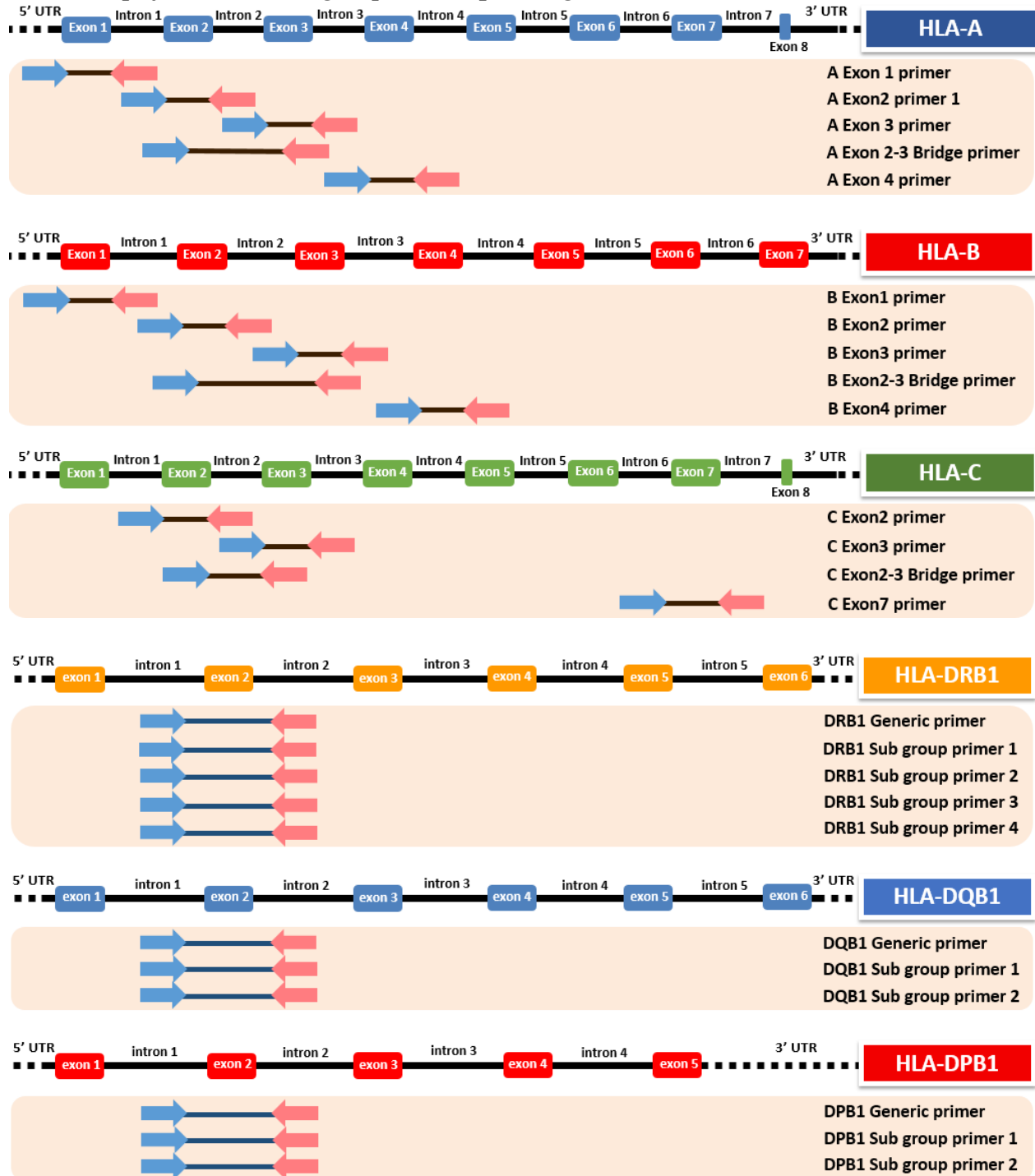
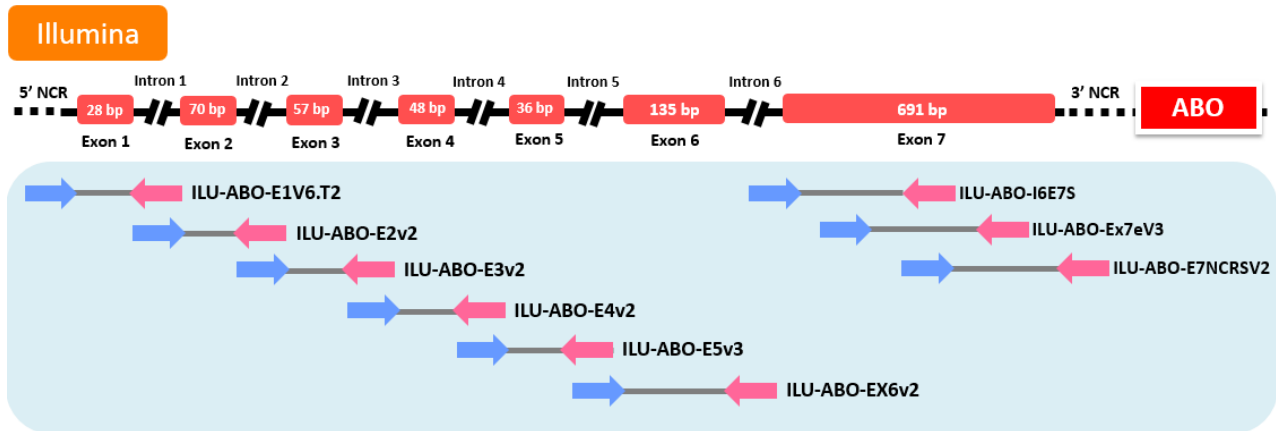


