

# Stanford

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## Kathleen Houlahan

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### Bio

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#### STANFORD ADVISORS

- Christina Curtis, Postdoctoral Faculty Sponsor

### Publications

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#### PUBLICATIONS

- **Deterministic evolution and stringent selection during preneoplasia.** *Nature*  
Karlsson, K., Przybilla, M. J., Kotler, E., Khan, A., Xu, H., Karagyzova, K., Sockell, A., Wong, W. H., Liu, K., Mah, A., Lo, Y. H., Lu, B., Houlahan, et al  
2023
- **Germline-mediated immunoediting sculpts breast cancer subtypes and metastatic proclivity.** *bioRxiv : the preprint server for biology*  
Houlahan, K. E., Khan, A., Greenwald, N. F., West, R. B., Angelo, M., Curtis, C.  
2023
- **A polygenic two-hit hypothesis for prostate cancer.** *Journal of the National Cancer Institute*  
Houlahan, K. E., Livingstone, J., Fox, N. S., Kurganova, N., Zhu, H., Sietsma Penington, J., Jung, C. H., Yamaguchi, T. N., Heisler, L. E., Jovelin, R., Costello, A. J., Pope, B. J., Kishan, et al  
2023
- **Prostate Cancer Transcriptomic Regulation by the Interplay of Germline Risk Alleles, Somatic Mutations, and 3D Genomic Architecture.** *Cancer discovery*  
Yuan, J., Houlahan, K. E., Ramanand, S. G., Lee, S., Baek, G., Yang, Y., Chen, Y., Strand, D. W., Zhang, M. Q., Boutros, P. C., Mani, R. S.  
2022; 12 (12): 2838-2855
- **Molecular classification and biomarkers of clinical outcome in breast ductal carcinoma in situ: Analysis of TBCRC 038 and RAHBT cohorts.** *Cancer cell*  
Strand, S. H., Rivero-Gutierrez, B., Houlahan, K. E., Seoane, J. A., King, L. M., Risom, T., Simpson, L. A., Vennam, S., Khan, A., Cisneros, L., Hardman, T., Harmon, B., Couch, et al  
2022
- **Targeted profiling of human extrachromosomal DNA by CRISPR-CATCH.** *Nature genetics*  
Hung, K. L., Luebeck, J., Dehkordi, S. R., Colon, C. I., Li, R., Wong, I. T., Coruh, C., Dharamipragada, P., Lomeli, S. H., Weiser, N. E., Moriceau, G., Zhang, X., Bailey, et al  
2022
- **Combinatorial immunotherapies overcome MYC-driven immune evasion in triple negative breast cancer.** *Nature communications*  
Lee, J. V., Housley, F., Yau, C., Nakagawa, R., Winkler, J., Anttila, J. M., Munne, P. M., Savelius, M., Houlahan, K. E., Van de Mark, D., Hemmati, G., Hernandez, G. A., Zhang, et al  
2022; 13 (1): 3671
- **A tumor "personality" test to guide therapeutic decision making.** *Cancer cell*  
Houlahan, K. E., Curtis, C.

2021

- **Do Breast Cancer Risk Scores Work for You?** *Journal of the National Cancer Institute*  
Houlahan, K. E.  
2021
- **CRISPR screens reveal a DNA methylation-mediated 3D genome dependent causal mechanism in prostate cancer.** *Nature communications*  
Ahmed, M., Soares, F., Xia, J. H., Yang, Y., Li, J., Guo, H., Su, P., Tian, Y., Lee, H. J., Wang, M., Akhtar, N., Houlahan, K. E., Bosch, et al  
2021; 12 (1): 1781
- **The landscape of RNA polymerase II-associated chromatin interactions in prostate cancer.** *The Journal of clinical investigation*  
Ramanand, S. G., Chen, Y., Yuan, J., Daescu, K., Lambros, M. B., Houlahan, K. E., Carreira, S., Yuan, W., Baek, G., Sharp, A., Paschalis, A., Kanchwala, M., Gao, et al  
2020; 130 (8): 3987-4005
- **The DNA methylation landscape of advanced prostate cancer.** *Nature genetics*  
Zhao, S. G., Chen, W. S., Li, H., Foye, A., Zhang, M., Sjöström, M., Aggarwal, R., Playdle, D., Liao, A., Alumkal, J. J., Das, R., Chou, J., Hua, et al  
2020; 52 (8): 778-789
- **Genome-wide germline correlates of the epigenetic landscape of prostate cancer.** *Nature medicine*  
Houlahan, K. E., Shiah, Y. J., Gusev, A., Yuan, J., Ahmed, M., Shetty, A., Ramanand, S. G., Yao, C. Q., Bell, C., O'Connor, E., Huang, V., Fraser, M., Heisler, et al  
2019; 25 (10): 1615-1626
- **Modelling the MYC-driven normal-to-tumour switch in breast cancer.** *Disease models & mechanisms*  
Lourenco, C., Kalkat, M., Houlahan, K. E., De Melo, J., Longo, J., Done, S. J., Boutros, P. C., Penn, L. Z.  
2019; 12 (7)
- **Molecular Hallmarks of Multiparametric Magnetic Resonance Imaging Visibility in Prostate Cancer.** *European urology*  
Houlahan, K. E., Salmasi, A., Sadun, T. Y., Pooli, A., Felker, E. R., Livingstone, J., Huang, V., Raman, S. S., Ahuja, P., Sisk, A. E., Boutros, P. C., Reiter, R. E.  
2019; 76 (1): 18-23
- **PLATYPUS: A Multiple-View Learning Predictive Framework for Cancer Drug Sensitivity Prediction.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*  
Graim, K., Friedl, V., Houlahan, K. E., Stuart, J. M.  
2019; 24: 136-147
- **BPG: Seamless, automated and interactive visualization of scientific data.** *BMC bioinformatics*  
P'ng, C., Green, J., Chong, L. C., Waggott, D., Prokopec, S. D., Shamsi, M., Nguyen, F., Mak, D. Y., Lam, F., Albuquerque, M. A., Wu, Y., Jung, E. H., Starmans, et al  
2019; 20 (1): 42
- **Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection.** *Genome biology*  
Lee, A. Y., Ewing, A. D., Ellrott, K., Hu, Y., Houlahan, K. E., Bare, J. C., Espiritu, S. M., Huang, V., Dang, K., Chong, Z., Caloian, C., Yamaguchi, T. N., Kellen, et al  
2018; 19 (1): 188
- **Valection: design optimization for validation and verification studies.** *BMC bioinformatics*  
Cooper, C. I., Yao, D., Sendorek, D. H., Yamaguchi, T. N., P'ng, C., Houlahan, K. E., Caloian, C., Fraser, M., Ellrott, K., Margolin, A. A., Bristow, R. G., Stuart, J. M., Boutros, et al  
2018; 19 (1): 339
- **MYC dephosphorylation by the PP1/PNUTS phosphatase complex regulates chromatin binding and protein stability.** *Nature communications*  
Dingar, D., Tu, W. B., Resetca, D., Lourenco, C., Tamachi, A., De Melo, J., Houlahan, K. E., Kalkat, M., Chan, P. K., Boutros, P. C., Raught, B., Penn, L. Z.  
2018; 9 (1): 3502
- **The Evolutionary Landscape of Localized Prostate Cancers Drives Clinical Aggression.** *Cell*  
Espirito, S. M., Liu, L. Y., Rubanova, Y., Bhandari, V., Holgersen, E. M., Szyca, L. M., Fox, N. S., Chua, M. L., Yamaguchi, T. N., Heisler, L. E., Livingstone, J., Wintersinger, J., Yousif, et al  
2018; 173 (4): 1003-1013.e15
- **Germline contamination and leakage in whole genome somatic single nucleotide variant detection.** *BMC bioinformatics*

