Read alignment

					answer(s) -
Question	Answer 1	Answer 2	Answer 3	Answer 4	choose at
1 Who maintains the human and other reference genomes?	NCBI	Genome Reference Consortium	Does not exist	UCSC	2
The reference file is a large Fasta file?	TRUE	FALSE			1
			An alignment with the highest mapping		
3 What is the optimal alignment?	An alignment with a MAPQ=60	differences	score	An alignment with the most matches	3
4 CA-CG is the optimal Smith-Waterman alignment for aligning CACG to CATCG. If the penalty matrix for scoring is a	1	2	3	4	3
	000 4040	700 4040	000 4040	500 4040	_
5 How many 150bp Illumina 10X reads do you expect in a 30X human sequencing project?	800x10^6	700x10^6	600x10^6	500x10^6	3
			5 " 0		
What is an example of a hash-based aligner?	MAQ	Bowtie	Bowtie2	bwa	1
7144 - 1 - 1 - 1 - 1 - 1 - 1 - 1	DRAGEN Aligner	MAQ	Eland	bwa	
7 What is an example of a BWT aligner?					4
8 What is a MAPQ of 30?	It is a 1/1000 probability that the read is incorrectly mapped	It is a 1/30 probability that the read is incorrectly mapped	It is a 1/100 probability that the read is incorrectly mapped	It is a 1/10000 probability that the read is incorrectly mapped	,
Wilders a WAPQ 0130?	, ,,				1
9 What is the difference between SAM. BAM and CRAM?	There is not difference all are the same alignment format	alignment format, BAM is the format of the SAM and CRAM is the	format, BAM is the format of the SAM and CRAM is the encrypted version of	SAM and BAM are alignment formats. CRAM is not an alignment format.	,
y What is the difference between SAM, DAM and CRAM?		of the SAW and CIVAW is the	and Civalvi is the encrypted version of	CIVAIN IS NOT AN ANGINNERT TOTAL.	2
10 What factors affect alignment?	Read Length and complexity of the genome	Alignment around indels	High density SNP regions	All of the above	4
To Mar accordance and more	genenic	7 mgrimont around indole	riigii delleky erti Teglerie	7 iii di tiid abdid	, i
	20	No score	0		_
What is the MAPQ score of an alignment that is placed equally on the reference elsewhere?	30	NO SCORE	0	'	3
	single end sequencing	paired end sequencing	none of the above		_
12 What type of sequencing is preferred in cases where you have repeats in the reference?	single end sequencing	palled end sequencing	none of the above		2
13 A 60Mbp bwa alignment takes 6 minutes. 1 human genome sequenced at 45x = 150 Gbp per HiSegX10 lane. Ho	1 25 hours	1 hour	.5 hours	2 hours	,
13 A downlop time alignment takes o minutes. I numan genome sequenced at 45x = 150 Gbp per hiseqx to lane, ho		Tiloui	.o nouis	Z Hours	2
14 What important steps are involved in BAM improvement?	Marking duplicates and base quality recalibration	Alignment around indels	All of the above	None of the above	1
What important steps are involved in DAW improvement:	recamplation	raigiment alound indes	All of the above	None of the above	ı*
15 What is needed in the base quality score recalibration process?	The reference	A list of known SNP sites	The alignments to be recalibrated	All of the above	4
Wilder is needed in the base quality score recalibration process:	The reference	A list of known of the sites	The diignifichts to be recalibrated		, I
16 What is the cause of library duplicates?	Misalignment	Library merging	Regions of SNPs near INDELs	The PCR amplification step in library preparation	4
What is the dade of library depricates:	bwa index	ziolary morging	//ref/GRCm38.68.dna.toplevel.chr7.fa	proparation	,
17 Which of these commands creates necessary BWA indexes?	GRCm38.68.dna.toplevel.chr7.fa.gz	samtools index md5638.sorted.bam	.gz md5638a_7_87000000_R1.fastq.gz	None of the above	1
Which of these commands deates necessary DWA indexes:	format and then sorted by	format, then converted to BAM and	format and then converted to an		
18 What does this command do? bwa mem//ref/GRCm38.68.dna.toplevel.chr7.fa.gz md5638a_7_87000000_R1.f		then sorted by coordinates	unsorted BAM	None of the above	2
That good and command go! Dwa mont at an order combot control control and provide an analyzing conducting the control and a cont	1000	It specifies the ReadGroup			Ĩ
19 What does the -R flag specify in the bwa command?	It specifies the reference	information	It specifies the ouput format	None of the above	2
	lane1/lane1.sorted.bam,	F	lane1/lane1.sorted.bam -l		_
20 Which of these commands merge lanes and then mark duplicates on them?	lane2/lane2.sorted.bam -O		lane2/lane2.sorted.bam -O	None of the above	2
21					