SBG RD168 WTx metadata

In addition to the metadata below, fastqs will be tagged with the library batch and sequencing run number, in this format: "Seq0x_Lib0x" (eg. Seq01_Lib01)

	FIXED VALUE	VARIABLE		FIXED VALUE	VARIABLE	
Experimental strategy	Total RNA-Seq		**Sample ID**		*CGR sample ID*	
Library ID		*CGR sample ID_with version # if not v1 (eg. "SC080048_v1")*	**Sample type**		*Tumor Tissue or Normal Tissue*	
Platform	Illumina HiSeq					
Platform Unit ID		*Runxx_Lanexx (eg "Run01_Lane01")*	**Investigation**	-	-	*leaving blank for now - may use it later on for variables like radiation dose, etc*
File Segment Number		*Lane number (integer only, eg "1")*	**Species**	Homo sapiens		
Quality Scale	illumina 18		**Batch number**		*Libxx_Seqxx (Library batch # and Sequencing Run #*	
Paired-end		*Set to 1 or 2 (R1 = 1, R2 = 2)*	**Case ID**		*Patient ID (from Nationwide spreadsheet; eg UA2124)*	
Reference genome	ucsc.hg19					

Green fields are consistent between all samples