Sendorek, D. H., Caloian, C., Ellrott, K., Bare, J. C., Yamaguchi, T. N., Ewing, A. D., Houlahan, K. E., Norman, T. C., Margolin, A. A., Stuart, J. M., Boutros, P. C.  
2018; 19 (1): 28

● **Pathogenic Germline Variants in 10,389 Adult Cancers.** *Cell*

Huang, K. L., Mashl, R. J., Wu, Y. n., Ritter, D. I., Wang, J. n., Oh, C. n., Paczkowska, M. n., Reynolds, S. n., Wyczalkowski, M. A., Oak, N. n., Scott, A. D., Krassowski, M. n., Cherniack, et al  
2018; 173 (2): 355–70.e14

● **Genomic hallmarks of localized, non-indolent prostate cancer.** *Nature*

Fraser, M., Sabelnykova, V. Y., Yamaguchi, T. N., Heisler, L. E., Livingstone, J., Huang, V., Shiah, Y. J., Yousif, F., Lin, X., Masella, A. P., Fox, N. S., Xie, M., Prokopec, et al  
2017; 541 (7637): 359-364

● **Compendium of TCDD-mediated transcriptomic response datasets in mammalian model systems.** *BMC genomics*

Prokopec, S. D., Houlahan, K. E., Sun, R. X., Watson, J. D., Yao, C. Q., Lee, J., P'ng, C., Pang, R., Wu, A. H., Chong, L. C., Smith, A. B., Harding, N. J., Moffat, et al  
2017; 18 (1): 78

● **Transcriptional profiling of rat white adipose tissue response to 2,3,7,8-tetrachlorodibenzo-#-dioxin.** *Toxicology and applied pharmacology*

Houlahan, K. E., Prokopec, S. D., Sun, R. X., Moffat, I. D., Lindén, J., Lensu, S., Okey, A. B., Pohjanvirta, R., Boutros, P. C.  
2015; 288 (2): 223-31

● **Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection.** *Nature methods*

Ewing, A. D., Houlahan, K. E., Hu, Y., Ellrott, K., Caloian, C., Yamaguchi, T. N., Bare, J. C., P'ng, C., Waggott, D., Sabelnykova, V. Y., Kellen, M. R., Norman, T. C., Haussler, et al  
2015; 12 (7): 623-30

● **Transcriptional profiling of rat hypothalamus response to 2,3,7,8-tetrachlorodibenzo-#-dioxin.** *Toxicology*

Houlahan, K. E., Prokopec, S. D., Moffat, I. D., Lindén, J., Lensu, S., Okey, A. B., Pohjanvirta, R., Boutros, P. C.  
2015; 328: 93-101

● **Cross-species transcriptomic analysis elucidates constitutive aryl hydrocarbon receptor activity.** *BMC genomics*

Sun, R. X., Chong, L. C., Simmons, T. T., Houlahan, K. E., Prokopec, S. D., Watson, J. D., Moffat, I. D., Lensu, S., Lindén, J., P'ng, C., Okey, A. B., Pohjanvirta, R., Boutros, et al  
2014; 15: 1053