A Single-Platform Custom Capture Array for Detection of Multiple Myeloma Variants

Background:
Multiple myeloma (MM) is a fatal malignancy of mature plasma B cells. MM has many genes associated with it and several common mutations, such as translocations, copy number alterations (CNAs), and single nucleotide variants (SNVs). Current methods, such as exome sequencing for genomic analysis of MM, are not capable of detecting these mutations in one generic platform analysis. This often requires heavy computational analysis, a longer time to receive clinical results, and is more expensive.

Technology Description:
Researchers at Washington University have developed a single platform, custom capture array sequencing platform that is capable of detecting SNVs, CNAs, and translocations. It makes use of oligonucleotide probes designed to be complementary to the coding regions of 467 genes expressed in myeloma. Due to its large number of genes, it can serve to identify canonical mutations, and reveal rarer mutations that are present only in some samples. Therefore, this platform is simple to use, comprehensive in delivery of results, and affordable.

Indications: Multiple Myeloma

Key Advantages:
- Capable of detecting SNVs, CNAs, and translocations in a single platform
- Affordable & easy to use
- More comprehensive
- Potential applications for other cancer diagnoses

Patent/Patent Application: Provisional Pending

Lead Inventor:
Michael Tomasson Ph.D, Scientific Director of Multiple Myeloma Program, Associate Professor, Washington University in St. Louis

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<tr>
<th>Licensing Contact</th>
<th>Application Space</th>
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<tr>
<td>Paul Hippenmeyer, Ph.D</td>
<td>Oncology, Diagnostics</td>
<td>016907</td>
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<tr>
<td><a href="mailto:hippenmeyerp@wustl.edu">hippenmeyerp@wustl.edu</a></td>
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