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PROFESSIONAL EXPERIENCE

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PUBLICATIONS (peer-reviewed journals):

1. Moon SY, Lee H, Kim S, Hong JH, Chun SH, Lee HY, **Kang K**, Kim HS, Won HS, Ko YH. Inhibition of STAT3 enhances sensitivity to tamoxifen in tamoxifen-resistant breast cancer cells. BMC Cancer. 2021 Aug 18;21(1):931. doi: 10.1186/s12885-021-08641-7.
2. Kim BJ *, Youn DH, Chang IB, **Kang K** *, Jeon JP. Identification of Differentially-Methylated Genes and Pathways in Patients with Delayed Cerebral Ischemia Following Subarachnoid Hemorrhage. J Korean Neurosurg Soc. 2021 Jul 29. doi: 10.3340/jkns.2021.0035. Online ahead of print. (***co-first author**)
3. Oh C, Kim HR, Oh S, Ko JY, Kim Y, **Kang K**, Yang Y, Kim J, Park JH, Roe JS, Yoo KH. Epigenetic Upregulation of MAGE-A Isoforms Promotes Breast Cancer Cell Aggressiveness. Cancers (Basel). 2021 Jun 25;13(13):3176. doi: 10.3390/cancers13133176.
4. Kim SY, Shen Q, Son K, Kim HS, Yang HD, Na MJ, Shin E, Yu S, **Kang K**, You JS, Yu KR, Jeong SM, Lee EK, Ahn YM, Park WS, Nam SW. SMARCA4 oncogenic potential via IRAK1 enhancer to activate Gankyrin and AKR1B10 in liver cancer. Oncogene. 2021 Jul;40(28):4652-4662. doi: 10.1038/s41388-021-01875-6. Epub 2021 Jun 17.

5. Chae S[*], Hong J[*], **Kang K**[*], Shin A, Kim DG, Lee S, Kim MY, Jung I, Kim D. Molecular laterality encodes stress susceptibility in the medial prefrontal cortex. Mol Brain. 2021 Jun 14;14(1):92. doi: 10.1186/s13041-021-00802-w. (***co-first author**)
6. **Kang K**[†], Choi Y, Moon H, You C, Seo M, Kwon G, Yun J, Bech BR, Kang K. Epigenomic analysis of RAD51 ChIP-seq data reveals cis-regulatory elements associated with autophagy in cancer cell lines. Cancers, 2021 (in press) ([†]**corresponding author**)
7. Kim S-K, Liu X, Park J, Um D, Kilaru G, Chiang C-M, Kang M, Huber KM, **Kang K**[†], Kim T-K[†]. Functional coordination of BET family proteins underlies altered transcription associated with memory impairment in fragile X syndrome. Sci Adv., 2021, 7(21):eabf7346 ([†]**corresponding author**)
8. Jeong J, Hamza MT, **Kang K**, Jo DS, Bae IJ, Kim D, Cho DH, Bunch H. Tetraarsenic oxide affects non-coding RNA transcriptome through deregulating polycomb complexes in MCF7 cells., Adv Biol Regul. 2021, 80:100809
9. Qiu K, Lee J, Kim H, Yoon S, **Kang K**. Machine learning based anti-cancer drug response prediction and search for predictor genes using cancer cell line gene expression. Genomics Inform. 2021, 19(1):e10
10. Mun S, Kim S, Lee W, **Kang K**, Meyer TJ, Han BG, Han K, Kim HS. A study of transposable element-associated structural variations (TASVs) using a de novo-assembled Korean genome. Exp Mol Med. 2021, 53(4):615-630
11. Lee S, Hong JH, Kim JS, Yoon JS, Chun SH, Hong SA, Kim EJ, **Kang K**, Lee Kang J, Ko YH, Ahn YH. Cancer-associated fibroblasts activated by miR-196a promote the migration and invasion of lung cancer cells. Cancer Lett. 2021, 508:92-103
12. Lee HK, Knabl L, Pipperger L, Volland A, Furth PA, **Kang K**, Smith HE, Knabl L Sr, Bellmann R, Bernhard C, Kaiser N, Gänzer H, Ströhle M, Walser A, von Laer D, Hennighausen L. Immune transcriptomes of highly exposed SARS-CoV-2 asymptomatic seropositive versus seronegative individuals from the Ischgl community. Sci Rep. 2021, 11(1):4243
13. Hong SH, Son KH, Ha SY, Wee TI, Choi SK, Won JE, Han HD, Ro Y, Park YM, Eun JW, Nam SW, Han JW, **Kang K**, You JS. Nucleoporin 210 Serves a Key Scaffold for SMARCB1 in Liver Cancer. Cancer Res. 2021, 81(2):356-370
14. Choi Y, Shin B, **Kang K**, Park S, Beck BR. Target-Centered Drug Repurposing Predictions of Human Angiotensin-Converting Enzyme 2 (ACE2) and Transmembrane Protease Serine Subtype 2 (TMPRSS2) Interacting Approved Drugs for Coronavirus Disease 2019 (COVID-19) Treatment through a Drug-Target Interaction Deep Learning Model., Viruses, 2020, 12(11):1325
15. Kim D, Park NY, **Kang K**, Calderwood SK, Cho DH, Bae IJ, Bunch H. Arsenic hexoxide has differential effects on cell proliferation and genome-wide gene expression in human primary mammary epithelial and MCF7 cells. Sci Rep. 2021, 11(1):3761
16. **Kang K**[†], Choi Y, Kim HH, Yoo KH, Yu S. Predicting FOXM1-Mediated Gene Regulation through the Analysis of Genome-Wide FOXM1 Binding Sites in MCF-7, K562, SK-N-SH, GM12878 and ECC-1 Cell Lines. Int J Mol Sci., 2020, 21(17):6141 ([†]**corresponding author**)