Schematic diagram shown below is the primers maps that is used for HiSeq/MiSeq sequencing. All amplicon sizes are ~300 to 450 base pairs.

Primer maps for Illumina G-group level Sequencing

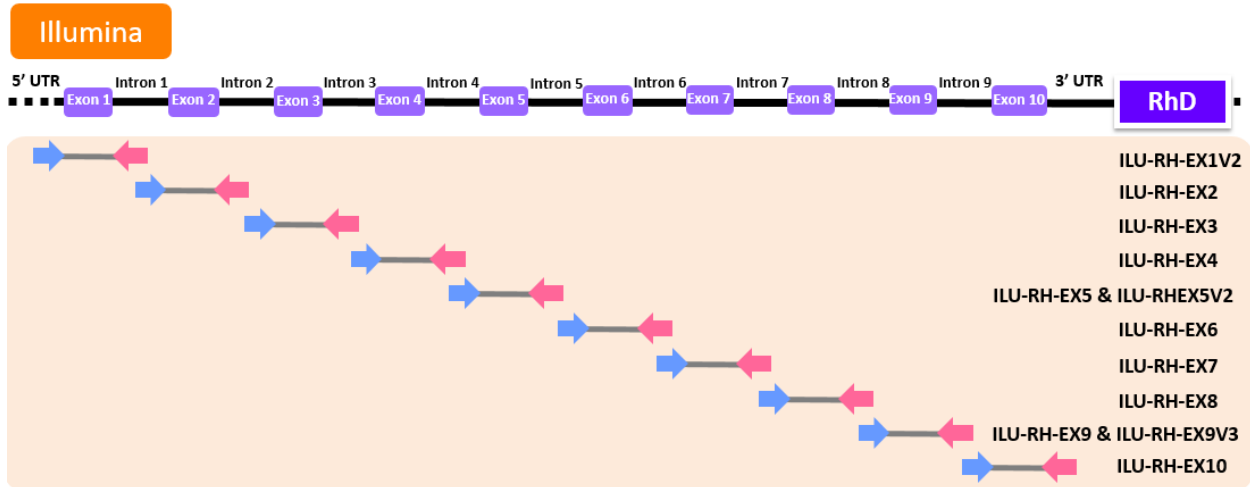


Schematic illustration of ABO Primer Maps for Illumina



A. RhD Blood group Typing

Schematic illustration of RhD Primer Maps for Illumina



B. CCR5 Δ 32 mutation

A set of amplification primers was designed to catch Delta 32 mutation which is located in exon 4. HiSeq/MiSeq platform enables to distinguish homozygous from heterozygous CCR5 Δ 32 mutation. Primer map for CCR5 Δ 32 mutation is shown below. This amplicon will be sequenced along with other amplicons in Illumina..

