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# CURRICULUM VITAE

## Personal Information


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## Professional Experience

- Jan 2015 – present: Assistant Professor, Saw Swee Hock School of Public Health, National University of Singapore, Singapore
- Oct 2011 – Dec 2014: Research fellow, Department of Biostatistics, Center for Statistical Genetics, University of Michigan, Ann Arbor, USA
  Advisor: Mike Boehnke (Ph.D.)
- July 2005 – Sept 2011: Research Assistant, Centre for Molecular Epidemiology, Yong Loo Lin School of Medicine, National University of Singapore
  Advisors: Kee-Seng Chia (MD), E-Shyong Tai (MD, Ph.D.), Yik-Ying Teo (Ph.D.)

## Education

- Aug 2007 – Sept 2011: Doctor of Philosophy, Saw Swee Hock School of Public Health, National University of Singapore, Singapore
  Advisors: Kee-Seng Chia (MD), E-Shyong Tai (MD, Ph.D.), Yik-Ying Teo (Ph.D.)
- Aug 2001 – May 2005: BSc. Hons. in Statistics, Department of Statistics and Applied Probability, National University of Singapore, Singapore

## Grants Held

NUS Startup
Principal Investigator S$180,000 April 15 – March 17
**Quantifying rare, deleterious coding variations in drug metabolism genes in Asian populations**

NIDDK/NIH
Principal Investigaor (Singapore) US$47,058 May 16 – April 17
**Proposal for the AMP T2D-GENES Data Coordination Center and Web Portal**

FNIH, USA
Principal Investigator US$297,971.14 Aug 16 – July 18
**Deposition of East Asian and South Asian individual-level data into Accelerating Medicines Partnership T2D Knowledge Portal**

## Academic Publications

(* indicates co-first author, as of 2017-01-05)


1. Blangero J, Teslovich TM, **Sim X**, Almeida MA, Jun G, Dyer TD, Johnson M, Peralta JM, Manning A, Wood AR, Fuchsberger C, Kent JW Jr, Aguilar DA, Below JE, Farook VS, Arya R, Fowler S, Blackwell TW, Puppala S, Kumar S, Glahn DC, Moses EK, Curran JE, Thameem F, Jenkinson CP, DeFronzo RA, Lehman DM, Hanis C, Abecasis G, Boehnke M, Göring H, Duggirala R, Almasy L; T2D-GENES Consortium. Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proc. 2016 Oct 18;10(Suppl 7):71-77. PubMed PMID: 27980614; PubMed Central PMCID: PMC5133484.

2. Dorajoo R, Ong RT, **Sim X**, Wang L, Liu W, Tai ES, Liu J, Saw SM. The contribution of recently identified adult BMI risk loci to paediatric obesity in a Singaporean Chinese childhood dataset. Pediatr Obes. 2016 Oct 25. doi:10.1111/ijpo.12175. [Epub ahead of print] PubMed PMID: 27780307.

3. Ehret GB, Ferreira T, Chasman DI, Jackson AU, Schmidt EM, Johnson T, Thorleifsson G, Luan J, Donnelly LA, Kanoni S, Petersen AK, Pihur V, Strawbridge RJ, Shungin D, Hughes MF, Meirelles O, Kaakinen M, Bouatia-Naji N, Kristiansson K, Shah S, Kleber ME, Guo X, Lyytikäinen LP, Fava C, Eriksson N, Nolte IM, Magnusson PK, Salfati EL, Rallidis LS, Theusch E, Smith AJ, Folkersen L, Witkowska K, Pers TH, Joehanes R, Kim SK, Lataniotis L, Jansen R, Johnson AD, Warren H, Kim YJ, Zhao W, Wu Y, Tayo BO, Bochud M; CHARGE-EchoGen Consortium; CHARGE-HF Consortium; Wellcome Trust Case Control Consortium, Absher D, Adair LS, Amin N, Arking DE, Axelsson T, Baldassarre D, Balkau B, Bandinelli S, Barnes MR, Barroso I, Bevan S, Bis JC, Bjornsdottir G, Boehnke M, Boerwinkle E, Bonnycastle LL, Boomsma DI, Bornstein SR, Brown MJ, Burnier M, Cabrera CP, Chambers JC, Chang IS, Cheng CY, Chines PS, Chung RH, Collins FS, Connell JM, Döring A, Dallongeville J, Danesh J, de Faire U, Delgado G, Dominiczak AF, Doney AS, Drenos F, Edkins S, Eicher JD, Elosua R, Enroth S, Erdmann J, Eriksson P, Esko T, Evangelou E, Evans A, Fall T, Farrall M, Felix JF, Ferrières J, Ferrucci L, Fornage M, Forrester T, Franceschini N, Franco OH, Franco-Cereceda A, Fraser RM, Ganesh SK, Gao H, Gertow K, Gianfagna F, Gigante B, Giulianini F, Goel A, Goodall AH, Goodarzi MO, Gorski M, Gräßler J, Groves CJ, Gudnason V, Gyllensten U, Hallmans G, Hartikainen AL, Hassinen M, Havulinna AS, Hayward C, Hercberg S, Herzig KH, Hicks AA, Hingorani AD, Hirschhorn JN, Hofman A, Holmen J, Holmen OL, Hottenga JJ, Howard P, Hsiung CA, Hunt SC, Ikram MA, Illig T, Iribarren C, Jensen RA, Kähönen M, Kang HM, Kathiresan S, Keating BJ, Khaw KT, Kim YK, Kim E, Kivimaki M, Klopp N, Kolovou G, Komulainen P, Kooner JS, Kosova G, Krauss RM, Kuh D, Kutalik Z, Kuusisto J, Kvaløy K, Lakka TA, Lee NR, Lee IT, Lee WJ, Levy D, Li X, Liang KW, Lin H, Lin L, Lindström J, Lobbens S, Männistö S, Müller G, Müller-Nurasyid M, Mach F, Markus HS, Marouli E, McCarthy MI, McKenzie CA, Meneton P, Menni C, Metspalu A, Mijatovic V, Moilanen L, Montasser ME, Morris AD, Morrison AC, Mulas A, Nagaraja R, Narisu N, Nikus K, O'Donnell CJ, O'Reilly PF, Ong KK, Paccaud F, Palmer CD, Parsa A, Pedersen NL, Penninx BW, Perola M, Peters A, Poulter N, Pramstaller PP, Psaty BM, Quertermous T, Rao DC, Rasheed A, Rayner NW, Renström F, Rettig R, Rice KM, Roberts R, Rose LM, Rossouw J, Samani NJ, Sanna S, Saramies J, Schunkert H, Sebert S, Sheu WH, Shin YA, **Sim X**, Smit JH, Smith AV, Sosa MX, Spector TD, Stančáková A, Stanton AV, Stirrups KE, Stringham HM, Sundstrom J, Swift AJ, Syvänen AC, Tai ES, Tanaka T, Tarasov KV, Teumer A, Thorsteinsdottir U, Tobin MD, Tremoli E, Uitterlinden AG, Uusitupa M, Vaez A, Vaidya D, van Duijn CM, van Iperen EP, Vasan RS, Verwoert GC, Virtamo J, Vitart V, Voight BF, Vollenweider P, Wagner A, Wain LV, Wareham NJ, Watkins H, Weder AB, Westra HJ, Wilks R, Wilsgaard T, Wilson JF, Wong TY, Yang TP, Yao J, Yengo L, Zhang W, Zhao JH, Zhu X, Bovet P, Cooper RS, Mohlke KL, Saleheen D, Lee JY, Elliott P, Gierman HJ, Willer CJ, Franke L, Hovingh GK, Taylor KD, Dedoussis G, Sever P, Wong A, Lind L, Assimes TL, Njølstad I, Schwarz PE, Langenberg C, Snieder H, Caulfield MJ, Melander O, Laakso M, Saltevo J, Rauramaa R, Tuomilehto J, Ingelsson E, Lehtimäki T, Hveem K, Palmas W, März W, Kumari M, Salomaa V, Chen YD, Rotter JI, Froguel P, Jarvelin MR, Lakatta EG, Kuulasmaa K, Franks PW, Hamsten A, Wichmann HE, Palmer CN, Stefansson K, Ridker PM, Loos RJ, Chakravarti A, Deloukas P, Morris AP, Newton-Cheh C, Munroe PB. The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nat Genet. 2016 Oct;48(10):1171-84. doi: 10.1038/ng.3667. Epub 2016 Sep 12. PubMed PMID: 27618452; PubMed Central PMCID: PMC5042863.

1. Surendran P[*], Drenos F[*], Young R[*], Warren H[*], Cook JP[*], Manning AK[*], Grarup N[*], **Sim X**[*], Barnes DR, Witkowska K, Staley JR, Tragante V, Tukiainen T, Yaghootkar H, Masca N, Freitag DF, Ferreira T,

Giannakopoulou O, Tinker A, Harakalova M, Mihailov E, Liu C, Kraja AT, Nielsen SF, Rasheed A, Samuel M, Zhao W, Bonnycastle LL, Jackson AU, Narisu N, Swift AJ, Southam L, Marten J, Huyghe JR, Stančáková A, Fava C, Ohlsson T, Matchan A, Stirrups KE, Bork-Jensen J, Gjesing AP, Kontto J, Perola M, Shaw-Hawkins S, Havulinna AS, Zhang H, Donnelly LA, Groves CJ, Rayner NW, Neville MJ, Robertson NR, Yiorkas AM, Herzig KH, Kajantie E, Zhang W, Willems SM, Lannfelt L, Malerba G, Soranzo N, Trabetti E, Verweij N, Evangelou E, Moayyeri A, Vergnaud AC, Nelson CP, Poveda A, Varga TV, Caslake M, de Craen AJ, Trompet S, Luan J, Scott RA, Harris SE, Liewald DC, Marioni R, Menni C, Farmaki AE, Hallmans G, Renström F, Huffman JE, Hassinen M, Burgess S, Vasan RS, Felix JF; CHARGE-Heart Failure Consortium, Uria-Nickelsen M, Malarstig A, Reilly DF, Hoek M, Vogt TF, Lin H, Lieb W; EchoGen Consortium, Traylor M, Markus HS; METASTROKE Consortium, Highland HM, Justice AE, Marouli E; GIANT Consortium, Lindström J, Uusitupa M, Komulainen P, Lakka TA, Rauramaa R, Polasek O, Rudan I, Rolandsson O, Franks PW, Dedoussis G, Spector TD; EPIC-InterAct Consortium, Jousilahti P, Männistö S, Deary IJ, Starr JM, Langenberg C, Wareham NJ, Brown MJ, Dominiczak AF, Connell JM, Jukema JW, Sattar N, Ford I, Packard CJ, Esko T, Mägi R, Metspalu A, de Boer RA, van der Meer P, van der Harst P; Lifelines Cohort Study, Gambaro G, Ingelsson E, Lind L, de Bakker PI, Numans ME, Brandslund I, Christensen C, Petersen ER, Korpi-Hyövälti E, Oksa H, Chambers JC, Kooner JS, Blakemore AI, Franks S, Jarvelin MR, Husemoen LL, Linneberg A, Skaaby T, Thuesen B, Karpe F, Tuomilehto J, Doney AS, Morris AD, Palmer CN, Holmen OL, Hveem K, Willer CJ, Tuomi T, Groop L, Käräjämäki A, Palotie A, Ripatti S, Salomaa V, Alam DS, Majumder AA, Di Angelantonio E, Chowdhury R, McCarthy MI, Poulter N, Stanton AV, Sever P, Amouyel P, Arveiler D, Blankenberg S, Ferrières J, Kee F, Kuulasmaa K, Müller-Nurasyid M, Veronesi G, Virtamo J, Deloukas P; Wellcome Trust Case Control Consortium, Elliott P; Understanding Society Scientific Group, Zeggini E, Kathiresan S, Melander O, Kuusisto J, Laakso M, Padmanabhan S, Porteous DJ, Hayward C, Scotland G, Collins FS, Mohlke KL, Hansen T, Pedersen O, Boehnke M, Stringham HM; EPIC-CVD Consortium, Frossard P, Newton-Cheh C; CHARGE+ Exome Chip Blood Pressure Consortium, Tobin MD, Nordestgaard BG; T2D-GENES Consortium; GoT2DGenes Consortium; ExomeBP Consortium; CHD Exome+ Consortium, Caulfield MJ, Mahajan A, Morris AP, Tomaszewski M, Samani NJ, Saleheen D, Asselbergs FW, Lindgren CM, Danesh J, Wain LV, Butterworth AS, Howson JM, Munroe PB. Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nat Genet. 2016 Oct;48(10):1151-61. doi:10.1038/ng.3654. Epub 2016 Sep 12. PubMed PMID: 27618447.

