Mark scheme - Manipulating Genomes

Question			Answer/Indicative content	Marks	Guidance
1			B	1	
			Total	**1**	
2			C ✓	1	
			Total	**1**	
3			D ✓	1	
			Total	**1**	
4			A ⟩	1	**Examiner's Comments** A little over half of candidates achieved this mark.
			Total	**1**	
5			D ✓	1 (AO1.1)	**Examiner's Comments** Only a few candidates scored the correct answer (D) with most common incorrect answer (C). It is possible that some candidates did not appreciate that D is not about genetic modification.
			Total	**0**	
6			C✓	1(AO2.4)	
			Total	**1**	
7			B✓	1(AO1.2)	
			Total	**1**	
8			C✓	1(AO2.2)	
			Total	**1**	
9			A✓	1(AO1.1)	
			Total	**1**	

10	a		B, D, C (1)(1)	2	One mark for D after B and one for C after D
	b		6 (1)(1)	2	Correct response = 2 marks If response incorrect **ALLOW** one mark for 600 nucleotides / bases **ALLOW** one mark for idea of one error every 100 nucleotides
	c		A C C T G C C C T G G	2	
			Total	**5**	
11	a		working out the sequence / AW , of nucleotides / bases ✓	1 (AO1.2)	**IGNORE** base pairs **Examiner's Comments** About half of responses were credited the mark for this straightforward definition. Candidates who used the irrelevant term 'base pairs', or who suggested that DNA was made of amino acids, received no credit. Some responses misinterpreted the question and attempted to describe the process of DNA sequencing. Occasionally, these responses included an accidental definition and gained a mark.
	b		100 000 000 / 100 million / 1.0 $\times 10^8$ / 1 $\times 10^8$ ✓✓	2(AO2.6)	**ALLOW** 1 mark for 100 000 / 1 $\times 10^5$ / 10^8 **Examiner's Comments** Candidates performed better on this than on other calculations and many answered in standard form. It is noteworthy that answers presented in standard form, although not required, were less likely to be accidentally out by a factor of 10.
	c	i	high throughput sequencing ✓ shotgun sequencing ✓ whole genome sequencing / WGS ✓ next generation sequencing / NGS ✓ pyrosequencing / use of luciferase ✓ massive parallel sequencing ✓	1 max (AO1.2)	**ALLOW** swapping radioactive tags for fluorescent tags **Examiner's Comments** A correct answer was seen only in about a quarter of responses; of those, pyrosequencing was the most common,

<table>
<tr><td></td><td></td><td></td><td></td><td></td><td>although all others were seen occasionally. Common incorrect responses included ‘PCR’, ‘electrophoresis’ and ‘use a computer’.</td></tr>
<tr><td></td><td></td><td>ii</td><td>
<table>
<tr><th>G</th><th>molecule of ATP</th><th></th></tr>
<tr><td>(contains) guanine / guanosine</td><td>(contains) adenine / adenosine</td><td>✓</td></tr>
<tr><td>(contains) deoxyribose</td><td>(contains) ribose</td><td>✓</td></tr>
<tr><td>1 phosphate</td><td>3 phosphates</td><td>✓</td></tr>
<tr><td>phosphate attached to C_3</td><td>no phosphate attached to C_3</td><td>✓</td></tr>
</table>
</td><td>2 max
(AO1.1)</td><td>Mark the first answer in each box.

