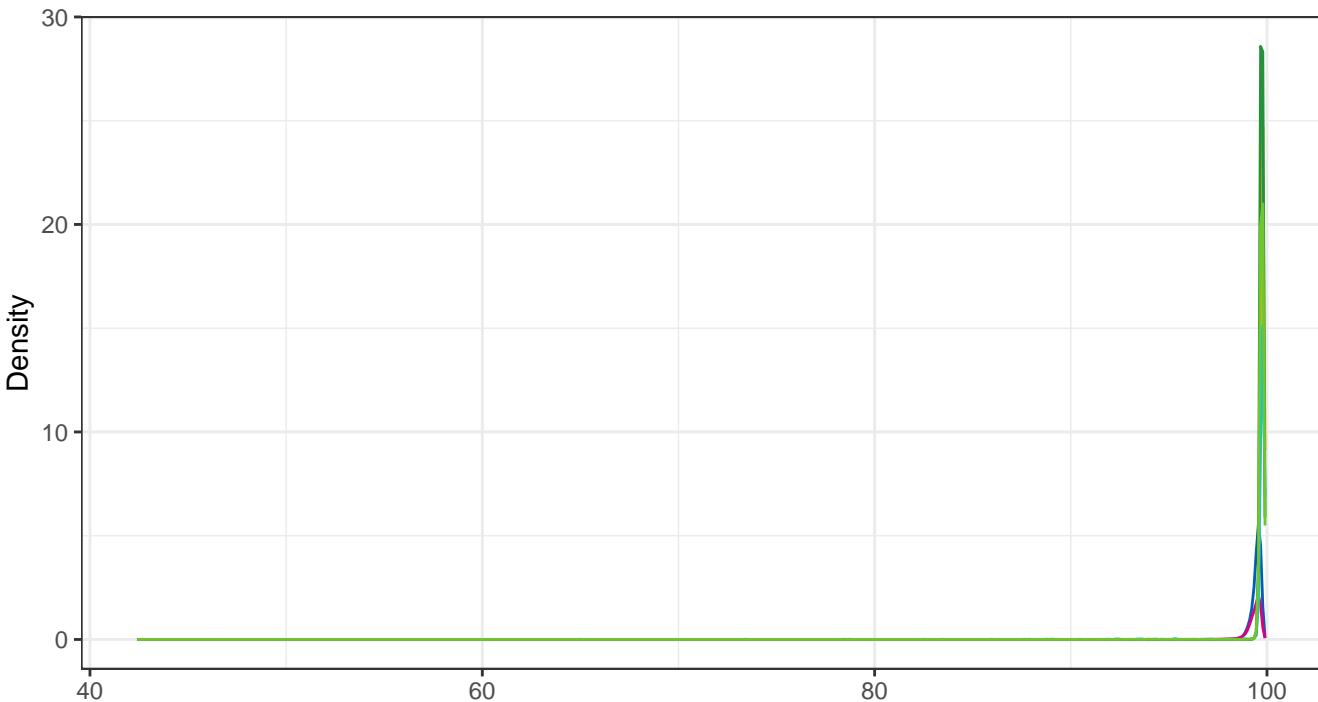
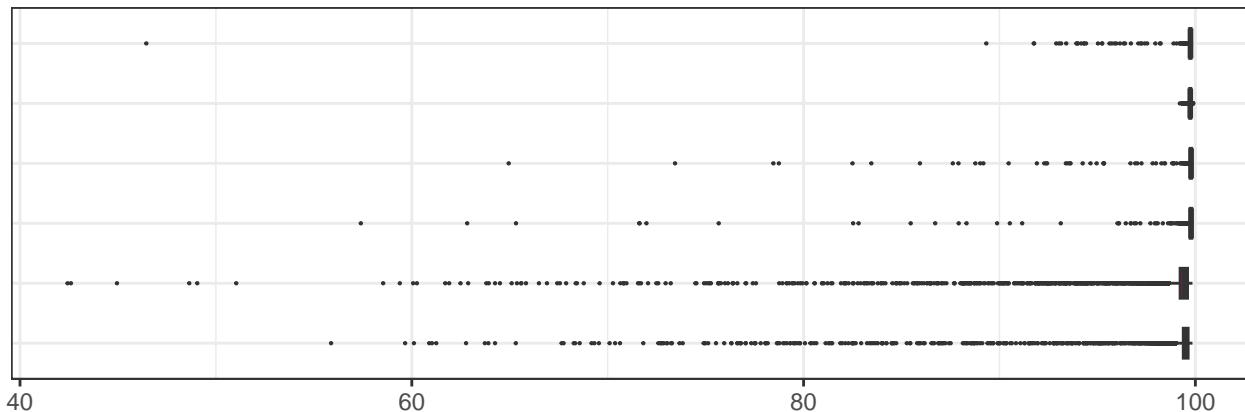