17. Yang M, Petralia F, Li Z, Li H, Ma W, Song X, Kim S, Lee H, Yu H, Lee B, Bae S, Heo E, Kaczmarczyk J, Stępniak P, Warchoł M, Yu T, Calinawan AP, Boutros PC, Payne SH, Reva B; NCI-CPTAC-DREAM Consortium, Boja E, Rodriguez H, Stolovitzky G, Guan Y, Kang J, Wang P, Fenyö D, Saez-Rodriguez J. Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. Cell Syst., 2020, 11(2):186-195
18. **Kang K**†, Kim HH, Choi Y. Tiotropium is Predicted to be a Promising Drug for COVID-19 Through Transcriptome-Based Comprehensive Molecular Pathway Analysis. Viruses, 2020, 12(7):776 (†**corresponding author**)
19. Kim JS, Chun SH, Park S, Lee S, Kim SE, Hong JH, **Kang K**, Ko YH, Ahn YH. Identification of Novel microRNA Prognostic Markers Using Cascaded Wx, a Neural Network-Based Framework, in Lung Adenocarcinoma Patients. Cancers, 2020, 12(7):1890
20. Kim BJ, Kim Y, Youn DH, Park JJ, Rhim JK, Kim HC, **Kang K**, Jeon JP. Genome-wide blood DNA methylation analysis in patients with delayed cerebral ischemia after subarachnoid hemorrhage. Sci Rep., 2020, 10(1):11419
21. Kim GC, Lee CG, Verma R, Rudra D, Kim T, **Kang K**, Nam JH, Kim Y, Im SH, Kwon HK. ETS1 Suppresses Tumorigenesis of Human Breast Cancer via Trans-Activation of Canonical Tumor Suppressor Genes. Front Oncol., 2020, 10:642
22. Yoon S, Won HS, **Kang K**, Qiu K, Park WJ, Ko YH. Hormone Receptor-Status Prediction in Breast Cancer Using Gene Expression Profiles and Their Macroscopic Landscape., Cancers, 2020, 12(5):1165
23. Kim TO, Park DI, Han YK, **Kang K**, Park SG, Park HR, Yi JM. Genome-Wide Analysis of the DNA Methylation Profile Identifies the Fragile Histidine Triad (FHIT) Gene as a New Promising Biomarker of Crohn's Disease. J Clin Med. 2020, 9(5):1338
24. Beck BR, Shin B, Choi Y, Park S, **Kang K**†**.** Predicting commercially available antiviral drugs that may act on the novel coronavirus (SARS-CoV-2) through a drug-target interaction deep learning model. Comput Struct Biotechnol J. 2020, 18:784-790 (†**corresponding author**)
25. Lee JD, Kim HY, **Kang K**, Jeong HG, Song MK, Tae IH, Lee SH, Kim HR, Lee K, Chae S, Hwang D, Kim S, Kim HS, Kim KB, Lee BM. Integration of transcriptomics, proteomics and metabolomics identifies biomarkers for pulmonary injury by polyhexamethylene guanidine phosphate (PHMG-p), a humidifier disinfectant, in rats. Arch Toxicol. 2020, 94(3):887-909
26. Kim GE, Kim NI, Lee JS, Park MH, **Kang K.** Differentially Expressed Genes in Matched Normal, Cancer, and Lymph Node Metastases Predict Clinical Outcomes in Patients With Breast Cancer. Appl Immunohistochem Mol Morphol. 2020, 28(2):111-122
27. Joung EK, Kim J, Yoon N, Maeng LS, Kim JH, Park S, **Kang K**, Kim JS, Ahn YH, Ko YH, Byun JH, Hong JH. Expression of EEF1A1 Is Associated with Prognosis of Patients with Colon Adenocarcinoma. J Clin Med., 2019, 8(11):1903
28. Hasan SN, Sharma A, Ghosh S, Hong SW, Roy-Chowdhuri S, Im SH, **Kang K**, Rudra D. Bcl11b prevents catastrophic autoimmunity by controlling multiple aspects of a regulatory T cell gene expression program. Sci Adv., 2019, 5(8):eaaw0706

