SOFTWARE TO ASSEMBLE HLA ALLELES USING SHORT PAIRED READS FROM EXOME SEQUENCING DATA

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Technology Description: In collaboration with the scientists at Broad Institute, WU scientists have developed a new software with a new algorithm that enables HLA high resolution typing from exome sequencing data. It will provide a significantly better tool to guide the bone marrow transplantation and inform research on a wide range of immune related diseases and pharmacogenetics.

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