2011

97. Bis, J. C., Kavousi, M., Franceschini, N., et al. (2011). Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. Nat Genet 43(10): 940-947.

98. Boger, C. A., Chen, M. H., Tin, A., et al. (2011). CUBN is a gene locus for albuminuria. J Am Soc Nephrol 22(3): 555-570.

99. Dehghan, A., Dupuis, J., Barbalic, M., et al. (2011). Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. Circulation 123(7): 731-738.

100. Ehret, G. B., Munroe, P. B., Rice, K. M., et al. (2011). Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature 478(7367): 103-109.

101. Evans, D. S., Snitker, S., Wu, S. H., et al. (2011). Habitual sleep/wake patterns in the Old Order Amish: heritability and association with non-genetic factors. Sleep 34(5): 661-669.

102. Fox, E. R., Young, J. H., Li, Y., et al. (2011). Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Hum Mol Genet 20(11): 2273-2284.

103. Gieger, C., Radhakrishnan, A., Cvejic, A., et al. (2011). New gene functions in megakaryopoiesis and platelet formation. Nature 480(7376): 201-208.

104. International Consortium for Blood Pressure Genome-Wide Association Studies, Ehret, G. B., Munroe, P. B., et al. (2011). Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature 478(7367): 103-109.

105. Kilpelainen, T. O., Qi, L., Brage, S., et al. (2011). Physical activity attenuates the influence of FTO variants on obesity risk: a meta-analysis of 218,166 adults and 19,268 children. PLoS Med 8(11): e1001116.

106. Kilpelainen, T. O., Zillikens, M. C., Stancakova, A., et al. (2011). Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nat Genet 43(8): 753-760.

107. Lanktree, M. B., Guo, Y., Murtaza, M., et al. (2011). Meta-analysis of dense genecentric association studies reveals common and uncommon variants associated with height. Am J Hum Genet 88(1): 6-18.

108. Lewis, J. P., Fisch, A. S., Ryan, K., et al. (2011). Paraoxonase 1 (PON1) gene variants are not associated with clopidogrel response. Clin Pharmacol Ther 90(4): 568-574.

109. Mitchell, B. D. and Yerges-Armstrong, L. M. (2011). The genetics of bone loss: challenges and prospects. J Clin Endocrinol Metab 96(5): 1258-1268.

110. Montasser, M. E., Douglas, J. A., Roy-Gagnon, M. H., et al. (2011). Determinants of blood pressure response to low-salt intake in a healthy adult population. J Clin Hypertens (Greenwich) 13(11): 795-800.

111. O'Donnell, C. J., Kavousi, M., Smith, A. V., et al. (2011). Genome-wide association study for coronary artery calcification with follow-up in myocardial infarction. Circulation 124(25): 2855-2864.

112. Parsa, A., Chang, Y. P., Kelly, R. J., et al. (2011). Hypertrophy-associated polymorphisms ascertained in a founder cohort applied to heart failure risk and mortality. Clin Transl Sci 4(1): 17-23.

113. Roghmann, M. C., Johnson, J. K., Stine, O. C., et al. (2011). Persistent Staphylococcus aureus colonization is not a strongly heritable trait in Amish families. PLoS One 6(2): e17368.

114. Shen, H., Damcott, C., Shuldiner, S. R., et al. (2011). Genome-wide association study identifies genetic variants in GOT1 determining serum aspartate aminotransferase levels. J Hum Genet 56(11): 801-805.

115. Speliotes, E. K., Yerges-Armstrong, L. M., Wu, J., et al. (2011). Genome-wide association analysis identifies variants associated with nonalcoholic fatty liver disease that have distinct effects on metabolic traits. PLoS Genet 7(3): e1001324.