

TABLE OF CONTENTS

| | |
|---|-----------|
| Breeding Objectives and Economics | 1 |
| Selection strategies for breeding objectives in growing pigs | 1 |
| <i>S. Hermesch, M.M.A. Arnal, V. Börner and S. Dominik</i> | |
| A genetic line of <i>Nile Tilapia</i> undergoing seven generations of selection under moderate salinity water environment | 5 |
| <i>N.P. Thoa, N.H. Ninh, W. Knibb and N.H. Nguyen</i> | |
| Non-linear calving difficulty weightings in the Irish dairy industry | 9 |
| <i>F.S. Hely, R. Evans, P.R. Amer and A. Cromie</i> | |
| Extended cow liveweight modelling for beef cattle breeding objectives | 13 |
| <i>B.J. Walmsley, M.L. Wolcott, W.S. Pitchford, D.J. Johnston and S.A. Barwick</i> | |
| Evaluation of alternative selection indexes for non-linear profit traits approaching their economic optimum | 17 |
| <i>D. Martin-Collado, B. Visser, T. Byrne, and P. Amer</i> | |
| A review of the national breeding objective and selection Indexes for the Australian dairy industry | 21 |
| <i>T. Byrne, D. Martin-Collado, B. Santos, P. Amer, J. Pryce, and M. Axford</i> | |
| Feed saved breeding values for Australian dairy cattle | 25 |
| <i>J.E. Pryce, O. Gonzalez-Recio, G. Nieuwhof, W.J. Wales, M.P. Coffey, B.J. Hayes, and M.E. Goddard</i> | |
| Breeding to improve meat eating quality in terminal sire sheep breeds | 29 |
| <i>A. Swan, T. Pleasants, and D. Pethick</i> | |
| Accounting for the cost of reproductive technologies during selection in sheep breeding programs | 33 |
| <i>T. Granleese, S.A. Clark, A.A. Swan, J.H.J. van der Werf</i> | |
| Genetic expressions and economic impact of performance Recording in multi-tiered sheep breeding schemes | 37 |
| <i>B.F.S. Santos, T.J. Byrne, B. Visser, J.H.J. van der Werf, J.P. Gibson and P.R. Amer</i> | |
| Detecting causal variants | 41 |
| Why can we impute some rare sequence variants and not others? | 41 |
| <i>B.J. Hayes, P.J. Bowman, H.D. Daetwyler and M.E. Goddard</i> | |
| From sheep SNP chips, genome sequences and transcriptomes via mechanisms to improved sheep breeding and management | 45 |
| <i>B.P. Dalrymple, V.H. Oddy, J.C. McEwan, J.W. Kijas, R. Xiang, J. Bond, N. Cockett, K. Worley, T. Smith and P.E. Vercoe</i> | |
| Pleiotropic multi-trait genome-wide association reveals putative candidate genes for fatty acid composition in Australian sheep | 49 |
| <i>S. Bolormaa, J.H.J. van der Werf, B.J. Hayes, M.E. Goddard, and H.D. Daetwyler</i> | |
| Fine-mapping single nucleotide polymorphisms on <i>bos taurus</i> chromosome 26 affecting adipose myristic acid | 53 |
| <i>Arthur R Gilmour</i> | |
| <i>D. Lu, S.M. Hickey, N.G. Cullen, S. Miller</i> | |
| Effects of <i>tex11</i> and <i>AR</i> polymorphisms on reproduction and Growth traits in Australian beef cattle | 57 |
| <i>L.T. Nguyen, G.M.F.D Camargo, R.E. Lyons, S.A. Lehnert and M.R.S. Fortes</i> | |

| | |
|---|-----------|
| Using protein QTL to disentangle variants effecting protein percentage in milk near the casein complex | 61 |
| <i>K.E. Kemper, M.J. Carrick and M.E. Goddard</i> | |
| A comparison of genotypes generated by infinium beadchips and a targeted genotype by sequencing method in cattle | 65 |
| <i>A.J. Chamberlain, P. Beatson, B.A. Mason, C. Prowse-Wilkins, C.M. Reich, C. Schrooten, B.J. Hayes, J. Tibbits, and M. Hayden</i> | |
| Identification of loci associated with parasite resistance in Australian sheep | 69 |
| <i>M. Al Kalaldehy, J.H.J. van der Werf and C. Gondro</i> | |
| Non-synonymous polymorphism in <i>HELB</i> is associated with male and female reproductive traits in cattle | 73 |