29. Kim S, Mun S, Kim T, Lee KH, **Kang K**, Cho JY, Han K. Transposable element-mediated structural variation analysis in dog breeds using whole-genome sequencing. Mamm Genome. 2019, 30(9-10):289-300
30. Kim S, Kim N, **Kang K**, Kim W, Won J, Cho J. Whole Transcriptome Analysis Identifies TNS4 as a Key Effector of Cetuximab and a Regulator of the Oncogenic Activity of KRAS Mutant Colorectal Cancer Cell Lines. Cells., 2019, 8(8):878
31. Kim SY, Han YK, Song JM, Lee CH, **Kang K**, Yi JM, Park HR. Aberrantly hypermethylated tumor suppressor genes were identified in oral squamous cell carcinoma (OSCC). Clin Epigenetics., 2019, 11(1):116
32. Shin B, Park S, Hong JH, An HJ, Chun SH, Kang K, Ahn YH, Ko YH, **Kang K**[†]. Cascaded Wx: A Novel Prognosis-Related Feature Selection Framework in Human Lung Adenocarcinoma Transcriptomes. Front Genet. 2019, 10:662 ([†]**corresponding author**)
33. Kang K, Bachu M, Park SH, **Kang K**, Bae S, Park-Min KH, Ivashkiv LB. IFN-ɣ selectively suppresses a subset of TLR4-activated genes and enhancers to potentiate macrophage activation. Nat Commun., 2019, 10(1):3320
34. Park S, Shin B, Sang Shim W, Choi Y, Kang K, **Kang K**[†]. Wx: a neural network-based feature selection algorithm for transcriptomic data. Sci Rep., 2019, 9(1):10500 ([†]**corresponding author**)
35. Hong M, Hwang JT, Shin EJ, Hur HJ, **Kang K**, Choi HK, Chung MY, Chung S, Sung MJ, Park JH. Genome-wide analysis of DNA methylation identifies novel differentially methylated regions associated with lipid accumulation improved by ethanol extracts of Allium tubersosum and Capsella bursa-pastoris in a cell model. PLoS One., 2019, 14(6):e0217877
36. Bunch H, Choe H, Kim J, Jo DS, Jeon S, Lee S, Cho DH, **Kang K**. P-TEFb Regulates Transcriptional Activation in Non-coding RNA Genes. Front Genet. 2019, 10:342
37. Kim EJ, Kim JS, Lee S, Lee H, Yoon JS, Hong JH, Chun SH, Sun S, Won HS, Hong SA, **Kang K**, Jo JY, Choi M, Shin DH, Ahn YH, Ko YH. QKI, a miR-200 target gene, suppresses epithelial-to-mesenchymal transition and tumor growth. Int J Cancer, 2019, 145(6):1585-1595
38. Lee CG, Kwon HK, Kang H, Kim Y, Nam JH, Won YH, Park S, Kim T, **Kang K**, Rudra D, Jun CD, Park ZY, Im SH. Ets1 suppresses atopic dermatitis by suppressing pathogenic T cell responses. JCI Insight, 2019, 4(5):e124202
39. Kim JS, Kim EJ, Lee S, Tan X, Liu X, Park S, **Kang K**, Yoon JS, Ko YH, Kurie JM, Ahn YH. MiR-34a and miR-34b/c have distinct effects on the suppression of lung adenocarcinomas. Exp Mol Med., 2019, 51(1):1-10
40. Son K, Yu S, Shin W, Han K, **Kang K**[†]. A Simple Guideline to Assess the Characteristics of RNA-Seq Data. Biomed Res Int., 2018, 4;2018:2906292 ([†]**corresponding author**)
41. Kim GC, Kwon HK, Lee CG, Verma R, Rudra D, Kim T, **Kang K**, Nam JH, Kim Y, Im SH. Upregulation of Ets1 expression by NFATc2 and NFKB1/RELA promotes breast cancer cell invasiveness. Oncogenesis, 2018, 7(11):91
42. Hwang SH, Hwang WM, **Kang K**, Ahn TY. Gramella fulva sp. nov., isolated from a dry surface of tidal flat. J Microbiol. 2019, 57(1):23-29

