Mark scheme - Patterns of Inheritance

Question	Answer/Indicative content	Marks	Guidance
1	C	1	
	Total	**1**	
2	A	1	
	Total	**1**	
3	C	1	
	Total	**1**	
4	A	1	
	Total	**1**	
5	C ⎫	1	**Examiner's Comments** The first question requiring a calculation proved challenging. Only a quarter of candidates worked out that a haploid number of 8 would give 2^8 different gametic possibilities.
	Total	**1**	
6	B ✓	1 (AO1.2)	**Examiner's Comments** Most responses were correct. The most common misconception was that antibiotic resistance is an example of genetic drift.
	Total	**1**	
7	**B** ✓	1	**Examiner's Comments** The differences between continuous and discontinuous variation can be difficult to spot for lower ability candidates. However, many candidates selected the correct response, B.
	Total	**1**	
8	C ✓	1 (AO2.1)	

			Total	**0**	
9			C ✓	1 (AO1.2)	**Examiner's Comments** Many candidates got the correct answer (C), suggesting that some candidates think that artificial selection causes mutations.
			Total	**0**	
10			D ✓	1 (AO2.4)	**Examiner's Comments** Candidates appeared not to have been put off by the erratum notice and many candidates were able to carry out the calculation correctly and achieve the mark. Many showed their working on the paper.
			Total	**0**	
11			B✓	1(AO2.4)	
			Total	**1**	
12			A ✓	1 AO2.2	
			Total	**1**	
13			no sexual reproduction (1) no / little, genetic variation (1) *idea of* susceptible to new diseases (1) *idea of* susceptible to changing environment (1)	3	**ALLOW** *idea of* limited gene pool
			Total	**3**	
14		i	***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***	6 AO1.1 AO1.2 AO2.5	**Indicative points include** *AO1.1 Demonstrate knowledge and understanding of scientific ideas* • genetic variation is the variety of alleles • offspring have alleles from more than one parent • random fertilisation • meiosis produces genetically unique gametes *AO1.2 Demonstrate knowledge and understanding of scientific processes*

			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)** Explains in detail how sexual reproduction leads to genetic variation with reference to more than one stage of meiosis and with reference to Hydra. *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)** Explains in some detail how sexual reproduction leads to genetic variation with reference to more than one stage of meiosis OR with reference to Hydra and one stage of meiosis. *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)** Mentions more than one reason why sexual reproduction leads to genetic variation. *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.*		• crossing over in prophase 1 • alleles swapped between non-sister chromatids • base sequence of chromosomes altered • independent assortment / random segregation • in metaphase 1 • also relevant in metaphase 2 if crossing over has occurred *AO2.5 Apply knowledge and understanding of scientific processes in a theoretical context when handling qualitative data* • the sperm from one *Hydra* can fertilise an egg from any other individual Hydra • the two *Hydra* can have different alleles • sperm carried in water • might travel large distances • to unrelated *Hydra*
		ii	(some offspring) might survive unfavourable conditions ✓	1 max AO2.1	**IGNORE** eggs can lie dormant as stated in question

<table>
<tr><td></td><td></td><td></td><td>(some) offspring have useful alleles ✓

(named) unfavourable conditions mean (all) offspring might die (if asexual) ✓</td><td></td><td>IGNORE less susceptible to unfavourable conditions</td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>7</td><td></td></tr>
<tr><td>15</td><td>a</td><td>i</td><td>parental genotypes
TtDd TtDd (1)

gametes
TD, Td, tD, td, (TD, Td, tD, td) (1)

offspring genotypes
TTDD TtDD TTDd TtDd TTdd Ttdd ttDD ttDd ttdd (1)

offspring phenotypes
curly / pink curly / black straight / pink straight / black (1)

phenotype ratio
9:3:3:1 (1)</td><td>5</td><td>ALLOW alternative letters only if clear key given.

Mark each line independently but offspring phenotypes must be correctly linked to genotype.

ALLOW phenotypes and genotypes in Punnett squares.</td></tr>
<tr><td></td><td></td><td>ii</td><td>higher proportion, heterozygous / like parents
OR
alleles not completely re-mixed / AW</td><td>1</td><td>DO NOT ALLOW genes.</td></tr>
<tr><td></td><td>b</td><td>i</td><td>
<table>
<tr><th>Phenotype</th><th>O</th><th>E</th><th>O – E</th><th>(O – E)^2</th><th>$\frac{(O-E)^2}{E}$</th></tr>
<tr><td>curly pink</td><td>20</td><td>26</td><td>6</td><td>36</td><td>1.38</td></tr>
<tr><td>curly black</td><td>30</td><td>26</td><td>4</td><td>16</td><td>0.62</td></tr>
<tr><td>straight pink</td><td>21</td><td>26</td><td>5</td><td>25</td><td>0.96</td></tr>
<tr><td>straight black</td><td>33</td><td>26</td><td>7</td><td>49</td><td>1.88</td></tr>
<tr><td></td><td></td><td></td><td></td><td>✓</td><td>✓</td></tr>
</table>
$\chi^2 = 4.84$ (1)</td><td>1</td><td>Correct answer with no working shown = 3 marks.

ALLOW correct answer in the working if the answer line is left blank.

