INTUITION EDUCATION

HSC 2026 · PREDICTED PRACTICE PAPER

2026 HSC Biology

Answers & marking notes

Paper total: 100 marks

Sit the paper first. These are worked answers with the marking notes behind them — what earns the mark, and the traps the marking centre has flagged in past years. Where a note names a band, it describes what a top-band response does, not a guaranteed mark.

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Answers & marking notes

Section I — answer key

Q	Answer	Note
1	B	Prions are infectious misfolded proteins with no DNA or RNA
2	C	Ovulation → fertilisation (in the fallopian tube) → implantation → placenta
3	B	Complement of CTAGGT with U replacing T: GAUCCA (option A is the DNA complement — the classic trap)
4	A	A = T = 30%, so G + C = 40% and G = C = 20%
5	A	I^A i and I^B i offspring only: groups A or B; group O (ii) is impossible — the AB parent has no i allele
6	A	Crossing over between homologues in meiosis I recombines linked alleles
7	D	Only germ-line (gamete-producing) mutations are heritable
8	C	Random survival + small population = genetic drift (bottleneck); selection is excluded by the stem
9	B	One enzyme, one recognition site ⇒ matching complementary sticky ends; ligase (not the restriction enzyme) joins them
10	A	Nuclear DNA comes from the somatic-cell donor X
11	A	Protozoan pathogen, insect vector, indirect (vector-borne) transmission
12	C	Memory cells are antigen-specific and adaptive; A, B, D are innate first/second line
13	D	Pre-formed antibodies given medically = artificial passive; no memory is formed
14	B	Plants have no phagocytes or antibodies; programmed cell death (with wall thickening, antimicrobial compounds) is an active response — the cuticle is passive
15	C	Correlation only; causation needs controlled evidence
16	B	New cases unchanged ⇒ incidence unchanged; longer survival ⇒ more people living with it ⇒ prevalence rises
17	C	Vasodilation increases heat loss by radiation; A, B, D conserve or generate heat
18	B	Conductive blockage with intact cochlea ⇒ bypass the outer/middle ear via bone conduction; a cochlear implant is for a damaged cochlea
19	B	Myopia: focal point in front of retina ⇒ diverging lens moves it back; increasing corneal curvature worsens it
20	B	Urea diffuses down its concentration gradient (28 → 0); glucose has no gradient

Section II — marking notes

Q21 (a). X = virus (non-cellular, has nucleic acid); Y = prion (non-cellular, no nucleic acid); Z = fungus (cellular, membrane-bound nucleus). 2 marks for all three; 1 mark for two.

(b). The toxin causes profuse watery diarrhoea, which expels enormous numbers of *V. cholerae* into the environment/water supply, contaminating water that new hosts drink — the symptom itself spreads the pathogen between hosts (transmission, not entry or survival).

Q22 (a). Mutation 1. It arose in the germ line (ovary lineage) before gamete formation, so it can be present in gametes and passed to the zygote; Mutation 2 is somatic — skin cells do not form gametes, so it dies with the individual. Both the identification and the gamete reasoning required for 2 marks.

(b). Any one: the mutation is copied into the descendants of that skin cell (a clone of mutant cells); if it disrupts control of the cell cycle it may lead to a cancer such as melanoma; or it may have no effect if the affected gene is not expressed in skin.

Q23 (a). Incomplete dominance: the heterozygote's phenotype (blue-grey) is intermediate between the two homozygotes, shown by the first cross producing ONLY blue-grey offspring from black × white parents (neither parental phenotype reappears in F1, so neither allele is completely dominant).

(b). Key: F^B = black allele, F^W = white allele; black = F^B F^B, blue-grey = F^B F^W, white = F^W F^W. Punnett square F^B F^W × F^B F^W → 1 F^B F^B : 2 F^B F^W : 1 F^W F^W = **1 black : 2 blue-grey : 1 white**. Marks: key (1), correct square (1), phenotypic ratio stated (1). A genotypic ratio alone, or indistinguishable allele symbols (e.g. B and b, which imply dominance), loses the ratio mark.