2. Fuchsberger C, Flannick J, Teslovich TM, Mahajan A, Agarwala V, Gaulton KJ, Ma C, Fontanillas P, Moutsianas L, McCarthy DJ, Rivas MA, Perry JR, **Sim X**, Blackwell TW, Robertson NR, Rayner NW, Cingolani P, Locke AE, Tajes JF, Highland HM, Dupuis J, Chines PS, Lindgren CM, Hartl C, Jackson AU, Chen H, Huyghe JR, van de Bunt M, Pearson RD, Kumar A, Müller-Nurasyid M, Grarup N, Stringham HM, Gamazon ER, Lee J, Chen Y, Scott RA, Below JE, Chen P, Huang J, Go MJ, Stitzel ML, Pasko D, Parker SC, Varga TV, Green T, Beer NL, Day-Williams AG, Ferreira T, Fingerlin T, Horikoshi M, Hu C, Huh I, Ikram MK, Kim BJ, Kim Y, Kim YJ, Kwon MS, Lee J, Lee S, Lin KH, Maxwell TJ, Nagai Y, Wang X, Welch RP, Yoon J, Zhang W, Barzilai N, Voight BF, Han BG, Jenkinson CP, Kuulasmaa T, Kuusisto J, Manning A, Ng MC, Palmer ND, Balkau B, Stančáková A, Abboud HE, Boeing H, Giedraitis V, Prabhakaran D, Gottesman O, Scott J, Carey J, Kwan P, Grant G, Smith JD, Neale BM, Purcell S, Butterworth AS, Howson JM, Lee HM, Lu Y, Kwak SH, Zhao W, Danesh J, Lam VK, Park KS, Saleheen D, So WY, Tam CH, Afzal U, Aguilar D, Arya R, Aung T, Chan E, Navarro C, Cheng CY, Palli D, Correa A, Curran JE, Rybin D, Farook VS, Fowler SP, Freedman BI, Griswold M, Hale DE, Hicks PJ, Khor CC, Kumar S, Lehne B, Thuillier D, Lim WY, Liu J, van der Schouw YT, Loh M, Musani SK, Puppala S, Scott WR, Yengo L, Tan ST, Taylor HA Jr, Thameem F, Wilson G, Wong TY, Njølstad PR, Levy JC, Mangino M, Bonnycastle LL, Schwarzmayr T, Fadista J, Surdulescu GL, Herder C, Groves CJ, Wieland T, Bork-

Jensen J, Brandslund I, Christensen C, Koistinen HA, Doney AS, Kinnunen L, Esko T, Farmer AJ, Hakaste L, Hodgkiss D, Kravic J, Lyssenko V, Hollensted M, Jørgensen ME, Jørgensen T, Ladenvall C, Justesen JM, Käräjämäki A, Kriebel J, Rathmann W, Lannfelt L, Lauritzen T, Narisu N, Linneberg A, Melander O, Milani L, Neville M, Orho-Melander M, Qi L, Qi Q, Roden M, Rolandsson O, Swift A, Rosengren AH, Stirrups K, Wood AR, Mihailov E, Blancher C, Carneiro MO, Maguire J, Poplin R, Shakir K, Fennell T, DePristo M, Hrabé de Angelis M, Deloukas P, Gjesing AP, Jun G, Nilsson P, Murphy J, Onofrio R, Thorand B, Hansen T, Meisinger C, Hu FB, Isomaa B, Karpe F, Liang L, Peters A, Huth C, O'Rahilly SP, Palmer CN, Pedersen O, Rauramaa R, Tuomilehto J, Salomaa V, Watanabe RM, Syvänen AC, Bergman RN, Bharadwaj D, Bottinger EP, Cho YS, Chandak GR, Chan JC, Chia KS, Daly MJ, Ebrahim SB, Langenberg C, Elliott P, Jablonski KA, Lehman DM, Jia W, Ma RC, Pollin TI, Sandhu M, Tandon N, Froguel P, Barroso I, Teo YY, Zeggini E, Loos RJ, Small KS, Ried JS, DeFronzo RA, Grallert H, Glaser B, Metspalu A, Wareham NJ, Walker M, Banks E, Gieger C, Ingelsson E, Im HK, Illig T, Franks PW, Buck G, Trakalo J, Buck D, Prokopenko I, Mägi R, Lind L, Farjoun Y, Owen KR, Gloyn AL, Strauch K, Tuomi T, Kooner JS, Lee JY, Park T, Donnelly P, Morris AD, Hattersley AT, Bowden DW, Collins FS, Atzmon G, Chambers JC, Spector TD, Laakso M, Strom TM, Bell GI, Blangero J, Duggirala R, Tai ES, McVean G, Hanis CL, Wilson JG, Seielstad M, Frayling TM, Meigs JB, Cox NJ, Sladek R, Lander ES, Gabriel S, Burtt NP, Mohlke KL, Meitinger T, Groop L, Abecasis G, Florez JC, Scott LJ, Morris AP, Kang HM, Boehnke M, Altshuler D, McCarthy MI. The genetic architecture of type 2 diabetes. Nature. 2016 Jul 11. doi: 10.1038/nature18642. [Epub ahead of print]. PMID: 27398621.

3. Horikoshi M, Pasquali L, Wiltshire S, Huyghe JR, Mahajan A, Asimit JL, Ferreira T, Locke AE, Robertson NR, Wang X, **Sim X**, Fujita H, Hara K, Young R, Zhang W, Choi S, Chen H, Kaur I, Takeuchi F, Fontanillas P, Thuillier D, Yengo L, Below JE, Tam CH, Wu Y; T2D-GENES Consortium, Abecasis G, Altshuler D, Bell GI, Blangero J, Burtt NP, Duggirala R, Florez JC, Hanis CL, Seielstad M, Atzmon G, Chan JC, Ma RC, Froguel P, Wilson JG, Bharadwaj D, Dupuis J, Meigs JB, Cho YS, Park T, Kooner JS, Chambers JC, Saleheen D, Kadowaki T, Tai ES, Mohlke KL, Cox NJ, Ferrer J, Zeggini E, Kato N, Teo YY, Boehnke M, McCarthy MI, Morris AP. Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Hum Mol Genet. 2016 Feb 23. pii: ddw048. [Epub ahead of print] PubMed PMID: 26911676.

4. Jensen RA, **Sim X**, Smith AV, Li X, Jakobsdóttir J, Cheng CY, Brody JA, Cotch MF, McKnight B, Klein R, Wang JJ, Kifley A, Harris TB, Launer LJ, Taylor KD, Klein BE, Raffel LJ, Li X, Ikram MA, Klaver CC, van der Lee SJ, Mutlu U, Hofman A, Uitterlinden AG, Liu C, Kraja AT; CHARGE Exome Chip Blood Pressure Consortium, Mitchell P, Gudnason V, Rotter JI, Boerwinkle E, van Duijn CM, Psaty BM, Wong TY. Novel Genetic Loci Associated with Retinal Microvascular Diameter. Circ Cardiovasc Genet. 2015 Nov 13. pii: CIRCGENETICS.115.001142. PubMed PMID: 26567291.

5. Wang X, Cheng CY, Liao J, **Sim X**, Liu J, Chia KS, Tai ES, Little P, Khor CC, Aung T, Wong TY, Teo YY. Evaluation of transethnic fine mapping with population-specific and cosmopolitan imputation reference panels in diverse Asian populations. Eur J Hum Genet. 2015 Jul 1. doi: 10.1038/ejhg.2015.150. PubMed PMID: 26130488.

6. He M, Xu M, Zhang B, Liang J, Chen P, Lee JY, Johnson TA, Li H, Yang X, Dai J, Liang L, Gui L, Qi Q, Huang J, Li Y, Adair LS, Aung T, Cai Q, Cheng CY, Cho MC, Cho YS, Chu M, Cui B, Gao YT, Go MJ, Gu D, Gu W, Guo H, Hao Y, Hong J, Hu Z, Hu Y, Huang J, Hwang JY, Ikram MK, Jin G, Kang DH, Khor CC, Kim BJ, Kim HT, Kubo M, Lee J, Lee J, Lee NR, Li R, Li J, Liu J, Longe J, Lu W, Lu X, Miao X, Okada Y, Ong RT, Qiu G, Seielstad M, **Sim X**, Song H, Takeuchi F, Tanaka T, Taylor PR, Wang L, Wang W, Wang Y, Wu C, Wu Y, Xiang YB, Yamamoto K, Yang H, Liao M, Yokota M, Young T, Zhang X, Kato N, Wang QK, Zheng

W, Hu FB, Lin D, Shen H, Teo YY, Mo Z, Wong TY, Lin X, Mohlke KL, Ning G, Tsunoda T, Han BG, Shu XO, Tai ES, Wu T, Qi L. Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Hum Mol Genet. 2015 Mar 15;24(6):1791-800. doi:10.1093/hmg/ddu583. Epub 2014 Nov 26. PubMed PMID: 25429064; PubMed Central PMCID: PMC4351379.

7. Hwang JY*, **Sim X***, Wu Y*, Liang J*, Tabara Y*, Hu C*, Hara K*, Tam CH*, Cai Q*, Zhao Q*, Jee S*, Takeuchi F*, Go MJ, Ong RT, Ohkubo T, Kim YJ, Zhang R, Yamauchi T, So WY, Long J, Gu D, Lee NR, Kim S, Katsuya T, Oh JH, Liu J, Umemura S, Kim YJ, Jiang F, Maeda S, Chan JC, Lu W, Hixson JE, Adair LS, Jung KJ, Nabika T, Bae JB, Lee MH, Seielstad M, Young TL, Teo YY, Kita Y, Takashima N, Osawa H, Lee SH, Shin MH, Shin DH, Choi BY, Shi J, Gao YT, Xiang YB, Zheng W, Kato N, Yoon M, He J, Shu XO, Ma RC, Kadowaki T, Jia W, Miki T, Qi L, Tai ES, Mohlke KL, Han BG, Cho YS, Kim BJ. Genome-Wide Association Meta-analysis Identifies Novel Variants Associated With Fasting Plasma Glucose in East Asians. Diabetes. 2015 Jan;64(1):291-8. Epub 2014 Sep 3. PubMed PMID: 25187374; PubMed Central PMCID: PMC4274808.

8. Mahajan A*, **Sim X***, Ng HJ*, Manning A, Rivas MA, Highland HM, Locke AE, Grarup N, Im HK, Cingolani P, Flannick J, Fontanillas P, Fuchsberger C, Gaulton KJ, Teslovich TM, Rayner NW, Robertson NR, Beer NL, Rundle JK, Bork-Jensen J, Ladenvall C, Blancher C, Buck D, Buck G, Burtt NP, Gabriel S, Gjesing AP, Groves CJ, Hollensted M, Huyghe JR, Jackson AU, Jun G, Justesen JM, Mangino M, Murphy J, Neville M, Onofrio R, Small KS, Stringham HM, Syvänen AC, Trakalo J, Abecasis G, Bell GI, Blangero J, Cox NJ, Duggirala R, Hanis CL, Seielstad M, Wilson JG, Christensen C, Brandslund I, Rauramaa R, Surdulescu GL, Doney AS, Lannfelt L, Linneberg A, Isomaa B, Tuomi T, Jørgensen ME, Jørgensen T, Kuusisto J, Uusitupa M, Salomaa V, Spector TD, Morris AD, Palmer CN, Collins FS, Mohlke KL, Bergman RN, Ingelsson E, Lind L, Tuomilehto J, Hansen T, Watanabe RM, Prokopenko I, Dupuis J, Karpe F, Groop L, Laakso M, Pedersen O, Florez JC, Morris AP, Altshuler D, Meigs JB, Boehnke M, McCarthy MI, Lindgren CM, Gloyn AL; On Behalf of the T2D-GENES consortium and GoT2D consortium. Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genet. 2015 Jan 27;11(1):e1004876. doi:10.1371/journal.pgen.1004876. eCollection 2015 Jan. PubMed PMID: 25625282; PubMed Central PMCID: PMC4307976.

