



UPPSALA  
UNIVERSITET

## Bioinformatics Engineering Program

Uppsala University School of Engineering

<b>UPTEC X 12 013</b>	<b>Date of issue 2012-06</b>	
Author	<b>Jesper Gådin</b>	
Title (English)	<b>basicASE: an R-statistics package to detect significant allelic imbalance in RNA-seq data</b>	
Title (Swedish)		
Abstract	<p>Investigation of allelic imbalance expression QTLs (aeQTLs) in RNA-seq data can increase the accuracy in the hunt for candidate genes susceptible as drug targets. The Bioconductor project has recently developed research tools to handle the massive amounts of data that come with next generation sequencing. The basicASE package has been developed to carry out aeQTL analyses in that environment. Many technical issues concerning a user friendly import, statistical testing and visualization of data are facilitated through the package, which also has a central design to accommodate integration of new functions and development.</p>	
Keywords	BasicASE, allelic imbalance, aeQTL, R, Bioconductor, NGS, RNA-seq	
Supervisor	<b>Lasse Folkersen</b> <b>The Center for Molecular Medicine at Karolinska Institute</b>	
Scientific reviewer	<b>Mikael Tholleson</b> <b>Department of Organismal Biology at Uppsala University</b>	
Project name	Sponsors	
Language	Security	
<b>English</b>	Secret until 2013-10	
<b>ISSN 1401-2138</b>	Classification	
Supplementary bibliographical information	Pages	
	<b>49</b>	
<b>Biology Education Centre</b> Box 592 S-75124 Uppsala	<b>Biomedical Center</b> Tel +46 (0)18 4710000	<b>Husargatan 3 Uppsala</b> Fax +46 (0)18 471 4687

