Accepted Manuscript

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PII: DOI: Reference:

S1874-9399(15)00216-3 doi: 10.1016/j.bbagrm.2015.10.010 ce: BBAGRM 948

To appear in: BBA - Gene Regulatory Mechanisms

Received date:30 June 2015Revised date:8 October 2015Accepted date:13 October 2015

Please cite this article as: Kaori Kashi, Lindsey Henderson, Alessandro Bonetti, Piero Carninci, Discovery and functional analysis of lncRNAs: Methodologies to investigate an uncharacterized transcriptome, *BBA - Gene Regulatory Mechanisms* (2015), doi: 10.1016/j.bbagrm.2015.10.010

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ACCEPTED MANUSCRIPT

Discovery and functional analysis of IncRNAs: methodologies to investigate an uncharacterized transcriptome

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Abstract

It is known that more than 70% of mammalian genomes are transcribed, yet the vast majority of transcripts do not code for proteins. Are these noncoding transcripts merely transcriptional noise, or do they serve a biological purpose? Recent developments in genomic analysis technologies, especially sequencing methods, have allowed researchers to create a large atlas of transcriptomes, study subcellular localization, and investigate potential interactions with proteins for a growing number of transcripts. Here, we review the current methodologies available for discovering and investigating functions of long noncoding RNAs (IncRNAs), which require a wide variety of applications to study their potential biological roles. Download English Version:

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