43. Ghosh S, Roy-Chowdhuri S, **Kang K**, Im SH, Rudra D. The transcription factor Foxp1 preserves integrity of an active Foxp3 locus in extrathymic Treg cells. Nat Commun. 2018, 9(1):4473
44. Lee IH, **Kang K**, Kang BW, Lee SJ, Bae WK, Hwang JE, Kim HJ, Park SY, Park JS, Choi GS, Kim JG. Genetic variations using whole-exome sequencing might predict response for neoadjuvant chemoradiotherapy in locally advanced rectal cancer. Med Oncol. 2018, 35(11):145
45. Yoon S, Kim D, **Kang K**†, Park WJ. TraRECo: a greedy approach based de novo transcriptome assembler with read error correction using consensus matrix. BMC Genomics, 2018, 19(1):653 (†**corresponding author**)
46. Hong KH, Song S, Shin W, **Kang K**, Cho CS, Hong YT, Han K, Moon JH. A case of interdigitating dendritic cell sarcoma studied by whole-exome sequencing. Genes Genomics, 2018, 40(12):1279-1285
47. Hong JH, Ko YH, **Kang K**† RNA variant identification discrepancy among splice-aware alignment algorithms. PLoS One, 2018, 13(8):e0201822 (†**corresponding author**)
48. Hwang WM, Ko Y, **Kang K**, Ahn TY. Paludirhabdus telluriireducens gen. nov., sp. nov. and Paludirhabdus pumila sp. nov., isolated from soil of a mountain wetland and emended description of Gorillibacterium massiliense. Int J Syst Evol Microbiol., 2018, 68(9):3040-3046
49. Lee HS, Hwang WM, **Kang K**, Ahn TY, *Flavobacterium parvum* sp. nov., isolated from soil polluted by sewer water., 2018, 56(8):542-548
50. Hwang WM, Ko Y, Kim JH, **Kang K**†. Ahniella affigens gen. nov., sp. nov., a gammaproteobacterium isolated from sandy soil near a stream. Int J Syst Evol Microbiol. 2018, 68(8):2478-2484 (†**corresponding author**)
51. Hong JH, Ko YH, **Kang K**†. RNA-seq data of invasive ductal carcinoma and adjacent normal tissues from a Korean patient with breast cancer. Data Brief, 2018, 18:736-739 (†**corresponding author**)
52. Nguyen DD, Lee DG, Kim S, **Kang K**, Rhee JK, Chang S. Integrative Bioinformatics and Functional Analyses of GEO, ENCODE, and TCGA Reveal FADD as a Direct Target of the Tumor Suppressor BRCA1., 2018, 19(5):1458 doi: 10.3390/ijms19051458
53. Hwang WM, Kim SM, **Kang K**, Ahn T. *Uliginosibacterium sediminicola* sp. nov., isolated from freshwater sediment., 2018, doi: 10.1099/ijsem.0.002611
54. Ko Y, Yim J, Hwang WM, **Kang K**, Ahn T. *Roseomonas fluminis* sp. nov. isolated from sediment of a shallow stream. Int J Syst Evol Microbiol., 2018, doi: 10.1099/ijsem.0.002578
55. Kim T, Seo DH, Hennighausen L, Lee D†, **Kang K**† Octopus-toolkit: a workflow to automate mining of public epigenomic and transcriptomic next-generation sequencing data. Nucleic Acids Res. 2018, 46(9):e53 https://doi.org/10.1093/nar/gky083 (†**corresponding author**)
56. Bae WK, Hong CS, Park MR, Sun EG, Lee JH, **Kang K**, Ryu KH, Shim HJ, Hwang JE, Cho SH, Chung IJ. TAp73 inhibits cell invasion and migration by directly activating KAI1 expression in colorectal carcinoma. Cancer Lett. 2018, 415:106-116.
57. Kwon HM, Kang EJ, **Kang K**, Kim SD, Yang K, Yi JM. Combinatorial effects of an epigenetic inhibitor and ionizing radiation contribute to targeted elimination of pancreatic cancer stem cell. Oncotarget, 2017, 8(51):89005-89020