If O − E incorrect, allow ecf for (O − E)^2 line only

If (O − E)^2 incorrect, allow ecf for $\frac{(O-E)^2}{E}$ line only</td></tr>
<tr><td></td><td></td><td>ii</td><td>(conclusion cannot be supported because results) not significantly different from expected (at 95% confidence) (1)</td><td>1</td><td>ALLOW not significant.
IGNORE ‘farmer wrong’, ‘due to chance’.
ALLOW ecf from incorrect chi-square result.</td></tr>
<tr><td></td><td></td><td></td><td>Total</td><td>10</td><td></td></tr>
</table>

16	a		<table><tr><td></td><td>Male</td><td>Female</td></tr><tr><td>Parental genotypes</td><td>$X^{Cr}X^{Cbl}$</td><td>$X^{Cbr}Y$</td></tr><tr><td>Gametes</td><td>X^{Cr} X^{Cbl}</td><td>X^{Cbr} Y</td></tr><tr><td>F1 genotype</td><td colspan="2">$X^{Cr}X^{Cbr}$ $X^{Cr}Y$ $X^{Cbr}X^{Cbl}$ $X^{Cbl}Y$</td></tr><tr><td>F1 Phenotype</td><td colspan="2">1red male : 1 red female : 1brown male : 1blue female</td></tr></table>	4	One mark for each parental genotype **ALLOW** ecf
	b	i	1.6 ✓✓	2	Two marks for correct answer If answer incorrect allow one mark for correct completion of table <table><tr><td>$(O-E)^2$</td><td>4</td><td>0</td><td>4</td><td></td></tr><tr><td>$(O-E)^2 / E$</td><td>0.8</td><td>0</td><td>0.8</td><td></td></tr></table>
		ii	there is no significant difference between the expected and observed results ✓	1	**ALLOW** the observed results are similar to the expected **ALLOW** ecf if value of chi-squared is calculated incorrectly
		iii	random fertilisation ✓	1	**DO NOT ALLOW** random mating
	c	i	value would rise to infinity ✓	1	
		ii	*idea of:* they were not monogamous / another bird was involved✓	1	
		iii	in female offspring the allele for feather colour comes from male parent✓ original male bird did not hold allele for brown feathers✓ brown feather allele in female would not produce brown female offspring✓	Max 2	
			Total	**12**	
17		i	YR, Yr, yR, yr ⎫	**1**	**ALLOW** ry, Ry, RY, rY **Examiner's Comments** Almost two thirds of candidates got the mark.
		ii	*genotypes* YyRr, Yyrr, yyRr, yyrr ⎫ *phenotypes*	**2**	**ALLOW** YRyr, Yryr, yRyr, yryr phenotypes must correspond to

			yellow round, yellow wrinkled, green round, green wrinkled ⟩		correct genotype **DO NOT CREDIT** if no or incorrect genotypes are given **Examiner's Comments** Just over half of candidates got full marks but many displayed the results of a dihybrid cross between two parents that were heterozygous for both characteristics – candidates are reminded of the need to read the question carefully. Without the correct genotypes, credit could not be given for any stated phenotypes. A surprising number of responses did not conform to convention, for example writing 'YRyr' instead of 'YyRr'. In the current series this approach did not result in lost marks but candidates are advised to follow convention in future.
			Total	**3**	
18	a	i	*idea* of greater susceptibility to, infection / pathogens ✓ no / fewer, plasma cells / effector cells / antibodies ✓	**2**	e.g. immune deficiency/ slower immune response/weakened immune system / longer time to recover from infection **IGNORE** ref to illness / disease / immunological memory **ALLOW** 'fewer lymphocytes to produce antibodies' **Examiner's Comments** This question was generally well answered, with the majority of candidates achieving 1 or 2 marks. Some candidates were not credited a mark for using the term 'illness' or 'disease' rather than referring to an increased risk of infection or susceptibility to pathogens. Fewer candidates were credited the second mark point, but for those that were, the majority stated 'less plasma cells' or 'less antibodies'. Some candidates missed out on this mark by stating what they knew about B cells, but not answering the actual question. For example, only saying 'fewer B

					lymphocytes are present' or that 'B cells make antibodies', rather than there being fewer B cells making fewer antibodies. There was a misconception amongst a few candidates that B lymphocytes were involved in phagocytosis.
		ii	(allele is) recessive (because) ✓ healthy parents produce children with the disease ✓ 2 / 5 / 2 and 5 / mothers , heterozygous / carrier ✓ (likely to be) sex-linked / described ✓ (because) on the X chromosome / X linked ✓ only males have the disease/no females have the disease/AW ✓	**4 max**	**ALLOW** '3 has the disease, but 1and 2 / parents, do not ' **ALLOW** '7, or / and, 8, has the disease, but, 5 and 6 /parents, do not' **ALLOW** 'allele found on the sex chromosomes' **Examiner's Comments** Again, a well answered question with plenty of opportunities to pick up marks. The majority of candidates were credited 3 or 4 marks here. Most were able to identify that the allele was recessive, sex linked and located on the X chromosome. Marks were lost when candidates misunderstood the reasoning behind only males being affected, and linking this to the Y chromosome. Some candidates gave imprecise answers which did not gain credit e.g. '2 and 5 were carriers' or saying 'males are more likely to have the disease' rather than 'only males have the disease'.
	b	i	*syndrome* 1 or 2 **and** *carriers* 3 ✓	**1**	**DO NOT ALLOW** 1.5 **IGNORE** 25% probability of a child having the syndrome and 50% probability of being a carrier.
		ii	0.25 / 25% / ¼ / 1 in 4 ✓	**1**	**IGNORE** 25 without % **IGNORE** 1:3

