willox B, Zhou H, Holthaus AM, Wang A, Shi TT, Maruo S, **Kharchenko PV**, Johannsen EC, Kieff E, Zhao B. Epstein-Barr virus nuclear antigen 3C binds to BATF/IRF4 or SPI1/IRF4 composite sites and recruits Sin3A to repress CDKN2A. *Proc Natl Acad Sci U S A*. 2014 Jan 7;111(1):421-6.
40. Alekseyenko AA, Gorchakov AA, **Kharchenko PV***, Kuroda MI*. Reciprocal interactions of human C10orf12 and C17orf96 with PRC2 revealed by BioTAP-XL cross-linking and affinity purification. *Proc Natl Acad Sci U S A*. 2014 Feb 18;111(7):2488-93.
41. **Kharchenko PV***, Silberstein L, Scadden DT, Bayesian approach to single-cell differential expression analysis. *Nature Methods*, 2014 Jul;11(7):740-2. doi: 10.1038/nmeth.2967
42. Alekseyenko AA, Gorchakov AA, Zee BM, Fuchs SM, **Kharchenko PV***, Kuroda MI*. Heterochromatin-associated interactions of Drosophila HP1a with dADD1, HIPPI, and repetitive RNAs. *Genes Dev*. 2014 Jul 1;28(13):1445-60. doi: 10.1101/gad.241950.114.
43. Ho JW et al. Comparative analysis of metazoan chromatin organization. *Nature*. 2014 Aug 28;512(7515):449-52. doi: 10.1038/nature13415.
44. Usoskin D, Furlan A, Islam S, Abdo H, Lönnerberg P, Lou D, Hjerling-Leffler J, Haeggström J, Kharchenko O, **Kharchenko PV**, Linnarsson S, Ernfors P. Unbiased classification of sensory neuron types by large-scale single-cell RNA sequencing. *Nat. Neurosci*. 2015 Jan;18(1):145-53. doi: 10.1038/nn.3881. Epub 2014 Nov 24.
45. Landau DA, Clement K, Ziller MJ, Boyle P, Fan J, Gu H, Stevenson K, Sougnez C, Wang L, Li S, Kotliar D, Zhang W, Ghandi M, Garraway L, Fernandes SM, Livak KJ, Gabriel S, Gnirke A, Lander ES, Brown JR, Neuberg D, **Kharchenko PV**, Hacohen N, Getz G, Meissner A, Wu CJ. Locally disordered methylation forms the basis of intratumor methylome variation in chronic lymphocytic leukemia. *Cancer Cell*. 2014 Dec 8;26(6):813-25. doi: 10.1016/j.ccell.2014.10.012
46. Schmidt SC, Jiang S, Zhou H, Willox B, Holthaus AM, **Kharchenko PV**, Johannsen EC, Kieff E, Zhao B. Epstein-Barr virus nuclear antigen 3A partially coincides with EBNA3C genome-wide and is tethered to DNA through BATF complexes. *Proc Natl Acad Sci U S A*. 2015 Jan 13;112(2):554-9. doi: 10.1073/pnas.1422580112
47. Alekseyenko AA, McElroy KA, Kang H, Zee BM, **Kharchenko PV**, Kuroda MI. BioTAP-XL: Cross-linking/Tandem Affinity Purification to Study DNA Targets, RNA, and Protein Components of Chromatin-Associated Complexes. *Curr Protoc Mol Biol*. 2015 Jan 5;109:21.30.1-21.30.32. doi: 10.1002/0471142727.mb2130s109.

48. Zhou H, Schmidt SC, Jiang S, Willox B, Bernhardt K, Liang J, Johannsen EC, **Kharchenko PV**, Gewurz BE, Kieff E, Zhao B. Epstein-Barr virus oncoprotein super-enhancers control B cell growth. *Cell Host Microbe*. 2015 Feb 11;17(2):205-16. doi: 10.1016/j.chom.2014.12.013
49. Welling M, Chen HH, Muñoz J, Musheev MU, Kester L, Junker JP, Mischerikow N, Arbab M, Kuijk E, Silberstein L, **Kharchenko PV**, Geens M, Niehrs C, van de Velde H, van Oudenaarden A, Heck AJ, Geijsen N. DAZL regulates Tet1 translation in murine embryonic stem cells. *EMBO Rep*. 2015 Jun 15. pii: e201540538.
50. Alekseyenko AA, Walsh EM, Wang X, Grayson AR, Hsi PT, **Kharchenko PV**, Kuroda MI, French CA. The oncogenic BRD4-NUT chromatin regulator drives aberrant transcription within large topological domains. *Genes Dev*. 2015 Jul 15;29(14):1507-23.