58. Shen Q, Eun JW, Lee K, Kim HS, Yang HD, Kim SY, Lee EK, Kim T, **Kang K**, Kim S, Min DH, Oh SN, Lee YJ, Moon H, Ro SW, Park WS, Lee JY, Nam SW. BANF1, PLOD3, SF3B4 as Early-stage Cancer Decision Markers and Drivers of Hepatocellular Carcinoma. Hepatology, 2017, doi: 10.1002/hep.29606 (**in press**)
59. Choi ES, Cheon Y, **Kang K**, Lee D. The Ino80 complex mediates epigenetic centromere propagation via active removal of histone H3. Nat Commun., 2017, 8(1):529
60. Ko Y, Hwang WM, Kim M, **Kang K**, Ahn TY. *Sphingomonas silvisoli* sp. nov., isolated from forest soil. Int J Syst Evol Microbiol., 2017, 67(8):2704-2710
61. Park SH, Kang K, Giannopoulou E, Qiao Y, **Kang K**, Kim G, Park-Min KH, Ivashkiv LB. Type I interferons and the cytokine TNF cooperatively reprogram the macrophage epigenome to promote inflammatory activation. Nat Immunol., 2017, 18(10):1104-1116
62. Kang K, Park SH, Chen J, Qiao Y, Giannopoulou E, Berg K, Hanidu A, Li J, Nabozny G, **Kang K**, Park-Min KH, Ivashkiv LB. Interferon-ɣ Represses M2 Gene Expression in Human Macrophages by Disassembling Enhancers Bound by the Transcription Factor MAF. Immunity, 2017, 47(2):235-250
63. Seo HD, Choi Y, Kim M, **Kang K**, Urano T, Lee D. The 19S proteasome is directly involved in the regulation of heterochromatin spreading in fission yeast. J Biol Chem., 2017, 292(41):17144-17155.
64. Kim D, **Kang K**, Ahn TY. *Chthonobacter albigriseus* gen. nov., sp. nov., isolated from grass-field soil. Int J Syst Evol Microbiol., 2017, 67(4):883-888
65. Yi JM, Kang EJ, Kwon HM, Bae JH, **Kang K**, Ahuja N, Yang K. Epigenetically altered miR-1247 functions as a tumor suppressor in pancreatic cancer. Oncotarget, 2017, 8(16):26600-26612
66. Yu S, Kim T, Yoo KH, **Kang K**[†] The T47D cell line is an ideal experimental model to elucidate the progesterone-specific effects of a luminal A subtype of breast cancer. Biochem Biophys Res Commun. 2017, 486(3):752-758. ([†]**corresponding author**)
67. Lee J, Choi ES, Seo HD, **Kang K**, Gilmore JM, Florens L, Washburn MP, Choe J, Workman JL, Lee D. Chromatin remodeller Fun30Fft3 induces nucleosome disassembly to facilitate RNA polymerase II elongation. Nat Commun. 2017, 8:14527.
68. Hwang WM, Kim D, **Kang K**, Ahn TY. *Flavobacterium eburneum* sp. nov., isolated from reclaimed saline land soil. Int J Syst Evol Microbiol. 67(1):55-59
69. Weidenfeld K, Schif-Zuck S, Abu-Tayeh H, **Kang K**, Kessler O, Weissmann M, Neufeld G, Barkan D. Dormant tumor cells expressing LOXL2 acquire a stem-like phenotype mediating their transition to proliferative growth. Oncotarget, 2016, 7(44):71362-71377
70. **Kang K**, Bae JH, Han K, Kim ES, Kim TO, Yi JM. A Genome-Wide Methylation Approach Identifies a New Hypermethylated Gene Panel in Ulcerative Colitis. Int J Mol Sci. 2016, **17**:E1291
71. Kim Y, Kim B, **Kang K**, Ahn TY. Sediminibacterium aquarii sp. nov., isolated from sediment in a fishbowl. Int J Syst Evol Microbiol. 2016, 66(11):4501-4505
72. *Alamri AM, ***Kang K**, Groeneveld S, Wang W, Zhong X, Kallakury B, Hennighausen L, Liu X, Furth PA. Primary cancer cell culture: mammary-optimized vs conditional reprogramming. Endocr Relat Cancer. 2016, **23**:535-554 **(*co-first author**)

