

How are you tomorrow?™

HIV-1 Tropism by Genotype Report

PATIENT AND SAMPLE DETAILS

Hospital/Clinic	HIV Hospital	Sample Date	03/01/2011
Sample ID	00000	Sample Received	04/01/2011
Patient ID	00000	Lab21 ID	00000
Date of Birth	01/01/1960	Report Date	08/01/2011

CLINIC DETAILS

Clinic	DD00000	Town	Imaginary Town
Hospital	HIV Hospital	Clinician	Dr Physician

RESULTS

CCR5 (R5) The predicted co-receptor tropism is CCR5 (R5).

COMMENTS

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In the HIV-1 Tropism Assay, RNA extracted from patient samples is transcribed into complementary DNA in triplicates, followed by amplification and genotyping of the V3 region of the HIV-1 gp120 gene sequence. The triplicate genotypes, together with lowest ever CD4 and CD8 results where available, are then analysed by the geno2pheno¹ software (Max Planck Institute, Germany) to predict the viral co-receptor tropism, with significance level set to optimized cutoffs based on analysis of clinical data from the MOTIVATE trial: 2% and 5.75% False Positive Rate. Please note that the software algorithm was generated from data for antiretroviral treatment naive patients.

In this report, viral tropism result is interpreted to be CCR5 (R5) when all triplicates are predicted to be CCR5 (R5), and CXCR4 (X4) when 1-3 triplicates are predicted to be CXCR4 (X4). In cases where neither is true, viral tropism is interpreted to be CCR5 (R5)/ CXCR4 (X4), and additional phenotyping should be considered. Since HIV-1 frequently evolves into an X4 phenotype during late stage disease, there is a strong predictive value associated with the patient's lowest recorded CD4 T cell levels. Please note that it is the responsibility of the physician to consider whether to act on the data presented in this report.

¹ Sing T et al. Predicting HIV co-receptor usage based on genetic and clinical covariates. Antivir Ther, 2007; 12(7):1097-106.