| <i>M.R.S. Fortes, F.B. Almughlliq, L.T. Nguyen, L.R. Porto Neto, S.A. Lehner</i> | |
| Detecting variants associated with complex traits through changing gene expression in cattle | 77 |
| <i>M. Khansefid, J.E. Pryce, S. Bolormaa, Y. Chen and M.E. Goddard</i> | |
| Multi-breed GWAS and meta-analysis using whole-genome sequences of five dairy cattle breeds | 81 |
| <i>I.van den Berg, D. Boichard and M.S. Lund</i> | |
| Feed efficiency, methane emission and fertility | 85 |
| Visualisation of rumen microbiome | 85 |
| <i>G.R. Wood, S. Kittelmann, C. Pinares-Patiño, K.G.Dodds, M.R. Kirk, S. Ganesh, S.M. Hickey, P.H. Janssen, J.C. McEwan and S.J. Rowe</i> | |
| Prediction of residual feed intake from genome and metagenome profiles in first lactation Holstein-Friesian dairy cattle | 89 |
| <i>M. Wang, J. E. Pryce, Keith Savin and B. J. Hayes</i> | |
| Associations of rumen volatile fatty acids with phenotypic and genetic variation in methane production traits in Angus cattle | 93 |
| <i>H.C. Smith, R.M. Herd, K.A. Donoghue, T. Bird-Gardiner, P.F. Arthur and R.F. Hegarty</i> | |
| Liver <i>microna</i> expression revealed the difference in fat Metabolism from cattle divergently selected for residual feed intake | 97 |
| <i>Y. Chen, W. AL-Husseini, I. Barchia, C. Gondro, R.M. Herd, and P.F. Arthur</i> | |
| Genetic selection for litter size in cattle | 101 |
| <i>L. R. Piper, B. M. Bindon, A. A. Swan, and H. G. Brewer</i> | |
| Towards a data set to investigate feed efficiency in New Zealand maternal sheep | 106 |
| <i>P.L. Johnson, S.P. Miller and K. Knowler</i> | |
| Repeatabilities for methane emission in merino ewes on pasture across different ages | 110 |
| <i>S. Dominik and V.H. Oddy</i> | |
| Genetic parameters for methane production and relationships with production traits in Australian beef cattle | 114 |
| <i>K.A. Donoghue, T.L. Bird-Gardiner, P.F. Arthur, R.M. Herd and R.F. Hegarty</i> | |
| Genomic estimated breeding values for methane production in Australian beef cattle | 118 |
| <i>B.J. Hayes, K.A. Donoghue, C. Reich, B. Mason, R.M. Herd and P.F. Arthur</i> | |
| Divergent selection for methane yield in beef cattle | 122 |
| <i>T. Bird-Gardiner, K.A. Donoghue, P.F. Arthur, R.M. Herd, and R.F. Hegarty</i> | |

| | |
|---|------------|
| Genomic prediction in practice | 126 |
| Big is beautiful: biology informed sequence exploitation | 126 |
| <i>M. Pérez-Enciso, M. Naval-Sánchez, J. Leno-Colorado and A. Reverter</i> | |
| High throughput genotyping-by-sequencing in livestock - ION AMPLISEQ™ | 133 |
| <i>Kristian Ridley, Jeremy Walker, Matthew Hickenbotham</i> | |
| Using genomic information to estimate genotype by environment interactions | 137 |
| <i>S.A. Clark, S.H. Lee and J.H.J. van der Werf</i> | |
| Lamb eating quality can be managed by using terminal sires with desirable breeding values for intramuscular fat and shear force | 141 |
| <i>J.E. Hocking Edwards, B. Hancock, S. Gill, R. Apps and A. Ball</i> | |
| Genomic best linear unbiased prediction using differential evolution | 145 |
| <i>H.A. Al-Mamun, P. Kwan, S. Clark, S.H. Lee, H.K. Lee, K.D. Song, S.H. Lee and C. Gondro</i> | |
| Improving the accuracy of across breed genomic predictions | 149 |
| <i>M.E. Goddard, I.M. MacLeod, S. Bolormaa, B.J. Hayes, and K.E. Kemper</i> | |
| Data compression: a new way to infer genomic relationship matrices and highlight regions of interest in commercial lines of broiler chicken | 153 |
| <i>N.J. Hudson, R. Hawken R. Sapp and A. Reverter</i> | |
| Relationships between change in trait definition and accuracy of genomic breeding value of type traits in Australian Holstein | 157 |