IGNORE phosphorus / phosphate molecule

IGNORE phosphorus / phosphate molecule

<u>Examiner’s Comments</u>

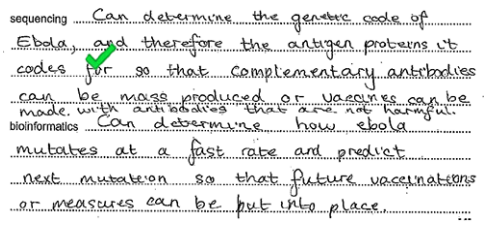
This AO2 question had very few candidates achieve full marks. A majority of candidates gained 1 mark but less than a third scored both. Many candidates were confused by the context: some answers suggested that candidates thought G was DNA. Many candidates thought that G was guanine. Such responses could gain the first two marking points but tended not to as the third marking point was the one most commonly attempted. The final marking point was never seen. Only a small minority of responses did not write comparative structural aspects in the same row. Those who, for example, wrote ‘guanosine’ next to ‘3 phosphates’ in the same row could not be credited.</td></tr>
<tr><td></td><td></td><td>iii</td><td>sequence / order , of bases <u>codes for</u> , sequence / order , of amino acids ✓

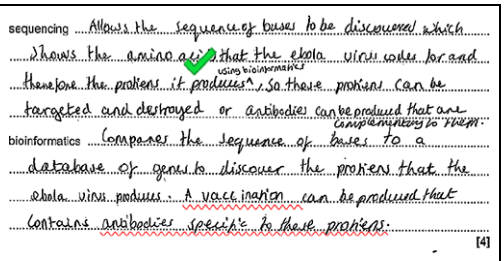
(each) triplet / three bases / codon , (codes) for , one amino acid ✓</td><td>2
(AO1.1)</td><td>IGNORE base pairs

IGNORE base pairs

<u>Examiner’s Comments</u>

Surprisingly few responses scored marks here. Those that did were most likely to be credited a mark for the idea that 3 bases represents the code for one amino acid. Linking the base sequence to the amino acid sequence was less common. Many responses gave detailed descriptions about DNA sequencing and appeared to be answering the question ‘Describe DNA sequencing’. Candidates are reminded to read the question carefully. Of those candidates who had read the question carefully, many confused bases with amino acids.</td></tr>
</table>

	d		*sequencing* 1 (high) mutation (rate) means many , strains / AW , of virus exist ✓ 2 can predict (viral) , strain / protein / antigen ✓ 3 (so) vaccine contains correct <u>antigen</u> ✓ *bioinformatics* 4 facilitates access to large amount of data ✓ 5 facilitates access to data on DNA **and** proteins ✓ 6 *idea that* format (of information) is universal ✓ 7 can identify source of outbreak ✓ 8 can identify vulnerable populations ✓ 9 vaccination program can target certain , area / individuals ✓	4 max (AO1.1) (AO2.1)	*Ignore prompts and mark as prose* **9 ALLOW** allows <u>specific</u> vaccines to be produced **<u>Examiner's Comments</u>** This was a very low scoring question. Although, all-in-all, it was quite a difficult question, candidates seemed to lack preparation in two areas: 1) The question mixed Module 6 topics – DNA sequencing and bioinformatics, with a Module 4 topic – vaccinations. Candidates seemed a little more comfortable with DNA sequencing but, unless they remembered and understood how vaccinations work, it was difficult to achieve many marks. It was not uncommon to see marking point 2 but candidates then often suggested that the vaccine would contain an antibody or that it was a drug that somehow affected the functioning of the virus. 2) Bioinformatics is a new topic on the specification and was very poorly understood by candidates. The vaccination-related marking points in the lower half of the mark scheme were occasionally given, most often marking point 9, but the exclusively bioinformatics points, 4,5 and 6, were almost never seen. Exemplar 11  sequencing Can determine the genetic code of Ebola, and therefore the antigen proteins it codes for so that complementary antibodies can be mass produced or vaccines can be made with antibodies that are not harmful. bioinformatics Can determine how ebola mutates at a fast rate and predict next mutation so that future vaccinations or measures can be put into place. This response achieves the regularly credited marking point 2 but misses out on marking point 3 as the response implies that vaccinations contain antibodies. Exemplar 12