51. Bersani F, Lee E, **Kharchenko PV**, Xu AW, Liu M, Xega K, MacKenzie OC, Brannigan BW, Wittner BS, Jung H, Ramaswamy S, Park PJ, Maheswaran S, Ting DT, Haber DA. Pericentromeric satellite repeat expansions through RNA-derived DNA intermediates in cancer. *Proc Natl Acad Sci U S A*. 2015 Dec 8;112(49):15148-53
52. Fan J, Salathia N, Liu R, Kaeser GE, Yung YC, Herman JL, Kaper F, Fan JB, Zhang K, Chun J, **Kharchenko PV**. Characterizing transcriptional heterogeneity through pathway and gene set overdispersion analysis. *Nature Methods*. 2016 Jan 18; 13:241-244
53. Masuda T, Wang X, Maeda M, Canver MC, Sher F, Funnell AP, Fisher C, Suciu M, Martyn GE, Norton LJ, Zhu C, Kurita R, Nakamura Y, Xu J, Higgs DR, Crossley M, Bauer DE, Orkin SH, **Kharchenko PV***, Maeda T*. Transcription factors LRF and BCL11A independently repress expression of fetal hemoglobin. *Science*. 2016 Jan 15;351(6270):285-9.
54. Burger JA, Landau DA, Taylor-Weiner A, Bozic I, Zhang H, Sarosiek K, Wang L, Stewart C, Fan J, Hoellenriegel J, Sivina M, Dubuc AM, Fraser C, Han Y, Li S, Livak KJ, Zou L, Wan Y, Konoplev S, Sougnez C, Brown JR, Abruzzo LV, Carter SL, Keating MJ, Davids MS, Wierda WG, Cibulskis K, Zenz T, Werner L, Dal Cin P, **Kharchenko P**, Neuberg D, Kantarjian H, Lander E, Gabriel S, O'Brien S, Letai A, Weitz DA, Nowak MA, Getz G, Wu CJ. Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. *Nat Commun*. 2016 May 20;7:11589
55. Silberstein L, Goncalves KA, **Kharchenko PV**, Turcotte R, Kfoury Y, Mercier F, Baryawno N, Severe N, Bachand J, Spencer JA, Papazian A, Lee D, Chitteti BR, Srour EF, Hoggatt J, Tate T, Lo Celso C, Ono N, Nutt S, Heino J, Sipilä K, Shioda T, Osawa M, Lin CP, Hu GF, Scadden DT. Proximity-Based Differential Single-Cell Analysis of the Niche to Identify Stem/Progenitor Cell Regulators. *Cell Stem Cell*. 2016 Aug 9.
56. Zhang X, Chen MH, Wu X, Kodani A, Fan J, Doan R, Ozawa M, Ma J, Yoshida N, Reiter JF, Black DL, **Kharchenko PV**, Sharp PA, Walsh CA. Cell-Type-Specific Alternative Splicing Governs Cell Fate in the Developing Cerebral Cortex. *Cell*. 2016 Aug 25;166(5):1147-1162.e15.
57. Wang L, Brooks AN, Fan J, Wan Y, Gambe R, Li S, Hergert S, Yin S, Freeman SS, Levin JZ, Fan L, Seiler M, Buonamici S, Smith PG, Chau KF, Cibulskis CL, Zhang W, Rassenti LZ, Ghia EM, Kipps TJ, Fernandes S, Bloch DB, Kotliar D, Landau DA, Shukla SA, Aster JC, Reed R, DeLuca DS, Brown JR, Neuberg D, Getz G, Livak KJ, Meyerson MM, **Kharchenko PV**, Wu CJ. Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. *Cancer Cell*. 2016 Nov 14;30(5):750-763.
58. Yu VW, Yusuf RZ, Oki T, Wu J, Saez B, Wang X, Cook C, Baryawno N, Ziller MJ, Lee E, Gu H, Meissner A, Lin CP, **Kharchenko PV***, Scadden DT*. Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells. *Cell*. 2016 Nov 17;167(5):1310-1322.e17
 - Mentions in the press:
 - i. North TE, Goesling W. Haematopoietic stem cells show their true colours, *Nature Cell Biol*. 19(1) 2017
 - ii. Research Highlights: Minot K. HSC function determined by epigenetic memory, *Nature Reviews Immunology* 17(5) 2016
59. Akle V, Stankiewicz AJ, Kharchenko V, Yu L, **Kharchenko PV**, Zhdanova IV. Circadian Kinetics of Cell Cycle Progression in Adult Neurogenic Niches of a Diurnal Vertebrate. *J Neurosci*. 2017 Feb 15; 37(7):1900-1909.