9. Wen W, Zheng W, Okada Y, Takeuchi F, Tabara Y, Hwang JY, Dorajoo R, Li H, Tsai FJ, Yang X, He J, Wu Y, He M, Zhang Y, Liang J, Guo X, Sheu WH, Delahanty R, Guo X, Kubo M, Yamamoto K, Ohkubo T, Go MJ, Liu JJ, Gan W, Chen CC, Gao Y, Li S, Lee NR, Wu C, Zhou X, Song H, Yao J, Lee IT, Long J, Tsunoda T, Akiyama K, Takashima N, Cho YS, Ong RT, Lu L, Chen CH, Tan A, Rice TK, Adair LS, Gui L, Allison M, Lee WJ, Cai Q, Isomura M, Umemura S, Kim YJ, Seielstad M, Hixson J, Xiang YB, Isono M, Kim BJ, **Sim X**, Lu W, Nabika T, Lee J, Lim WY, Gao YT, Takayanagi R, Kang DH, Wong TY, Hsiung CA, Wu IC, Juang JM, Shi J, Choi BY, Aung T, Hu F, Kim MK, Lim WY, Wang TD, Shin MH, Lee J, Ji BT, Lee YH, Young TL, Shin DH, Chun BY, Cho MC, Han BG, Hwu CM, Assimes TL, Absher D, Yan X, Kim E, Kuo JZ, Kwon S, Taylor KD, Chen YD, Rotter JI, Qi L, Zhu D, Wu T, Mohlke KL, Gu D, Mo Z, Wu JY, Lin X, Miki T, Tai ES, Lee JY, Kato N, Shu XO, Tanaka T. Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. Hum Mol Genet. 2014 Oct 15;23(20):5492-504. Epub 2014 May 26.

10. Simino J, Shi G, Bis JC, Chasman DI, Ehret GB, Gu X, Guo X, Hwang SJ, Sijbrands E, Smith AV, Verwoert GC, Bragg-Gresham JL, Cadby G, Chen P, Cheng CY, Corre T, de Boer RA, Goel A, Johnson T, Khor CC; LifeLines Cohort Study, Lluís-Ganella C, Luan J, Lyytikäinen LP, Nolte IM, **Sim X**, Sõber S, van

der Most PJ, Verweij N, Zhao JH, Amin N, Boerwinkle E, Bouchard C, Dehghan A, Eiriksdottir G, Elosua R, Franco OH, Gieger C, Harris TB, Hercberg S, Hofman A, James AL, Johnson AD, Kähönen M, Khaw KT, Kutalik Z, Larson MG, Launer LJ, Li G, Liu J, Liu K, Morrison AC, Navis G, Ong RT, Papanicolau GJ, Penninx BW, Psaty BM, Raffel LJ, Raitakari OT, Rice K, Rivadeneira F, Rose LM, Sanna S, Scott RA, Siscovick DS, Stolk RP, Uitterlinden AG, Vaidya D, van der Klauw MM, Vasan RS, Vithana EN, Völker U, Völzke H, Watkins H, Young TL, Aung T, Bochud M, Farrall M, Hartman CA, Laan M, Lakatta EG, Lehtimäki T, Loos RJ, Lucas G, Meneton P, Palmer LJ, Rettig R, Snieder H, Tai ES, Teo YY, van der Harst P, Wareham NJ, Wijmenga C, Wong TY, Fornage M, Gudnason V, Levy D, Palmas W, Ridker PM, Rotter JI, van Duijn CM, Witteman JC, Chakravarti A, Rao DC. Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. Am J Hum Genet. 2014 Jul 3;95(1):24-38.

11. Lim ET, Würtz P, Havulinna AS, Palta P, Tukiainen T, Rehnström K, Esko T, Mäg R, Inouye M, Lappalainen T, Chan Y, Salem RM, Lek M, Flannick J, **Sim X**, Manning A, Ladenvall C, Bumpstead S, Hämäläinen E, Aalto K, Maksimow M, Salmi M, Blankenberg S, Ardissino D, Shah S, Horne B, McPherson R, Hovingh GK, Reilly MP, Watkins H, Goel A, Farrall M, Girelli D, Reiner AP, Stitziel NO, Kathiresan S, Gabriel S, Barrett JC, Lehtimäki T, Laakso M, Groop L, Kaprio J, Perola M, McCarthy MI, Boehnke M, Altshuler DM, Lindgren CM, Hirschhorn JN, Metspalu A, Freimer NB, Zeller T, Jalkanen S, Koskinen S, Raitakari O, Durbin R, MacArthur DG, Salomaa V, Ripatti S, Daly MJ, Palotie A; Sequencing Initiative Suomi (SISu) Project. Distribution and medical impact of loss-of-function variants in the Finnish founder population. PLoS Genet. 2014 Jul 31;10(7):e1004494.

12. DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium; Asian Genetic Epidemiology Network Type 2 Diabetes (AGEN-T2D) Consortium; South Asian Type 2 Diabetes (SAT2D) Consortium; Mexican American Type 2 Diabetes (MAT2D) Consortium; Type 2 Diabetes Genetic Exploration by Next-generation sequencing in multi-Ethnic Samples (T2D-GENES) Consortium, Mahajan A, Go MJ, Zhang W, Below JE, Gaulton KJ, Ferreira T, Horikoshi M, Johnson AD, Ng MC, Prokopenko I, Saleheen D, Wang X, Zeggini E, Abecasis GR, Adair LS, Almgren P, Atalay M, Aung T, Baldassarre D, Balkau B, Bao Y, Barnett AH, Barroso I, Basit A, Been LF, Beilby J, Bell GI, Benediktsson R, Bergman RN, Boehm BO, Boerwinkle E, Bonnycastle LL, Burtt N, Cai Q, Campbell H, Carey J, Cauchi S, Caulfield M, Chan JC, Chang LC, Chang TJ, Chang YC, Charpentier G, Chen CH, Chen H, Chen YT, Chia KS, Chidambaram M, Chines PS, Cho NH, Cho YM, Chuang LM, Collins FS, Cornelis MC, Couper DJ, Crenshaw AT, van Dam RM, Danesh J, Das D, de Faire U, Dedoussis G, Deloukas P, Dimas AS, Dina C, Doney AS, Donnelly PJ, Dorkhan M, van Duijn C, Dupuis J, Edkins S, Elliott P, Emilsson V, Erbel R, Eriksson JG, Escobedo J, Esko T, Eury E, Florez JC, Fontanillas P, Forouhi NG, Forsen T, Fox C, Fraser RM, Frayling TM, Froguel P, Frossard P, Gao Y, Gertow K, Gieger C, Gigante B, Grallert H, Grant GB, Grrop LC, Groves CJ, Grundberg E, Guiducci C, Hamsten A, Han BG, Hara K, Hassanali N, Hattersley AT, Hayward C, Hedman AK, Herder C, Hofman A, Holmen OL, Hovingh K, Hreidarsson AB, Hu C, Hu FB, Hui J, Humphries SE, Hunt SE, Hunter DJ, Hveem K, Hydrie ZI, Ikegami H, Illig T, Ingelsson E, Islam M, Isomaa B, Jackson AU, Jafar T, James A, Jia W, Jöckel KH, Jonsson A, Jowett JB, Kadowaki T, Kang HM, Kanoni S, Kao WH, Kathiresan S, Kato N, Katulanda P, Keinanen-Kiukaanniemi KM, Kelly AM, Khan H, Khaw KT, Khor CC, Kim HL, Kim S, Kim YJ, Kinnunen L, Klopp N, Kong A, Korpi-Hyövälti E, Kowlessur S, Kraft P, Kravic J, Kristensen MM, Krithika S, Kumar A, Kumate J, Kuusisto J, Kwak SH, Laakso M, Lagou V, Lakka TA, Langenberg C, Langford C, Lawrence R, Leander K, Lee JM, Lee NR, Li M, Li X, Li Y, Liang J, Liju S, Lim WY, Lind L, Lindgren CM, Lindholm E, Liu CT, Liu JJ, Lobbens S, Long J, Loos RJ, Lu W, Luan J, Lyssenko V, Ma RC, Maeda S, Mägi R, Männisto S, Matthews DR, Meigs JB, Melander O, Metspalu A, Meyer J, Mirza G, Mihailov E, Moebus S, Mohan V, Mohlke KL, Morris AD, Mühleisen TW, Müller-Nurasyid M, Musk B, Nakamura J, Nakashima E,

Navarro P, Ng PK, Nica AC, Nilsson PM, Njølstad I, Nöthen MM, Ohnaka K, Ong TH, Owen KR, Palmer CN, Pankow JS, Park KS, Parkin M, Pechlivanis S, Pedersen NL, Peltonen L, Perry JR, Peters A, Pinidiyapathirage JM, Platou CG, Potter S, Price JF, Qi L, Radha V, Rallidis L, Rasheed A, Rathman W, Rauramaa R, Raychaudhuri S, Rayner NW, Rees SD, Rehnberg E, Ripatti S, Robertson N, Roden M, Rossin EJ, Rudan I, Rybin D, Saaristo TE, Salomaa V, Saltevo J, Samuel M, Sanghera DK, Saramies J, Scott J, Scott LJ, Scott RA, Segrè AV, Sehmi J, Sennblad B, Shah N, Shah S, Shera AS, Shu XO, Shuldiner AR, Sigurđsson G, Sijbrands E, Silveira A, **Sim X**, Sivapalaratnam S, Small KS, So WY, Stančáková A, Stefansson K, Steinbach G, Steinthorsdottir V, Stirrups K, Strawbridge RJ, Stringham HM, Sun Q, Suo C, Syvänen AC, Takayanagi R, Takeuchi F, Tay WT, Teslovich TM, Thorand B, Thorleifsson G, Thorsteinsdottir U, Tikkanen E, Trakalo J, Tremoli E, Trip MD, Tsai FJ, Tuomi T, Tuomilehto J, Uitterlinden AG, Valladares-Salgado A, Vedantam S, Veglia F, Voight BF, Wang C, Wareham NJ, Wennauer R, Wickremasinghe AR, Wilsgaard T, Wilson JF, Wiltshire S, Winckler W, Wong TY, Wood AR, Wu JY, Wu Y, Yamamoto K, Yamauchi T, Yang M, Yengo L, Yokota M, Young R, Zabaneh D, Zhang F, Zhang R, Zheng W, Zimmet PZ, Altshuler D, Bowden DW, Cho YS, Cox NJ, Cruz M, Hanis CL, Kooner J, Lee JY, Seielstad M, Teo YY, Boehnke M, Parra EJ, Chambers JC, Tai ES, McCarthy MI, Morris AP. Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nat Genet. 2014 Mar;46(3):234-44.

13. Lange LA, Hu Y, Zhang H, Xue C, Schmidt EM, Tang ZZ, Bizon C, Lange EM, Smith JD, Turner EH, Jun G, Kang HM, Peloso G, Auer P, Li KP, Flannick J, Zhang J, Fuchsberger C, Gaulton K, Lindgren C, Locke A, Manning A, **Sim X**, Rivas MA, Holmen OL, Gottesman O, Lu Y, Ruderfer D, Stahl EA, Duan Q, Li Y, Durda P, Jiao S, Isaacs A, Hofman A, Bis JC, Correa A, Griswold ME, Jakobsdottir J, Smith AV, Schreiner PJ, Feitosa MF, Zhang Q, Huffman JE, Crosby J, Wassel CL, Do R, Franceschini N, Martin LW, Robinson JG, Assimes TL, Crosslin DR, Rosenthal EA, Tsai M, Rieder MJ, Farlow DN, Folsom AR, Lumley T, Fox ER, Carlson CS, Peters U, Jackson RD, van Duijn CM, Uitterlinden AG, Levy D, Rotter JI, Taylor HA, Gudnason V Jr, Siscovick DS, Fornage M, Borecki IB, Hayward C, Rudan I, Chen YE, Bottinger EP, Loos RJ, Sætrom P, Hveem K, Boehnke M, Groop L, McCarthy M, Meitinger T, Ballantyne CM, Gabriel SB, O'Donnell CJ, Post WS, North KE, Reiner AP, Boerwinkle E, Psaty BM, Altshuler D, Kathiresan S, Lin DY, Jarvik GP, Cupples LA, Kooperberg C, Wilson JG, Nickerson DA, Abecasis GR, Rich SS, Tracy RP, Willer CJ; NHLBI Grand Opportunity Exome Sequencing Project. Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. Am J Hum Genet. 2014 Feb 6;94(2):233-45.

14. Gao H, Kim YM, Chen P, Igase M, Kawamoto R, Kim MK, Kohara K, Lee J, Miki T, Ong RT, Onuma H, Osawa H, **Sim X**, Teo YY, Tabara Y, Tai ES, van Dam RM. Genetic variation in CDH13 is associated with lower plasma adiponectin levels but greater adiponectin sensitivity in East Asian populations. Diabetes. 2013 Dec;62(12):4277-83.

15. Dorajoo R, Li R, Ikram MK, Liu J, Froguel P, Lee J, **Sim X**, Ong RT, Tay WT, Peng C, Young TL, Blakemore AI, Cheng CY, Aung T, Mitchell P, Wang JJ, Klaver CC, Boerwinkle E, Klein R, Siscovick DS, Jensen RA, Gudnason V, Smith AV, Teo YY, Wong TY, Tai ES, Heng CK, Friedlander Y. Are C-reactive protein associated genetic variants associated with serum levels and retinal markers of microvascular pathology in Asian populations from Singapore? PLoS One. 2013 Jul 2;8(7):e67650.