					 sequencing Allows the sequence of bases to be discovered which shows the amino acids that the ebola virus codes for and therefore the protein it produces, so these proteins can be targeted and destroyed or antibodies can be produced that are complementary to them. bioinformatics Compares the sequence of bases to a database of genes to discover the proteins that the ebola virus produces. A vaccination can be produced that contains antibodies specific to these proteins. [4] This response also achieves marking point 2 but misses out on marking point 3 as the response implies that vaccinations are drugs that directly target the biochemistry of the virus or, again, contain antibodies.
			Total	**12**	
12		i	1/8 or 0.125 (1)(1)	2	Correct response = 2 marks If response incorrect **ALLOW** one mark for working e.g. 3/24 **ALLOW** 12.5%
		ii	Sanger / chain termination technique (1) Only 5 errors per 100 000 nucleotides compared to, 50 in Roche pyrosequencing / 500 in SOLiD / 1000 in Helicos (1)	2	
		iii	base sequence of normal allele and (known) alternatives held (in database) (1) computational analysis allows rapid comparison of sequences with newly sequenced allele (1) amino acid sequence / protein structures, also held (in database) (1) *idea of* computer modelling of new protein structure from base sequence (1)	2	
			Total	**6**	
13		i	60 (cm^3) ✓	1 (AO2.2)	1.44 dm^3 = 1440 cm^3 1440 / 24 = 60
		ii	inbreeding / AW, reduces genetic diversity ✓	1 max (AO 2.5)	**ALLOW** 'inbreeding creates smaller gene pool' **ALLOW** 'more homozygous recessive

			(more) homozygous recessive alleles (for CPF) ✓ *idea of* allele for CPF linked to gene for desirable trait (so inherited together) ✓		genotypes (for CPF)' **ALLOW** (leads to) inbreeding depression e.g. 'CPF gene on same chromosome as (named) desirable trait '
		iii	*idea of* compare genomes of, dog breeds / individual dogs ✓ *idea of* identify, alleles / genotypes / base sequences (in WHTs), that are present (only) in dogs with CPF ✓ *idea of* identify dogs that are carrying (the allele for) CPF ✓ (use of) computational biology / bioinformatics, to link genes with CPF ✓ *idea of* linking DNA sequences to specific proteins (i.e. proteomics) ✓	2 max (AO 2.5)	e.g. 'compare DNA of dogs with and without CPF' e.g. 'identify, allele / gene, that causes CPF' e.g. 'can identify mutated protein from DNA sequence'
		iv	weakened / dead / inactivated, (parvo)virus ✓ antigens from the (parvo)virus ✓ mRNA to produce(parvo)virus proteins ✓	1 max (AO2.1)	**IGNORE** 'dormant form of virus' **ALLOW** 'attenuated form of virus' **ALLOW** viral coat proteins
		v	memory cells have, reduced in number / AW ✓	1 (AO2.5)	**ALLOW** to produce more memory cells (to improve immunity) **DO NOT ALLOW** 'no memory cells left'
			Total	**6**	
14			in most people, the genome is very similar / most genes the same (1) using coding sequences would not provide unique profiles (1) (parts of) non-coding DNA contains variable numbers of, short tandem repeats / repeating sequences (1)	3	
			Total	**3**	