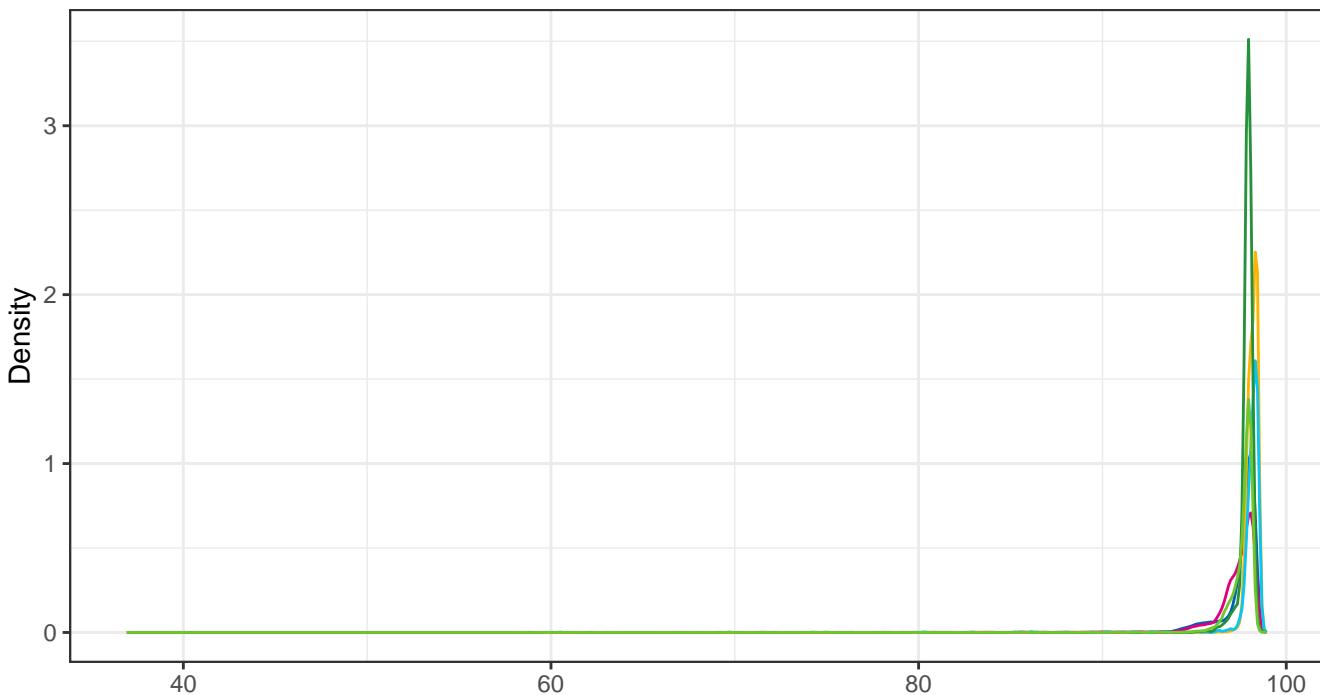
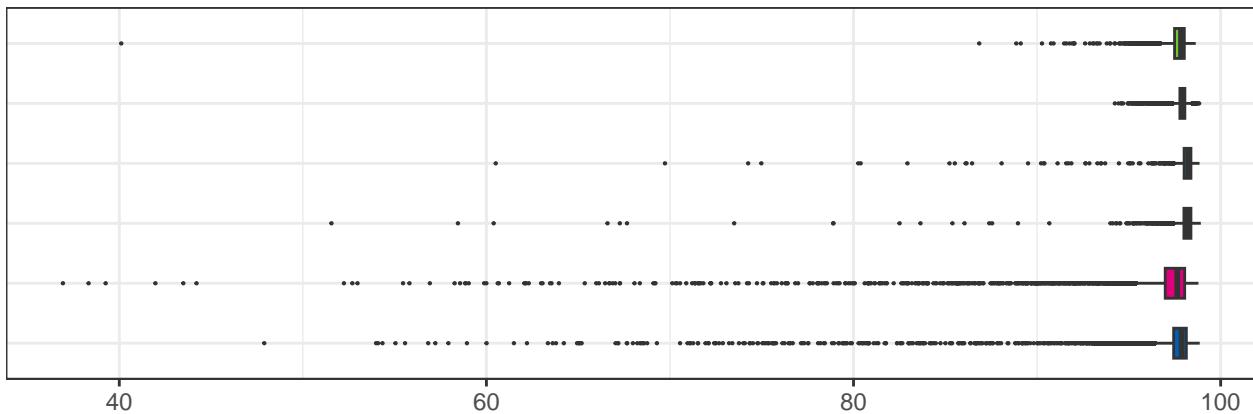