					• Probability of each genotype in couple Z's offspring: VV = 0.25, Vv = 0.5, vv = 0.25. • Probability that mother is VV and child is vv = 0 x 0.25 = 0 • Probability that mother is Vv and child is vv = 0.25 x 0.5 = 0.125 • Probability that mother is vv and child is vv = 0.5 x 0.25 = 0.125 • 0.125 + 0.125 = **0.25** **Examiner's Comments** The calculations in Q4(b) were challenging. Generally, Q4 (b) (i) was well answered, with most errors occurring because of 1.5 children being produced, rather than the answer being rounded to either 1 or 2 children. Q4(b)(ii) was designed as a stretch and challenge question, but most candidates attempted to produce an answer and many successfully gave the correct answer of 25%.
			Total	**8**	
19		i	aaBB ✓ AAbb ✓ white / no pigment ✓	**2**	**ALLOW** BBaa / aBaB **ALLOW** bbAA /AbAb **DO NOT ALLOW** colourless **Examiner's Comments** The majority of candidates gained at least one mark for this question, with a high proportion gaining 2 or 3 marks. Where marks were not credited it was often for candidates selecting one copy of each allele instead of two (AB,ab) or for giving the heterozygous genotypes (AaBb , Aabb).
		ii	(dominant) epistasis ✓	**1**	**DO NOT ALLOW** recessive epistasis **DO NOT ALLOW** complementary

					epistasis **ALLOW** antagonistic epistasis **Examiner's Comments** The majority of candidates correctly identified the type of gene interaction as epistasis, though co dominance was a common incorrect term seen. A few candidates gave recessive epistasis as the answer which was not credited.
		ii	B, produces / codes for, repressor protein / repressor polypeptide / enzyme / transcription factor ✓ (protein / polypeptide / product of B) binds to, promoter (of A) / mRNA / ribosome ✓ (product of allele B) stops, transcription / translation (of allele A) / protein synthesis / described✓ product of B inhibits the enzyme (encoded by A) ✓	**2 max**	**IGNORE** ref to genes instead of alleles **IGNORE** B is a regulatory gene **IGNORE** binds to operator **IGNORE** 'allele B turns off allele A' **ALLOW** 'product of allele B stops production of (named) product of allele A' **DO NOT ALLOW** 'B produces an enzyme which breaks down pigment produced by A'(as this is happening after expression of allele A) **Examiner's Comments** This question proved to be a good discriminator. Many candidates talked about 'allele B turning off allele A', rather than 'allele B producing a product that prevented the expression of allele A', and so did not gain credit. A few candidates mentioned allele B coding for repressor proteins or transcription factors which can bind to promoter regions and prevent transcription of allele A.
			Total	**6**	
20	a	i	(bird) females have two different (sex) chromosomes / AW **ora**	1(AO2.1)	**ALLOW** human females are homozygous **IGNORE** male mammals have X and Y chromosomes

					DO NOT CREDIT chromosomes described as , alleles / genes
		ii	*Parents' phenotype* red male blue female ✓ *Gametes* Z^A, Z^b Z^B, W ✓ *Offspring genotypes* Z^AZ^B, Z^BZ^b, Z^AW, Z^b W ✓ *Offspring phenotypes* red male, blue male, red female, brown female ✓	4(AO2.1)	**ALLOW ECF** if no sexes given for mp1 or mp4 but colours correct **Examiner's Comments** Most candidates could do the genetic cross successfully, but few appreciated that the sex of the individual birds, i.e., male or female, was an important part of the description of the phenotype. Many candidates get 3 marks because they don't include the sex as part of the phenotype so the first marking point cannot be given but the final one can.
	b		(hypophosphatemic rickets allele is) dominant ✓ because occurs in daughter of an affected father ✓ on X chromosome / not on Y chromosome , because , it occurs in females (and males) / affected fathers always pass to daughters ✓	2 max(AO3.1)	**ALLOW** it / gene , is dominant **Examiner's Comments** This question was challenging but differentiated well between candidates. Only a minority of candidates gained marks – usually for stating that the allele in question was dominant or that it was carried on the X-chromosome with a supporting statement. Most responses either attempted to describe the results, rather than drawing a conclusion from them, or assumed the allele was recessive and attempted to find evidence to support that assumption.
			Total	**7**	
21		i	8.73 or 8.8 ⟩⟩⟩ **O** | **E** | **$(O-E)^2$ / E** 58 | 63 | 0.40 | 25/63 31 | 21 | 4.76 | 100/21 21 | 21 | 0 | 0 2 | 7 | 3.57 | 25/7	**3**	**ALLOW** correct answers up to 4 s.f. **ALLOW** 2 marks any answer **between** 8.73 and 8.8 *If answer is incorrect* **ALLOW** 1 mark for correct expected numbers: 63, 21, 21, 7 **ALLOW** 1 mark for correctly calculated $(O-E)^2/E$ numbers: 0.40, 4.76, 0, 3.57

