

## The Koala Genome Consortium

REBECCA N. JOHNSON,\*<sup>1</sup> MATTHEW HOBBS,<sup>1</sup> MARK D. B. ELDRIDGE,<sup>2</sup> ANDREW G. KING,<sup>1</sup>  
DONALD J. COLGAN,<sup>2</sup> MARC R. WILKINS,<sup>3</sup> ZHILIANG CHEN,<sup>3</sup> PETER J. PRENTIS,<sup>4</sup>  
ANA PAVASOVIC,<sup>4</sup> ADAM POLKINGHORNE,<sup>4,5</sup> AND PETER TIMMS<sup>4,5</sup>

<sup>1</sup> Australian Centre for Wildlife Genomics, Australian Museum Research Institute,  
6 College Street, Sydney NSW 2010, Australia

<sup>2</sup> Australian Museum Research Institute, 6 College Street, Sydney NSW 2010, Australia

<sup>3</sup> NSW Systems Biology Initiative, School of Biotechnology and Biomolecular Sciences,  
University of New South Wales, Sydney NSW 2052, Australia

<sup>4</sup> Queensland University of Technology, Brisbane Queensland 4000, Australia

<sup>5</sup> Current address: University of the Sunshine Coast,  
Sippy Downs Queensland 4556, Australia  
[rebecca.johnson@austmus.gov.au](mailto:rebecca.johnson@austmus.gov.au)

**ABSTRACT.** The koala (*Phascolarctos cinereus*) is an iconic Australian animal. Koalas are both biologically unique and evolutionarily distinct as the only living representative of the marsupial family Phascolarctidae. Their unique and highly specific diet of eucalyptus leaves, combined with the increasing threats of predation and habitat loss through urbanisation, mean that koalas are particularly vulnerable to the deleterious effects of fragmented habitat and population bottlenecks. They are further threatened by disease such as *Chlamydia* and there is increasing interest in the varying strains of the Koala Retrovirus. We present preliminary transcriptome and genome data for the koala and introduce the Koala Genome Consortium (KGC), a group working towards the production of a high quality draft assembly of the koala genome. The KGC is currently comprised of several Australian research institutes and Universities although our intention is to recruit researchers from around the world to contribute to the genome assembly and annotation process and ultimately make use of the assembled genome. Once available as an annotated draft, we anticipate the genome sequence will add significant value to the extensive body of existing research for koalas.

JOHNSON, REBECCA N., MATTHEW HOBBS, MARK D. B. ELDRIDGE, ANDREW G. KING, DONALD J. COLGAN, MARC R. WILKINS, ZHILIANG CHEN, PETER J. PRENTIS, ANA PAVASOVIC, ADAM POLKINGHORNE AND PETER TIMMS. 2014. The Koala Genome Consortium. In *The Koala and its Retroviruses: Implications for Sustainability and Survival*, ed. Geoffrey W. Pye, Rebecca N. Johnson and Alex D. Greenwood. *Technical Reports of the Australian Museum, Online* 24: 91–92.

### Overview of the Koala Genome Consortium

The purpose of the Koala Genome Consortium is to generate a high quality draft assembly of the koala genome, which will be useful to all koala researchers and have real and measurable conservation outcomes for koalas. Prior to the sequencing of the koala genome, we also undertook to determine the transcriptome from several tissues from two

separate koalas. The Koala Genome Consortium is a project co-led by the Australian Museum and Queensland University of Technology but since this is a large undertaking, demanding the expertise of a wide group of researchers in the fields of koala biology, bioinformatics and marsupial genomics, we are currently seeking expressions of interest from potential new Consortium members and will continue to do so over the course of the project.

\* author for correspondence