15		i	(protease) digests / breaks down / hydrolyses, proteins associated with DNA / histones ✓	**1**	**IGNORE** digests / breaks down, enzymes / nucleases / contaminating proteins **Examiner's Comments** Another challenging question. Some candidates did not get credit due to a lack of detail in answers, e.g. 'protease breaks down protein in the mixture', or 'breaks peptide bonds in DNA'. To gain credit answers needed to refer to the breakdown of proteins associated with the DNA, such as histones.
		ii	$10^{3.61}$ ✓ ✓	**2**	**ALLOW** 4096 /3.61/ 3.612 for 1 mark **ALLOW** $10^{3.612}$ for 2 marks **Examiner's Comments** Few candidates got this question entirely correct. Some achieved one mark for stating 4096 or 3.61. Candidates seemed unable to convert logs to give the correct response.
		iii	temperature damage to, template / strand / fragment ✓ (sometimes, once separated) template / strands, may rejoin (rather than bonding to primers) ✓ lack of, primers / (free) nucleotides ✓ primers fail to, join / attach / anneal (to fragment) ✓	**1 max**	**IGNORE** 'temperature damage to DNA' **IGNORE** 'damage to fragment' **ALLOW** 'strands fail to separate' **IGNORE** lack of, enzymes / bases **Examiner's Comments** A small proportion of candidates achieved the mark in this question, with the majority of correct responses being credited for a lack of primers or free nucleotides, or the primers failing to anneal. Common incorrect responses included 'DNA is lost', 'DNA is not replicated correctly' or 'RNA/DNA polymerase is denatured at high temperatures'.

		iv	(Taq DNA) polymerase ✓ **Examiner's Comments** The majority of candidates got this question correct, giving either polymerase or DNA polymerase as their answer. Incorrect responses included 'RNA polymerase', 'DNA ligase' and 'DNA helicase'.	**1**	**DO NOT ALLOW RNA** polymerase **Examiner's Comments** Not many candidates achieved full marks on this question as many were unable to fully explain the changes they suggested. Many candidates identified the need for a buffer, running it for longer or adding a stain, but often lost the mark because they did not explain why the change was needed. The extra time was often linked to the DNA needing to move further, rather than to separate more. The buffer was to keep the pH constant, rather than allow current to flow, and many did not link the dye to better visualisation of the bands/patterns. There was also a lot of confusion between anode and cathode and which way the DNA moved.
		v	use, alkaline solution /buffer (solution) **AND** Solution carries charge / current (to separate fragments)✓ (use) Southern blotting / described **AND** to transfer fragments to a membrane ✓ use (radioactive / fluorescent) probes / tags / dyes / labels /stains **AND** to , visualise / AW , bands/ patterns ✓ *idea* of testing for longer than one minute **or** carrying out preliminary tests to assess the optimum run time **AND** *idea of* (ensures) separation (of DNA fragments / bands) ✓	**2 max**	**Mark first two changes described** **ALLOW to see the position of the fragments**
			Total	**7**	
16			thermostable **OR** does not, denature / AW, at 95 °C (during DNA strand separation) (1)	2	**ALLOW** temperature values 93 – 97 °C in correct context. **DO NOT ALLOW** "killed" for denatured.

			so PCR can be cycled repeatedly without stopping (to reload with enzyme) (1)		**IGNORE** refs to optimum working temperature, which would apply equally to less thermostable polymerases.
			Total	**2**	
17		i	**R** used to label a phosphodiester bond ✓	1	
		ii	**p** used to label a hydrogen bond ✓	1	
			Total	**2**	
18	a	i	radioactive, labels / tags (1) fluorescent, labels / tags (1) UV, light / radiation (1) (named) visible stain (1)	2	
		ii	X placed on any fragment below Y (1)	1	X can be placed in any of the 9 lanes, but must be touching a DNA band that is lower in the image (nearer the cathode) than Y
	b	i	denature / unfold, protein **AND** *idea of* exposes charges or hydrophobic region (1)	1	
		ii	*idea that* different proteins have different overall charges (1) *idea that* (binding of) SDS makes all proteins negatively charged (1) *idea that* proteins will be separated by, mass / length (1) *idea that* proteins move in the same direction (1)	2	
			Total	**6**	
19			electrophoresis	1	
			Total	**1**	
20			*Fertility* breed GM stock with non-modified stock (1) see if offspring fertile (1) if so they should be classed as the same species (1) **ora** *Morphology* Compare several individuals from GM and non-GM groups (1) in respect of several physical structures (1)	3	Marks awarded should be from **one** outlined investigation **and** the conclusion from its results. If more than one investigation suggested, mark the first investigation and **IGNORE** the others.