| <i>M. Haile-Mariam, J.E. Pryce and B.J. Hayes</i> | |
| Predicting genomic selection accuracy from heterogeneous sources | 161 |
| <i>J.H.J. van der Werf, S.A. Clark and S.H. Lee</i> | |
| Accuracy of genomic prediction for merino wool traits using high-density marker genotypes | 165 |
| <i>N. Moghaddar, A.A. Swan and J.H.J. van der Werf</i> | |
| Genetics on the ground | 169 |
| Considerations in the use of commercial data for genetic evaluation in beef and sheep in Australia | 169 |
| <i>R. G. Banks and B. Tier</i> | |
| What causes the negative genetic correlation between maternal and direct effects for lamb birth weight? | 173 |
| <i>H.T. Blair</i> | |
| Genetic correlations between purebred and crossbred performance of Poll Dorset sheep | 177 |
| <i>D.J. Brown and J.H.J. van der Werf</i> | |
| Using hump height to estimate <i>Bos indicus</i> content in the MSA beef grading model which predicts eating quality | 181 |
| <i>M. Kelly, J.M. Thompson, L.R. Porto-Neto, R.E. Lyons and S. S. Moore</i> | |
| Are high Australian profit ranking sires best in all herds? Findings from the feeding the genes project | 185 |
| <i>J.M. Morton, R.R. Woolaston, P. Brightling, S. Little, K.L. Macmillan, J.E. Pryce and G.J. Nieuwhof</i> | |
| Selection for reduced mature cow weight will reduce body condition unless accompanied by selection for increased fat | 189 |
| <i>W.S. Pitchford, S.J. Lee, K.A. Donoghue and B.J. Walmsley</i> | |

| | |
|---|------------|
| Estimates of genetic parameters for seasonal weight changes of beef cows <i>Karin Meyer and Ian G. Colditz</i> | 193 |
| Effects of productions level on the expression of breed and heterosis for lactation yields of milk, fat and protein in cows milked once and twice daily <i>F. Lembeye, N. Lopez-Villalobos, J.L. Burke and S.R. Davis</i> | 197 |
| Revisiting total weaning weight as a selection criterion <i>K.L. Bunter and D.J. Brown</i> | 201 |
| Is fibre comfort factor required in Merino breeding programs? <i>S. Hatcher and D.J. Brown</i> | 205 |
| Genetic parameters for eating quality traits of Australian lamb <i>S.I. Mortimer, A.A. Swan, L. Pannier, A.J. Ball, R.H. Jacob, J.H.J. van der Werf and D.W. Pethick</i> | 209 |
| Industry focus | 213 |
| A public: private collaboration to evaluate the potential value of genomic information to a vertically-integrated commercial beef cattle enterprise <i>B.T Welly, M.D. MacNeil, A.R. McClain, R.C. Raymond, E.B. Simpson, and A.L. Van Eenennaam</i> | 213 |
| Production performance of merino and Dohne Merino and lambs in pure or crossbreeding systems <i>S.W.P. Cloete and J.J.E. Cloete</i> | 217 |
| Has the beef genetic improvement pipeline been effective? <i>P.F Parnell</i> | 221 |
| Detailing a beef genetics extension strategy <i>S.J. Lee and W.S. Pitchford</i> | 225 |
| Evaluating dairy herd genetic progress <i>M.M. Axford, P.W. Williams, D.P. Abernethy, and G.J. Nieuwhof</i> | 229 |
| Realising genetic improvement for the extensive livestock Industries as a whole <i>R. G. Banks</i> | 233 |
| Inheritance of tail length in merino sheep <i>J.C.Greeff, L.J.E.Karlsson and A.C.Schlink</i> | 237 |
| Testing an approach to account for daughter misidentification In the estimation of breeding values <i>N. Lopez-Villalobos, J.R. Bryant, B.L Harris and D.J. Garrick</i> | 241 |
| Merino breeding objectives under climate change <i>P. Graham, A.A. Swan and R.G. Banks</i> | 245 |
| SNP-based parentage in an Australian cattle industries context: does one size fit all? <i>R.E. Lyons, S. Buttsworth, D. Waine and M. Kelly</i> | 249 |
