

## Publications

- [1] D. Tang, M. Fakiola, G. Syn, D. Anderson, H. J. Cordell, E. S. H. Scaman, E. Davis, S. J. Miles, T. McLeay, S. E. Jamieson, T. Lassmann, and J. M. Blackwell. Arylsulphatase A Pseudodeficiency (ARSA-PD), hypertension and chronic renal disease in Aboriginal Australians. *Sci Rep*, 8(1):10912, Jul 2018. URL: <http://www.ncbi.nlm.nih.gov/pubmed/30026549>.
- [2] K. M. Rothacker, K. L. Ayers, D. Tang, K. Joshi, J. A. van den Bergen, G. Robevska, N. Samnakay, L. Nagarajan, K. Francis, A. H. Sinclair, and C. S. Choong. A novel, homozygous mutation in desert hedgehog (DHH) in a 46, XY patient with dysgenetic testes presenting with primary amenorrhoea: a case report. *Int J Pediatr Endocrinol*, 2018:2, 2018. URL: <https://www.ncbi.nlm.nih.gov/pubmed/29507583>.
- [3] F. Roudnický, L. C. Dieterich, C. Poyet, L. Buser, P. Wild, D. Tang, P. Camenzind, C. Hsien Ho, V. I. Otto, and M. Detmar. High expression of insulin receptor on tumor-associated blood vessels in invasive bladder cancer predicts poor overall and progression-free survival. *J. Pathol.*, Mar 2017. URL: <http://www.ncbi.nlm.nih.gov/pubmed/28295307>.
- [4] C. C. Hon, J. A. Ramilowski, J. Harshbarger, N. Bertin, O. J. Rackham, J. Gough, E. Denisenko, S. Schmeier, T. M. Poulsen, J. Severin, M. Lizio, H. Kawaji, T. Kasukawa, M. Itoh, A. M. Burroughs, S. Noma, S. Djebali, T. Alam, Y. A. Medvedeva, A. C. Testa, L. Lipovich, C. W. Yip, I. Abugessaisa, M. Mendez, A. Hasegawa, D. Tang, et al. An atlas of human long non-coding RNAs with accurate 5' ends. *Nature*, Mar 2017. URL: <http://www.ncbi.nlm.nih.gov/pubmed/28241135>.
- [5] M. B. Abraham, D. Li, D. Tang, S. M. O'Connell, F. McKenzie, E. M. Lim, H. Hakonarson, M. A. Levine, and C. S. Choong. Short stature and hypoparathyroidism in a child with Kenny-Caffey syndrome type 2 due to a novel mutation in FAM111A gene. *Int J Pediatr Endocrinol*, 2017:1, 2017. URL: <http://www.ncbi.nlm.nih.gov/pubmed/28138333>.
- [6] G. Baynam, N. Pachter, F. McKenzie, S. Townshend, J. Slee, C. Kiraly-Borri, A. Vasudevan, A. Hawkins, S. Broley, L. Schofield, H. Verhoef, C. E. Walker, C. Molster, J. M. Blackwell, S. Jamieson, D. Tang, T. Lassmann, K. Mina, J. Beilby, M. Davis, N. Laing, L. Murphy, T. Weeramanthri, H. Dawkins, and J. Goldblatt. The rare and undiagnosed diseases diagnostic service - application of massively parallel sequencing in a state-wide clinical service. *Orphanet J Rare Dis*, 11(1):77, 2016. URL: <http://www.ncbi.nlm.nih.gov/pubmed/27287197>.
- [7] D. Tang, D. Anderson, R. W. Francis, G. Syn, S. E. Jamieson, T. Lassmann, and J. M. Blackwell. Reference genotype and exome data from an Australian Aboriginal population for health-based research. *Sci Data*, 3:160023, 2016. URL: <http://www.ncbi.nlm.nih.gov/pubmed/27070114>.
- [8] Y. Hasegawa, D. Tang, N. Takahashi, Y. Hayashizaki, A. R. Forrest, et al. CCL2 enhances pluripotency of human induced pluripotent stem cells by activating hypoxia related genes. *Sci Rep*, 4:5228, 2014. URL: <http://www.ncbi.nlm.nih.gov/pubmed/24957798>.
- [9] D. T. Tang, C. Plessy, M. Salimullah, A. M. Suzuki, R. Calligaris, S. Gustincich, and P. Carninci. Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. *Nucleic Acids Res.*, 41(3):e44, Feb 2013. URL: <http://www.ncbi.nlm.nih.gov/pubmed/23180801>.
- [10] A. Saxena, D. Tang, and P. Carninci. piRNAs warrant investigation in Rett Syndrome: an omics perspective. *Dis. Markers*, 33(5):261–275, 2012. URL: <http://www.ncbi.nlm.nih.gov/pubmed/22976001>.
- [11] S. Francia, F. Michelini, A. Saxena, D. Tang, M. de Hoon, V. Anelli, M. Mione, P. Carninci, and F. d'Adda di Fagagna. Site-specific DICER and DROSHA RNA products control the DNA-damage response. *Nature*, 488(7410):231–235, Aug 2012. URL: <http://www.ncbi.nlm.nih.gov/pubmed/22722852>.

