NGS_21_QC_Data_Formats

Quiz template

Add questions, at least two answer alternatives and choose correct answers (at least one). Have fun creating your awesome quiz!
See an example question below (don't forget to overwrite this with your first question!)

	Question	*Answer 1*	*Answer 2*	*Answer 3*	*Answer 4*	*Correct answer(s) - choose at least one*
1	Raw read sequence information is stored in:	BAM format	FASTA format	VCF format	**FASTQ format**	4
2	Quality scores are included in the raw read sequer	As values from 1- 30	**As a measure of the quality of**	**As ASCII encoded values**	As alphabet characters	2 & 3
3	A Phred quality score of Q30 is considered good b	Q30 is the highest quality sco	**Q30 is equivalent to s 99.9% cc**	Error probabilities are equal t	**It is equal to a 0.1% error ra**	2&4
4	The following CIGAR string 1M2I4M1D3M corresp	1 mismatches, 2 inversions, 4	**1 match, 2 insertions, 4 matche**	2 matches, 4 insertions. 1 ma	3 matches, 4, mismatches, 1	2
5	The flow of data formats from raw reads to called \	**FASTQ -> SAM -> BAM -> VC**	FASTA -> SAM -> BAM -> VCF	**FASTQ -> BAM -> CRAM ->**	FASTA -> BAM -> SAM -> VC	1 & 3
6	In the practical session for this module, you made	**SM:i:23, RG:Z:ERR003762, I**	SM:i:37, RG:Z:ERR003762, MQ:i	SM:i:37, RG:Z:ERR0015472,	SM:i:37, RG:Z:ERR003814, M	1
7	In the practical session for this module you made u	GRCh38	GRCh37.1	GRCh38.1	**hs37d5**	4
8	In the practical session for this module you made u	10029	7398	**2702**	10043	3
9	In the practical session for this module you made u	53	25	32	**60**	4
10	In the practical session for this module you made u	Ref T Alt A, Genotype T/T, Re	Ref A Alt G, Genotype G/A, Read	Ref G Alt A, Genotype G/G, R	**Ref A Alt G, Genotype G/G,**	4
11	What is a FastQC	a quality check of your FAST	a tool used to obtain your FASTQ	a tool used by the sequencing platform to check the sequencing data	a file containing your raw sequencing data	1
12	When would a FastQC step be need in a NGS Bioinformatics analysis	file from the sequencing platform	after the variant calling	file and after running the alignment	file and before running the alignment	4
13	The FastQC report allows you to	obtain metrics to use for variant calling	obtain metrics to decide on potential data filtering / trimming	obtain metrics to skip later alignment stages	obtain metrics to generate a FASTQ file	2
14						
15						
16						
17						
18						