

Standard Operating Procedures (SOP) for: WAIT Trial QA/QC				
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Authorisation:		
Name / Position	Dr Tom Vulliamy	
Signature		
Date		

## Purpose and Objective:

To document quality assurance/quality control (QA/QC) procedures taking place within the WAIT trial.

## SOP Text

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	Responsibility	Activity	
1.	Lab Technician	Sample Receipt – When a sample arrives, it is checked over for packaging, labelling and for any leaks. This is documented for	
		each sample in the 'WAIT Sample Receipt' log, kept in filing	
		cabinet GWHD-6, in the paediatric write-up area.	
2.	Lab Technician	Sample Processing – All samples are amplified in duplicate. All samples are also run alongside positive standards. Three of these	
		standards were used to validate the method (see 'Method Validation' in the WAIT trial lab site file) and were sequenced to	
		confirm their genotype. They are as follows:	
		S1-W001– 5/5 genotype	
		S2-2535 – 4/5 genotype	
		S3-2551 – 3/5 genotype	
		A fourth standard with the 5/6 genotype is also run with all	
		samples. This standard originated from a trial sample which was	
		found to have the 5/6 genotype. DNA from this saliva sample was	
		re-extracted and is labelled with the same trial number followed	
		by a (2), e.g. LO-140(2). As a standard, it will therefore appear on	
		the genotyping worksheet as, for example, S4-LO140(2).	
3.	Lab Technician	Repeat Testing – When there is a low number of samples to be	
		analysed and space on the genotyping plate, randomly picked old	
		trial samples are re-amplified and re-genotyped. This is	
		demonstrated on the genotyping worksheet by 'QA/QC' in the	
		margins next to the samples being re-run. Periodically, a whole	
		'QA/QC' run may take place where all the samples on the plate	
		are re-genotyped. This again will denoted by 'QA/QC' on the worksheet.	
4.	Lab Technician	<b>Results Reporting</b> – All results in the WAIT trial are double	
		checked by another member of the lab staff, Dr. Tom Vulliamy.	
		Before a report or sample result is sent out, Dr. Vulliamy will	
		look over the raw data and double check the genotype result, as	
		well as the stratification. Please see the 'Results Reporting SOP',	