**Automating NEBNext® Enzymatic Methyl-seq Kit Using the Biomek i7 Hybrid NGS Workstation for Whole Genome Methylation sequencing**

**Siva Chavadi** (schavadi@neb.com), New England Biolabs, **Michael Benway**, New England Biolabs, **Zach Herbert**, Dana-Farber Cancer Institute, **Raga Vadhi**, Dana Farber Cancer Institute Molecular Biology Core Facilities., **Zach Smith**, Beckman Coulter Life Sciences

DNA methylation is one of the most important epigenetic regulatory mechanisms, and epigenomic changes are recognized as factors that influence tumor initiation, growth and progression. Accurate identification of 5mC and 5hmC in DNA increases insight into potential gene regulatory mechanisms. Traditionally, Bisulfite sequencing which chemically converts cytosines to uracils is commonly used method for DNA methylation analysis. This chemical-based conversion damages and degrades DNA, resulting in shorter insert sizes as well as introducing bias into the data. NEBNext® Enzymatic Methyl-seq (EM-seq™) addresses the drawbacks of bisulfite sequencing by minimizing the damage to DNA, enabling longer insert sizes, lower duplication rates and reduced GC bias resulting in more accurate quantification of methylation in the DNA. Advances in next generation sequencing, in particular, automating sample preparation workflows, have aided large scale quantification of DNA methylation. In this poster, we describe the automation of whole genome methylation sequencing using NEBNext® Enzymatic Methyl-seq Kit on the Biomek i7 Hybrid NGS Workstation, which allows higher throughput and less hands-on time for researchers to map genome wide methylome markers without resourcing to bisulfite conversion.