60. Yuan GC, Cai L, Elowitz M, Enver T, Fan G, Guo G, Irizarry R, **Kharchenko P**, Kim J, Orkin S, Quackenbush J, Saadatpour A, Schroeder T, Shivdasani R, Tirosh I. Challenges and emerging directions in single-cell analysis. *Genome Biol*. 2017 May 8;18(1):84

61. Alekseyenko AA, Walsh EM, Zee BM, Pakozdi T, Hsi P, Lemieux ME, Dal Cin P, Ince TA, **Kharchenko PV**, Kuroda MI, French CA. Ectopic protein interactions within BRD4-chromatin complexes drive oncogenic megadomain formation in NUT midline carcinoma. *Proc Natl Acad Sci U S A*. 2017 May 23;114(21):E4184-E4192
62. Wang L, Fan J, Francis JM, Georghiou G, Hergert S, Li S, Gambe R, Zhou CW, Yang C, Xiao S, Cin PD, Bowden M, Kotliar D, Shukla SA, Brown JR, Neuberg D, Alessi DR, Zhang CZ, **Kharchenko PV**, Livak KJ, Wu CJ. Integrated single-cell genetic and transcriptional analysis suggests novel drivers of chronic lymphocytic leukemia. *Genome Res*. 2017 Aug;27(8):1300-1311
63. Furlan A, Dyachuk V, Kastri ME, Calvo-Enrique L, Abdo H, Hadjab S, Chontorotzea T, Akkuratova N, Usoskin D, Kamenev D, Petersen J, Sunadome K, Memic F, Marklund U, Fried K, Topilko P, Lallemand F, **Kharchenko PV**, Ernfors P, Adameyko I. Multipotent peripheral glial cells generate neuroendocrine cells of the adrenal medulla. *Science*. 2017 Jul 7;357(6346)
64. Lake BB, Codeluppi S, Yung YC, Gao D, Chun J, **Kharchenko PV***, Linnarsson S*, Zhang K*. A comparative strategy for single-nucleus and single-cell transcriptomes confirms accuracy in predicted cell-type expression from nuclear RNA. *Sci Rep*. 2017 Jul 20;7(1):6031
65. Hoggatt J, Singh P, Tate TA, Chou BK, Datari SR, Fukuda S, Liu L, **Kharchenko PV**, Schajnovitz A, Baryawno N, Mercier FE, Boyer J, Gardner J, Morrow DM, Scadden DT, Pelus LM. Rapid Mobilization Reveals a Highly Engraftable Hematopoietic Stem Cell. *Cell*. 2017 Nov 17. pii: S0092-8674(17)31312-0
66. Lake BB, Chen S, Sos BC, Fan J, Kaeser GE, Yung YC, Duong TE, Gao D, Chun J*, **Kharchenko PV***, Zhang K*. Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. *Nature Biotechnology*. 2018 Jan; 36(1):70-80. doi: 10.1038/nbt.4038
 - Mentions in Press:
 - i. News and Views: Satija R.: Strength in numbers from integrated single-cell neuroscience. *Nature Biotech* 36(1) 2017
67. Fan J, Lee H, Lee S, Ryu D, Lee S, Xue C, Kim SJ, Kim K, Barkas N, Park PJ, Park WY*, **Kharchenko PV***. Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. *Genome Res*. 2018 June 13, doi: 10.1101/gr.228080.117
68. Petukhov V, Guo J, Baryawno N, Severe N, Scadden DT, Samsonova MG, **Kharchenko PV**. dropEst: pipeline for accurate estimation of molecular counts in droplet-based single-cell RNA-seq experiments. *Genome Biol*. 2018 Jun 19;19(1):78
69. La Manno G, Soldatov R, Zeisel A, Braun E, Hochgerner H, Petukhov V, Lidschreiber K, Kastri ME, Lönnerberg P, Furlan A, Fan J, Borm LE, Liu Z, van Bruggen D, Guo J, He X, Barker R, Sundström E, Castelo-Branco G, Cramer P, Adameyko I, Linnarsson S*, **Kharchenko PV***. RNA velocity of single cells. *Nature*. 2018 Aug 8, 10.1038/s41586-018-0414-6
 - Mentions in Press:
 - i. News and Views: Klein A.: Technique to measure the expression dynamics of each gene in a single cell. *Nature* Aug 8, 2018
 - ii. Research Highlights: Burgess D: Full speed ahead for single-cell analysis. *Nature Reviews Genetics* Aug 28, 2018
 - iii. Spotlight: Svensson V, Pachter L: Molecular kinetics from single-cell RNA-seq. *Molecular Cell*, October 4, 2018
70. Soldatov R, Kaucka M, Kastri ME, Petersen J, Chontorotzea T, Englmaier L, Akkuratova N, Yang Y, Haring M, Daychuk V, Bock C, Farlik M, Piacentino M, Boismoreau F, Hilscher MM, Yokota C, Qian X, Nilsson M, Bronner ME, Croci L, Hsiao W, Guertin DA, Brunet JF, Consalez GG, Enfors P, Fried K, **Kharchenko PV***, Adameyko I*. Spatiotemporal structure of cell fate decisions in murine neural crest. *Science*. 2019 Jun 7 10.1126/science.aas9536
71. Barkas N, Petukhov V, Nikolaeva D, Lozinsky Y, Demharther S, Khodosevich K, **Kharchenko PV**. Joint analysis of heterogeneous single-cell RNA-seq dataset collections. *Nature Methods*. 2019 Aug;16(8):695-698.