73. *Yoo K., *Oh S., ***Kang K.**, Wang C., Robinson G.W., Ge K., Hennighausen L. The histone demethylase KDM6A controls the mammary luminal lineage through enzyme-independent mechanisms. *Mol. Cell. Biol.* 2016, **36**:2108-2120 **(*co-first author**)
74. Kim W., Kim D., **Kang K.**, Ahn T. *Dankookia rubra* gen. nov., sp. nov., an alphaproteobacterium isolated from sediment of a shallow stream. *Journal of Microbiology* 2016, **54**:420-425
75. Sakamoto K., Wehde B.L., Yoo K.H., Kim T., Rajbhandari N., Shin H.Y., Triplett A.A., Rädler P.D., Schuler F., Villunger A., **Kang K.**, Hennighausen L., Wagner K.U. Janus kinase 1 is essential for inflammatory cytokine signaling and mammary gland remodeling. *Mol. Cell. Biol.* 2016, **36**:1673-1690
76. Kim T, Yang S.J., Hwang D., Song J., Kim M., Kyum Kim S., **Kang K.**, Ahn J., Lee D., Kim M.Y., Kim S., Seung Koo J., Seok Koh S., Kim S.Y., Lim D.S. A basal-like breast cancer-specific role for SRF-IL6 in YAP-induced cancer stemness. *Nat Commun*. 2015, 10186
77. Metser G., Shin H.Y., Wang C., Yoo K.H., Oh S., Villarino A.V., O'Shea J.J., **Kang K.**, Hennighausen L. An autoregulatory enhancer controls mammary-specific STAT5 functions. *Nucleic Acids Res.* 2016, 44:1052-1063
78. *Yoo K.H., *Oh S., ***Kang K.**, Hensel T., Robinson G.W., Hennighausen L. Loss of EZH2 results in precocious mammary gland development and activation of STAT5-dependent genes. *Nucleic Acids Res.* 2015, **43**:8774-8789 **(*co-first author**)
79. *Bae W., ***Kang K.**, *Yu J.H., *Yoo K.H., Hennighausen L. The methyltransferases enhancer of zeste homolog (EZH) 1 and EZH2 control hepatocyte homeostasis and regeneration. *The FASEB Journal* 2015, **29**:1653-1662 **(*co-first author**)
80. Lee W., Mun S., **Kang K.**, Hennighausen L, Han K. Genome-wide target site triplication of Alu elements in the human genome. *Gene* 2015, 561:283-291
81. Kim T., Lee W., Han K., **Kang K**†. An automated analysis pipeline for a large set of ChIP-seq data: AutoChIP. *Genes & Genomics* 2015, **37**:305-311
82. Han T., Oh S., **Kang K†.** ETS family protein GABP is a novel co-factor strongly associated with genomic YY1 binding sites in various cell lines. *Genes & Genomics* 2015, 1-7
83. Dabydeen S.A., ***Kang K.**, Diaz-Crus E.S., Alamri A., Axelrod M.L., Bouker K.B., Al-Kharboosh R., Clarke R., Hennighausen L., Furth P.A. Comparison of tamoxifen and letrozole response in mammary preneoplasia of ER and aromatase overexpressing mice defines an immune-associated gene signature linked to tamoxifen resistance. *Carcinogenesis* 2014, **36**:122-132 **(*co-first author**)
84. Yoo K.H., ***Kang K.**, Feuermann Y., Jang S.J., Robinson G.W., Hennighausen L. The STAT5-regulated miR-193b locus restrains mammary stem and progenitor cell activity and alveolar differentiation. *Developmental Biol.* 2014, **395**:245-254 **(*co-first author**)
85. *Assefnia S., ***Kang K.**, Groeneveld S., Yamaji D., Dabydeen S., Alamri A.M., Liu X., Hennighausen L., Furth P.A. Trp63 is regulated by STAT5 in mammary tissue and subject to differentiation in cancer. *Endocr. Relat. Cancer* 2014, **21**:443-457 **(*co-first author**)
86. Lee S., Oh S., **Kang K.**, Han K. BLAT-Based Comparative Analysis for Transposable Elements: BLATCAT. *BioMed research international* 2014, **2014**:7