Percentage Mapped Reads



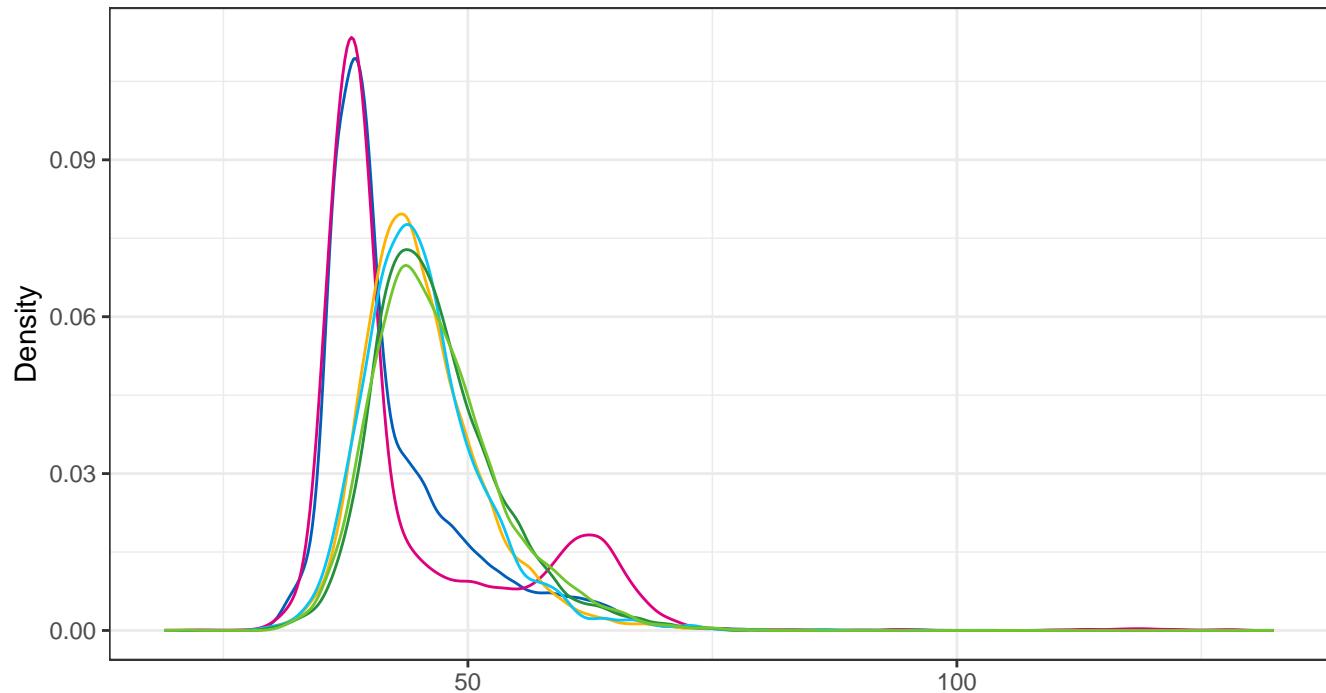
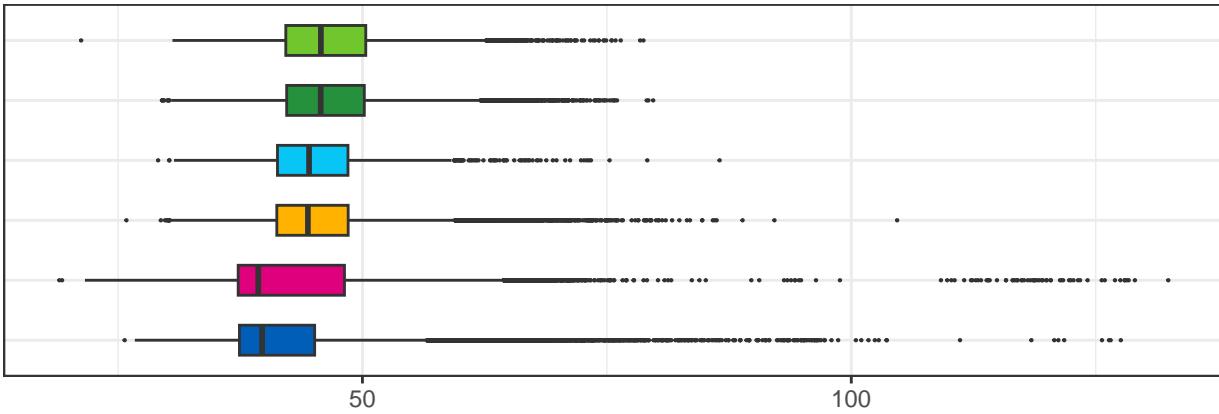
Percentage Properly Paired Reads