16. Stambolian D, Wojciechowski R, Oexle K, Pirastu M, Li X, Raffel LJ, Cotch MF, Chew EY, Klein B, Klein R, Wong TY, Simpson CL, Klaver CC, van Duijn CM, Verhoeven VJ, Baird PN, Vitart V, Paterson AD, Mitchell P, Saw SM, Fossarello M, Kazmierkiewicz K, Murgia F, Portas L, Schache M, Richardson A, Xie J, Wang JJ, Rochtchina E; DCCT/EDIC Research Group, Viswanathan AC, Hayward C, Wright AF,

Polasek O, Campbell H, Rudan I, Oostra BA, Uitterlinden AG, Hofman A, Rivadeneira F, Amin N, Karssen LC, Vingerling JR, Hosseini SM, Döring A, Bettecken T, Vatavuk Z, Gieger C, Wichmann HE, Wilson JF, Fleck B, Foster PJ, Topouzis F, McGuffin P, **Sim X**, Inouye M, Holliday EG, Attia J, Scott RJ, Rotter JI, Meitinger T, Bailey-Wilson JE. Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFOX1, a regulator of tissue-specific splicing, associated with refractive error. Hum Mol Genet. 2013 Jul 1;22(13):2754-64.

17. **Sim X**[*], Jensen RA[*], Ikram MK[*], Cotch MF[*], Li X, MacGregor S, Xie J, Smith AV, Boerwinkle E, Mitchell P, Klein R, Klein BE, Glazer NL, Lumley T, McKnight B, Psaty BM, de Jong PT, Hofman A, Rivadeneira F, Uitterlinden AG, van Duijn CM, Aspelund T, Eiriksdottir G, Harris TB, Jonasson F, Launer LJ; Wellcome Trust Case Control Consortium 2, Attia J, Baird PN, Harrap S, Holliday EG, Inouye M, Rochtchina E, Scott RJ, Viswanathan A; Global BPGen Consortium, Li G, Smith NL, Wiggins KL, Kuo JZ, Taylor KD, Hewitt AW, Martin NG, Montgomery GW, Sun C, Young TL, Mackey DA, van Zuydam NR, Doney AS, Palmer CN, Morris AD, Rotter JI, Tai ES, Gudnason V, Vingerling JR, Siscovick DS, Wang JJ, Wong TY. Genetic loci for retinal arteriolar microcirculation. PLoS One. 2013 Jun 12;8(6):e65804.

18. Lam VK, Ma RC, Lee HM, Hu C, Park KS, Furuta H, Wang Y, Tam CH, **Sim X**, Ng DP, Liu J, Wong TY, Tai ES, Morris AP; DIAGRAM Consortium, Tang NL, Woo J, Leung PC, Kong AP, Ozaki R, Jia WP, Lee HK, Nanjo K, Xu G, Ng MC, So WY, Chan JC. Genetic associations of type 2 diabetes with islet amyloid polypeptide processing and degrading pathways in asian populations. PLoS One. 2013 Jun 11;8(6):e62378.

19. Olden M, Teumer A, Bochud M, Pattaro C, Köttgen A, Turner ST, Rettig R, Chen MH, Dehghan A, Bastardot F, Schmidt R, Vollenweider P, Schunkert H, Reilly MP, Fornage M, Launer LJ, Verwoert GC, Mitchell GF, Bis JC, O'Donnell CJ, Cheng CY, **Sim X**, Siscovick DS, Coresh J, Kao WH, Fox CS, O'Seaghdha CM; AortaGen, CARDIoGRAM, CHARGE Eye, CHARGE IMT, ICBP, NeuroCHARGE, and CKDGen Consortia. Overlap between common genetic polymorphisms underpinning kidney traits and cardiovascular disease phenotypes: the CKDGen consortium. Am J Kidney Dis. 2013 Jun;61(6):889-98.

20. Ma RC, Hu C, Tam CH, Zhang R, Kwan P, Leung TF, Thomas GN, Go MJ, Hara K, **Sim X**, Ho JS, Wang C, Li H, Lu L, Wang Y, Li JW, Wang Y, Lam VK, Wang J, Yu W, Kim YJ, Ng DP, Fujita H, Panoutsopoulou K, Day-Williams AG, Lee HM, Ng AC, Fang YJ, Kong AP, Jiang F, Ma X, Hou X, Tang S, Lu J, Yamauchi T, Tsui SK, Woo J, Leung PC, Zhang X, Tang NL, Sy HY, Liu J, Wong TY, Lee JY, Maeda S, Xu G, Cherny SS, Chan TF, Ng MC, Xiang K, Morris AP; DIAGRAM Consortium, Keildson S; MuTHER Consortium, Hu R, Ji L, Lin X, Cho YS, Kadowaki T, Tai ES, Zeggini E, McCarthy MI, Hon KL, Baum L, Tomlinson B, So WY, Bao Y, Chan JC, Jia W. Genome-wide association study in a Chinese population identifies a susceptibility locus for type 2 diabetes at 7q32 near PAX4. Diabetologia. 2013 Jun;56(6):1291-305.

21. Wang X, Chua HX, Chen P, Ong RT, **Sim X**, Zhang W, Takeuchi F, Liu X, Khor CC, Tay WT, Cheng CY, Suo C, Liu J, Aung T, Chia KS, Kooner JS, Chambers JC, Wong TY, Tai ES, Kato N, Teo YY. Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. Hum Mol Genet. 2013 Jun 1;22(11):2303-11.

22. Saxena R, Saleheen D, Been LF, Garavito ML, Braun T, Bjonnes A, Young R, Ho WK, Rasheed A, Frossard P, **Sim X**, Hassanali N, Radha V, Chidambaram M, Liju S, Rees SD, Ng DP, Wong TY, Yamauchi T, Hara K, Tanaka Y, Hirose H, McCarthy MI, Morris AP; DIAGRAM; MuTHER; AGEN, Basit A, Barnett AH, Katulanda P, Matthews D, Mohan V, Wander GS, Singh JR, Mehra NK, Ralhan S,

Kamboh MI, Mulvihill JJ, Maegawa H, Tobe K, Maeda S, Cho YS, Tai ES, Kelly MA, Chambers JC, Kooner JS, Kadowaki T, Deloukas P, Rader DJ, Danesh J, Sanghera DK. Genome-wide association study identifies a novel locus contributing to type 2 diabetes susceptibility in Sikhs of Punjabi origin from India. Diabetes. 2013 May;62(5):1746-55.

23. French JD, Ghoussaini M, Edwards SL, Meyer KB, Michailidou K, Ahmed S, Khan S, Maranian MJ, O'Reilly M, Hillman KM, Betts JA, Carroll T, Bailey PJ, Dicks E, Beesley J, Tyrer J, Maia AT, Beck A, Knoblauch NW, Chen C, Kraft P, Barnes D, González-Neira A, Alonso MR, Herrero D, Tessier DC, Vincent D, Bacot F, Luccarini C, Baynes C, Conroy D, Dennis J, Bolla MK, Wang Q, Hopper JL, Southey MC, Schmidt MK, Broeks A, Verhoef S, Cornelissen S, Muir K, Lophatananon A, Stewart-Brown S, Siriwanarangsan P, Fasching PA, Loehberg CR, Ekici AB, Beckmann MW, Peto J, dos Santos Silva I, Johnson N, Aitken Z, Sawyer EJ, Tomlinson I, Kerin MJ, Miller N, Marme F, Schneeweiss A, Sohn C, Burwinkel B, Guénel P, Truong T, Laurent-Puig P, Menegaux F, Bojesen SE, Nordestgaard BG, Nielsen SF, Flyger H, Milne RL, Zamora MP, Arias Perez JI, Benitez J, Anton-Culver H, Brenner H, Müller H, Arndt V, Stegmaier C, Meindl A, Lichtner P, Schmutzler RK, Engel C, Brauch H, Hamann U, Justenhoven C; GENICA Network, Aaltonen K, Heikkilä P, Aittomäki K, Blomqvist C, Matsuo K, Ito H, Iwata H, Sueta A, Bogdanova NV, Antonenkova NN, Dörk T, Lindblom A, Margolin S, Mannermaa A, Kataja V, Kosma VM, Hartikainen JM; kConFab Investigators, Wu AH, Tseng CC, Van Den Berg D, Stram DO, Lambrechts D, Peeters S, Smeets A, Floris G, Chang-Claude J, Rudolph A, Nickels S, Flesch-Janys D, Radice P, Peterlongo P, Bonanni B, Sardella D, Couch FJ, Wang X, Pankratz VS, Lee A, Giles GG, Severi G, Baglietto L, Haiman CA, Henderson BE, Schumacher F, Le Marchand L, Simard J, Goldberg MS, Labrèche F, Dumont M, Teo SH, Yip CH, Ng CH, Vithana EN, Kristensen V, Zheng W, Deming-Halverson S, Shrubsole M, Long J, Winqvist R, Pylkäs K, Jukkola-Vuorinen A, Grip M, Andrulis IL, Knight JA, Glendon G, Mulligan AM, Devilee P, Seynaeve C, García-Closas M, Figueroa J, Chanock SJ, Lissowska J, Czene K, Klevebring D, Schoof N, Hooning MJ, Martens JW, Collée JM, Tilanus-Linthorst M, Hall P, Li J, Liu J, Humphreys K, Shu XO, Lu W, Gao YT, Cai H, Cox A, Balasubramanian SP, Blot W, Signorello LB, Cai Q, Pharoah PD, Healey CS, Shah M, Pooley KA, Kang D, Yoo KY, Noh DY, Hartman M, Miao H, Sng JH, **Sim X**, Jakubowska A, Lubinski J, Jaworska-Bieniek K, Durda K, Sangrajrang S, Gaborieau V, McKay J, Toland AE, Ambrosone CB, Yannoukakos D, Godwin AK, Shen CY, Hsiung CN, Wu PE, Chen ST, Swerdlow A, Ashworth A, Orr N, Schoemaker MJ, Ponder BA, Nevanlinna H, Brown MA, Chenevix-Trench G, Easton DF, Dunning AM. Functional variants at the 11q13 risk locus for breast cancer regulate cyclin D1 expression through long-range enhancers. Am J Hum Genet. 2013 Apr 4;92(4):489-503.

24. Fritsche LG, Chen W, Schu M, Yaspan BL, Yu Y, Thorleifsson G, Zack DJ, Arakawa S, Cipriani V, Ripke S, Igo RP Jr, Buitendijk GH, **Sim X**, Weeks DE, Guymer RH, Merriam JE, Francis PJ, Hannum G, Agarwal A, Armbrecht AM, Audo I, Aung T, Barile GR, Benchaboune M, Bird AC, Bishop PN, Branham KE, Brooks M, Brucker AJ, Cade WH, Cain MS, Campochiaro PA, Chan CC, Cheng CY, Chew EY, Chin KA, Chowers I, Clayton DG, Cojocaru R, Conley YP, Cornes BK, Daly MJ, Dhillon B, Edwards AO, Evangelou E, Fagerness J, Ferreyra HA, Friedman JS, Geirsdottir A, George RJ, Gieger C, Gupta N, Hagstrom SA, Harding SP, Haritoglou C, Heckenlively JR, Holz FG, Hughes G, Ioannidis JP, Ishibashi T, Joseph P, Jun G, Kamatani Y, Katsanis N, N Keilhauer C, Khan JC, Kim IK, Kiyohara Y, Klein BE, Klein R, Kovach JL, Kozak I, Lee CJ, Lee KE, Lichtner P, Lotery AJ, Meitinger T, Mitchell P, Mohand-Saïd S, Moore AT, Morgan DJ, Morrison MA, Myers CE, Naj AC, Nakamura Y, Okada Y, Orlin A, Ortube MC, Othman MI, Pappas C, Park KH, Pauer GJ, Peachey NS, Poch O, Priya RR, Reynolds R, Richardson AJ, Ripp R, Rudolph G, Ryu E, Sahel JA, Schaumberg DA, Scholl HP, Schwartz SG, Scott WK, Shahid H, Sigurdsson H, Silvestri G, Sivakumaran TA, Smith RT, Sobrin L, Souied EH, Stambolian DE, Stefansson H, Sturgill-Short GM, Takahashi A, Tosakulwong N, Truitt BJ, Tsironi EE, Uitterlinden AG, van Duijn CM, Vijaya L,

Vingerling JR, Vithana EN, Webster AR, Wichmann HE, Winkler TW, Wong TY, Wright AF, Zelenika D, Zhang M, Zhao L, Zhang K, Klein ML, Hageman GS, Lathrop GM, Stefansson K, Allikmets R, Baird PN, Gorin MB, Wang JJ, Klaver CC, Seddon JM, Pericak-Vance MA, Iyengar SK, Yates JR, Swaroop A, Weber BH, Kubo M, Deangelis MM, Léveillard T, Thorsteinsdottir U, Haines JL, Farrer LA, Heid IM, Abecasis GR; AMD Gene Consortium. Seven new loci associated with age-related macular degeneration. Nat Genet. 2013 Apr;45(4):433-9, 439e1-2.