87. *Robinson G.W., ***Kang K.**, *Yoo K.H., *Yong T., Zhu B., Yamaji D., Colditz V., Jang S.J., Gronostajski R.M., Hennighausen L. Co-regulation of genetic programs by the transcription factors NFIB and STAT5. *Mol. Endocrinol.* 2014, **5**:758-767 **(*co-first author**)
88. Feuermann Y., **Kang K.**, Shamay A., Robinson G.W., Hennighausen L. MiR-21 is under control of STAT5 but is dispensable for mammary development and lactation. *PLoS One 2014*, **9**:e85123
89. *Feuermann Y., ***Kang K.**, *Gavrilova O., *Haetscher N., Jang S.J., Yoo K.H., Changtao J., Gonzalez F., Robinson G.W., Hennighausen L. MiR-193b and miR-365-1 are not required for the development and function of brown fat in the mouse. *RNA biol.* 2013, **10**:1807-1814 **(*co-first author**)
90. **Kang K.**, Yamaji D., Yoo K.H., Robinson G.W., Hennighausen L. Mammary-Specific Gene Activation Is Defined by Progressive Recruitment of STAT5 during Pregnancy and the Establishment of H3K4me3 Marks. *Mol. Cell Biol.* 2014, **34**:464-473
    This paper is selected by Editors as "Spotlights in the Current Issue"

91. **Kang K**†**.**, Robinson G.W., Hennighausen L†. Comprehensive meta-analysis of Signal Transducers and Activators of Transcription (STATs) genomic binding patterns discerns cell-specific cis-regulatory modules. *BMC genomics* 2013, **14**:4 (†**corresponding author**)
92. *Yamaji D., ***Kang K.**, Robinson G.W., Hennighausen L. Sequential activation of genetic programs in mouse mammary epithelium during pregnancy depends on STAT5A/B concentrations. *Nucleic Acids Res.* 2012, **41**:1622-1636 (***co-first author**)
93. Yu J.H., Zhu B., Riedlinger G., **Kang K.**, Hennighausen L. The liver-specific tumor suppressor STAT5 controls expression of the ROS generating enzyme NOX4 and the pro-apoptotic proteins PUMA and BIM. *Hepatology* 2012, **56**:2375-2386
94. Shim Y.S., Choi Y., **Kang K.**, Cho K., Oh S., Grewal S., Lee, D. Hrp3 controls nucleosome positioning to suppress non-coding transcription in eu- and heterochromatin. ***EMBO J.*** 2012, **31**:4375-4387 (**IF: 9.21**)
    This paper is highlighted by "Nucleosome positioning and transcription: fission yeast CHD remodellers make their move" EMBO J. 2012; 31, 4371-4372

