Termites are renowned as pests as they can cause major damage to properties. However, not all termite species consume lignocellulose in the form of wood - many Australian termites feed on grass, plant debris or soil, thereby providing a range of crucial ecosystem services. This diversity in feeding habits suggests that the intestinal tracts of these insects are an untapped resource for enzymes with the potential to breakdown regional sources of lignocellulose for the production of biofuels. Utilising this resource requires knowledge of the diet and endosymbionts of the termite species local to the biofuel process and the adaptation of one or the other to optimise the conversion of cellulose into ethanol. Therefore this study aims to: (1) profile the natural gut microbiota of several Western Australian termites and (2) perform feeding experiments to investigate whether the gut population can be selected for efficient breakdown of wheat crop residue and eucalyptus wood, two potential sources of feedstock for future biofuel production in WA. We optimised a metagenomics pipeline, including sample preparation, paired-end sequencing of the V4 hypervariable region of the 16S rRNA gene on the Illumina MiSeq platform and a bioinformatics analysis using the USEARCH and QIIME software packages. We profiled the gut bacteria from the lower termite *Coptotermes acinaciformis*, and two higher termites, *Tumilitermes westraliensis* and *Amitermes obeuntis*. We found that WA termites indeed harbour a large number of novel bacterial species while retaining the major phyla present in other termite species. Furthermore, there are differences between the gut microbiota of individuals from different *T. westraliensis* colonies, suggesting local adaptations of gut bacterial populations. Our findings indicate that there is a rich diversity and natural variation of gut communities present in Western Australian termites, warranting further experiments to understand the functioning and adaptability of these gut communities.