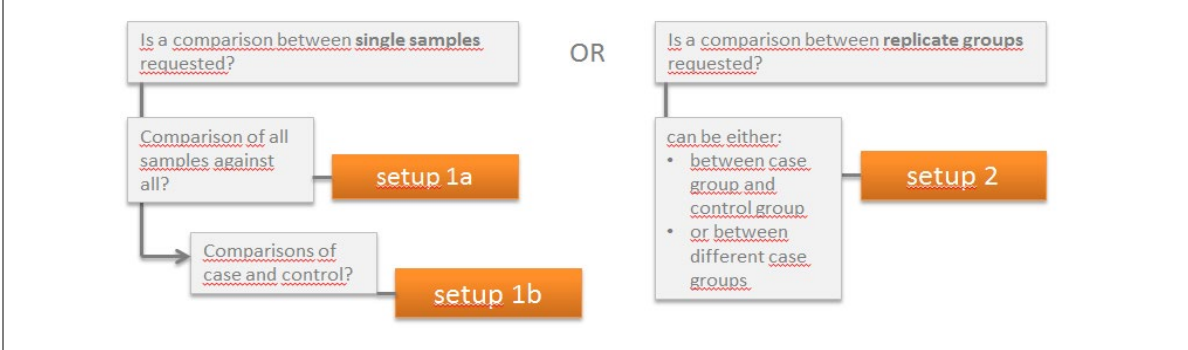


INFORMATION REQUEST FORM

This information is mandatory for performing the Transcriptome or Methylation Analysis.
Please fill in this form electronically and send it back to GATC Biotech by e-mail

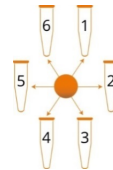
Information about the experimental design

Find the right setup for your analysis



Setup 1a: sample wise comparison, all against all

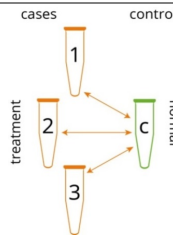
Samples will be compared singlewise, all against all.



Setup 1b: sample wise case / control setup

Sample assignment to case / control

sample name	case	control
normal		x
treatment_1	x	
treatment_2	x	
treatment_3	x	

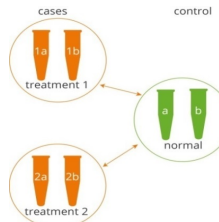


Setup 2: Group wise comparison for replicates

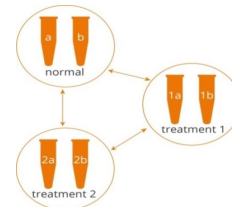
Sample assignment to groups

sample name	group name
sample_a	normal
sample_b	normal
sample_1_a	treatment_1
sample_1_b	treatment_1
sample_2_a	treatment_2
sample_2_b	treatment_2

- valid characters for group names: 0 to 9, Aa-Zz _
- invalid characters will be converted to "_"



OR



Groups to be compared

case group	vs.	control group or alt. case group
normal		treatment_1
normal		treatment_2
treatment_1		treatment_2

Setup 2: Group wise comparison for replicates

Groups to be compared

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Information about your experimental design

Your offer number: _____

Please, choose which setup your experiment is designed for and fill in the relevant table (add lines if necessary)

For alternative splicing analysis in Transcriptome Analysis (eucaryotes) a case/control setup has to be defined. Please choose setup 1b or setup 2 for Transcriptome Analysis.



Setup 1:
sample wise comparison, all against all.



Setup 1b:
sample wise case/control setup



Setup 2:
group wise comparison for replicates
can be case/control groups

Setup 1a: sample wise comparison, all against all
The list of comparing sample pairs will be created automatically for this setup.

Setup 1b: sample wise case / control setup
- sample names and group names must have at least 3 characters, valid characters: 0 to 9, Aa-Zz_

sample name	case	control
	x	
		x