95. Kim S.K., Jung I., Kim M., Lee H., **Kang K.**, Han Y.M., Kim Y.S., Kim D., Lee D. Human histone H3K79 methyltransferase DOT1L binds actively transcribing RNA polymerase II to regulate gene expression. *J. Biol. Chem.* 2012, **287**:39698-39709
96. Feuermann Y., Robinson G.W., Zhu B.M., **Kang K.**, Raviv N., Yamaji D., Hennighausen L. The miR-17/92 cluster is targeted by STAT5 but dispensable for mammary development. Genesis 2012, **50**:665-671
97. **Kang K.**, Hennighausen L. Genomic and bioinformatics tools to understand the biology of signal transducers and activators of transcription. *Horm. Mol. Biol. Clin. Invest.* 2012, **10**:207-210

98. Zhu B., **Kang K.**, Yu J., Chen W., Smith H., Lee D., Sun H., Wei L., Hennighausen L. Genome-wide analyses reveal the extent of opportunistic STAT5 binding that does not yield transcriptional activation of neighboring genes. *Nucleic Acids Res.* 2012, **40**:4461-4472
99. Ekram M.B., **Kang K.**, Kim H., Kim J. Retrotransposons as a major source of epigenetic variations in the mammalian genome. *Epigenetics* 2012, **7**:370-382
100. Park S.Y., Lee S.H., Kawasaki N., Itoh S., **Kang K.**, Ryu S., Hashii N., Kim J.M., Kim J.Y., Kim J.H., α1-3/4 fucosylation at Asn 241 of β-haptoglobin is a novel marker for colon cancer: a combinatorial approach for development of glycan biomarkers, *Int. J. Cancer* 2012, **130**:2366-2376
101. Kim H., **Kang K.**, Ekram M.B., Roh T., Kim J. Aebp2 as an epigenetic regulator for neural crest cells. PLoS One 2011, **6**:e25174
102. Ryu S.H., Yoo T., **Kang K.**, Park S.Y., Joe C.O., Chung J.H. Transcriptional changes of secreted Wnt antagonists in hindlimb skeletal muscle during the lifetime of the C57BL/6J mouse. *Mech Ageing Dev.* 2011, **132**:511-514
103. Ryu S.H., **Kang K.**, Yoo T., Joe C.O., Chung J.H. Transcriptional repression of repeat-derived transcripts correlates with histone hypoacetylation at repetitive DNA elements in aged mice brain. *Exp Gerontol.* 2011, **46**:811-818 (IF: 3.74)
104. **Kang K[†].**, Kim J., Chung J.H., Lee D[†]. Decoding the genome with an integrative analysis tool: Combinatorial CRM Decoder. *Nucleic Acids Res.* 2011, **39**:e116 ([†]**corresponding author**)
105. *Kim J.D., ***Kang K.**, Kim J. YY1's role in DNA methylation of Peg3 and Xist. *Nucleic Acids Res.* 2009, **37**:5656-5664 (***co-first author**)
106. Kim H., **Kang K.**, Kim J. AEBP2 as a potential targeting protein for Polycomb Repression Complex PRC2. *Nucleic Acids Res.* 2009, **37**:2940-2950
107. **Kang K.**, Chung J.H., Kim J. Evolutionary Conserved Motif Finder (ECMFinder) for genome-wide identification of clustered YY1- and CTCF- binding sites. *Nucleic Acids Res.* 2009, **37**:2003-2013
108. Yoon Y.S., Choo J.H., Yoo T., **Kang K.**, Chung J.H. RhoB is epigenetically regulated in an age- and tissue- specific manner. *Biochem Biophys Res Comm.* 2007, **362**: 164-169

RESEACH INTEREST:

- **Artificial intelligence**
- **Computational Epigenetics**
- **Next-generation sequencing (NGS) based approaches**
- **Epigenetics and diseases**
- Gene regulation via transcription factors and histone modifications
- SNPs, genomic instability, copy number variation and personalized medicine
- Novel computational algorithms for NGS data processing
- Integrative analysis of available BIG data in biological and medical sciences

HONORS AND SERVICE:

09/06 – 02/11	KAIST National Scholarship
09/06 – 02/11	Brain Korea 21 Scholarship
09/09 – 12/09	Analysis of cytokine profile of in vitro cultured stem cells, LG Household & Health

	Care Ltd, Daejeon, South Korea
09/07 – 09/08	Brain Korea 21 Overseas Scholarship
09/02 – 10/04	KATUSA Sergeant in the U.S. army (military service), HQ, 4-7 Cavalry Squadron