72. HuBMAP Consortium. The human body at cellular resolution: the NIH Human Biomolecular Atlas Program. *Nature*. 2019;574(7777):187-192. doi: 10.1038/s41586-019-1629-x. PMID: 31597973.

73. Bachireddy P, Ennis C, Nguyen VN, Gohil SH, Clement K, Shukla SA, Forman J, Barkas N, Freeman S, Bavli N, Elagina L, Leshchiner I, Mohammad AW, Mathewson ND, Keskin DB, Rassenti LZ, Kipps TJ, Brown JR, Getz G, Ho VT, Gnirke A, Neuberger D, Soiffer RJ, Ritz J, Alyea EP, **Kharchenko PV**, Wu CJ. Distinct evolutionary paths in chronic lymphocytic leukemia during resistance to the graft-versus-leukemia effect. *Sci Transl Med.* 2020 Sep 16;12(561):eabb7661
74. Krivanek J, Soldatov RA, Kastri ME, Chontorotzea T, Herdina AN, Petersen J, Szarowska B, Landova M, Matejova VK, Holla LI, Kuchler U, Zdrilic IV, Vijaykumar A, Balic A, Marangoni P, Klein OD, Neves VCM, Yianni V, Sharpe PT, Harkany T, Metscher BD, Bajénoff M, Mina M, Fried K, **Kharchenko PV***, Adameyko I*. Dental cell type atlas reveals stem and differentiated cell types in mouse and human teeth. *Nature Communications* . 2020 Sep 23;11(1):4816.
75. Pfisterer U, Petukhov V, Demharter S, Meichsner J, Thompson JJ, Batiuk MY, Asenjo-Martinez A, Vasistha NA, Thakur A, Mikkelsen J, Adorjan I, Pinborg LH, Pers TH, von Engelhardt J, **Kharchenko PV***, Khodosevich K*. Identification of epilepsy-associated neuronal subtypes and gene expression underlying epileptogenesis. *Nature Communications* . 2020 Oct 7;11(1):5038.
76. Kagan J, Moritz RL, Mazurchuk R, Lee JH, **Kharchenko PV**, Rozenblatt-Rosen O, Ruppén E, Edfors F, Ginty F, Goltsev Y, Wells JA, LaCava J, Riesterer JL, Germain RN, Shi T, Chee MS, Budnik BA, Yates JR, Chait BT, Moffitt JR, Smith RD, Srivastava S. National Cancer Institute Think-Tank Meeting Report on Proteomic Cartography and Biomarkers at the Single-Cell Level: Interrogation of Premalignant Lesions. *J Proteome Res.* 2020;19(5):1900-1912. doi: 10.1021/acs.jproteome.0c00021. PMID: 32163288.
77. Specht H, Emmott E, Petelski AA, Huffman RG, Perlman DH, Serra M, **Kharchenko P**, Koller A, Slavov N. Single-cell proteomic and transcriptomic analysis of macrophage heterogeneity using SCoPE2. *Genome Biology.* 2021 Jan 27;22(1):50.
78. Kupari J, Usoskin D, Parisien M, Lou D, Hu Y, Fatt M, Lönnerberg P, Spångberg M, Eriksson B, Barkas N, **Kharchenko PV**, Loré K, Khoury S, Diatchenko L, Ernfors P. Single cell transcriptomics of primate sensory neurons identifies cell types associated with chronic pain. *Nature Communnications.* 2021 Mar 8;12(1):1510.
79. Kameneva P, Artemov AV, Kastri ME, Faure L, Olsen TK, Otte J, Erickson A, Semsch B, Andersson ER, Ratz M, Frisén J, Tischler AS, de Krijger RR, Boudierlique T, Akkuratova N, Vorontsova M, Gusev O, Fried K, Sundström E, Mei S, Kogner P, Baryawno N, **Kharchenko PV***, Adameyko I*. Single-cell transcriptomics of human embryos identifies multiple sympathoblast lineages with potential implications for neuroblastoma origin. *Nature Genetics.* 2021 May;53(5):694-706.