Q24 (a). Autosomal recessive. Justification citing individuals: II-3 is affected although her parents I-1 and I-2 are both unaffected, so the allele is recessive (both parents are carriers). It cannot be X-linked recessive: an affected female (II-3, or III-2) must be homozygous and must therefore have received an affected X from her father, but her father (I-1, or II-4 respectively) is unaffected. Marks: recessive with individuals cited (1), autosomal exclusion argument with individuals cited (1), correct mode stated (1). "Somatic" for "autosomal" scores zero for that mark.

(b). Key: A = normal allele, a = disorder allele. II-3 is aa (affected); II-4 is Aa (his father I-3 is affected aa, so II-4 must carry a; he is unaffected so he is Aa — also required by the affected child III-2). Punnett: aa × Aa → ½ Aa (unaffected) : ½ aa (affected). **Probability = ½ (50%)**. Marks: keyed square with justified parental genotypes (1), probability (1).

Q25. A comparison on shared criteria (a table is ideal): Enzyme — DNA polymerase (replication) vs RNA polymerase (transcription); helicase unwinds in both/replication. Template — both strands of the entire DNA molecule (replication) vs one strand (template strand) of a single gene (transcription). Product — two identical double-stranded DNA molecules, each half original and half new (semi-conservative) vs a single-stranded mRNA molecule. Base pairing — A–T (replication) vs A–U (transcription); both use C–G. Marks: one per correct compared criterion up to 4; two separate descriptions that never align the criteria cap at 2 (2024 Q30(a) feedback).

Q26 (a). mRNA from the normal template: **AUG CCU AAA UGU UAA**; amino acids: **methionine (start) – proline – lysine – cysteine – (stop)**. 1 mark mRNA (U not T; complementary), 1 mark

amino acid chain read from the supplied table.

(b). A substitution (point) mutation: the seventh template base T → A changes the third codon from AAA (lysine) to UAA (STOP) — a **nonsense mutation**. Translation terminates early, producing a truncated polypeptide of only two amino acids after methionine instead of the full chain; the shortened polypeptide cannot fold into its functional tertiary shape, so the protein loses its function. Marks: substitution identified (1), premature stop/truncation from the chart (1), link to folding/function (1). Note the frameshift trap: only one base is REPLACED, not inserted or deleted, so the reading frame is unchanged.

Q27 (a). Trisomy 21 (three copies of chromosome 21; Down syndrome) — 47 chromosomes.

(b). During meiosis in one parent, the two homologous copies of chromosome 21 failed to separate at anaphase I (or sister chromatids failed to separate at anaphase II) — non-disjunction. This produced a gamete containing two copies of chromosome 21 (24 chromosomes) instead of one. Fertilisation of this gamete by a normal gamete (23 chromosomes, one copy of 21) produced a zygote with three copies of chromosome 21 and 47 chromosomes in every body cell. Marks: non-disjunction named (1), meiosis I/II mechanics of failed separation (1), abnormal gamete with 24 chromosomes (1), fertilisation step completing the trisomy (1). "Error in mitosis" scores at most 1.

Q28 (a). Stimulus: blood glucose rising above the set point — from 5.0 to 7.6 mmol L^{-1} at 30 min. Response: insulin secretion rises (40 → 280 pmol L^{-1}, peaking at 45 min, just after the glucose peak) while glucagon falls (90 → 55 ng L^{-1}). Data values required.

(b). Beta cells of the pancreatic islets detect the raised glucose and secrete insulin; insulin causes the liver (and muscle) to take up glucose and convert it to glycogen, and body cells to increase glucose uptake, so blood glucose falls (7.6 → 5.2 by 120 min). Alpha cells reduce glucagon secretion, so glycogen breakdown slows. As glucose returns to the set point, the stimulus for insulin release is removed and insulin falls back toward 40–60 pmol L^{-1} — the response counteracts the original change and switches itself off, which is negative feedback. Marks: beta cells as detector (1), liver/glycogen effector action (1), the counteracting direction of change referenced to the graphs (1), the feedback loop closed (falling glucose removes the stimulus) (1). Naming insulin without glucagon-suppression or without the loop closing caps at 3.

