## Mark schemes

## Q1.

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	(a)	1.	Comparing (measurable/observable) features/characteristics;		
		2.	Comparing amino acid sequences/primary structures (of a/named/the same protein);		
			Must have idea of comparison/ differences/similarities		
			Ignore courtship/ behaviour/mutations/		
			number of chromosomes/allele		
			frequency/species richness/index of		
			diversity		
			Accept comparing amount of antibody bound to antigen/protein (in different		
			species)		
				2 max	
	(h)	26 to			
	(b)	36 tC	o 36.4;	1	
				-	
	(c)	В, А,	С;		
				1	
	(d)	1.	Student's t-test;		
		0			
		2.	Comparing mean of data sets/histograms <b>OR</b>		
			Comparing (2) means		
			OR		
			Data are normally distributed;		
			Accept average for 'mean'		
			Ignore difference between means		
				2	[6]
					[6]
Q2	2.				
	(a)	1.	Kingdom, Phylum, Class, Order, Family;		
		2.	Luscinia svecica.		
			1 mark for each correct column		
			Allow Genus and Species if both placed in box for		
			species but not if both placed in genus box	2	
	(b)	Num	ber of different alleles of each gene.		
			Accept number of different base sequences (found)		
			in each gene	1	
				•	
	(c)	1.	Has greater proportion of genes / percentage of genes showing		
			diversity;		

2. Percentage is 35% compared with 28% / proportion is 0.35

compared with 0.28. Allow correct figures that are not rounded up, i.e., 34.9% / 0.349 and 27.8% / 0.278 2 [5] Q3. (a) PKNJ. 1 (b) Lutra lutra. 1 (c) Bone / skin / preserved remains / museums. 1 (d) 1. (Hunting) reduced population size(s), so (much) only few alleles left: Accept bottleneck 2. Otters today from one / few surviving population(s); Accept founder effect 3. Inbreeding. Allow any two 2 max Population might have been very small / genetic bottleneck; (e) 1. 2. Population might have started with small number of individuals / by one pregnant female / founder effect; 3. Inbreeding. Allow any two 2 max [7]