			if similar they should be classed as one species (1) **ora** *Ecology* observe how both function in the wild (1) occupy the same or different niche(s) (1) if same niche they should be classed as one species (1) **ora** *Genetics* compare DNA (1) by electrophoresis (1) same pattern should be classed as one species (1) **ora**		
			Total	**3**	
21			1. separates by (relative) , adsorption / solubility / interaction with the stationary phase in TLC **and** (separates) by size in electrophoresis ✓ 2. TLC separates non - charged particles **and** electrophoresis (only) separates charged particles ✓ 3. electricity, used for electrophoresis / not used for TLC ✓ 4. buffer solution, used for electrophoresis / not used for TLC ✓ 5. dyes used in TLC **OR** radioactive / fluorescent , tags / nucleotides, used in electrophoresis ✓ 6. *Idea of* electrophoresis is ,	**3 max**	**Read as prose and look for any three correct mp's** **for mp1 and 2** **IGNORE** separates by size of charge on molecule **ACCEPT** mass / length for size **ACCEPT** electrophoresis uses, current / voltage / charge / (named) electrode(s) **Examiner's Comments** The differences between thin layer chromatography and the form of electrophoresis used to sequence DNA were well understood by the majority of candidates. Most appreciated that electrophoresis required electricity in order to separate the DNA fragments. Many also stated that in electrophoresis, DNA would be separated by mass or length, while in TLC, molecules would be separated by solubility or interaction with the stationary phase. There were several references to fluorescent or radioactive tags being needed to visualise the DNA fragments, or the use of dyes, such

			automated / computerised / uses laser scanning (to analyse sequence) / TLC is not automated ✓		as ninhydrin, in TLC. Some commented on the need for a buffer in electrophoresis although there was little mention of electrophoresis being computerised or automated. Hardly any mention of the separation of charged particles in electrophoresis and non-charged particles in TLC was seen.
			Total	**3**	
22	a		base sequence in genes is unchanged ✓ *idea that* mRNA is inhibited, therefore translation does not occur ✓ gene is not expressed ✓	2 max	
	b		***Please refer to the marking instructions on page 4 of this mark scheme for guidance on how to mark this question.*** ***In summary:*** *Read through the whole answer. (Be prepared to recognise and credit unexpected approaches where they show relevance.)* *Using a 'best−fit' approach based on the science content of the answer, first decide which of the level descriptors,* ***Level 1****,* ***Level 2*** *or* ***Level 3****, best describes the overall quality of the answer.* *Then, award the higher or lower mark within the level, according to the* ***Communication Statement****(shown in italics):* • *award the higher mark where the Communication Statement has been met.* • *award the lower mark where aspects of the Communication Statement have been missed*		

			• ***The science content determines the level.*** • ***The Communication Statement determines the mark within a level.*** **Level 3 (5−6 marks)** Describes the process in detail, with no significant errors. *There is a well-developed line of reasoning, which is clear and logically-structured and uses scientific terminology at an appropriate level. All the information presented is relevant and forms a continuous narrative.* **Level 2 (3−4 marks)** Describes some details of the process, with only minor errors. *There is a line of reasoning presented with some structure and use of appropriate scientific language. The information presented is mostly relevant.* **Level 1 (1−2 marks)** Describes aspects of the process, but with significant omissions or errors. *The information is communicated with only a little structure. Communication is hampered by the inappropriate use of technical terms.* **0 marks** No response or no response worthy of credit.	6	**Indicative scientific points may include:** • method for gene extraction from the bacterium (e.g. conversion of mRNA to cDNA with reverse transcriptase, or removal of gene with restriction enzymes) • use of appropriate vector (e.g. *Ti* plasmid of *Agrobacteriumtumefaciens*) • electroporation • use of DNA ligase • reference to marker genes and their purpose • electrofusion
			Total	**8**	
23	a		restriction, enzyme / endonuclease ⟩ same ⟩	**3 max**	**ALLOW** restriction (endonuclease) **IGNORE** sticky ends