					OR **ALLOW 2 marks for 636 to 638 (ECF** from incorrect expected numbers – 9, 3, 3, 1) **Examiner's Comments** Around half of candidates got full marks, but it was hard to give credit for incorrect answers if no working was given. Many candidates made good use of the grid provided. A significant minority of candidates used 9, 3, 3, 1 as the expected numbers but were still able to access two of the three marks. Candidates should be aware answers given to an inappropriate number of significant figures are unlikely to attract full marks.
		ii	*supports because…* **1** (critical / table, value =) 7.82 ⟩ **2** difference is significant as (X^2), higher than, 7.82 / critical value ⟩ **3** (less than) 5% / 1 in 20, probability / chance, that difference is due to chance ⟩ ora **4** X^2 / calculated value is, smaller than, 9.35 / value at p=0.025 ⟩ **5** greater than, 2.5% / 1 in 40, probability that difference is due to chance ⟩ ora	**3 max**	**ALLOW** correct interpretation of significance of incorrect X^2 value in part (i) If candidate has miscalculated degrees of freedom **CREDIT only** mps 2 and 3 **IGNORE** reject null hypothesis **1 ALLOW** 7.82 highlighted in table **2 ALLOW** difference is not significant as (selected number) less than (selected) critical value **3 ALLOW** > 5% chance that difference is due to chance (if consistent with candidate's X^2 and critical value) **4 ACCEPT** X^2 / calculated value is, close to critical value / 7.82 / value at p=0.05 **4 ACCEPT** X^2 / calculated value, <, 11.34 / value at p=0.01 **5 ACCEPT** > 1% probability that difference is due to chance **Examiner's Comments** This question differentiated well and candidates who had incorrectly calculated the chi squared value in part (i) were not penalised here. Many candidates gained one mark, invariably for identifying the correct critical value at 3 degrees of freedom. Those who chose the wrong critical

					value were still able to access two of the three available marks. A reasonable minority of candidates gained a mark for correctly stating the relationship between their calculated chi squared value and their chosen critical value in terms of significant difference. Candidates who simply stated 'the results are significant' were not awarded marking point 2. The command word 'discuss' ought to have encouraged candidates to address the implication of the chi squared test in terms of the numerical probability that any difference observed was due to chance but most did not attempt this and only a few were credited with a mark for it.
		ii i	**1** (autosomal) linkage ⟩ **2** (both) genes / alleles, occur on same, chromosome / autosome / chromatid ⟩ **3** no independent assortment ⟩ **4** (so) <u>alleles</u>, inherited together / end up in same <u>gamete</u> ⟩ **5** (unless) crossing over occurs / chiasma forms between gene loci ⟩	**3 max**	**1 IGNORE sex linkage /** mutations **1 ALLOW** *idea of* lethal genes **1 ALLOW** genetic drift if number of individuals is small (in suggestion or explanation) **5 ALLOW** if the genes are close together there is less chance of crossing over **Examiner's Comments** This question also differentiated well between candidates of differing ability. Around a third of candidates recognised linkage and most of these went on to achieve two or three marks. Many candidates cited mutations or random fertilization as a possible explanation, with no credit.
			Total	**9**	
22		i	<table><tr><th>phenotypes</th><th>observed number (O)</th><th>expected number (E)</th><th>O-E</th><th>$(O-E)^2$</th><th>$\frac{(O-E)^2}{E}$</th></tr></table>	2(AO2.6)	**IGNORE** decimal places **<u>Examiner's Comments</u>**

			<table><tr><td>healthy female</td><td>5</td><td>4.5</td><td>0.5</td><td>0.25</td><td>0.056</td></tr><tr><td>healthy male</td><td>3</td><td>2.25</td><td>0.75</td><td>0.56</td><td>0.249</td></tr><tr><td>haemophilia male</td><td>1</td><td>2.25</td><td>-1.25</td><td>1.56</td><td>0.693</td></tr><tr><td></td><td>✓</td><td>✓</td><td></td><td>X^2=</td><td>0.998</td></tr></table>		Around half of candidates achieved full marks. Very few scored 1 mark.
		ii	5.991 ✓		1(AO2.2)		**ALLOW** number circled or otherwise indicated in table **Examiner's Comments** Very few candidates could select a critical value from a statistical table.
		iii	student is incorrect because , chi-squared / calculated , number below critical value ✓ greater than , 5% / 10% , probability that any difference is due to chance ✓ *idea that* statistical tests only gives a probability ✓		2 max(AO3.2)		**ALLOW** no significant difference between observed and expected **ALLOW** numbers too low to be confident about conclusion **Examiner's Comments** Around half of candidates achieved 1 mark in this challenging question about interpreting the results of a statistical test. Most appreciated that a calculated value below the critical value meant the student was incorrect and the null hypothesis ought to be accepted but few could use the idea of probability to discuss this further.
			Total		**5**		
23			<table><tr><td>Feature</td><td>Cause of feature</td><td>Number of genes involved</td><td>Type of graph used to present data</td></tr><tr><td>Circum-ference (mm)</td><td>environ-ment **and** genes / genetics</td><td>many / several / poly-genic / AW</td><td>line graph</td></tr></table>		3		**One mark per correct column** **ALLOW** histogram instead of line graph

