

• **Name:**

Seong-Eui Hong

• **Current Position:**

General Manager, Theragen BioInstitute

• **Country:**

Republic of Korea

• **Educational Background:**

2002. 3 ~ 2007. 2 The Doctoral Degree (Major in Bioinformatics) Pusan National University,
Busan, Republic of Korea
Thesis Advisor: Dr. Hae Young Chung

2000. 3 ~ 2002. 2 Master of Science (Major in Biotechnology)
Handong University, Pohang, Republic of Korea
Thesis Advisor: Dr. Myong-sool Do

1995. 3 ~ 2000. 2 Bachelor of Engineering (Major in Food and Biotechnology)
Handong University, Pohang, Republic of Korea

• **Professional Experience:**

2015. 11 ~ Manager, Theragen Etex

2015. 5 ~ 2015 Senior Consultant, Insilicogen

2014. 8 ~ 2015 Research fellow, Physiology lab, Aju University, Suwon, Republic of Korea

2012. 9 ~ 2014 Research fellow, Systems Biology Research Center, Gwangju Institute of Science and
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2007 ~ 2012. 9 Postdoctoral Researcher, Systems Biology Research Center, Gwangju Institute of
Science and Technology, Gwangju, Republic of Korea

2004 ~ 2007 Research Assistant, Systems biology, Gwangju Institute of Science and Technology,
Gwangju, Republic of Korea

2003 ~ 2004 Research Assistant, [Korea Research Institute of Bioscience and Biotechnology,
Daejeon, Republic of Korea](http://www.krib.ac.kr)

• **Main Scientific Publications:**

2018

1. A novel system-level approach using RNA-sequencing data identifies miR-30-5p and miR-142a-5p as key regulators of apoptosis in myocardial infarction. Kim JO, Park, JH, Kim T, **Hong SE**, Lee JY, Nho KJ, Cho C, Kim YS, Kang WS, Ahn Y, Kim DH. Sci Report 2018 Oct 2;8(1):14638. doi: 10.1038/s41598-018-33020-x.

2017

2. Pathway profiles based on gene-set enrichment analysis in the honey bee *Apis mellifera* under brood rearing-suppressed conditions. Kim K, Kim JH, Kim YH, **Hong SE**, Lee SH. Genomics. 2017 Aug 10. pii: S0888-7543(17)30071-X. doi: 10.1016/j.ygeno.2017.08.004.
3. Pan-cancer analysis of systematic batch effects on somatic sequence variations. Choi JH, **Hong SE**, Woo HG. BMC Bioinformatics. 2017 Apr 11;18(1):211. doi: 10.1186/s12859-017-1627-7.

2015

4. Deep sequencing-generated modules demonstrate coherent expression patterns for various cardiac diseases. **Hong SE**, Nho KJ, Song HK, Kim do H. *Gene*. 2015 Dec 10;574(1):53-60. doi: 10.1016/j.gene.2015.07.080. Epub 2015 Jul 29.
5. miR-185 plays an anti-hypertrophic role in the heart via multiple targets in the calcium-signaling pathways. Kim JO, Song DW, Kwon EJ, **Hong SE**, Song HK, Min CK, Kim do H. *PLoS One*. 2015 Mar 13;10(3):e0122509. doi: 10.1371/journal.pone.0122509. eCollection 2015.