25. Huyghe JR, Jackson AU, Fogarty MP, Buchkovich ML, Stančáková A, Stringham HM, **Sim X**, Yang L, Fuchsberger C, Cederberg H, Chines PS, Teslovich TM, Romm JM, Ling H, McMullen I, Ingersoll R, Pugh EW, Doheny KF, Neale BM, Daly MJ, Kuusisto J, Scott LJ, Kang HM, Collins FS, Abecasis GR, Watanabe RM, Boehnke M, Laakso M, Mohlke KL. Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. Nat Genet. 2013 Feb;45(2):197-201.

26. Schache M, Richardson AJ, Mitchell P, Wang JJ, Rochtchina E, Viswanathan AC, Wong TY, Saw SM, Topouzis F, Xie J, **Sim X**, Holliday EG, Attia J, Scott RJ, Baird PN. Genetic association of refractive error and axial length with 15q14 but not 15q25 in the Blue Mountains Eye Study cohort. Ophthalmology. 2013 Feb;120(2):292-7.

27. Chen P, Ong RT, Tay WT, **Sim X**, Ali M, Xu H, Suo C, Liu J, Chia KS, Vithana E, Young TL, Aung T, Lim WY, Khor CC, Cheng CY, Wong TY, Teo YY, Tai ES. A study assessing the association of glycated hemoglobin A1C (HbA1C) associated variants with HbA1C, chronic kidney disease and diabetic retinopathy in populations of Asian ancestry. PLoS One. 2013 Nov 7;8(11):e79767.

28. Jensen RA[*], **Sim X**[*], Li X[*], Cotch MF[*], Ikram MK[*], Holliday EG[*], Eiriksdottir G, Harris TB, Jonasson F, Klein BE, Launer LJ, Smith AV, Boerwinkle E, Cheung N, Hewitt AW, Liew G, Mitchell P, Wang JJ, Attia J, Scott R, Glazer NL, Lumley T, McKnight B, Psaty BM, Taylor K, Hofman A, de Jong PT, Rivadeneira F, Uitterlinden AG, Tay WT, Teo YY, Seielstad M, Liu J, Cheng CY, Saw SM, Aung T, Ganesh SK, O'Donnell CJ, Nalls MA, Wiggins KL, Kuo JZ; Blue Mountains Eye Study GWAS Team; CKDGen Consortium, van Duijn CM, Gudnason V, Klein R, Siscovick DS, Rotter JI, Tai ES, Vingerling J, Wong TY. Genome-wide association study of retinopathy in individuals without diabetes. PLoS One. 2013;8(2):e54232.

29. Holliday EG[*], Smith AV[*], Cornes BK[*], Buitendijk GH[*], Jensen RA[*], **Sim X**[*], Aspelund T, Aung T, Baird PN, Boerwinkle E, Cheng CY, van Duijn CM, Eiriksdottir G, Gudnason V, Harris T, Hewitt AW, Inouye M, Jonasson F, Klein BE, Launer L, Li X, Liew G, Lumley T, McElduff P, McKnight B, Mitchell P, Psaty BM, Rochtchina E, Rotter JI, Scott RJ, Tay W, Taylor K, Teo YY, Uitterlinden AG, Viswanathan A, Xie S; Wellcome Trust Case Control Consortium 2, Vingerling JR, Klaver CC, Tai ES, Siscovick D, Klein R, Cotch MF, Wong TY, Attia J, Wang JJ. Insights into the genetic architecture of early stage age-related macular degeneration: a genome-wide association study meta-analysis. PLoS One. 2013;8(1):e53830.

30. Vithana EN, Khor CC, Qiao C, Nongpiur ME, George R, Chen LJ, Do T, Abu-Amero K, Huang CK, Low S, Tajudin LS, Perera SA, Cheng CY, Xu L, Jia H, Ho CL, Sim KS, Wu RY, Tham CC, Chew PT, Su DH, Oen FT, Sarangapani S, Soumittra N, Osman EA, Wong HT, Tang G, Fan S, Meng H, Huong DT, Wang H, Feng B, Baskaran M, Shantha B, Ramprasad VL, Kumaramanickavel G, Iyengar SK, How AC, Lee KY, Sivakumaran TA, Yong VH, Ting SM, Li Y, Wang YX, Tay WT, **Sim X**, Lavanya R, Cornes BK, Zheng YF, Wong TT, Loon SC, Yong VK, Waseem N, Yaakub A, Chia KS, Allingham RR, Hauser MA, Lam DS, Hibberd ML, Bhattacharya SS, Zhang M, Teo YY, Tan DT, Jonas JB, Tai ES, Saw SM, Hon do N, Al-

Obeidan SA, Liu J, Chau TN, Simmons CP, Bei JX, Zeng YX, Foster PJ, Vijaya L, Wong TY, Pang CP, Wang N, Aung T. Genome-wide association analyses identify three new susceptibility loci for primary angle closure glaucoma. Nat Genet. 2012 Oct;44(10):1142-6.

31. Verhoeven VJ, Hysi PG, Saw SM, Vitart V, Mirshahi A, Guggenheim JA, Cotch MF, Yamashiro K, Baird PN, Mackey DA, Wojciechowski R, Ikram MK, Hewitt AW, Duggal P, Janmahasatian S, Khor CC, Fan Q, Zhou X, Young TL, Tai ES, Goh LK, Li YJ, Aung T, Vithana E, Teo YY, Tay W, **Sim X**, Rudan I, Hayward C, Wright AF, Polasek O, Campbell H, Wilson JF, Fleck BW, Nakata I, Yoshimura N, Yamada R, Matsuda F, Ohno-Matsui K, Nag A, McMahon G, St Pourcain B, Lu Y, Rahi JS, Cumberland PM, Bhattacharya S, Simpson CL, Atwood LD, Li X, Raffel LJ, Murgia F, Portas L, Despriet DD, van Koolwijk LM, Wolfram C, Lackner KJ, Tönjes A, Mägi R, Lehtimäki T, Kähönen M, Esko T, Metspalu A, Rantanen T, Pärssinen O, Klein BE, Meitinger T, Spector TD, Oostra BA, Smith AV, de Jong PT, Hofman A, Amin N, Karssen LC, Rivadeneira F, Vingerling JR, Eiríksdóttir G, Gudnason V, Döring A, Bettecken T, Uitterlinden AG, Williams C, Zeller T, Castagné R, Oexle K, van Duijn CM, Iyengar SK, Mitchell P, Wang JJ, Höhn R, Pfeiffer N, Bailey-Wilson JE, Stambolian D, Wong TY, Hammond CJ, Klaver CC. Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. Hum Genet. 2012 Sep;131(9):1467-80.

32. Okada Y[*], **Sim X**[*], Go MJ[*], Wu JY[*], Gu D[*], Takeuchi F[*], Takahashi A, Maeda S, Tsunoda T, Chen P, Lim SC, Wong TY, Liu J, Young TL, Aung T, Seielstad M, Teo YY, Kim YJ, Lee JY, Han BG, Kang D, Chen CH, Tsai FJ, Chang LC, Fann SJ, Mei H, Rao DC, Hixson JE, Chen S, Katsuya T, Isono M, Ogihara T, Chambers JC, Zhang W, Kooner JS; KidneyGen Consortium; CKDGen Consortium, Albrecht E; GUGC consortium, Yamamoto K, Kubo M, Nakamura Y, Kamatani N, Kato N, He J, Chen YT, Cho YS, Tai ES, Tanaka T. Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. Nat Genet. 2012 Jul 15;44(8):904-9.

33. Lee W, Gusnanto A, Salim A, Magnusson P, **Sim X**, Tai ES, Pawitan Y. Estimating the number of true discoveries in genome-wide association studies. Stat Med. 2012 May 20;31(11-12):1177-89.

34. Wang X, Liu X, **Sim X**, Xu H, Khor CC, Ong RT, Tay WT, Suo C, Poh WT, Ng DP, Liu J, Aung T, Chia KS, Wong TY, Tai ES, Teo YY. A statistical method for region-based meta-analysis of genome-wide association studies in genetically diverse populations. Eur J Hum Genet. 2012 Apr;20(4):469-75.

35. Wen W, Cho YS, Zheng W, Dorajoo R, Kato N, Qi L, Chen CH, Delahanty RJ, Okada Y, Tabara Y, Gu D, Zhu D, Haiman CA, Mo Z, Gao YT, Saw SM, Go MJ, Takeuchi F, Chang LC, Kokubo Y, Liang J, Hao M, Le Marchand L, Zhang Y, Hu Y, Wong TY, Long J, Han BG, Kubo M, Yamamoto K, Su MH, Miki T, Henderson BE, Song H, Tan A, He J, Ng DP, Cai Q, Tsunoda T, Tsai FJ, Iwai N, Chen GK, Shi J, Xu J, **Sim X**, Xiang YB, Maeda S, Ong RT, Li C, Nakamura Y, Aung T, Kamatani N, Liu JJ, Lu W, Yokota M, Seielstad M, Fann CS; Genetic Investigation of ANthropometric Traits (GIANT) Consortium, Wu JY, Lee JY, Hu FB, Tanaka T, Tai ES, Shu XO. Meta-analysis identifies common variants associated with body mass index in east Asians. Nat Genet. 2012 Feb 19;44(3):307-11.

36. Cornes BK, Khor CC, Nongpiur ME, Xu L, Tay WT, Zheng Y, Lavanya R, Li Y, Wu R, **Sim X**, Wang YX, Chen P, Teo YY, Chia KS, Seielstad M, Liu J, Hibberd ML, Cheng CY, Saw SM, Tai ES, Jonas JB, Vithana EN, Wong TY, Aung T. Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. Hum Mol Genet. 2012 Jan 15;21(2):437-45.

37. Suo C, Xu H, Khor CC, Ong RT, **Sim X**, Chen J, Tay WT, Sim KS, Zeng YX, Zhang X, Liu J, Tai ES, Wong TY, Chia KS, Teo YY. Natural positive selection and north-south genetic diversity in East Asia. Eur J Hum Genet. 2012 Jan;20(1):102-10.

38. Dorajoo R, Blakemore AI, **Sim X**, Ong RT, Ng DP, Seielstad M, Wong TY, Saw SM, Froguel P, Liu J, Tai ES. Replication of 13 obesity loci among Singaporean Chinese, Malay and Asian-Indian populations. Int J Obes (Lond). 2012 Jan;36(1):159-63.