			complementary ⟩		**Examiner's Comments** This was generally well answered by most candidates. The most common incorrect response was the third, where several candidates put 'sticky' or 'exposed'.
	b		the gene / the DNA fragment, inserted into plasmid ⟩ complementary bases (pair / anneal) ⟩ formation of hydrogen bonds ⟩ formation of phosphodiester bonds ⟩ using (DNA) ligase ⟩	**3 max**	**ALLOW** the bit of DNA combines with ring of bacterial DNA **ALLOW** complementary sticky ends **DO NOT CREDIT** in context of making hydrogen bonds **Examiner's Comments** This question differentiated well between candidates with all marking points seen. Common responses that were not credited included referring to the plasmid imprecisely as DNA, or incorrectly as a bacterium. Many candidates also stated that the DNA ligase was used to form hydrogen bonds and were not credited for mentioning the ligase. Some candidates described the events occurring in step D, as opposed to C, and gained no marks. Precise and correct use of key terms is essential when answering knowledge and understanding questions such as this.
	c		use of marker (gene) ⟩ (genes for) fluorescence / colour change ⟩ (examine fluorescence under) UV, light / radiation ⟩ antibiotic resistance (gene) ⟩ (then) grow on agar containing antibiotic ⟩	**3 max**	**IGNORE** replica plating **ALLOW** (gene for) glowing **ALLOW** use GFP **ALLOW** test for survival in antibiotic **Examiner's Comments** Around half of candidates achieved at least one mark. All marking points were seen. A number of candidates used extra space to describe in detail the process of replica plating. As these candidates often achieved

					full marks anyway, their time might have been better spent on other questions. A minority of candidates discussed testing to see if the donor gene was expressed and received no credit.
	d		make, single stranded DNA / cDNA / complementary DNA ⟩ using, reverse transcriptase / reverse transcription ⟩ make double-stranded DNA using DNA polymerase ⟩	**2 max**	**IGNORE** mRNA **ALLOW** make copy DNA **Examiner's Comments** Around half of candidates achieved one mark and a quarter got two, usually the first two points on the mark scheme. Some failed to gain the first mark by referring simply to DNA rather than cDNA or single-stranded DNA. Some candidates discussed mRNA or PCR and electrophoresis and gained no credit.
			Total	**11**	
24		i	**X** <u>restriction</u> (endonuclease) ✓ **Y** (DNA) ligase ✓ **Z** electroporation / culture heating / heat shock / calcium salts ✓	3 (AO1.2)	**ALLOW** electric shock **ALLOW** calcium ions
		ii	(acts as) marker / reporter, gene ✓ *idea of* to indicate which bacteria have taken up the plasmid ✓	1 max (AO2.5)	e.g. 'can identify transgenic bacteria'
		iii	0.00025 or 2.5×10^{-4} ✓✓	2 (AO2.6)	**FIRST CHECK ON ANSWER LINE** **If answer = 0.00025 or 2.5×10^{-4} award 2 marks** **If the answer is incorrect, award one mark for** 1/400 = 0.0025 or 2.5×10^{-3} **OR** 0.0025/1000 = 0.0000025 or $2,5 \times 10^{-6}$ **OR** 0.0000025 x 100 (= 0.00025 or 2.5×10^{-4})
		iv	*idea of* extract DNA from cancerous liver and (named) healthy tissue ✓ choose primers for, E coli / β-galactosidase, DNA ✓ *idea of* comparing rate of DNA amplification ✓	2 max (AO3.4)	e.g. 'compare amount of DNA after 30 cycles of PCR'