| Impact of scanning lean cattle on the genetic correlation between scan and carcass intramuscular fat in Angus and Hereford cattle <i>S.F.Walkom, M.G.Jeyaruban and D.J.Johnston</i> | 253 |
| Plenary Presentations | 257 |
| Integration of genomic information into national cattle and sheep evaluations – past, present and future <i>D.P. Berry, J.F. Kearney, N. McHugh, E. Wall, D. Purfield, and A.R. Cromie</i> | 257 |

| | |
|---|------------|
| Sole haemorrhage, dermatitis and co. - how genomic information and precise phenotypes help to unscramble Genetic background of health traits in dairy cattle <i>K. Schöpke</i> | 261 |
| The opportunities and challenges of integrating genomics in a broiler breeding program <i>R.J. Hawken, R.L. Sapp, R. Okimoto, J. Chen, R. Borg, C-H. Huang, T. Wing, C. Wang, J. Henshall, and M. Abrahamsen</i> | 266 |
| Genomic prediction using sequence data in a multibreed context <i>M.S. Lund, I. van den Berg and D. Boichard</i> | 270 |
| Poster Presentations | 274 |
| Selection patterns for Holstein sires in production-recorded Holstein herds with differing feeding systems <i>K.L. Macmillan, J.M. Morton and J.E. Pryce</i> | 274 |
| Mildly penalized maximum likelihood estimation of genetic covariances matrices without tuning <i>Karin Meyer</i> | 278 |
| Efficiency of a tactical phenotyping strategy for multi-stage selection <i>C Massault and J.H.J van der Werf</i> | 282 |
| A commercial comparison of ewe breeds for reproduction, wool and lamb growth <i>K. P. Ransom, F. D. Brien and W.S. Pitchford</i> | 286 |
| Reproductive performance of Holstein and Jersey heifers and cows in a pasture-based system in South Africa <i>C.J.C. Muller, J.P. Potgieter, S.W.P Cloete and J.A. Botha</i> | 290 |
| Genetic diversity and population structure of four South African sheep breeds <i>L. Sandenbergh, S.W.P. Cloete, R. Roodt-Wilding, M.A. Snyman and A.E. Van der Merwe</i> | 294 |
| Sheep phylogeography and domestication as inferred from complete genome sequences <i>M. Naval-Sanchez, S. McWilliam, A. Reverter, M. Perez-Enciso, N. J. Hudson, J. Kijas</i> | 298 |
| Assessing imputation accuracy using a 15k low density panel in a multi-breed New Zealand sheep population <i>R.V. Ventura M. Lee, S.P. Miller, S.M. Clarke and J.C. McEwan</i> | 302 |
| Estimating the genetic (co)variance explained per chromosome for two growth traits using a half sib data structure in sheep <i>C. Esquivelzeta-Rabell, N. Moghaddar, S. Clark and J.H.J. van der Werf</i> | 306 |
| Runs of homozygosity in swakara pelt producing sheep: Implications on sub-vital performance <i>F.C. Muchadeyi, M.T. Malesa, P. Soma and E.F. Dzomba</i> | 310 |
| Genetic diversity and effective population size of eight Iranian cattle breeds <i>E.M. Strucken, K. Karimi, A.K. Esmailzadeh, N. Moghaddar and C. Gondro</i> | 314 |
| <i>Arthrospira platensis</i> : a novel feed supplement influences gene expression in the heart, kidney and liver of prime lambs <i>A.E.O. Malau-Aduli and A. Kashani</i> | 318 |
| Environmental effects on post weaning fleece traits of a Merino sire evaluation flock <i>S.I. Mortimer and A.E. Casey</i> | 322 |

| | |
|---|------------|
| Methane emissions estimated based on milk fatty acids of jersey and Fleckvieh x Jersey cows in a pasture-based system | 326 |
| <i>S. Abel, C.J.C. Muller and B. Sasanti</i> | |
| Comparison of survival phenotypes in specific dairy production systems | 330 |
| <i>B. Visser, K. Stachowicz, J.R. Bryant and P.R. Amer</i> | |
| Modelling of longitudinal liveweight data using regression with legendre and eigenvector functions | 334 |
| <i>M. D. Price, M. E. Olayemi and J. B. Bryant</i> | |