80. Kameneva P, V Artemov A, Kastri ME, Sundström E, **Kharchenko PV***, Adameyko I*. Evolutionary switch in expression of key markers between mouse and human leads to mis-assignment of cell types in developing adrenal medulla. *Cancer Cell.* 2021 May 10;39(5):590-591. (communication)
81. **Kharchenko PV.** The triumphs and limitations of computational methods for scRNA-seq. *Nature Methods.* 2021 Jul;18(7):723-732. (review)
82. Seplyarskiy VB, Soldatov RA, Koch E, McGinty RJ, Goldmann JM, Hernandez RD, Barnes K, Correa A, Burchard EG, Ellinor PT, McGarvey ST, Mitchell BD, Vasan RS, Redline S, Silverman E, Weiss ST, Arnett DK, Blangero J, Boerwinkle E, He J, Montgomery C, Rao DC, Rotter JJ, Taylor KD, Brody JA, Chen YI, de Las Fuentes L, Hwu CM, Rich SS, Manichaikul AW, Mychaleckyj JC, Palmer ND, Smith JA, Kardia SLR, Peyser PA, Bielak LF, O'Connor TD, Emery LS; NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium; TOPMed Population Genetics Working Group, Gilissen C, Wong WSW, **Kharchenko PV**, Sunyaev S. Population sequencing data reveal a compendium of mutational processes in the human germ line. *Science.* 2021 Aug 12:eaba7408.
83. Petukhov V, Xu RJ, Soldatov RA, Cadinu P, Khodosevich K, Moffitt JR, **Kharchenko PV.** Cell segmentation in imaging-based spatial transcriptomics. *Nature Biotechnology.* 2021 Oct 14. doi: 10.1038/s41587-021-01044-w.
84. Bergen V, Soldatov RA, **Kharchenko PV**, Theis FJ. RNA velocity-current challenges and future perspectives. *Mol Syst Biol.* 2021 Aug;17(8):e10282.
85. Tasdemir-Yilmaz OE, Druckenbrod NR, Olukoya OO, Dong W, Yung AR, Bastille I, Pazyra-Murphy MF, Sitko AA, Hale EB, Vigneau S, Gimelbrant AA, **Kharchenko PV**, Goodrich LV, Segal RA. Diversity of developing peripheral glia revealed by single-cell RNA sequencing. *Developmental Cell.* 2021 Sep 13;56(17):2516-2535.e8.
86. Girskis KM, Stergachis AB, DeGennaro EM, Doan RN, Qian X, Johnson MB, Wang PP, Sejourne GM, Nagy MA, Pollina EA, Sousa AMM, Shin T, Kenny CJ, Scotellaro JL, Debo BM, Gonzalez DM, Rento LM, Yeh RC, Song JHT, Beaudin M, Fan J, **Kharchenko PV**, Sestan N, Greenberg ME, Walsh CA. Rewiring of human

neurodevelopmental gene regulatory programs by human accelerated regions. *Neuron*. 2021 Oct 20;109(20):3239-3251.e7.

87. Bedoya-Reina OC, Li W, Arceo M, Plescher M, Bullova P, Pui H, Kaucka M, **Kharchenko P**, Martinsson T, Holmberg J, Adameyko I, Deng Q, Larsson C, Juhlin CC, Kogner P, Schlisio S. Single-nuclei transcriptomes from human adrenal gland reveal distinct cellular identities of low and high-risk neuroblastoma tumors. *Nat Commun*. 2021 Sep 7;12(1):5309.
88. Bakken et al. Comparative cellular analysis of motor cortex in human, marmoset and mouse. *Nature*. 2021 Oct;598(7879):111-119.
89. Yao et al. A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. *Nature*. 2021 Oct;598(7879):103-110.
90. BRAIN Initiative Cell Census Network (BICCN). A multimodal cell census and atlas of the mammalian primary motor cortex. *Nature*. 2021 Oct;598(7879):86-102.
91. Kfoury Y, Baryawno N, Severe N, Mei S, Gustafsson K, Hirz T, Brouse T, Scadden EW, Igoalkina AA, Kokkalis K, Choi BD, Barkas N, Randolph MA, Shin JH, Saylor PJ, Scadden DT, Sykes DB, **Kharchenko PV**. Human prostate cancer bone metastases have an actionable immunosuppressive microenvironment. *Cancer Cell*. 2021 Oct 15:S1535-6108(21)00494-3.
92. Osumi-Sutherland D, Xu C, Keays M, Levine AP, **Kharchenko PV**, Regev A, Lein E, Teichmann SA. Cell type ontologies of the Human Cell Atlas. *Nat Cell Biol*. 2021 Nov;23(11):1129-1135.
93. Purroy Zuriguel N, Tong YE, Lemvigh CK, Cieri N, Li S, Parry EM, Zhang W, Rassenti LZ, Kipps TJ, Slager SL, Kay NE, Lesnick C, Shanafelt TD, Ghia P, Scarfò L, Livak KJ, **Kharchenko PV**, Neuberg D, Olsen LR, Fan J, Gohil SH, Wu CJ. Single cell analysis reveals immune dysfunction from the earliest stages of CLL that can be reversed by ibrutinib. *Blood*. 2022 Jan 12:blood.2021013926.