			<table><tr><td>Containing seeds or seedless</td><td>genes / genetics</td><td>one / two</td><td>bar chart / graph</td></tr><tr><td></td><td>(1)</td><td>(1)</td><td>(1)</td></tr></table>		
			Total	**3**	
24		i	*two from* babies / infants (1) elderly / infirm (1) immuno-compromised / on immunosuppressant drugs / HIV positive (1) known to have been exposed (to the infection) (1)	2	
		ii	*two from* (antibiotic is) selective pressure (1) (bacterial) gene pool / AW, has variation (1) (only) some bacteria have resistance / some bacteria are more resistant than others (1) *two from* when exposed (to antibiotic) most-resistant survive (1) surviving bacteria continue to reproduce to make a resistant population (1) *idea that* over many generations there is an increase in proportion of resistant bacteria (under continued antibiotic pressure) (1) antibiotic becomes ineffective / new antibiotic needed (1)	4	**IGNORE** increase in number of resistant bacteria.
			Total	**6**	
25			* **Level 3 (7–9 marks)** Extensive reference has been made to the (pre-) historical circumstances of both populations. Inferences have been clearly drawn in terms of natural selection. Learner demonstrates a holistic grasp of the Darwinian theory and the information given; reaching reasoned conclusions that explain how the different phenotypic frequencies occurred. *There is a well-developed line of reasoning which is clear and logically structured. The information presented is relevant and substantiated.* **Level 2 (4–6 marks)** Reference has been made to the (pre-) historical circumstances of both populations.	9	**Indicative scientific principles may include:** **Europeans:** • (pre-agricultural) gene pool / genetic variation, included mutant / non-intolerance, allele • availability of milk acted as (positive) selection pressure • individuals / groups, with mutant / non-intolerance, allele had better, chance of survival / success in reproduction • directional selection

			Some inferences have been drawn in terms of natural selection. There is partial structuring of the ideas with the connections between Darwinian theory and information generally clear. Conclusions are used to explain how the different phenotypic frequencies occurred. *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 (1–3 marks)** Reference has been made to the (pre-) historical circumstances of at least one of the populations. At least one inference has been stated in terms of natural selection. The ideas expressed are poorly structured but some relevant points are made. *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.		• mutant / non-intolerance, allele accumulated (in gene pool) • genetic drift (in small prehistoric population) • mutant / non-intolerance, allele is dominant • so expressed in heterozygotic individuals (increasing phenotype frequency). **Australian aborigines:** • ancestral population pre-agricultural • so no selection for mutant / non-intolerance, allele • no suitable mammals to domesticate / milk • island, so no borders for suitable mammals to come in • no contact / breeding, with non-Aboriginal peoples • no gene flow (from other human populations) • no selection pressure • to increase mutant / non-intolerance, allele / phenotype, frequency.
			Total	**9**	
26			<u>adapted</u> to occupy the (oil spill) , <u>niche</u> / <u>environment</u> ✓ outcompete other , bacteria / species ✓ oil is acting as <u>selective agent</u> / <u>selection</u> of bacteria that were able to digest oil ✓	1 max (AO2.5)	**<u>Examiner's Comments</u>** This was also a challenging contextual question for candidates to achieve a mark in as responses had to offer something not already included in the question. Many candidates did not appreciate from the context that there would not always be oil present in the area, merely that oil spills happened with some regularity, hence answers like 'they can gain nutrition from the

					oil' were not credited without further explanation.
			Total	**1**	
27		i	genetic polymorphism / proportion of heterozygotes / proportion of gene variants ✓	1 (AO1.1)	**CREDIT** number of polymorphic genes **Examiner's Comments** Less than 1 in 4 responses achieved this relatively straightforward AO1 mark.. Some candidates appeared to miss the significance of 'genetic' and suggested various sampling techniques or Simpson's index of diversity. Others appeared to attach little significance to 'diversity' and described DNA sequencing techniques or the Hardy-Weinberg principle.
		ii	(many) alleles lost (when population dropped) ✓ **ora** (modern population) descended from few survivors / AW ✓	2 (AO2.5)	**ALLOW** few alleles were left after drop in population **ALLOW** cheetahs still alive descended from a small gene pool **IGNORE** founder effect unqualified **Examiner's Comments** This was a relatively low scoring question. Most responses did not address the question that was asked but rather attempted to explain what a genetic bottleneck was or to discuss the consequences of low genetic diversity. Those candidates that did address the question usually achieved 1 mark, often for referencing the loss of alleles when the population crashed. However, some such responses did not achieve this mark because of imprecise references to reductions in allele frequency, rather than number of alleles or because of conflation of 'genes' with 'alleles'. Fewer candidates discussed the idea that the modern population were all descended from the diminished original. Some responses hinted that candidates thought the genetic bottleneck had occurred within the last

					100 years, perhaps misunderstanding the significance of 'relatively recently' in terms of the existence of the species.
		ii i	*idea that* one individual or allele has proportionally higher effect on small population ✓ (more likely that) <u>alleles</u> will be lost from population ✓ (population) more vulnerable / likely to become extinct due , to environmental change / AW ✓	2 max (AO1.2)	**IGNORE** founder effect unqualified **ALLOW** example of environmental change E.g. might become extinct because of (new) disease **IGNORE** event **<u>Examiner's Comments</u>** Genetic drift seems to be poorly understood on the part of candidates. Many responses appeared to confuse genetic drift with speciation or inbreeding depression; others discussed the decreased likelihood of meeting another cheetah. Around a quarter of responses achieved 1 mark and very few scored both. Some of the candidates that appeared to know what genetic drift was went no further than stating that genetic drift affects small populations, which added little or nothing to the information given in the question.
			Total	**5**	
28	a	i	-1.8 ✓	1(AO2.2)	The minus sign is required for the mark.
		ii	**FIRST CHECK ON ANSWER LINE** **If answer = 0.24 award 2 marks** 0.8 / 3.4 ✓	2(AO2.2)	*If answer incorrect…* **ALLOW** max 1 mark for 0.2 / correct answer to >2 s.f. / 24% **Examiner's Comments** This was the most challenging calculation question with fewer than half of candidates gaining both marks. Many candidates calculated the *G.fortis* range as a proportion of *G.fuliginosa*, giving their answer as 4.25. Some gave their answer to only one significant figure, or as a percentage, despite the instruction.