| Fibre diameter measured in the post-weaning age window is genetically the same trait as yearling fibre diameter | 338 |
| <i>Andrew Swan</i> | |
| Measurement of methane traits in the beef information nucleus cattle | 342 |
| <i>P.F. Arthur, R.M. Herd, C. Weber, H. Smith and R.F. Hegarty</i> | |
| Reproduction, behaviour and health | 346 |
| Regions impacting inbreeding depression and their association with additive genetic effects for jersey cattle from the United States of America and Australia | 346 |
| <i>J. T. Howard, J. E. Pryce, M. Haile-Mariam, C. Maltecca</i> | |
| Genetic and phenotypic relationships between kid survival and birth weight in Australian meat goats | 350 |
| <i>M.N. Aldridge, D.J. Brown, W.S. Pitchford</i> | |
| Genetic relationships between breech cover, wrinkle and lamb survival in merino sheep | 354 |
| <i>S. Hatcher, D.J. Brown, F.D. Brien and M.L. Hebart</i> | |
| A genome-wide association study of non-additive effects for milk yield and fertility in Holstein and Jersey dairy cattle | 358 |
| <i>H. Aliloo, J.E. Pryce, O. González-Recio, B.G. Cocks, B.J. Hayes</i> | |
| Effects of selection for fertility on lactation curves | 362 |
| <i>E.M. Strucken, Y.C.S.M. Laurenson and G.A. Brockmann</i> | |
| Benchmarking cow health status with dairy herd summary data | 366 |
| <i>K.L. Parker Gaddis, J.B. Cole, J.S. Clay, and C. Maltecca</i> | |
| Proposed changes in the genetic evaluation of dairy fertility in New Zealand | 370 |
| <i>K. Stachowicz, G.M. Jenkins, P.R. Amer, J.R. Bryant and S. Meier</i> | |
| Using sequence data to improve accuracy of genomic prediction and QTL discovery for dairy cow fertility | 374 |
| <i>I.M. MacLeod, B.J. Hayes, M. Haile-Mariam, P. Bowman, A.J. Chamberlain, C.J. Vander Jagt, C. Schrooten and M.E. Goddard</i> | |
| Genomic breeding values of heat tolerance in Australian dairy cattle | 378 |
| <i>T.T.T. Nguyen, P.J. Bowman, M. Haile-Mariam, J.E. Pryce, B.J. Hayes</i> | |
| Improving the accuracy of genomic selection for lactation anoestrous interval in Brahman cattle | 382 |
| <i>M.L. Wolcott, Y.D. Zhang and D.J. Johnston</i> | |
| Australian sheep breeding values for worm egg count retain predictive power across flocks in the presence of GxE | 386 |
| <i>L. Li, A.A. Swan, D.J. Brown and J.H.J. van der Werf</i> | |

| | |
|--|------------|
| Speed Talks | 390 |
| Bessie: a program for multivariate linear model BLUP and Bayesian analysis of larger scale genomic data | 390 |
| <i>V. Boerner and B. Tier</i> | |
| Collection of data for the genetic improvement of health traits in Australian dairy cattle | 393 |
| <i>M. Abdelsayed, P. Douglas and J.E. Pryce</i> | |
| Quantifying between animal variation for male semen traits and female egg traits in an ostrich flock used to develop an artificial insemination protocol | 397 |
| <i>S.W.P Cloete, M. Bonato, A.M.J. Smith and I.A. Malecki</i> | |
| Genomic predictions for meat colour traits in New Zealand sheep | 401 |
| <i>L.F. Brito, S.P. Miller, M.A. Lee, D. Lu, K.G. Dodds, N.K. Pickering, W.E. Bain, F.S. Schenkel, J.C. McEwan, S.M. Clarke</i> | |
| Genotype by birth or rearing type interaction in Merino sheep | 405 |
| <i>A. Dakhlan, N. Moghaddar and J.H.J. van der Werf</i> | |
| Genetic analyses on carcass characters of Australian Wagyu beef cattle | 409 |
| <i>Yuandan Zhang, Bruce Tier and Robert Banks</i> | |
| Change in accuracy of estimated breeding values for Viascan lean-meat yield when estimated from half-sib records | 413 |
| <i>H.J.B. Craig, N.B. Jopson and M.J. Young</i> | |
| Effect of different data exclusion policies on the heritability of fat depth in maternal, Merino and terminal sheep | 417 |