- [12] R. D. Thiagarajan, N. Cloonan, B. B. Gardiner, T. R. Mercer, G. Kolle, E. Nourbakhsh, S. Wani, D. Tang, K. Krishnan, K. M. Georgas, B. A. Rumballe, H. S. Chiu, J. A. Steen, J. S. Mattick, M. H. Little, and S. M. Grimmond. Refining transcriptional programs in kidney development by integration of deep RNA-sequencing and array-based spatial profiling. *BMC Genomics*, 12:441, 2011. URL: <http://www.ncbi.nlm.nih.gov/pubmed/21888672>.
- [13] R. D. Thiagarajan, K. M. Georgas, B. A. Rumballe, E. Lesieur, H. S. Chiu, D. Taylor, D. T. Tang, S. M. Grimmond, and M. H. Little. Identification of anchor genes during kidney development defines ontological relationships, molecular subcompartments and regulatory pathways. *PLoS ONE*, 6(2):e17286, 2011. URL: <http://www.ncbi.nlm.nih.gov/pubmed/21386911>.
- [14] H. S. Chiu, J. C. Szucsik, K. M. Georgas, J. L. Jones, B. A. Rumballe, D. Tang, S. M. Grimmond, A. G. Lewis, B. J. Aronow, J. L. Lessard, and M. H. Little. Comparative gene expression analysis of genital tubercle development reveals a putative appendicular Wnt7 network for the epidermal differentiation. *Dev. Biol.*, 344(2):1071–1087, Aug 2010. URL: <http://www.ncbi.nlm.nih.gov/pubmed/20510229>.
- [15] N. Cloonan, Q. Xu, G. J. Faulkner, D. F. Taylor, D. T. Tang, G. Kolle, and S. M. Grimmond. RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. *Bioinformatics*, 25(19):2615–2616, Oct 2009. URL: <http://www.ncbi.nlm.nih.gov/pubmed/19648138>.
- [16] K. Georgas, B. Rumballe, M. T. Valerius, H. S. Chiu, R. D. Thiagarajan, E. Lesieur, B. J. Aronow, E. W. Brunskill, A. N. Combes, D. Tang, D. Taylor, S. M. Grimmond, S. S. Potter, A. P. McMahon, and M. H. Little. Analysis of early nephron patterning reveals a role for distal RV proliferation in fusion to the ureteric tip via a cap mesenchyme-derived connecting segment. *Dev. Biol.*, 332(2):273–286, Aug 2009. URL: <http://www.ncbi.nlm.nih.gov/pubmed/19501082>.
- [17] D. T. Tang, E. A. Glazov, S. M. McWilliam, W. C. Barris, and B. P. Dalrymple. Analysis of the complement and molecular evolution of tRNA genes in cow. *BMC Genomics*, 10:188, 2009. URL: <http://www.ncbi.nlm.nih.gov/pubmed/19393063>.
- [18] J. W. Kijas, D. Townley, B. P. Dalrymple, M. P. Heaton, J. F. Maddox, A. McGrath, P. Wilson, R. G. Ingersoll, R. McCulloch, S. McWilliam, D. Tang, et al. A genome wide survey of SNP variation reveals the genetic structure of sheep breeds. *PLoS ONE*, 4(3):e4668, 2009. URL: <http://www.ncbi.nlm.nih.gov/pubmed/19270757>.