94. Buonomo E, Mei S, Guinn S, Leo I, Peluso M, Nolan MA, Schildberg F, Zhao L, Lian C, Xu S, Misdraji J, **Kharchenko P**, Sharpe A. Liver Stromal Cells Restrict Macrophage Maturation and Stromal IL-6 Limits the Differentiation of Cirrhosis-linked Macrophages. *J Hepatol*. 2022 Jan 21:S0168-8278(22)00007-1.
95. Verhoeven BM, Mei S, Olsen TK, Gustafsson K, Valind A, Lindström A, Gisselsson D, Fard SS, Hagerling C, **Kharchenko PV**, Kogner P, Johnsen JI, Baryawno N. The immune cell atlas of human neuroblastoma. *Cell Rep Med*. 2022 Jun 21;3(6):100657.
96. Alchahin AM, Mei S, Tsea I, Hirz T, Kfoury Y, Dahl D, Wu CL, Subtelny AO, Wu S, Scadden DT, Shin JH, Saylor PJ, Sykes DB, **Kharchenko PV***, Baryawno N*. A transcriptional metastatic signature predicts survival in clear cell renal cell carcinoma. *Nat Commun*. 2022 Sep 30;13(1):5747. doi: 10.1038/s41467-022-33375-w
97. Batiuk M, Tyler T, Dragicevic K, Mei S, Rydbirk R, Petukhov V, Devitiarov R, Sedmak D, Frank E, Feher V, Habek N, Hu Q, Igoalkina A, Roszik L, Pfisterer U, Garcia-Gonzalez D, Petanjek Z, Adorjan I*, **Kharchenko PV***, Khodosevich K*. Upper cortical layer-driven network impairment in schizophrenia. *Science Advances*. 2022 Oct 14;8(41):eabn8367. PMID: 36223459.
98. Haase C, Gustafsson K, Mei S, Yeh SC, Richter D, Milosevic J, Turcotte R, **Kharchenko PV**, Sykes DB, Scadden DT, Lin CP. Image-seq: spatially-resolved single cell sequencing guided by in situ and in vivo imaging. *Nat Methods*. 2022 Dec;19(12):1622-1633.
99. Faure L, Soldatov R, **Kharchenko PV**, Adameyko I. scFates: a scalable python package for advanced pseudotime and bifurcation analysis from single-cell data. *Bioinformatics*. 2023 Jan 1;39(1):btac746.
100. Huebner AJ, Gorelov RA, Devitiarov R, Demharter S, Kull T, Walsh RM, Taylor MS, Steiger S, Mullen JT, **Kharchenko PV***, Hochedlinger K*. Dissection of gastric homeostasis in vivo facilitates permanent capture of isthmus-like stem cells in vitro. *Nature Cell Biology*. 2023 Jan 30.
101. Hirz T, Mei S, Sarkar H, Kfoury Y, Wu S, Verhoeven BM, Subtelny AO, Zlatev DV, Wszolek MW, Salari K, Murray E, Chen F, Macosko EZ, Wu CL, Scadden DT, Dahl DM, Baryawno N*, Saylor PJ*, **Kharchenko PV***, Sykes DB*. Dissecting the immune suppressive human prostate tumor microenvironment via integrated single-cell and spatial transcriptomic analyses. *Nat Commun*. 2023 Feb 7;14(1):663.
102. Gao T, Soldatov R, Sarkar H, Kurkiewicz A, Biederstedt E, Loh PR, **Kharchenko PV**. Haplotype-aware analysis of somatic copy number variations from single-cell transcriptomes. *Nature Biotechnology* 2023 Mar;41(3):417-426. doi: 10.1038/s41587-022-01468-y.

103. Lake BB, et al. An atlas of healthy and injured cell states and niches in the human kidney. *Nature* 2023 Jul;619(7970):585-594.
104. Jain S., et al. Advances and prospects for the Human BioMolecular Atlas Program (HuBMAP). *Nature Cell Biology*. 2023 Aug;25(8):1089-1100
105. Gao T, Kastriti ME, Ljungström V, Heinzel A, Tischler AS, Oberbauer R, Loh PR, Adameyko I, Park PJ, **Kharchenko PV**. A pan-tissue survey of mosaic chromosomal alterations in 948 individuals. *Nature Genetics*. 2023 Nov;55(11):1901-1911.
 - i. Parry EM, Lemvigh CK, Deng S, Dangle N, Ruthen N, Knisbacher BA, Broséus J, Hergalant S, Guiéze R, Li S, Zhang W, Johnson C, Long JM, Yin S, Werner L, Anandappa A, Purroy N, Gohil S, Oliveira G, Bachireddy P, Shukla SA, Huang T, Khoury JD, Thakral B, Dickinson M, Tam C, Livak KJ, Getz G, Neuberg D, Feugier P, **Kharchenko P**, Wierda W, Olsen LR, Jain N, Wu CJ. ZNF683 marks a CD8+ T cell population associated with anti-tumor immunity following anti-PD-1 therapy for Richter syndrome. *Cancer Cell*. 2023;41(10):1803-1816.e8. doi: 10.1016/j.ccell.2023.08.013. PMID: 37738974.