| <i>A.J. McMillan and D.J. Brown</i> | |
| How precise are enteric methane emission phenotypes or breeding values estimated from spot flux measures? | 421 |
| <i>D.J. Cottle, J.I. Velazco, D. Mayer, R.S. Hegarty and R.M. Herd</i> | |
| Implications of manipulating the ewe live weight penalty in maternal sheep indexes in New Zealand | 425 |
| <i>J.I. Kerslake, P.R. Amer, M.J. Young and T.J. Byrne</i> | |
| Statistical methods and computation | 429 |
| Computing for multi-trait single-step genomic evaluation of Australian sheep | 429 |
| <i>Karin Meyer, Andrew Swan and Bruce Tier</i> | |
| Using random forests to identify SNP associated with leg defect in broiler chicken: impact of correcting for population structures | 433 |
| <i>Y. Li, A. George, R. Hawken, R. Sapp, S. Lehnert, and A. Reverter</i> | |
| Missing heritability of adaptation phenotypes in tropical cattle | 437 |
| <i>Laercio R. Porto-Neto, Nicholas J. Hudson, William Barendse, Sigrid A. Lehnert and Antonio Reverter</i> | |
| Imputation accuracy measurement and post-imputation quality in imputed SNP genotypes for dairy cattle | 441 |
| <i>K.M. Tiplady and R.G. Sherlock</i> | |
| Inbreeding depression in adaptation phenotypes of tropical beef cattle using genome wide data | 445 |
| <i>L.R. Porto-Neto, N.J. Hudson, W. Barendse, M.A.R. de Cara, S.A. Lehnert and A. Reverter</i> | |

| | |
|---|------------|
| Optbr: computationally efficient genomic predictions and QTL mapping in multi-breed populations | 449 |
| <i>Tingting Wang, Yi-Ping Phoebe Chen, Kathryn E. Kemper, Michael E. Goddard and Ben J. Hayes</i> | |
| The impact of fitting incorrect models on the partitioning of genetic variance components for binomial lamb traits | 453 |
| <i>P.R. Amer K. Stachowicz, P. Pierard and G.M. Jenkins</i> | |
| Backfat as an environmental descriptor in defining growth rate of the pig: a G×E analysis | 457 |
| <i>S.Z.Y. Guy, S. Hermesch and P.C. Thomson</i> | |
| Which genomic relationship matrix? | 461 |
| <i>B. Tier, K. Meyer and M. H. Ferdosi</i> | |
| Detection and validation of structural variation in cattle whole-genome sequence data | 465 |
| <i>L. Chen, A.J. Chamberlain, C.M. Reich, H.D. Daetwyler and B.J. Hayes</i> | |
| A comparison of genetic connectedness measures using data from the NZ sheep industry | 469 |
| <i>J.B. Holmes, B. Auvray, S.A. Newman, K.G. Dodds and M.A. Lee</i> | |
| Evolving to the best SNP panel for Hanwoo breed proportion estimates | 473 |
| <i>C. Esquivelzeta-Rabell, H.A. Al-Mamun, S.H. Lee, H.K. Lee, K.D. Song and C. Gondro</i> | |
| Systems biology | 477 |
| What's next in genomics? functional annotation of animal Genomes | 477 |
| <i>C.J. Vander Jagt, A.J. Chamberlain, B.J. Hayes, L.C. Marett, M.E. Goddard</i> | |
| A map of bovine long non coding RNA across 18 tissues | 481 |
| <i>Lambros T. Koufariotis, Yi-Ping Phoebe Chen, Amanda Chamberlian, Christy Vander Jagt, Ben J. Hayes</i> | |
| Potential role of lncrna cyp2c91-protein interactions on immune diseases and obesity | 485 |
| <i>P. Suravajhala, L.J.A. Kogelman, G. Mazzoni and H.N. Kadarmideen</i> | |
| Allele specific expression is pervasive in cattle | 489 |
| <i>J. Kijas, B. Barendse, C. Bottema, R. Brauning, A. Chamberlain, S. Clarke, B. Dalrymple, R. Tellam, B. Hayes, J. McEwan, S. Moore</i> | |
| Connecting gene expression and phenotype – preliminary results from RNA sequencing of 150 lambs | 493 |
| <i>S. Bolormaa, R. Behrendt, M.I. Knight, B.A. Mason, C.P. Prowse-Wilkins, L. Slocombe, C.J. Vander Jagt, B.J. Hayes, A.J. Chamberlain and H.D. Daetwyler</i> | |