

Required Processing Information for Sequencing Projects

Please indicate the workflows you would like to be applied at your data.

Whole Genome (WGS): (paired-end)	Alignment	<input type="checkbox"/>
	InDel	<input type="checkbox"/>
	SNV	<input type="checkbox"/>
	SV (SOPHIA)	<input type="checkbox"/>
	CNV (ACEseq)	<input type="checkbox"/>

Exome (WES): (paired-end)	Alignment	<input type="checkbox"/>
	InDel	<input type="checkbox"/>
	SNV	<input type="checkbox"/>

RNA: (single- & paired-end)	Alignment	<input type="checkbox"/>
--------------------------------	-----------	--------------------------

ChIP-seq: (paired-end)	Alignment	<input type="checkbox"/>
---------------------------	-----------	--------------------------

Whole Genome Bisulfite: (WGBS) (paired-end)	Alignment	<input type="checkbox"/>
---	-----------	--------------------------

Please indicate if you want your data processed with the same parameters as a former project	<input type="checkbox"/>
---	--------------------------

name of former project:

Please send the form electronically to: odcf-service@dkfz.de