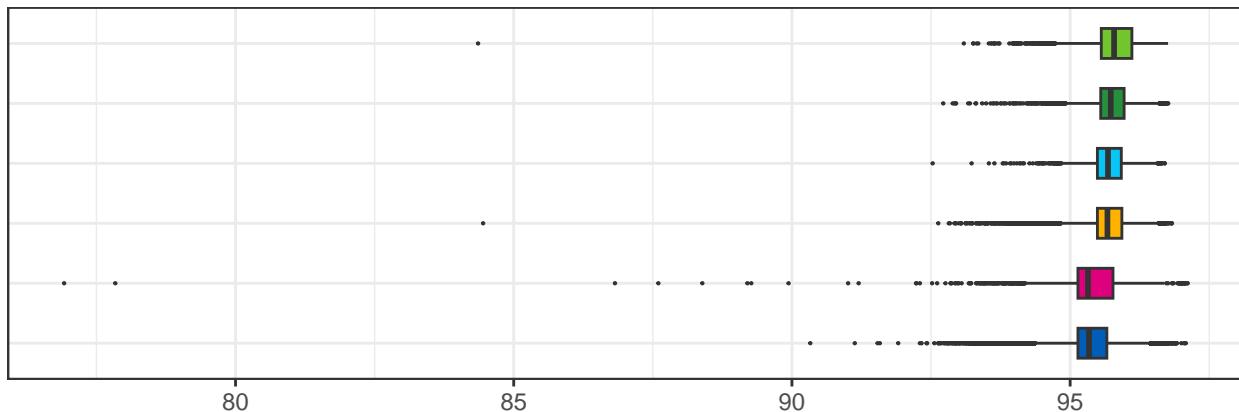
Programme Type

 MP100K Rare Disease	 GMS Rare Disease	 COVID Mild
 MP100K Cancer	 GMS Cancer	 COVID Severe