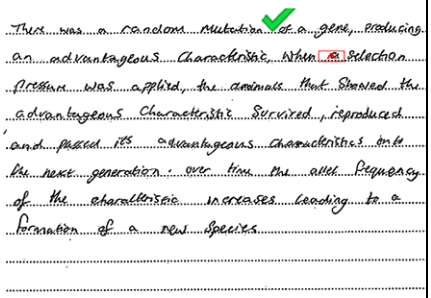
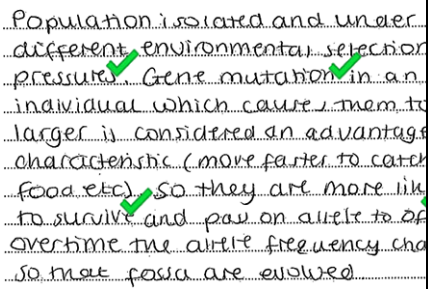
		iii	*supports because...* **1** two peaks ✓ **2** (at) 0 and , 1.2 / 1.4 ✓ *does not support because...* **3** second / AW , peak is not much higher than background ✓ **4** second / AW , peak represents a small number of birds ✓ **5** *idea that* there could be other explanations for more birds between 1.2 and 1.4 (a.u.) ✓ **OR if marking points 3, 4 or 5 have not been awarded** *does not support because...* **6** there is <u>only one</u> peak ✓ **7** *idea that* more likely directional selection as peak closer to left hand side ✓	3 max(AO3.1 3.2)	**1 ALLOW** not a normal distribution **<u>Examiner's Comments</u>** This was a challenging question in which candidates were required to apply their knowledge of the expected shape of a disruptive selection graph to some real data about finches. Real data rarely matches the textbook ideal and most candidates struggled to perceive two peaks in the graph they were presented with. It was rare to award more than one mark and those candidates that did achieve the mark tended to do so for challenging the scientists' conclusion and describing the graph as having only one peak. Few candidates attempted to consider reasons why the conclusion might be supported.
	b		***Please refer to the marking instructions on page 4 of this mark scheme for guidance on how to mark this question.*** **Level 3 (5–6 marks)** Explains how genetic variation, differential survival and the passing on of alleles to the next generation act to increase the proportion of the population with a beak length of around 11mm and makes appropriate use of the graph data to support explanation. *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)** Explains how natural selection acts to increase the proportion of the population with a beak length of around 11mm. *There is a line of reasoning presented with some structure. The information presented is relevant and supported by some evidence.* **Level 1 (1–2 marks)**	6(AO2.5 3.2)	**Indicative points may include** *AO2.5* Genetic variation • pre-existing • sexual reproduction • meiosis • mutation Differential survival • overproduction of offspring • finches with extreme beak depth less likely to survive • reason for birds with very small or large beaks not surviving Inheritance • survivors possess alleles for average beak depth

			Explains how natural selection favours those in the population with an average phenotype **OR** that natural selection favours finches with a beak length of around 11 mm. *There is an attempt at a logical structure with a line of reasoning. The information is in the most part relevant.* *0 marks* *No response or no response worthy of credit.*		• alleles for average beak depth more likely to be inherited by offspring • increase frequency of these alleles from one generation to the next *AO3.2* Use of figures from graph • bell-shaped curve • skewed to right • beak depth with peak survival is 11.2 mm • no birds survived with beaks of 7.4 mm or less • no birds survived with beaks of 11.6 mm or more **Examiner's Comments** The majority of the candidates were able to use the data in the graph correctly and they were able to outline that birds with very small or very large beaks did not survive whereas those with average beak sizes did. Most of the candidates had to explain the process in more detail, by including details about the importance of genetic variation or inheritance of alleles for average beak size. Many candidates successfully referred to the graph within their answers and so were able to access the higher levels. A few candidates did not seem to appreciate the fact that extremely large beak sizes were being selected against as well as extremely small ones. There was a small but significant number of candidates that discussed the data in the graph as if the x-axis represented time, rather than beak size.
			Total	**12**	
29	a	i	4.7 ✓✓	2 (AO2.6)	*Max 1 if answer not given to 2 s.f.* **IGNORE** sign

					If answer incorrect **ALLOW** 1 mark for 4.8 or 4.9 **Examiner's Comments** Most candidates scored on this question, either getting the full 2 marks for 4.7 or getting one mark for 4.8 or 4.9 as a result of dividing by the female length rather than the male. The majority of candidates answered to 2 significant figures as instructed.
		ii	little / nothing (can be concluded) ✓ because no (named) statistical test done ✓	2 max (AO3.1)	**IGNORE** 'not significant' *If no other marks awarded*, **ALLOW** *1 mark only for*… (probably) not significant because , error bars / standard deviations , overlap **Examiner's Comments** Less than 1% of candidates gave the full correct answer, i.e. that, without performing a statistical test, nothing can be concluded. However, around a third of responses gained 1 mark by stating that the difference was probably not significant because the error bars overlapped. Although not strictly true, this approach is obviously being taught by centres. Many responses included phrases like 'low significance' or 'not very significant'. These largely meaningless terms gained no credit. Candidates are advised to stick with the absolute term: the difference is or is not significant. A number of candidates confused the percentage difference in height (4.7%) with the 5% probability used to determine significance and gained no marks.
		iii	*No, because…* *idea that* standard deviation is not the same as range ✓	1 (AO3.2)	**ALLOW** e.g. SD does not include all outliers / error bars don't show range

