Mark schemes

Q1.

(a) 1. Mutation (in *KRAS* gene)

OR

Change in base sequence (of *KRAS* gene);

Accept named mutation e.g. substitution.

Accept mutation in promoter gene.

Ignore epigenetic modifications.

2. Change in (signalling) protein

OR

More (signalling) protein/K-Ras produced;

Accept change in amino acid sequence (of protein).

Reject 'no protein produced' or suggests a non-functional protein is produced.

3. (Results in) rapid/uncontrollable cell division;

Accept cell division cannot be regulated.

Ignore growth.

Reject meiosis for cell division, but accept mitosis.

3

(b) 1. **A**/untreated (type II diabetes) lowest survival (time)

OR

A/untreated (type II diabetes) lowers/reduces survival (time compared with control group);

*1 to 6 Accept descriptions of each group e.g. **A** = no drugs, **B** = metformin, **C** = combined drugs.*

2. **B**/metformin increases survival (time) the most

OR

B/metformin has the highest survival (time);

3. **C**/combined drugs increases survival (time);

4. Groups **A and B** have a significant difference (in survival time compared with control);

*4 and 5 Reject 'results are significant' or 'results are not significant' **once**, but **only** where there is no indication that these results are 'different', 'greater', 'reduced' etc.*

4 and 5 Accept 'not due to chance' for 'significant' and converse for 'not significant'.

5. Group **C** has no significant difference (in survival time compared with control);

6. (In group **C**) other drugs have reduced effect of metformin

OR

B/metformin is more effective (treatment/drug) than **C/**combined drugs;

Ignore reference to sample size, repeats or a single study.

5 max

[8]

Q2.

(a) 1. (The vesicle) fuses/binds with a lysosome;

2. Lysozyme/s hydrolyses/digests (SCFR)

OR

Hydrolytic enzyme/s breaks down/hydrolyses/ digests (SCFR);

Accept protease hydrolyses/digests (SCFR);

2

(b) **Control**

1. Cardiomyocytes/(cardiac muscle) cells have **not** been replaced

OR

Infarcted tissue is **not** repaired/replaced

OR

(The contraction of the ventricle is weak as) there is a small number of cardiomyocytes/ (cardiac muscle) cells still alive

OR

(The ventricular pressure is low as) cardiomyocytes/(cardiac muscle) cells are damaged/dead;

Reject 'some stem cells from bone marrow moved to the infarcted tissue'

2. (Pressure is not zero as) not **all** cardiomyocytes/(cardiac muscle) cells died

OR

(Pressure is not zero as) not **all** cardiomyocytes/(cardiac muscle) cells became infarcted tissue;

c-KIT–

3. Higher than control, **so** (some) stem cells (must) have been able to differentiate

OR

Higher than control, **so** (some) cardiomyocytes/(cardiac muscle) cells have been replaced/infarcted tissues have been repaired;

4. (So) *c-KIT* is not the only gene responsible for differentiation

OR

(So) SCF must be able to bind to something other than SCFR
OR

(So) something else must be able to activate TK in cells;

5. Increase is less than **c-KIT+** group as they could not make SCFR
OR

Increase is less than **c-KIT+** group as they could not activate TK;

4

(c) A correct answer 34% **= 2 marks**;;

Evidence of 2 and 1 **= 1 mark**

An answer of 42.8/43% **= 1 mark** (answer that did not subtract the 'control' from read values)

2

(d) **Connexin-43**

1. (Connexin-43) allows impulses to pass to the bottom/apex of the heart/ventricles
OR

(Connexin-43) allows impulses to pass through Purkyne tissue/the bundle of His;

Accept (connexin-43) allows diffusion/movement of ions (between cardiomyocytes)

Ignore references to signals/information/messages

GATA-4

2. More actinomyosin bridges
OR

More binding sites on actin

OR

More myosin filaments/heads;

Accept cross bridges for actinomyosin bridges

Accept more binding of myosin to actin

2

[10]

Q3.

(a) 1. Change in DNA base sequence/triplet;

2. Change in (sequence of) amino acids
OR
Change in primary/tertiary/3^0 structure;
Ignore reference to protein not being formed.
Reject (different) amino acids formed.
Ignore 3D structure.

3. (Results in) rapid/uncontrollable cell division;
Accept cell division cannot be regulated.
Ignore growth.
Accept cell replication but ignore cell reproduction.

3

(b) 1. Use of PCR to amplify (DNA sample);
Accept description of amplification.

2. Cut (DNA) using restriction endonuclease/enzymes;

3. Separate (DNA fragments) using electrophoresis;
Accept use of microarray for electrophoresis.

4. Addition of (labelled) DNA probes **and** binding (by DNA hybridisation);
Ignore primers.
Reference to probe being complementary is insufficient.

5. (Mutations) identified by fluorescence/radioactivity
OR
Compare positions/bands (to known) DNA sample with (all harmful) mutations;
Accept identification using X-ray/photographic/film/autoradiography or UV light.

***Note if only DNA sequencing** is used award **max 3 marks** for the following.*
1 Use of PCR to amplify (DNA/sample);
2. Sequence the DNA sample;
3. Compare DNA sequence with known DNA sequence of mutation;

4 max

(c) 1. (Drug) binds to (oestrogen/ER) receptor;
Accept (inactive) transcription factor for receptor.

2. Prevents binding of oestrogen/hormone;
Reject active site/enzyme-substrate complex once only.

3. No/fewer transcription factor(s) bind to promoter
OR
RNA polymerase not stimulated/activated;

3

(d) 1. High/increased (concentration of) PSA not always linked to (prostate) cancer
OR
High/increased (concentration of) PSA could be a false positive;

2. 2.(Could be) due to urinary infection
OR
(Could be) due to enlarged prostate;
Accept 'urine infection'.

2

(e) 1. (Drugs could) increase methylation of oncogene(s);

2. (Drugs could) decrease methylation of tumour suppressor gene(s);

3. (Increased) methylation of DNA/gene(s) inhibits transcription/expression (of genes)
OR
Decreased methylation of DNA/gene(s) stimulates transcription/expression (of genes);
Accept promoter (region) for DNA/gene

4. Decreased acetylation of histones inhibits transcription/expression (of genes)
OR
(Increased) acetylation of histones stimulates transcription/expression (of genes);
Ignore 'switching on' and 'switching off' genes once but accept as alternative(s) for 1 mark if used correctly in context of transcription/ expression for both points 3 and 4.

Ignore methylation of histones and acetylation of DNA/genes.
Ignore proto-oncogenes.

3 max

[15]