39. Dastani Z, Hivert MF, Timpson N, Perry JR, Yuan X, Scott RA, Henneman P, Heid IM, Kizer JR, Lyytikäinen LP, Fuchsberger C, Tanaka T, Morris AP, Small K, Isaacs A, Beekman M, Coassin S, Lohman K, Qi L, Kanoni S, Pankow JS, Uh HW, Wu Y, Bidulescu A, Rasmussen-Torvik LJ, Greenwood CM, Ladouceur M, Grimsby J, Manning AK, Liu CT, Kooner J, Mooser VE, Vollenweider P, Kapur KA, Chambers J, Wareham NJ, Langenberg C, Frants R, Willems-Vandijk K, Oostra BA, Willems SM, Lamina C, Winkler TW, Psaty BM, Tracy RP, Brody J, Chen I, Viikari J, Kähönen M, Pramstaller PP, Evans DM, St Pourcain B, Sattar N, Wood AR, Bandinelli S, Carlson OD, Egan JM, Böhringer S, van Heemst D, Kedenko L, Kristiansson K, Nuotio ML, Loo BM, Harris T, Garcia M, Kanaya A, Haun M, Klopp N, Wichmann HE, Deloukas P, Katsareli E, Couper DJ, Duncan BB, Kloppenburg M, Adair LS, Borja JB; DIAGRAM+ Consortium; MAGIC Consortium; GLGC Investigators; MuTHER Consortium, Wilson JG, Musani S, Guo X, Johnson T, Semple R, Teslovich TM, Allison MA, Redline S, Buxbaum SG, Mohlke KL, Meulenbelt I, Ballantyne CM, Dedoussis GV, Hu FB, Liu Y, Paulweber B, Spector TD, Slagboom PE, Ferrucci L, Jula A, Perola M, Raitakari O, Florez JC, Salomaa V, Eriksson JG, Frayling TM, Hicks AA, Lehtimäki T, Smith GD, Siscovick DS, Kronenberg F, van Duijn C, Loos RJ, Waterworth DM, Meigs JB, Dupuis J, Richards JB, Voight BF, Scott LJ, Steinthorsdottir V, Dina C, Welch RP, Zeggini E, Huth C, Aulchenko YS, Thorleifsson G, McCulloch LJ, Ferreira T, Grallert H, Amin N, Wu G, Willer CJ, Raychaudhuri S, McCarroll SA, Hofmann OM, Segrè AV, van Hoek M, Navarro P, Ardlie K, Balkau B, Benediktsson R, Bennett AJ, Blagieva R, Boerwinkle E, Bonnycastle LL, Boström KB, Bravenboer B, Bumpstead S, Burtt NP, Charpentier G, Chines PS, Cornelis M, Crawford G, Doney AS, Elliott KS, Elliott AL, Erdos MR, Fox CS, Franklin CS, Ganser M, Gieger C, Grarup N, Green T, Griffin S, Groves CJ, Guiducci C, Hadjadj S, Hassanali N, Herder C, Isomaa B, Jackson AU, Johnson PR, Jørgensen T, Kao WH, Kong A, Kraft P, Kuusisto J, Lauritzen T, Li M, Lieverse A, Lindgren CM, Lyssenko V, Marre M, Meitinger T, Midthjell K, Morken MA, Narisu N, Nilsson P, Owen KR, Payne F, Petersen AK, Platou C, Proença C, Prokopenko I, Rathmann W, Rayner NW, Robertson NR, Rocheleau G, Roden M, Sampson MJ, Saxena R, Shields BM, Shrader P, Sigurdsson G, Sparsø T, Strassburger K, Stringham HM, Sun Q, Swift AJ, Thorand B, Tichet J, Tuomi T, van Dam RM, van Haeften TW, van Herpt T, van Vliet-Ostaptchouk JV, Walters GB, Weedon MN, Wijmenga C, Witteman J, Bergman RN, Cauchi S, Collins FS, Gloyn AL, Gyllensten U, Hansen T, Hide WA, Hitman GA, Hofman A, Hunter DJ, Hveem K, Laakso M, Morris AD, Palmer CN, Rudan I, Sijbrands E, Stein LD, Tuomilehto J, Uitterlinden A, Walker M, Watanabe RM, Abecasis GR, Boehm BO, Campbell H, Daly MJ, Hattersley AT, Pedersen O, Barroso I, Groop L, Sladek R, Thorsteinsdottir U, Wilson JF, Illig T, Froguel P, van Duijn CM, Stefansson K, Altshuler D, Boehnke M, McCarthy MI, Soranzo N, Wheeler E, Glazer NL, Bouatia-Naji N, Mägi R, Randall J, Elliott P, Rybin D, Dehghan A, Hottenga JJ, Song K, Goel A, Lajunen T, Doney A, Cavalcanti-Proença C, Kumari M, Timpson NJ, Zabena C, Ingelsson E, An P, O'Connell J, Luan J, Elliott A, McCarroll SA, Roccasecca RM, Pattou F, Sethupathy P, Ariyurek Y, Barter P, Beilby JP, Ben-Shlomo Y, Bergmann S, Bochud M, Bonnefond A, Borch-Johnsen K, Böttcher Y, Brunner E, Bumpstead SJ, Chen YD, Chines P, Clarke R, Coin LJ, Cooper MN, Crisponi L, Day IN, de Geus EJ, Delplanque J, Fedson AC, Fischer-Rosinsky A, Forouhi NG, Franzosi MG, Galan P, Goodarzi MO, Graessler J, Grundy S, Gwilliam R, Hallmans G, Hammond N, Han X, Hartikainen AL, Hayward C, Heath SC, Hercberg S, Hillman DR, Hingorani AD, Hui J, Hung J, Kaakinen M, Kaprio J, Kesaniemi YA, Kivimaki M, Knight B, Koskinen S,

Kovacs P, Kyvik KO, Lathrop GM, Lawlor DA, Le Bacquer O, Lecoeur C, Li Y, Mahley R, Mangino M, Martínez-Larrad MT, McAteer JB, McPherson R, Meisinger C, Melzer D, Meyre D, Mitchell BD, Mukherjee S, Naitza S, Neville MJ, Orrù M, Pakyz R, Paolisso G, Pattaro C, Pearson D, Peden JF, Pedersen NL, Pfeiffer AF, Pichler I, Polasek O, Posthuma D, Potter SC, Pouta A, Province MA, Rayner NW, Rice K, Ripatti S, Rivadeneira F, Rolandsson O, Sandbaek A, Sandhu M, Sanna S, Sayer AA, Scheet P, Seedorf U, Sharp SJ, Shields B, Sigurðsson G, Sijbrands EJ, Silveira A, Simpson L, Singleton A, Smith NL, Sovio U, Swift A, Syddall H, Syvänen AC, Tönjes A, Uitterlinden AG, van Dijk KW, Varma D, Visvikis-Siest S, Vitart V, Vogelzangs N, Waeber G, Wagner PJ, Walley A, Ward KL, Watkins H, Wild SH, Willemsen G, Witteman JC, Yarnell JW, Zelenika D, Zethelius B, Zhai G, Zhao JH, Zillikens MC; DIAGRAM Consortium; GIANT Consortium; Global B Pgen Consortium, Borecki IB, Meneton P, Magnusson PK, Nathan DM, Williams GH, Silander K, Bornstein SR, Schwarz P, Spranger J, Karpe F, Shuldiner AR, Cooper C, Serrano-Ríos M, Lind L, Palmer LJ, Hu FB, Franks PW, Ebrahim S, Marmot M, Kao WH, Pramstaller PP, Wright AF, Stumvoll M, Hamsten A; Procardis Consortium, Buchanan TA, Valle TT, Rotter JI, Penninx BW, Boomsma DI, Cao A, Scuteri A, Schlessinger D, Uda M, Ruokonen A, Jarvelin MR, Peltonen L, Mooser V, Sladek R; MAGIC investigators; GLGC Consortium, Musunuru K, Smith AV, Edmondson AC, Stylianou IM, Koseki M, Pirruccello JP, Chasman DI, Johansen CT, Fouchier SW, Peloso GM, Barbalic M, Ricketts SL, Bis JC, Feitosa MF, Orho-Melander M, Melander O, Li X, Li M, Cho YS, Go MJ, Kim YJ, Lee JY, Park T, Kim K, **Sim X**, Ong RT, Croteau-Chonka DC, Lange LA, Smith JD, Ziegler A, Zhang W, Zee RY, Whitfield JB, Thompson JR, Surakka I, Spector TD, Smit JH, Sinisalo J, Scott J, Saharinen J, Sabatti C, Rose LM, Roberts R, Rieder M, Parker AN, Pare G, O'Donnell CJ, Nieminen MS, Nickerson DA, Montgomery GW, McArdle W, Masson D, Martin NG, Marroni F, Lucas G, Luben R, Lokki ML, Lettre G, Launer LJ, Lakatta EG, Laaksonen R, Kyvik KO, König IR, Khaw KT, Kaplan LM, Johansson Å, Janssens AC, Igl W, Hovingh GK, Hengstenberg C, Havulinna AS, Hastie ND, Harris TB, Haritunians T, Hall AS, Groop LC, Gonzalez E, Freimer NB, Erdmann J, Ejebe KG, Döring A, Dominiczak AF, Demissie S, Deloukas P, de Faire U, Crawford G, Chen YD, Caulfield MJ, Boekholdt SM, Assimes TL, Quertermous T, Seielstad M, Wong TY, Tai ES, Feranil AB, Kuzawa CW, Taylor HA Jr, Gabriel SB, Holm H, Gudnason V, Krauss RM, Ordovas JM, Munroe PB, Kooner JS, Tall AR, Hegele RA, Kastelein JJ, Schadt EE, Strachan DP, Reilly MP, Samani NJ, Schunkert H, Cupples LA, Sandhu MS, Ridker PM, Rader DJ, Kathiresan S. Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. PLoS Genet. 2012;8(3):e1002607.

40. Cho YS[*], Chen CH[*], Hu C, Long J[*], Ong RT[*], **Sim X**[*], Takeuchi F[*], Wu Y[*], Go MJ[*], Yamauchi T, Chang YC, Kwak SH, Ma RC, Yamamoto K, Adair LS, Aung T, Cai Q, Chang LC, Chen YT, Gao Y, Hu FB, Kim HL, Kim S, Kim YJ, Lee JJ, Lee NR, Li Y, Liu JJ, Lu W, Nakamura J, Nakashima E, Ng DP, Tay WT, Tsai FJ, Wong TY, Yokota M, Zheng W, Zhang R, Wang C, So WY, Ohnaka K, Ikegami H, Hara K, Cho YM, Cho NH, Chang TJ, Bao Y, Hedman ÅK, Morris AP, McCarthy MI; DIAGRAM Consortium; MuTHER Consortium, Takayanagi R, Park KS, Jia W, Chuang LM, Chan JC, Maeda S, Kadowaki T, Lee JY, Wu JY, Teo YY, Tai ES, Shu XO, Mohlke KL, Kato N, Han BG, Seielstad M. Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. Nat Genet. 2011 Dec 11;44(1):67-72.

41. Xu H, Poh WT, **Sim X**, Ong RT, Suo C, Tay WT, Khor CC, Seielstad M, Liu J, Aung T, Tai ES, Wong TY, Chia KS, Teo YY. SgD-CNV, a database for common and rare copy number variants in three Asian populations. Hum Mutat. 2011 Dec;32(12):1341-9.

42. Fan Q, Zhou X, Khor CC, Cheng CY, Goh LK, **Sim X**, Tay WT, Li YJ, Ong RT, Suo C, Cornes B, Ikram MK, Chia KS, Seielstad M, Liu J, Vithana E, Young TL, Tai ES, Wong TY, Aung T, Teo YY, Saw SM. Genome-

wide meta-analysis of five Asian cohorts identifies PDGFRA as a susceptibility locus for corneal astigmatism. PLoS Genet. 2011 Dec;7(12):e1002402.

43. Sobrin L, Green T, **Sim X**, Jensen RA, Tai ES, Tay WT, Wang JJ, Mitchell P, Sandholm N, Liu Y, Hietala K, Iyengar SK; Family Investigation of Nephropathy and Diabetes-Eye Research Group, Brooks M, Buraczynska M, Van Zuydam N, Smith AV, Gudnason V, Doney AS, Morris AD, Leese GP, Palmer CN; Wellcome Trust Case Control Consortium 2, Swaroop A, Taylor HA Jr, Wilson JG, Penman A, Chen CJ, Groop PH, Saw SM, Aung T, Klein BE, Rotter JI, Siscovick DS, Cotch MF, Klein R, Daly MJ, Wong TY. Candidate gene association study for diabetic retinopathy in persons with type 2 diabetes: the Candidate gene Association Resource (CARe). Invest Ophthalmol Vis Sci. 2011 Sep 29;52(10):7593-602.

44. Han S, Chen P, Fan Q, Khor CC, **Sim X**, Tay WT, Ong RT, Suo C, Goh LK, Lavanya R, Zheng Y, Wu R, Seielstad M, Vithana E, Liu J, Chia KS, Lee JJ, Tai ES, Wong TY, Aung T, Teo YY, Saw SM. Association of variants in FRAP1 and PDGFRA with corneal curvature in Asian populations from Singapore. Hum Mol Genet. 2011 Sep 15;20(18):3693-8.