		v	*idea of* safety of genetic engineering (in bacteria) has been established ✓ *idea of* few animal rights issues to consider ✓	1 max (AO3.2)	e.g. 'It's been done for many years without any problems' / 'genetic engineering is safe' e.g. 'bacteria do not have emotions like animals that can be engineered' / 'bacteria do not feel pain' / 'bacteria are not conscious' **Examiner's Comments** Most candidates gave appropriate suggestions for the functions of proteins A and C, based on the information given in Table 4.1, and could recognise that antibiotic A22 could cause problems in humans by binding to actin in muscles. Likewise, many candidates used the data in Table 4.2 to evaluate the advantages and disadvantages of the two antibiotics, gaining both marks. However, some candidates lost marks by not being precise in their responses, for instance by saying oritavancin cures fewer bacterial infections without naming the specific infection *Streptococcus*, or by saying it has fewer side effects without naming the side effects. Many candidates correctly identified X and Y in **(c)(i)** but few could name Z correctly. Few candidates knew why antibiotic genes are used in plasmids for **(c)(ii)**. Many candidates referred to the gene providing bacteria with protection from antibiotics without stating why this was done in this case. Many candidates struggled to gain both marks for the two- step calculation in **(c)(iii)**, although many gained a mark for working out one of the steps correctly. Candidates often understood the technique of PCR, but could not apply this technique to compare growth rates of *E.coli* in different tissues for **(c)(iv)**. Those that suggested taking DNA samples from both tissues and using PCR to compare the amounts of DNA produced after a fixed number of cycles gained credit here.

			Total	**9**	
25			(increase in antibiotic) <u>resistance</u> ⟩	**1**	**DO NOT CREDIT** immune **Examiner's Comments** Antibiotic resistance was correctly identified by a little under half of candidates. As this is a science qualification, candidates who discussed 'playing God' or ethical concerns about bacterial rights received no credit.
			Total	**1**	
26	a		* **Level 3 (5–6 marks)** A complete explanation detailing objections and improvements for validity, accuracy and control. The evaluation of the data / procedures is critical, providing refinements that address all the significant issues concerned. *There is a well-developed line of reasoning which is clear and logically structured. The information presented is relevant and substantiated.* **Level 2 (3–4 marks)** A partial explanation detailing objections and improvements for some of the teachers concerns **OR** objections and improvements for all of the teachers concerns. A range of aspects of the data / procedures are evaluated resulting in sound but not comprehensive refinements. *There is a line of reasoning presented with some structure. The information presented is in the most-part relevant and supported by some evidence.* **Level 1 (1–2 marks)** A simple explanation, linking some objections or improvements to some of the teachers concerns.	6	**IGNORE** professions of agreement with the tutor. **Indicative scientific points may include:** **Results not valid** **Objections:** • cause of collapse not recorded / plants may have collapsed for different reasons • number of collapsed less meaningful than percent **Improvements:** • determine which plants collapsed due to corn borer • dissect stems to seek larvae • use percent collapsed out of, original / still standing, numbers. **Results may not be accurate** **Objections:** • collapsed plants may have been counted twice from plot-edge • some collapsed plants may not have been noticed from plot-edge • students may have counted differently from each other **Improvements:** • remove / mark, collapsed when counted

<table>
<tr>
<td></td><td></td><td></td>
<td>Evaluation and / or refinement, links to data / procedure in some respects but links are not clearly shown.

The information is basic and communicated in an unstructured way. The information is supported by limited evidence and the relationship to the evidence may not be clear.

0 marks
No response or no response worthy of credit.</td>
<td></td>
<td>• use narrow strips as plots so that collapsed not missed
• have all plots counted by the same student
• have more than one student counting
• average the counts.

Variables not controlled
Objections:

• no account of natural variation in plant susceptibility
• genetic variations between Bt and regular corn

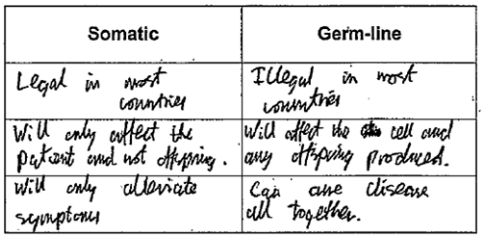
Improvements:

• use, cloned / genetically identical, plants in each plot.
• perform genetic modification to Bt on same clones as used for other plots.