106. Mei S, Alchahin AM, Tsea I, Kfoury Y, Hirz T, Jeffries NE, Zhao T, Xu Y, Zhang H, Sarkar H, Wu S, Subtelny AO, Johnsen JI, Zhang Y, Salari K, Wu CL, Randolph MA, Scadden DT, Dahl DM, Shin J, **Kharchenko PV**, Saylor PJ, Sykes DB, Baryawno N. Single-cell analysis of immune and stroma cell remodeling in clear cell renal cell carcinoma primary tumors and bone metastatic lesions. *Genome Med*. 2024 Jan 29;16(1):1.
107. Zhang Y, Petukhov V, Biederstedt E, Que R, Zhang K, **Kharchenko PV**. Gene panel selection for targeted spatial transcriptomics. *Genome Biol*. 2024 Jan 25;25(1):35. doi: 10.1186/s13059-024-03174-1
108. Mei S, Alchahin AM, Embaie BT, Gavriliuc IM, Verhoeven BM, Zhao T, Li X, Jeffries NE, Pepich A, Sarkar H, Olsen TK, Wickström M, Stenman J, Reina-Bedoya O, **Kharchenko PV**, Saylor PJ, Johnsen JI, Sykes DB, Kogner P, Baryawno N. Single-cell analyses of metastatic bone marrow in human neuroblastoma reveals microenvironmental remodeling and metastatic signature. *JCI Insight*. 2024 Feb 15;9(6):e173337.
109. Kalhor K, Chen CJ, Lee HS, Cai M, Nafisi M, Que R, Palmer C, Yuan Y, Zhang Y, Song J, Knoten A, Lake BB, Gaut JP, Keene D, Lein E, **Kharchenko PV**, Chun J, Jain S, Fan JB, Zhang K. Mapping Human Tissues with Highly Multiplexed RNA in situ Hybridization. *Nat Commun*. 2024 Mar 20;15(1):2511
110. Olsen TK, Otte J, Mei S, Embaie BT, Kameneva P, Cheng H, Gao T, Zachariadis V, Tsea I, Björklund Å, Kryukov E, Hou Z, Johansson A, Sundström E, Martinsson T, Fransson S, Stenman J, Fard SS, Johnsen JI, Kogner P, Adameyko I, Enge M, **Kharchenko PV***, Baryawno N*. Joint single-cell genetic and transcriptomic analysis reveal pre-malignant SCP-like subclones in human neuroblastoma. *Mol Cancer*. 2024 Aug 31;23(1):180.
111. Keller MS, Gold I, McCallum C, Manz T, **Kharchenko PV**, Gehlenborg N. Vitesse: integrative visualization of multimodal and spatially resolved single-cell data. *Nature Methods*. 2025 Jan;22(1):63-67. doi: 10.1038/s41592-024-02436-x.
112. Mitchel J, Gordon MG, Perez RK, Biederstedt E, Bueno R, Ye CJ, **Kharchenko PV**. Coordinated, multicellular patterns of transcriptional variation that stratify patient cohorts are revealed by tensor decomposition. *Nature Biotechnology*. 2025 Jul;43(7):1192-1201. doi: 10.1038/s41587-024-02411-z.
113. Toghani D, Gupte S, Zeng S, Mahammadov E, Crosse EI, Seyedhassantehrani N, Burns C, Gravano D, Radtke S, Kiem HP, Rodriguez S, Carlesso N, Pradeep A, Georgiades A, Lucas F, Wilson NK, Kinston SJ, Göttgens B, Zong L, Beerman I, Park B, Janssens DH, Jones D, Toghani A, Nerlov C, Pietras EM, Mesnieres M, Maes C, Kumanogoh A, Worzfeld T, Cheong JG, Josefowicz SZ, **Kharchenko P**, Scadden DT, Scialdone A, Spencer JA, Silberstein L. Niche-derived Semaphorin 4A safeguards functional identity of myeloid-biased hematopoietic stem cells. *Nature Aging*. 2025 Apr;5(4):558-575. doi: 10.1038/s43587-024-00798-7.
114. Embaie BT, Sarkar H, Alchahin AM, Otte J, Olsen TK, Tümmeler C, Kameneva P, Artemov AV, Akkuratova N, Adameyko I, Stukenborg JB, Wickström M, Kogner P, Johnsen JI, Mei S, **Kharchenko PV**, Baryawno N. Comparative Single-Cell Transcriptomics of Human Neuroblastoma and Preclinical Models Reveals Conservation of an Adrenergic Cell State. *Cancer Research* 2025 Mar 14;85(6):1015-1034. doi: 10.1158/0008-5472.CAN-24-1507.