Mean Autosome Coverage



Percentage of genome with coverage above 15X



80

85

90

95

1.5

1.0

0.5

0.0

80

85

90

95

Programme Type



MP100K Rare Disease



GMS Rare Disease



COVID Mild



MP100K Cancer

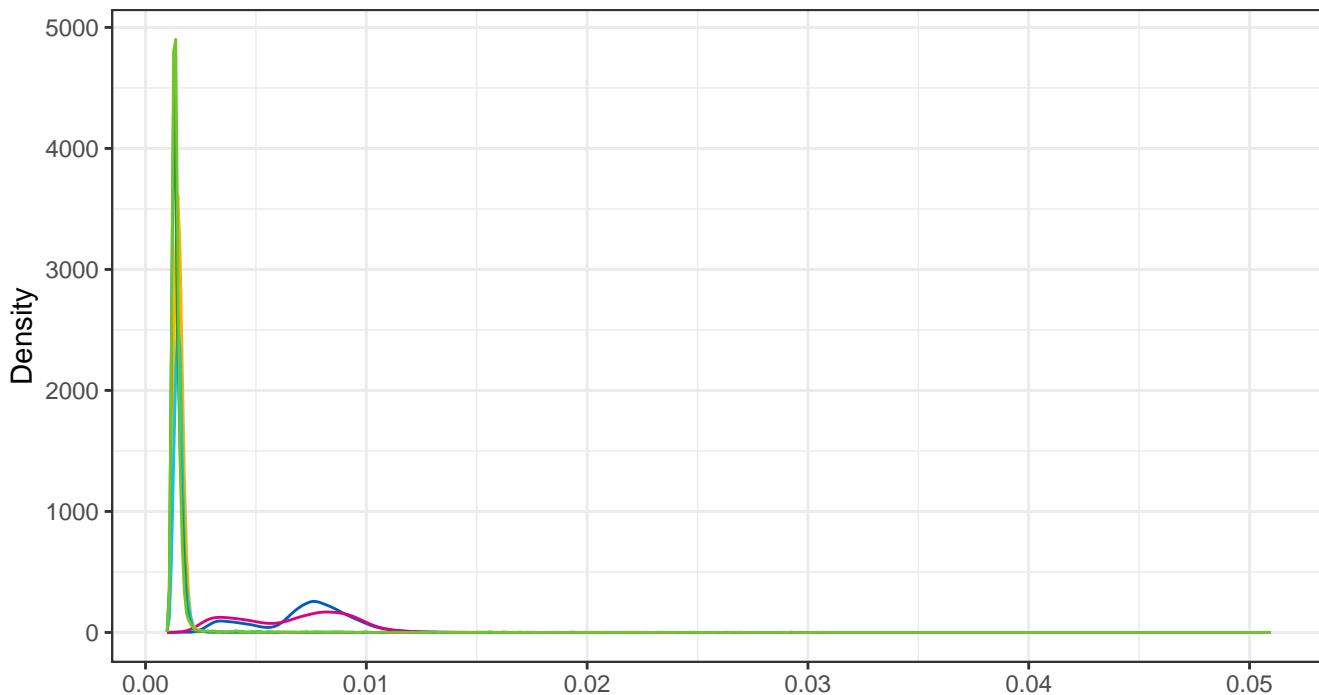
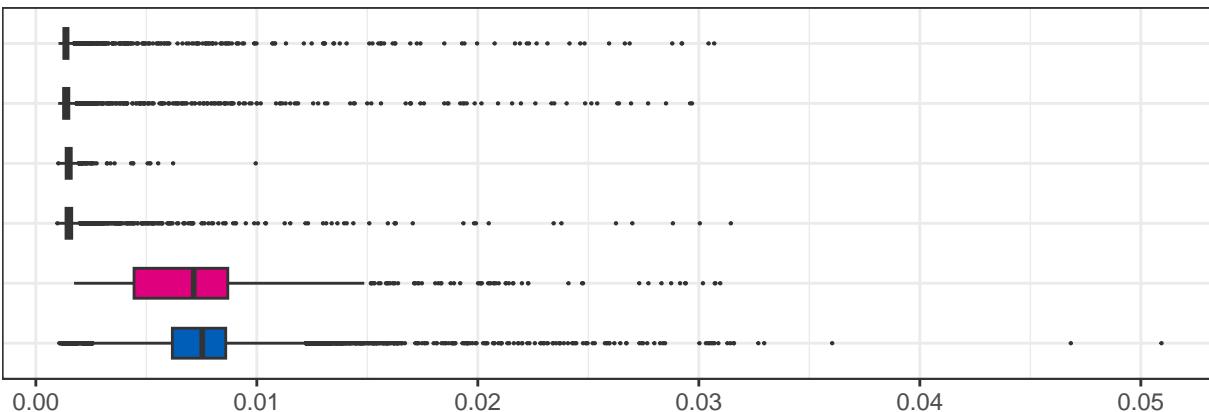