45. International Consortium for Blood Pressure Genome-Wide Association Studies, Ehret GB, Munroe PB, Rice KM, Bochud M, Johnson AD, Chasman DI, Smith AV, Tobin MD, Verwoert GC, Hwang SJ, Pihur V, Vollenweider P, O'Reilly PF, Amin N, Bragg-Gresham JL, Teumer A, Glazer NL, Launer L, Zhao JH, Aulchenko Y, Heath S, Sõber S, Parsa A, Luan J, Arora P, Dehghan A, Zhang F, Lucas G, Hicks AA, Jackson AU, Peden JF, Tanaka T, Wild SH, Rudan I, Igl W, Milaneschi Y, Parker AN, Fava C, Chambers JC, Fox ER, Kumari M, Go MJ, van der Harst P, Kao WH, Sjögren M, Vinay DG, Alexander M, Tabara Y, Shaw-Hawkins S, Whincup PH, Liu Y, Shi G, Kuusisto J, Tayo B, Seielstad M, **Sim X**, Nguyen KD, Lehtimäki T, Matullo G, Wu Y, Gaunt TR, Onland-Moret NC, Cooper MN, Platou CG, Org E, Hardy R, Dahgam S, Palmen J, Vitart V, Braund PS, Kuznetsova T, Uiterwaal CS, Adeyemo A, Palmas W, Campbell H, Ludwig B, Tomaszewski M, Tzoulaki I, Palmer ND; CARDIoGRAM consortium; CKDGen Consortium; KidneyGen Consortium; EchoGen consortium; CHARGE-HF consortium, Aspelund T, Garcia M, Chang YP, O'Connell JR, Steinle NI, Grobbee DE, Arking DE, Kardia SL, Morrison AC, Hernandez D, Najjar S, McArdle WL, Hadley D, Brown MJ, Connell JM, Hingorani AD, Day IN, Lawlor DA, Beilby JP, Lawrence RW, Clarke R, Hopewell JC, Ongen H, Dreisbach AW, Li Y, Young JH, Bis JC, Kähönen M, Viikari J, Adair LS, Lee NR, Chen MH, Olden M, Pattaro C, Bolton JA, Köttgen A, Bergmann S, Mooser V, Chaturvedi N, Frayling TM, Islam M, Jafar TH, Erdmann J, Kulkarni SR, Bornstein SR, Grässler J, Groop L, Voight BF, Kettunen J, Howard P, Taylor A, Guarrera S, Ricceri F, Emilsson V, Plump A, Barroso I, Khaw KT, Weder AB, Hunt SC, Sun YV, Bergman RN, Collins FS, Bonnycastle LL, Scott LJ, Stringham HM, Peltonen L, Perola M, Vartiainen E, Brand SM, Staessen JA, Wang TJ, Burton PR, Soler Artigas M, Dong Y, Snieder H, Wang X, Zhu H, Lohman KK, Rudock ME, Heckbert SR, Smith NL, Wiggins KL, Doumatey A, Shriner D, Veldre G, Viigimaa M, Kinra S, Prabhakaran D, Tripathy V, Langefeld CD, Rosengren A, Thelle DS, Corsi AM, Singleton A, Forrester T, Hilton G, McKenzie CA, Salako T, Iwai N, Kita Y, Ogihara T, Ohkubo T, Okamura T, Ueshima H, Umemura S, Eyheramendy S, Meitinger T, Wichmann HE, Cho YS, Kim HL, Lee JY, Scott J, Sehmi JS, Zhang W, Hedblad B, Nilsson P, Smith GD, Wong A, Narisu N, Stančáková A, Raffel LJ, Yao J, Kathiresan S, O'Donnell CJ, Schwartz SM, Ikram MA, Longstreth WT Jr, Mosley TH, Seshadri S, Shrine NR, Wain LV, Morken MA, Swift AJ, Laitinen J, Prokopenko I, Zitting P, Cooper JA, Humphries SE, Danesh J, Rasheed A, Goel A, Hamsten A, Watkins H, Bakker SJ, van Gilst WH, Janipalli CS, Mani KR, Yajnik CS, Hofman A, Mattace-Raso FU, Oostra BA, Demirkan A, Isaacs A, Rivadeneira F, Lakatta EG, Orru M, Scuteri A, Ala-Korpela M, Kangas AJ, Lyytikäinen LP, Soininen P, Tukiainen T, Würtz P, Ong RT, Dörr M, Kroemer HK, Völker U, Völzke H, Galan P, Hercberg S, Lathrop M, Zelenika D, Deloukas P,

Mangino M, Spector TD, Zhai G, Meschia JF, Nalls MA, Sharma P, Terzic J, Kumar MV, Denniff M, Zukowska-Szczechowska E, Wagenknecht LE, Fowkes FG, Charchar FJ, Schwarz PE, Hayward C, Guo X, Rotimi C, Bots ML, Brand E, Samani NJ, Polasek O, Talmud PJ, Nyberg F, Kuh D, Laan M, Hveem K, Palmer LJ, van der Schouw YT, Casas JP, Mohlke KL, Vineis P, Raitakari O, Ganesh SK, Wong TY, Tai ES, Cooper RS, Laakso M, Rao DC, Harris TB, Morris RW, Dominiczak AF, Kivimaki M, Marmot MG, Miki T, Saleheen D, Chandak GR, Coresh J, Navis G, Salomaa V, Han BG, Zhu X, Kooner JS, Melander O, Ridker PM, Bandinelli S, Gyllensten UB, Wright AF, Wilson JF, Ferrucci L, Farrall M, Tuomilehto J, Pramstaller PP, Elosua R, Soranzo N, Sijbrands EJ, Altshuler D, Loos RJ, Shuldiner AR, Gieger C, Meneton P, Uitterlinden AG, Wareham NJ, Gudnason V, Rotter JI, Rettig R, Uda M, Strachan DP, Witteman JC, Hartikainen AL, Beckmann JS, Boerwinkle E, Vasan RS, Boehnke M, Larson MG, Järvelin MR, Psaty BM, Abecasis GR, Chakravarti A, Elliott P, van Duijn CM, Newton-Cheh C, Levy D, Caulfield MJ, Johnson T. Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature. 2011 Sep 11;478(7367):103-9.

46. Kooner JS*, Saleheen D*, **Sim X***, Sehmi J*, Zhang W*, Frossard P*, Been LF, Chia KS, Dimas AS, Hassanali N, Jafar T, Jowett JB, Li X, Radha V, Rees SD, Takeuchi F, Young R, Aung T, Basit A, Chidambaram M, Das D, Grundberg E, Hedman AK, Hydrie ZI, Islam M, Khor CC, Kowlessur S, Kristensen MM, Liju S, Lim WY, Matthews DR, Liu J, Morris AP, Nica AC, Pinidiyapathirage JM, Prokopenko I, Rasheed A, Samuel M, Shah N, Shera AS, Small KS, Suo C, Wickremasinghe AR, Wong TY, Yang M, Zhang F; DIAGRAM; MuTHER, Abecasis GR, Barnett AH, Caulfield M, Deloukas P, Frayling TM, Froguel P, Kato N, Katulanda P, Kelly MA, Liang J, Mohan V, Sanghera DK, Scott J, Seielstad M, Zimmet PZ, Elliott P, Teo YY, McCarthy MI, Danesh J, Tai ES, Chambers JC. Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nat Genet. 2011 Aug 28;43(10):984-9.

47. Ku CS, Teo SM, Naidoo N, **Sim X**, Teo YY, Pawitan Y, Seielstad M, Chia KS, Salim A. Copy number polymorphisms in new HapMap III and Singapore populations. J Hum Genet. 2011 Aug;56(8):552-60.

48. Kato N*, Takeuchi F*, Tabara Y*, Kelly TN*, Go MJ*, **Sim X***, Tay WT*, Chen CH*, Zhang Y*, Yamamoto K*, Katsuya T*, Yokota M, Kim YJ, Ong RT, Nabika T, Gu D, Chang LC, Kokubo Y, Huang W, Ohnaka K, Yamori Y, Nakashima E, Jaquish CE, Lee JY, Seielstad M, Isono M, Hixson JE, Chen YT, Miki T, Zhou X, Sugiyama T, Jeon JP, Liu JJ, Takayanagi R, Kim SS, Aung T, Sung YJ, Zhang X, Wong TY, Han BG, Kobayashi S, Ogihara T, Zhu D, Iwai N, Wu JY, Teo YY, Tai ES, Cho YS, He J. Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. Nat Genet. 2011 Jun;43(6):531-8.

49. Khor CC, Ramdas WD, Vithana EN, Cornes BK, **Sim X**, Tay WT, Saw SM, Zheng Y, Lavanya R, Wu R, Wang JJ, Mitchell P, Uitterlinden AG, Rivadeneira F, Teo YY, Chia KS, Seielstad M, Hibberd M, Vingerling JR, Klaver CC, Jansonius NM, Tai ES, Wong TY, van Duijn CM, Aung T. Genome-wide association studies in Asians confirm the involvement of ATOH7 and TGFBR3, and further identify CARD10 as a novel locus influencing optic disc area. Hum Mol Genet. 2011 May 1;20(9):1864-72.

50. **Sim X***, Ong RT*, Suo C, Tay WT, Liu J, Ng DP, Boehnke M, Chia KS, Wong TY, Seielstad M, Teo YY, Tai ES. Transferability of type 2 diabetes implicated loci in multi-ethnic cohorts from Southeast Asia. PLoS Genet. 2011 Apr;7(4):e1001363.

51. Ong RT, Liu X, Poh WT, **Sim X**, Chia KS, Teo YY. A method for identifying haplotypes carrying the causative allele in positive natural selection and genome-wide association studies. Bioinformatics. 2011 Mar 15;27(6):822-8.

52. Vithana EN, Aung T, Khor CC, Cornes BK, Tay WT, **Sim X**, Lavanya R, Wu R, Zheng Y, Hibberd ML, Chia KS, Seielstad M, Goh LK, Saw SM, Tai ES, Wong TY. Collagen-related genes influence the glaucoma risk factor, central corneal thickness. Hum Mol Genet. 2011 Feb 15;20(4):649-58.

53. Li YJ, Goh L, Khor CC, Fan Q, Yu M, Han S, **Sim X**, Ong RT, Wong TY, Vithana EN, Yap E, Nakanishi H, Matsuda F, Ohno-Matsui K, Yoshimura N, Seielstad M, Tai ES, Young TL, Saw SM. Genome-wide association studies reveal genetic variants in CTNND2 for high myopia in Singapore Chinese. Ophthalmology. 2011 Feb;118(2):368-75.

54. Teo YY, Ong RT, **Sim X**, Tai ES, Chia KS. Identifying candidate causal variants via trans-population fine-mapping. Genet Epidemiol. 2010 Nov;34(7):653-64.

55. Ikram MK*, **Sim X***, Jensen RA*, Cotch MF*, Hewitt AW*, Ikram MA, Wang JJ, Klein R, Klein BE, Breteler MM, Cheung N, Liew G, Mitchell P, Uitterlinden AG, Rivadeneira F, Hofman A, de Jong PT, van Duijn CM, Kao L, Cheng CY, Smith AV, Glazer NL, Lumley T, McKnight B, Psaty BM, Jonasson F, Eiriksdottir G, Aspelund T; Global BPgen Consortium, Harris TB, Launer LJ, Taylor KD, Li X, Iyengar SK, Xi Q, Sivakumaran TA, Mackey DA, Macgregor S, Martin NG, Young TL, Bis JC, Wiggins KL, Heckbert SR, Hammond CJ, Andrew T, Fahy S, Attia J, Holliday EG, Scott RJ, Islam FM, Rotter JI, McAuley AK, Boerwinkle E, Tai ES, Gudnason V, Siscovick DS, Vingerling JR, Wong TY. Four novel Loci (19q13, 6q24, 12q24, and 5q14) influence the microcirculation in vivo. PLoS Genet. 2010 Oct 28;6(10):e1001184.

56. Shu XO, Long J, Cai Q, Qi L, Xiang YB, Cho YS, Tai ES, Li X, Lin X, Chow WH, Go MJ, Seielstad M, Bao W, Li H, Cornelis MC, Yu K, Wen W, Shi J, Han BG, **Sim XL**, Liu L, Qi Q, Kim HL, Ng DP, Lee JY, Kim YJ, Li C, Gao YT, Zheng W, Hu FB. Identification of new genetic risk variants for type 2 diabetes. PLoS Genet. 2010 Sep 16;6(9):e1001127.