ALLOW references to repeating the procedure.</td>
</tr>
<tr>
<td></td><td>b</td><td></td>
<td>recommend GM Bt corn, because spray may not reach all larvae / larvae are inside plant (stem) / shielded from spray (1)</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td></td><td></td><td></td>
<td>Total</td>
<td>7</td>
<td></td>
</tr>
<tr>
<td>27</td><td></td><td>i</td>
<td>
<table>
<tr><th>Somatic</th><th>Germ-line</th></tr>
<tr><td>cannot be, inherited / passed to offspring</td><td>can be, inherited / passed to offspring</td></tr>
<tr><td>(gene introduced into) / body /</td><td>(gene introduced into) sperm /</td></tr>
</table>
✓ ✓ ✓ ✓
</td>
<td>3 max
(AO 2.5)</td>
<td>IGNORE refs to legality or ethics

IGNORE affects / does not affect (offspring)

IGNORE adult / diploid
DO NOT CREDIT alters DNA
ALLOW gamete producing cell
ALLOW somatic cell / germ-line cell</td>
</tr>
</table>

			<table><tr><td>non-reproductive, cell</td><td>egg / gamete / sex cell / embryo / zygote</td></tr><tr><td>only some cells get (functional), gene / allele</td><td>all cells get (functional), gene / allele</td></tr><tr><td>short-term / temporary / needs repeating / non-permanent</td><td>long-term / permanent / does not need repeating</td></tr></table>		**Examiner's Comments** Most candidates gained at least one mark but only a few scored full marks. References to inheritability, the type of cell involved, or the longevity of treatment were regularly credited but relatively few candidates discussed inserting genes or alleles. Many responses were not awarded marks because of lack of clarity, for example referring to the treatment 'affecting' the offspring rather than being passed on. A few candidates discussed legal and ethical issues and were not credited for this. **Exemplar 3**  <table><tr><th>Somatic</th><th>Germ-line</th></tr><tr><td>Legal in most countries</td><td>Illegal in most countries</td></tr><tr><td>Will only affect the patient and not offspring.</td><td>Will affect the the cell and any offspring produced.</td></tr><tr><td>Will only alleviate symptoms</td><td>Can cure disease all together.</td></tr></table> Exemplar 3 didn't score any marks. The first row addresses legal issues which are not covered by the mark scheme. The second row is vague about inheritances, merely stating that offspring are (or are not) 'affected' by the treatment. The third row hints at the idea of permanent and temporary but, again, is not explicit enough.
		ii	frameshift ✓ altered triplet(s) ✓ adjacent / nearby, genes (on same chromosome) switched, on / off ✓ *idea that* new gene could disable a functioning gene if inserted into it ✓	2 max (AO 2.1)	**IGNORE** mutation without further qualification **ALLOW** altered codons **ALLOW** affects, transcription / expression, of the next gene along **ALLOW** inserted into promoter **Examiner's Comments** This was a synoptic question about mutations and gene expression but only a few candidates scored any marks. Many candidates did not appear to appreciate the

					significance of 'in that chromosome'. A number of candidates discussed epistasis and a minority discussed aspects of meiosis, which were not credited.
		iii	(Huntington's) protein / Huntingtin, still, synthesized / present ✓	1 (AO 2.1)	**Examiner's Comments** This stretch and challenge question was answered correctly by very few high ability candidates. Most responses tended to reword the question without adding to the information given; for example, writing 'because the Huntington's disease allele is dominant'. Few candidates seemed to appreciate that alleles are dominant because they synthesize a particular protein and, in the case of Huntington's disease, huntingtin would continue to be synthesised even in the presence of a healthy allele.
			Total	**0**	