					Examiner's Comments Around half of responses stated, correctly, that the information did not support the candidate's answer and a majority of these gained a mark. A minority, however, believed that the reason the candidate's answer was not supported was that the mean length was that of the longest cheetah. The other half of responses incorrectly stated that the information did support the candidate's answer, usually because they interpreted the error bars as range bars.
		iv	environment ✓ genes / genetic / alleles , and environment ✓ many genes / polygenic ✓ age ✓	2 max (AO2.1)	**ALLOW** suitable example, e.g. diet **Note** 'genes and environment' = 2 marks **IGNORE** refs to mutation **Examiner's Comments** About half of responses achieved 2 marks. However, many wrote unnecessarily long explanations. The command word 'state' ought to have directed candidates to answer quickly with short, direct, statements. On this occasion a three-word answer 'genes and environment' easily achieved both marks. Many candidates missed the significance of the context of the question, i.e. that body length displays continuous variation and that any contribution from genes is likely to be minimal in the relatively genetically homogenous cheetah population; hence, answers that focussed on genetic variation alone achieved no credit. Responses that did not answer the question, such as lengthy discussions of the potential advantage of longer body length in males, received no credit.
	b	i		1 max (AO2.3)	*Mark the first response only* *Assume 'it' refers to mongoose* **IGNORE** references head / body /

			Fossa has … longer , legs ✓ different (shaped / size) , ears ✓ (proportionally) bigger eyes ✓		shape **ALLOW ora** for mongoose throughout **ALLOW** longer tail / larger jaw **Examiner's Comments** The vast majority of candidates achieved this mark. Some were even able to correctly refer to proportional sizes. Those few responses that did not gain a mark tended to refer to differences not visible in the figure or vague differences in body shape.
		ii	**1** allopatric speciation ✓ **2** different , selection pressure / environmental conditions (from mainland) ✓ **3** (random) mutation ✓ **4** (fossa-like) individuals with , mutation / (new) feature , survive / reproduce ✓ **ora** **5** beneficial / AW , <u>alleles</u> passed on ✓ **6** <u>directional</u> selection	4 max (AO2.5)	**3 ALLOW** pre-existing genetic variation **4 IGNORE** best adapted / fittest **Examiner's Comments** This question differentiated well between candidates of differing abilities and two marks were most commonly scored. The best responses outlined the natural selection of cat-like features using technical terms. Many responses were not credited marks because they did not use the term 'alleles' correctly. Some conflated 'alleles' with 'genes' while others merely referred to traits, characteristics or features. Answers that ignored the context completely struggled to gain full marks as generic references to selection pressures or survival of the best adapted were not credited without a link to the Madagascar/fossa-like context. A minority of responses did not address the question, which the evolution of the fossa, and devoted their entire

					answer to issues of speciation, gaining little credit. Use of the A Level key term, 'directional selection', was rare. Exemplar 9  This response ignores the context of the question and simply discusses natural selection in generic terms. One mark has been credited for discussing mutations but, although the response alludes to marking points 2 and 4, as these are context-dependent, the marks have not been given. Exemplar 10  This response achieves full marks for the following marking points: 2 – recognising the context of an environment different from the African mainland, 3, 4 – recognising the context of a vacant large predator niche, and 5.
		ii i	mutation / genetic diversity ✓ natural / directional , selection ✓	3 max (AO1.2)	**IGNORE** refs to isolation **ALLOW** genetically different / large gene pool **ALLOW** e.g. different food source

			idea that environment / selection pressure , is <u>different</u> from the 'other' population ✓ time ✓		**ALLOW** many generations **<u>Examiner's Comments</u>** This question was poorly answered with many candidates failing to appreciate the significance of 'other' in the question and, hence, listing methods of reproductive isolation. Mutation and different environmental conditions were the most commonly seen correct answers but references to natural selection and time were rare.
			Total	**15**	
3 0		i	bar chart drawn **AND** x-axis labelled 'phenotype' **AND** linear y-axis scale labelled 'frequency' ✓ bars correct height and same width ✓ bars fill half the available (vertical) space ✓ bars labelled / key **AND** tongue rolling and non-tongue-rolling bars do not touch ✓	4 AO3.3	**DO NOT CREDIT** stacked bars Y-axis must start at 0 **ALLOW** all 4 bars not touching
		ii	**FIRST CHECK ON ANSWER LINE** **If answer = 0.5 or 0.49 or 0.493 or 0.494 award 3 marks** q^2 = 77/248 = 0.31 ✓ q = √ 0.31 = 0.557 ✓ p = 1 – 0.557 = 0.443 $2pq$ = 2 x 0.443 x 0.557 = 0.494 ✓	3 AO2.4	**IGNORE** sig. figs for working marks **If answer incorrect, ALLOW** either half of working equations for 1 mark each up to a maximum of 2. **ALLOW e.g**. 'q^2 = 77/248' or '77/248 = 0.31'
		ii i	(population) not (sufficiently) large ✓ (population) not randomly mating / not subject to selection ✓	2 AO2.3	*Mark the first answer on each prompt line* **ALLOW ora** in context of Hardy-Weinberg assumptions **ALLOW** mutations might occur **IGNORE** immigration / emigration