115. Gustafsson K, Isaev S, Mirsanaye K, Hofmann J, Kooshesh KA, Baryawno N, Kiem A, Severe N, Zhao T, Scadden EW, Spencer JA, Burns C, Akilan K, Barkas N, Gessesew H, Kokkalis KD, Lin CP, **Kharchenko PV**, Scadden DT. Mesenchymal thymic niche cells enable regeneration of the adult thymus and T cell immunity. *Nature Biotechnology*. 2025 Oct 30. doi: 10.1038/s41587-025-02864-w.

116. Mitchell J, Gao T, Petukhov V, Cole E, **Kharchenko PV**. Impact and correction of segmentation errors in spatial transcriptomics. *Nature Genetics*. 2026 Jan 20. doi: 10.1038/s41588-025-02497-4. Online ahead of print.
117. Palmer CR, Song J, Yang B, Chen CJ, Diep D, Conklin K, Plongthongkum N, Indralingam HS, Liu CS, Kurtz J, Hu Q, Ransom L, Shahnaee A, Hiniker A, Hodge RD, Dirk Keene C, Lein E, **Kharchenko P**, Zemke NR, Chun J, Ren B, Zhang K. Single-cell multiomic human brain atlas reveals regulatory drivers of cortical regionality. *Nat Commun*. 2026;17(1):3051. doi: 10.1038/s41467-026-69368-2. PMID: 41723114.
118. Poverennaya I, Murtazina A, Li L, Maili L, Sourada L, Montano-Gutierrez LF, Galimullina R, Steinschaden T, Kaiser M, Zikmund T, Goralija A, Gao T, Attina A, Clara O, Bartenhagen C, Erickson A, Gershtein Y, Chen S, Polaskova K, Sterba J, Semasch B, Anderson ER, Prakash V, Vincent T, Arceo M, Kogner P, Schlisio S, **Kharchenko PV**, David A, Kaiser J, Fischer M, Skoda J, Trainor PA, Chagin AS, Adameyko I. Ribosomal modifications are associated with mesenchymal fate selection in the neural crest lineage. *Nat Commun*. 2026;17(1):2326. doi: 10.1038/s41467-026-70375-6. PMID: 41803115.
119. Rydbirk R, Sørensen FNF, Folke J, Haukedal H, Martinez AA, Vargas IL, McGarry S, Hollmann OC, Gherardelli C, Sepulveda S, Szafran AT, Mancini MA, Kaalund SS, Brudek T, Salvesen L, Bech S, Okarmus J, **Kharchenko P**, Meyer M, Soto C, Freude K, Mukherjee A, Aznar S, Khodosevich K. Single-nucleus brain transcriptomics reveals microglia dysfunction in multiple system atrophy. *Nat Commun*. 2026;17(1):5234. doi: 10.1038/s41467-026-71525-6. PMID: 41986335.
120. Schwarz LA, Dotter CP, Isaev S, Lisi M, Malzl D, Büschl C, Ladstätter S, Oliveira B, Barel M, Basilico B, Chintaluri C, Gorkiewicz S, Goudarzi M, Belinova T, Reichl S, Sendžikaitė G, Jayaram SA, Koppensteiner P, Sommer C, Vogels TP, Menche J, Adameyko I, **Kharchenko PV**, Bock C, Novarino G. Cortical development dynamics across autism spectrum disorder mouse models. *Nature*. 2026;656(8126):159-172. doi: 10.1038/s41586-026-10679-1. PMID: 42310454.
121. Gonzalez Lopez M, Katsura KA, Neves VCM, Soldatov R, Lavicky J, Azam M, Kavkova M, Cigosova K, Tamsamrit B, Bonnardel J, Gong H, Nemec KM, Bennett FC, Tuaima H, Yianni V, Sharpe PT, Bajenoff M, **Kharchenko P**, Bennett ML, Adameyko I, Krivanek J. Embryonic and postnatal macrophages are necessary for proper tooth development and homeostasis. *Nat Commun*. 2026;17(1):6537. doi: 10.1038/s41467-026-75576-7. PMID: 42469240.
122. Kastriti ME, Maksimov D, Krupinova J, Utkina M, Beltsevich D, Roslyakova A, Glazova O, Kaziakhmedova S, Ryabova A, Kuznetsova A, Shcherbakova A, Bondarenko E, Antysheva Z, Albert E, Urusova L, Lapshina A, Chevais A, Avsievich E, Trofimov V, Melnichenko G, Mokrysheva N, Dedov I, Englmaier L, Petersen J, Gusev O, Heinzl A, Oberbauer R, Volchkov P, **Kharchenko PV***, Adameyko I*. Human and mouse adrenal glands are characterized by species-specific steroidogenic states and tissue turnover. *Nature Genetics*. 2026. doi: 10.1038/s41588-026-02737-1.