Q29 (a). The plant detects the INTERNAL change — falling water content/turgor of its cells (not the hot weather itself). Abscisic acid (ABA) is produced and signals the guard cells; guard cells lose turgor and the stomata close, reducing transpiration so water loss no longer exceeds uptake and internal water is kept within tolerance limits. Marks: internal detection (1), ABA/guard-cell mechanism (1), stomatal closure reducing transpiration linked back to water balance (1). Structural adaptations (sunken stomata, thick cuticle) are not responses to a change and score zero here — the 2019 Q29 trap.

(b). In negative feedback the response counteracts the stimulus and returns the variable to a set point. Here the response (contractions) INCREASES the stimulus (pressure on the cervix), which increases oxytocin release, which strengthens contractions — the loop amplifies the original change rather than opposing it, escalating until an endpoint (birth) removes the stimulus entirely.

Marks: negative feedback defined by counteraction (1), amplification loop traced in the stimulus (1), endpoint/contrast completed (1).

Q30 (a). Urea diffuses from the blood (28 mmol L $^{-1}$) across the semi-permeable dialyser membrane into the dialysate (0 mmol L $^{-1}$) down its concentration gradient; constant replacement of dialysate maintains the gradient, so urea keeps leaving (28 → 9). Glucose shows no net movement because its concentration is equal (5.0 mmol L $^{-1}$) on both sides — no gradient. Plasma proteins and red blood cells are too large to cross the membrane's pores, so they are retained. Marks: urea gradient + diffusion (1), glucose equal concentrations (1), size exclusion of proteins/cells (1). "The machine cleans the blood" or "urea moves by osmosis" scores zero for that mark — the 2020 Q24(c) traps.

(b). If the dialysate contained no glucose, glucose would diffuse out of the blood down a gradient; matching the dialysate glucose to normal blood concentration prevents the loss of this useful solute.

Q31 (a). Sample answer: Collect equal-volume water samples from several sites along the creek using sterile containers. Spread a fixed volume of each sample onto separate sterile nutrient agar plates. Controls: one plate spread with sterile distilled water, and one unopened sterile plate, to show any growth comes from the creek water and not the equipment or air. Controlled variables: volume of water per plate, type/depth of agar, incubation temperature (about 25–30 °C) and time (48 h), same sealing (tape, not fully airtight). Reliability: at least three plates per site, count colonies and compare with the controls. Marks: valid method with sterile technique (1), control treatment(s) (1), at least two controlled variables (1), repetition/replication for reliability (1). Confusing reliability (repeats agree) with validity (only the tested variable differs) loses a mark — flagged 2022 and 2024.

(b). Incubation may have multiplied harmful (pathogenic) microorganisms to enormous numbers; opening the plate would expose students to them. Plates are sealed, examined through the lid, and sterilised before disposal.

(c). The same bacterium must be found in all sufferers (and not in healthy people); it must be isolated from a sufferer and grown in pure culture; the cultured bacterium must cause the same disease when introduced into a healthy host; and it must be re-isolated from that host and shown to be identical. Any two postulate steps applied to this scenario for 2 marks.

Q32 (a). Points plotted accurately with axes labelled (1); a single smooth line/curve of best fit — NOT dot-to-dot — rising to the 2018 peak (138) then falling after 2019 (1); a dashed extrapolation beyond 2024 shown ON the graph, reading off a 2026 prediction of roughly 10–20 cases per 100 000 (1). The even-year graphing fixture: dot-to-dot and unshown extrapolation were the flagged errors in 2020, 2022 and 2024.