57. Teslovich TM, Musunuru K, Smith AV, Edmondson AC, Stylianou IM, Koseki M, Pirruccello JP, Ripatti S, Chasman DI, Willer CJ, Johansen CT, Fouchier SW, Isaacs A, Peloso GM, Barbalic M, Ricketts SL, Bis JC, Aulchenko YS, Thorleifsson G, Feitosa MF, Chambers J, Orho-Melander M, Melander O, Johnson T, Li X, Guo X, Li M, Shin Cho Y, Jin Go M, Jin Kim Y, Lee JY, Park T, Kim K, **Sim X**, Twee-Hee Ong R, Croteau-Chonka DC, Lange LA, Smith JD, Song K, Hua Zhao J, Yuan X, Luan J, Lamina C, Ziegler A, Zhang W, Zee RY, Wright AF, Witteman JC, Wilson JF, Willemsen G, Wichmann HE, Whitfield JB, Waterworth DM, Wareham NJ, Waeber G, Vollenweider P, Voight BF, Vitart V, Uitterlinden AG, Uda M, Tuomilehto J, Thompson JR, Tanaka T, Surakka I, Stringham HM, Spector TD, Soranzo N, Smit JH, Sinisalo J, Silander K, Sijbrands EJ, Scuteri A, Scott J, Schlessinger D, Sanna S, Salomaa V, Saharinen J, Sabatti C, Ruokonen A, Rudan I, Rose LM, Roberts R, Rieder M, Psaty BM, Pramstaller PP, Pichler I, Perola M, Penninx BW, Pedersen NL, Pattaro C, Parker AN, Pare G, Oostra BA, O'Donnell CJ, Nieminen MS, Nickerson DA, Montgomery GW, Meitinger T, McPherson R, McCarthy MI, McArdle W, Masson D, Martin NG, Marroni F, Mangino M, Magnusson PK, Lucas G, Luben R, Loos RJ, Lokki ML, Lettre G, Langenberg C, Launer LJ, Lakatta EG, Laaksonen R, Kyvik KO, Kronenberg F, König IR, Khaw KT, Kaprio J, Kaplan LM, Johansson A, Jarvelin MR, Janssens AC, Ingelsson E, Igl W, Kees Hovingh G, Hottenga JJ, Hofman A, Hicks AA, Hengstenberg C, Heid IM, Hayward C, Havulinna AS, Hastie ND, Harris TB, Haritunians T, Hall AS, Gyllensten U, Guiducci C, Groop LC, Gonzalez E, Gieger

C, Freimer NB, Ferrucci L, Erdmann J, Elliott P, Ejebe KG, Döring A, Dominiczak AF, Demissie S, Deloukas P, de Geus EJ, de Faire U, Crawford G, Collins FS, Chen YD, Caulfield MJ, Campbell H, Burtt NP, Bonnycastle LL, Boomsma DI, Boekholdt SM, Bergman RN, Barroso I, Bandinelli S, Ballantyne CM, Assimes TL, Quertermous T, Altshuler D, Seielstad M, Wong TY, Tai ES, Feranil AB, Kuzawa CW, Adair LS, Taylor HA Jr, Borecki IB, Gabriel SB, Wilson JG, Holm H, Thorsteinsdottir U, Gudnason V, Krauss RM, Mohlke KL, Ordovas JM, Munroe PB, Kooner JS, Tall AR, Hegele RA, Kastelein JJ, Schadt EE, Rotter JI, Boerwinkle E, Strachan DP, Mooser V, Stefansson K, Reilly MP, Samani NJ, Schunkert H, Cupples LA, Sandhu MS, Ridker PM, Rader DJ, van Duijn CM, Peltonen L, Abecasis GR, Boehnke M, Kathiresan S. Biological, clinical and population relevance of 95 loci for blood lipids. Nature. 2010 Aug 5;466(7307):707-13.

58. Ku CS, Pawitan Y, **Sim X**, Ong RT, Seielstad M, Lee EJ, Teo YY, Chia KS, Salim A. Genomic copy number variations in three Southeast Asian populations. Hum Mutat. 2010 Jul;31(7):851-7.

59. Chia SE, Tan CS, Lim GH, **Sim X**, Lau W, Chia KS. Incidence, mortality and five-year relative survival ratio of prostate cancer among Chinese residents in Singapore from 1968 to 2002 by metastatic staging. Ann Acad Med Singapore. 2010 Jun;39(6):466-71.

60. Teo YY, **Sim X**. Patterns of linkage disequilibrium in different populations: implications and opportunities for lipid-associated loci identified from genome-wide association studies. Curr Opin Lipidol. 2010 Apr;21(2):104-15.

61. Zhang Z, Liu J, Kwoh CK, **Sim X**, Tay WT, Tan Y, Yin F, Wong TY. Learning in glaucoma genetic risk assessment. Conf Proc IEEE Eng Med Biol Soc. 2010;2010:6182-5.

62. Teo YY[*], **Sim X**[*], Ong RT[*], Tan AK, Chen J, Tantoso E, Small KS, Ku CS, Lee EJ, Seielstad M, Chia KS. Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. Genome Res. 2009 Nov;19(11):2154-62.

63. Tai ES, **Sim XL**, Ong TH, Wong TY, Saw SM, Aung T, Kathiresan S, Orho-Melander M, Ordovas JM, Tan JT, Seielstad M. Polymorphisms at newly identified lipid-associated loci are associated with blood lipids and cardiovascular disease in an Asian Malay population. J Lipid Res. 2009 Mar;50(3):514-20.

64. Chia SE, Tan CS, Lim GH, **Sim X**, Pawitan Y, Reilly M, Mohamed Ali S, Lau W, Chia KS. Incidence, mortality and survival patterns of prostate cancer among residents in Singapore from 1968 to 2002. BMC Cancer. 2008 Dec 16;8:368.

65. Tan JT, Dorajoo R, Seielstad M, **Sim XL**, Ong RT, Chia KS, Wong TY, Saw SM, Chew SK, Aung T, Tai ES. FTO variants are associated with obesity in the Chinese and Malay populations in Singapore. Diabetes. 2008 Oct;57(10):2851-7. doi:10.2337/db08-0214. Epub 2008 Jul 3.

66. de Kok IM, Wong CS, Chia KS, Sim X, Tan CS, Kiemeney LA, Verkooijen HM. Gender differences in the trend of colorectal cancer incidence in Singapore, 1968-2002. Int J Colorectal Dis. 2008 May;23(5):461-7. doi:10.1007/s00384-007-0421-9. Epub 2008 Jan 9.

67. Sim X, Ali RA, Wedren S, Goh DL, Tan CS, Reilly M, Hall P, Chia KS. Ethnic differences in the time trend of female breast cancer incidence: Singapore, 1968-2002. BMC Cancer. 2006 Nov 2;6:261.

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## Invited/Conference Presentations

- Sim X. Genomics and Type 2 Diabetes. Invited speaker for the c-BIG Symposium, November 11, 2016, Exploration Theatrette, Matrix, Biopolis, Singapore.
- **Sim X**, Wang C, Chai JF, Kao SL, Podgornaia AI, Chothani S, Liu X, Cheng CY, Sabanayagam C, Teo YY, Wong TY, van Dam RM, Liu J, Reilly DF, Paterson A, Tai ES. A coding 27bp deletion in SLC4A1 is associated with 0.53% lower HbA1c in Malays. Presented at the 66th Annual Meeting of The American Society of Human Genetics, October 21, 2016, Vancouver, Canada. (**Poster Presentation; Reviewers' Choice Abstract**)
- **Sim X** on behalf of AGEN and DIAMANTE consortia. Type 2 diabetes genetics in East Asians. Invited speaker for the 12th KOGO Winter Symposium 2016, February 2, 2016, Hong-Cheon, Korea. (**Invited Presentation**).
- **Sim X**, Welch RP, Jackson AU, Stringham HM, Teslovich TM, Chines PS, Narisu N, Fuchsberger C, Huyghe JR, Locke AE, Cannon ME, Ala-Korpela M, Boehnke M, Mohlke KL, Laakso M. Identification of novel and rare coding variants associated with free fatty acids and serum fatty acid profile. Presented at the 64th Annual Meeting of The American Society of Human Genetics, October 21, 2014, San Diego, CA, USA. (**Poster Presentation**).
- **Sim X**, Highland HM, Rivas MA, Im HK, Manning AK, Mahajan A, Locke AE, Grarup N, Fontanillas P, Teslovich TM, Flannick J, Fuchsberger C, Gaulton K, Kang HM, Meigs JB, Lindgren CM, T2D-GENES and GoT2D Consortia, Contribution of coding variation to type 2 diabetes-related quantitative traits in 13,000 exomes from multiple ancestries. Presented at the 63th Annual Meeting of The American Society of Human Genetics, October 24, 2013, Boston, MA, USA. (**Oral Presentation**).
- **Sim X**, Mahajan A, Manning AK, Rivas MA, Grarup N, Locke AE, Highland HM, Im HK, Meigs JB, Lindgren CM, T2D-GENES and GoT2D Consortia, Exome chip genotyping in >30,000 non-diabetic European individuals identifies low frequency coding variants associated with glycemic traits. Selected for poster presentation at The Genomics of Common Diseases 2013, September, Oxford, UK. (**Poster Presentation**).
- **Sim X**, Rivas MA, Manning AK, Locke AE, Lindgren CM, GoT2D Consortium, Mapping quantitative traits with integrated whole exome/genome/array panel in individuals of European descent. Presented at the 62th Annual Meeting of The American Society of Human Genetics, November 8, 2012, San Francisco, CA, USA. (**Oral Presentation**).
- **Sim X**, Highland HM, Manning AK, Rivas MA, Im HK, .., McCarthy MI, The impact of genetic variation on diabetes-related quantitative traits from whole exome sequences, the T2D-GENES Consortium. Presented at The Genomics of Common Diseases 2012, September 21, Potomac, MD, USA. (**Poster Presentation**).
- **Sim X**, Ong RTH, Tay WT, Suo C, Wong TY, Tai ES, Chia KS, Teo YY, Combining signatures of selection and disease-associated loci in three ethnic groups. Presented at the 60th Annual Meeting of The American Society of Human Genetics, November, 2010, Washington, DC, USA. (**Poster Presentation**).
- Teo YY, **Sim X**, Ku CS, Ong RTH, Tan ATS, Tantoso E, Pawitan Y, Seielstad M, Lee EJD, Chia KS, The Singapore Genome Variation Project. Presented at the Integrative Molecular Cancer Epidemiology, An IARC-EACR-AACR-ECNIS Symposium, July, 2008, Lyon, France. (**Poster Presentation**).
- **Sim X**, Ali RA, Wedren S, Goh DLM, Tan CS, Hall P, Chia KS, Ethnic differences in the time trend of breast cancer incidence: Singapore 1968 – 2002. Presented at the AACR American Association for Cancer Research, April 1 – 5, 2006, Washington, DC, USA. (**Poster Presentation**).

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## Teaching Record

- Quantitative Epidemiological Methods CO5103 AY15/16. Course coordinator and lecturer
- Community Health Project (CHP) statistical advisor, 2015. Title: Knowledge, Attitudes and Perceptions (KAP) Influencing the Utilization of Home-based Intermediate and Long Term Care Services in Singapore.
- Course Instructor, Genetics and Genomics of Complex Phenotypes, April 26 – 30, 2010
- Teaching Assistant, Quantitative Epidemiological Methods, Masters of Public Health, National University of Singapore (2007 – 2010)
- Teaching Assistant, Advanced Quantitative Epidemiological Methods, Masters of Public Health, National University of Singapore (2008 – 2011)

## Students Advising

- Yeli Wang, PhD in PH, SSHSPH (2015 – present; Project title): co-advisor

### PhD examiner

- Jin Zhou, PhD in Statistics, Department of Statistics and Applied Probability (15 Dec 2015; Statistical challenges in next generation genomics study): examiner

### PhD qualifying examination

- Ying Chen, PhD in PH, SSHSPH (2016-07-29; oral; Assessing inpatient diabetes mellitus care with data science and analytics: Chair
- Raymond Boon Tar Lim, PhD in PH, SSHSPH (2016-01-18; oral; Efficacy of a health promotion and sexually transmitted infection (STI) prevention program for entertainment: Chair
- Woei-Yuh Saw, PhD in PH, SSHSPH (2015-08-17; oral; Mapping the genetic architecture of global populations): Examiner
- Neelakantan Nithya, PhD in PH, SSHSPH (2015-03-20; oral; Assessment of dietary intakes and identification of dietary patterns to reduce risk of coronary heart disease in the Singapore population): Chair

### Thesis advisory committee

- Wei-Chuen Tan-Koi, PhD in PH, SSHSPH (2016 – present; Project title): Chair
- Xiaohe Li, PhD in PH, SSHSPH (2015 – present; Project title): Chair
- Woei-Yuh Saw, PhD in PH, SSHSPH (2015 – present; Project title): Chair

### MPH practicum

- Yafang Dou, MPH full time 2015/2016. The association of physical activity and sedentary behavior with incident cardiovascular disease.

### Independent Study Module

- Wei-Chuen Tan-Koi, PhD in PH, SSHSPH (2016-04-01; Applications of pharmacogenomics in regulatory science: a product life cycle review): Examiner

### Community Health Project (CHP) for medical students

- [2015/2016] Statistical advisor for two Community Health Project groups. CHP group 4: A Study of Public Perspectives on the Concept of a Tobacco Endgame and Tobacco Endgame Strategies in Singapore and CHP group 3: Prevalence and Epidemiology of Common Skin Conditions and the Disease Burden on Quality of Life in the Singaporean Population. Both groups were among the top three scoring groups for presentation.

## Courses Attended

- Pathogen Genomics Capacity Building Workshop (02 Feb – 06 Feb 2015)

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## Awards

- Best Research Publication Award Academic Year 2011 – 2012. 2nd Annual Graduate Scientific Congress 2012. Yong Loo Lin School of Medicine. National University of Singapore, Singapore.

## Journal Editor

Genes and Genomics

## Journal Reviewer

BMC Medical Genomics, BMC Genetics, Diabetes, Diabetologia, European Journal of Human Genetics, Gene, Human Heredity, Journal of Human Genetics, PLoS One, Sage Open, Scientific Reports