2014

6. Identification of tissue-enriched novel transcripts and novel exons in mice. **Hong SE**, Song HK, Kim DH. *BMC Genomics* 2014,
7. Sumoylation regulates ER stress response by modulating calreticulin gene expression in XBP-1-dependent mode in *Caenorhabditis elegans*. Lim Y, Lee D, Kalichamy K, **Hong SE**, Michalak M, Ahn J, Kim DH and Lee SK. *Int J Biochem Cell Biol*. 2014,
8. Identification of the modules for heart-enriched genes. **Hong SE**, Nho KJ and Kim DH. *Exp. Clin. Cardiol*. 2014,
9. Pressure-overload cardiac hypertrophy is associated with distinct alternative splicing due to altered expression of splicing factors. Kim T, Kim JO, Oh JG, **Hong SE*** and Kim DH*. *Molecules and Cells* 2014, 37:81-87 * co-corresponding
10. Exon 9 skipping of apoptotic caspase-2 pre-mRNA is promoted by SRSF3 through interaction with exon 8. Jang HN, Lee M, Loh TJ, Choi SW, Oh HK, Moon H, Cho S, **Hong SE**, Kim DH, Sheng Z, Green MR, Park D, Zheng X, Shen H. *Biochim. Biophys. Acta* 2014, 1839:25-32
11. SC35 promotes splicing of the C5-V6-C6 isoform of CD44 pre-mRNA. Loh TJ, Moon H, Cho S, Jung DW, **Hong SE**, Kim DH, Green MR, Zheng X, Zhou J, Shen H. *Oncol. Rep*. 2014, 31:273-279.

2013

12. Meta-analysis of multiple interspecies microarray sets of cardiac diseases revealed common and disease-specific signatures. Kim T, Song HK, **Hong SE*** and Kim DH*. *Animal Cells and Systems* 2013, * co-corresponding

2012

13. Deep RNA sequencing reveals novel cardiac transcriptomic signatures for physiological and pathological hypertrophy. Song HK*, **Hong SE***, Kim T, Kim DH. *Plos One* 2012, e35552 *co-first
14. Identification of the dichotomous role of age-related LCK in calorie restriction revealed by integrative analysis of cDNA microarray and interactome. Park D, Lee EK, Jang EJ, Jeong HO, Kim BC, Ha YM, **Hong SE**, Yu, BP Chung HY. *AGE*. 2012, 35:1045-1060 (SCIE)

2011

15. Alteration of the transcriptional profile of human embryonic kidney cells by transient overexpression of mouse TRPM7 channels. Lee BC, **Hong SE**, Lim HH, Kim do H, Park CS. *Cell Physiol. Biochem*. 2011, 27:313-326 (Scopus)

2010

16. Revealing System-level Correlations between Aging and Calorie Restriction using a Mouse Transcriptome. **Hong SE**, Kim DH, Heo HS, Kim MS, Kim CH, Yu BP, Leeuwenburgh C, Chung HY. *AGE*. 2010, 32:15-30

2008

17. Identification of mouse heart transcriptomic network sensitive to various heart diseases. **Hong SE**, Park I, Cha H, Rho SH, Park WJ, Cho C, Kim DH. *Biotechnol J*. 2008, 3:648-58

2007

18. Comprehensive identification and characterization of novel cardiac genes in mouse. Park I, **Hong SE**, Kim TW, Lee J, Oh J, Choi E, Han C, Lee H, Han Kim DH, Cho C. *J Mol Cell Cardiol*. 2007, 43:93-106
19. Gene profiling during regression of pressure overload-induced cardiac hypertrophy. Yang DK, Choi BY, Lee YH, Kim YG, Cho MC, **Hong SE**, Kim DH, Hajjar RJ, Park WJ. *Physiol Genomics*. 2007, 19:30:1-7

2006

20. HCNNet: a database of heart and calcium functional network. **Hong SE**, Rho SH, Yeom YI, Kim DH. *Bioinformatics*. 2006, 22:2053-4

2004

21. Effect of retinoic acid on leptin, glycerol, and glucose levels in mature rat adipocytes in vitro. **Hong SE**, Ahn IS, Jung HS, Rayner DV, Do MS. J Med Food. 2004, 7:320-6

2003

22. AgingDB: A database for oxidative stress and calorie restriction in the study of aging. Dae Ui Park, Chul Hong Kim, **Hong SE**, Byung Pal Yu and Hae Young Chung. Journal of the American Aging Association. 2003, 26:11

2002

23. Metallothionein gene expression in human adipose tissue from lean and obese subjects. Do MS, Nam SY, **Hong SE**, Kim KW, Duncan JS, Beattie JH, Trayhurn P. Horm Metab Res. 2002, 34:348-51