(b). Judgement plus data: the program is effective — incidence rose steadily to 138 per 100 000 in 2018 but fell every year after the 2019 introduction, to 31 in 2024, a fall of about 78% while coverage rose from 74% to 94% (2). Herd immunity: at 94% coverage, so few susceptible hosts remain that chains of transmission are broken; an infected person is unlikely to contact an unvaccinated susceptible person, so even the ~6% unvaccinated are rarely exposed (2). Restating numbers without an explicit judgement caps at 2 — the 2021/2023 Q30 trap.

Q33 (a). Genetic drift (a bottleneck). Justification from data: the island frequency of B was stable (0.60–0.61) until the 2016 cyclone cut the population from ~1500 to 38; among the few random survivors the allele frequencies differed by chance from the original population (0.60 → 0.22), and the stem states survivors were no better adapted, ruling out natural selection. The mainland population (~60 000) is large, so chance deaths cannot appreciably shift its frequencies (0.59–0.61 throughout), and isolation means no gene flow between the populations. Marks: drift named (1), bottleneck/small-sample chance reasoning with data cited (1), selection excluded using the stem (1), population-size contrast for the mainland (1). Gene flow vs drift confusion is the most-flagged error in this topic (2022, 2025).

(b). This introduces gene flow: alleles carried by migrating lizards enter the island gene pool, so the island's allele frequencies are expected to move back toward the mainland's (B rising from ~0.19 toward ~0.60) and the island population's genetic diversity increases. Process named (1), predicted direction/effect justified (1).

Q34 (a). Incidence 2025 = 150/50 000 = 0.3% = **300 per 100 000 per year**. Prevalence = 1200/50 000 = **2.4%**. One mark each; incidence counts NEW cases, prevalence counts all existing cases.

(b). Weaknesses: self-reported symptoms in an online survey are subjective and unverified (measurement validity); no directly measured dust exposure; no matched control group of similar adults away from the quarry — state-wide rates differ in age, smoking and occupation; confounders (smoking, occupational dust) not recorded although smoking is the leading cause of COPD; 8 months is far too short for a chronic disease that develops over decades; 350 people from one suburb is a small, localised sample (any three, 3 marks). Reliability vs validity distinguished: repetition/consistency of results was not addressed, and reliability cannot rescue an invalid design (1). Judgement: the study can at best show a correlation; it cannot establish that quarry dust causes COPD — a longitudinal cohort with measured exposure, spirometry diagnosis, a matched unexposed control group and smoking data would be needed (1). No explicit judgement caps the response — flagged 2021, 2023, 2025.

Q35 (a). The resistance gene is cut out of the wild banana's DNA using a restriction enzyme, producing fragments with sticky ends; the same restriction enzyme cuts open a plasmid vector so its sticky ends are complementary; DNA ligase joins the gene into the plasmid (recombinant plasmid); the plasmid is inserted into bacteria (e.g. *Agrobacterium*), which are cultured to amplify the gene and then used to deliver it into Cavendish banana cells; transformed cells are grown by tissue culture into whole plants, so every cell of the regenerated plant — including its reproductive cells — carries the resistance gene. Marks: restriction enzyme/sticky ends (1), ligase + plasmid vector (1), amplification and delivery into plant cells (1), regeneration so ALL cells carry the gene, making the trait heritable (1). "Place the gene into the banana" without process terminology caps at 1 — the 2025 Q30(a) trap.

(b). Technology 1: one bull fathers every calf, so the variety of paternal alleles collapses — genetic diversity falls sharply. Technology 2: clones are genetically identical to one cow, so diversity among breeding females falls to near zero for those animals. Technology 3: introduces alleles from a different breed's gene pool — diversity increases (gene flow). Overall judgement: used together, Technologies 1 and 2 leave the herd genetically uniform; a new disease or environmental change to which the champion genotypes are susceptible could affect almost

every animal at once, so long-term vulnerability is high. Marks: one per technology judged on DIVERSITY (not on productivity) (3), explicit overall judgement linking uniformity to vulnerability (1). Effects on the organism instead of on the gene pool score zero per row — the 2023 Q34 trap.