			Total	**9**	
3 1			2 ✓✓✓	**3**	**Max 2 marks for calculation if answer not to one significant figure** (q^2 = 1 in 10,000 = 0.0001) q = 0.01 ✓ (p = 1 – 0.01 = 0.99) 2pq = 0.0198 ✓ 0.02 = **2 marks** 1.98 = **2 marks** **Examiner's Comments** Most candidates failed to give the correct final result but managed to score at least one of the three marks available. A high proportion of candidates were able to correctly calculate the value of p and q but then got lost trying to substitute them into the equation. A few candidates calculated 2pq correctly but did not go on to calculate the percentage, while some others followed the calculation to the end but did not round up the result to one significant figure.
			Total	**3**	
3 2		i	sympatric ✓	1(AO1.2)	
		ii	*idea that* individuals choose to mate only with other individuals with similar sized beaks ✓	1(AO1.2)	**CREDIT** sexual selection **ALLOW** different , mating seasons / courtship rituals
		ii i	(DNA) found in all organisms ✓ some / AW , sequences highly conserved ✓ comparison (of DNA between species) ✓ similar (base) sequence indicates recent common ancestor ✓ **ora**	2(AO1.1)	**ALLOW** look at similarities in DNA **IGNORE** closely related
			Total	**4**	
3 3	a	i	artificial selection ✓	1	
		ii	suitable named plant **and** adaptation ✓	1	e.g. wheat / barley / corn / oats , large seeds

	b		wolf is the result of natural selection ✓ selected / evolved to survive in habitat ✓ no extreme features ✓ dogs bred by artificial selection ✓ dogs have extreme features ✓ example of extreme features ✓ not well adapted to survive in wild ✓	Max 4	**ALLOW** able to reproduce well in wild e.g. long body / short legs of dachshund large ears / creased face of blood hound **ALLOW** not able to reproduce well in wild
	c		artificial breeding / selection can exaggerate features ✓ other characteristics may be ignored ✓ (may be) detrimental to health (of dog) ✓ club provides guidance / advice to maintain welfare ✓	Max 3	
			Total	**9**	
34		i	60 (cm^3) ✓	1 (AO2.2)	1.44 dm^3 = 1440 cm^3 1440 / 24 = 60
		ii	inbreeding / AW, reduces genetic diversity ✓ (more) homozygous recessive alleles (for CPF) ✓ *idea of* allele for CPF linked to gene for desirable trait (so inherited together) ✓	1 max (AO 2.5)	**ALLOW** 'inbreeding creates smaller gene pool' **ALLOW** 'more homozygous recessive 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 ✓	2 max (AO 2.5)	e.g. 'compare DNA of dogs with and without CPF' e.g. 'identify, allele / gene, that causes CPF'

			idea of linking DNA sequences to specific proteins (i.e. proteomics) ✓		e.g. 'can identify mutated protein from DNA sequence'
		i v	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**	
3 5			**Level 3 (5–6 marks)** Provides a detailed explanation of the benefits to selective breeding of maintaining a viable wild population. *The answer contains well-developed lines of reasoning which are clear and logically structured and uses scientific terminology at an appropriate level. All the information presented is broadly relevant.* **Level 2 (3–4 marks)** Provides an explanation of the benefits to selective breeding of maintaining a viable wild population. *The answer contains some reasoning, structure and use of appropriate scientific language. The information presented is mostly relevant.* **Level 1 (1–2 marks)** Lists at least one benefit to selective breeding of maintaining a viable wild population. *The information is communicated with only a little structure. Communication is hampered by the inappropriate use of technical terms or substantial irrelevant material.* *0 marks* *No response or no response worthy of credit.*	6 (AO1.2)	**Indicative points** *These could be described in terms of problems associated with selective breeding and solutions offered by maintaining a wild population* • genetic variation • genetic resource / gene bank • source of useful alleles • can be cross bred with crop varieties • allows introduction of different traits • unknown future requirements • potentially useful in changing climate • prevention of inbreeding depression • promotion of hybrid vigour • prevent dwindling gene pool • source of replacement if cultivated population is in danger • plausible example(s) of any of the above **Examiner's Comments** Most candidates gave answers that indicated they had a good understanding of the problems associated with selective breeding, i.e.

					that selection of desired characteristics results in reduced genetic diversity. Most were then able to exemplify the consequences of a reduced gene pool in terms of susceptibility to the same disease. Fewer candidates were able to show that they understood that the existence of a wild variety of the same species could alleviate this problem. Only occasionally did responses include discussion of potential environmental changes that may happen in the future, to which the resource of alleles in the wild population of plants may provide a solution. It was noted by examiners that, when discussing selective breeding, many candidates displayed a fundamental misunderstanding of a lot of related biology. Commonly seen errors included: conflating genes with alleles, referring to resistance as immunity, suggesting that selective breeding caused mutations, conflating genetic diversity and biodiversity and misuse of 'species' to mean 'variety'. Such responses often meant that the upper mark within a level could not be credited and sometimes limited the level that the response was able to access. Many answers included a lot of irrelevant material about ethics, aesthetics and medicinal drugs and were therefore unable to access the upper mark within a level.
			Total	**6**	