Prediction provenance

Which consensus prediction each part of this paper realises. Full evidence panels: intuitioneducation.com.au/hsc-2026

Paper item	Prediction	Agreement
Section I Q1	`topic-level consensus`	0.56 cluster · 6 (all)
Section I Q2	`topic-level consensus`	rested: P(substantial) 0.51 · 3 models rest it
Section I Q3	`topic-level consensus`	0.70 (grok) · 2 (grok, fable)
Section I Q4	`topic-level consensus`	0.45 (fable) · 2 (fable, grok)
Section I Q5	`topic-level consensus`	0.55–0.58 · 2 (grok, opus)
Section I Q7	`topic-level consensus`	0.49 (gpt-5.6-sol) · 2 (gpt-5.6-sol, deepseek)
Section I Q8	`topic-level consensus`	0.50 (grok) · 2 (grok, opus)
Section I Q9	`topic-level consensus`	0.45 (grok) · 1 (grok)
Section I Q11	`topic-level consensus`	0.45 (grok) · 1 (grok)
Section I Q12	`watch list`	0.85 (fable) · 4 (fable, opus, grok, deepseek)
Section I Q13	`watch list`	0.50 (grok) · 2 (grok, opus)
Section I Q14	`watch list`	0.30 (opus) · 2 (opus, fable)
Section I Q15	`topic-level consensus`	0.55 (fable) · 2 (fable, gpt-5.6-sol)
Section I Q16	`watch list`	0.60 (fable) · 4 (fable, opus, grok, deepseek)
Section I Q17	`topic-level consensus`	0.40 (grok) · 1 (grok)
Section I Q18	`bio-q14-hearing-technologies`	0.52 cluster · 6 (all)
Section I Q19	`topic-level consensus`	0.38 (grok) · 3 (grok, gemini-3.1-pro, opus)
Section I Q20	`topic-level consensus`	0.53 cluster · 5

Paper item	Prediction	Agreement
Q21	`bio-q10-pathogen-classification-adaptation`	0.56 · 6 (all)
Q22	`bio-q4-somatic-vs-germline`	0.59 · 5 (fable, opus, gpt-5.6-sol, gemini-3.1-pro, deepseek)
Q23	`bio-q12-non-mendelian-cross`	0.55 · 4 (fable, opus, grok, deepseek)
Q24	`bio-q1-pedigree-mode-of-inheritance`	0.71 · 6 (all)
Q25	`bio-q9-dna-replication-written-return`	0.57 · 6 (all)
Q26	`bio-q3-codon-chart-mutation`	0.64 · 5 (fable, opus, gpt-5.6-sol, gemini-3.1-pro, deepseek; grok contrarian)
Q27	`watch list`	0.75 / 0.55 / 0.60 · 3 (gemini-3.1-pro, grok, deepseek)
Q28	`bio-q7-glucose-negative-feedback`	0.57 · 5 (fable, opus, gpt-5.6-sol, grok, deepseek)
Q29	`watch list`	0.45–0.75 / 0.32–0.55 · 5 / 3
Q30	`bio-q13-kidney-dialysis`	0.53 · 5 (fable, opus, gpt-5.6-sol, grok, deepseek)
Q31	`watch list`	0.42–0.58 / 0.45–0.50 · 5 / 3
Q32	`bio-q5-vaccination-program-analysis`	0.60 / 0.60 (fable) · 5 / 2
Q33	`bio-q8-gene-pool-processes`	0.57 · 5 (fable, opus, gpt-5.6-sol, gemini-3.1-pro, grok)
Q34	`bio-q2-epidemiology-study-evaluation`	0.67 · 6 (all)
Q35	`bio-q6-transgenic-production-process`	0.57 / 0.55 · 6 / 5

Built by an AI panel and backtested against the hidden 2025 papers before publication — method at intuitioneducation.com.au/hsc-2026/how-we-did-it. Scored publicly in November 2026. Independent Intuition Education material from publicly available NESA documents; not affiliated with or endorsed by NESA.