GMS Cancer



COVID Severe

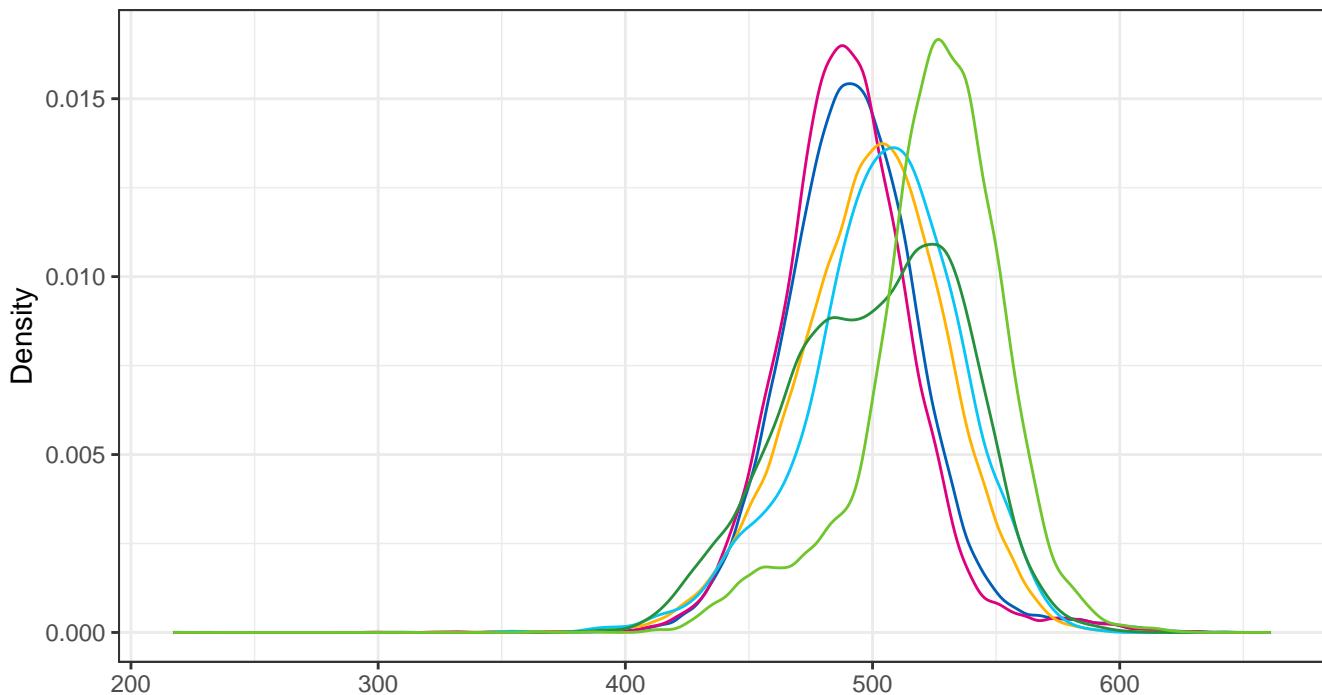
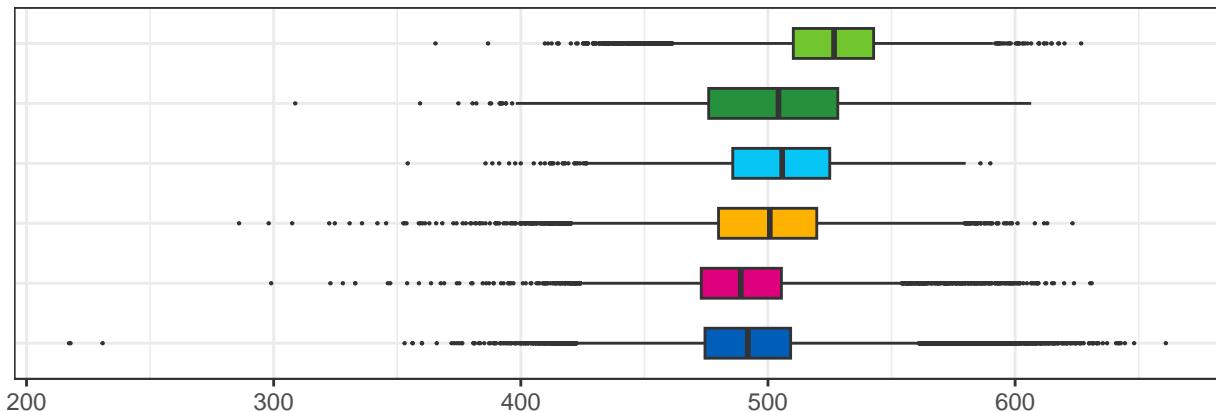
CHARR Score



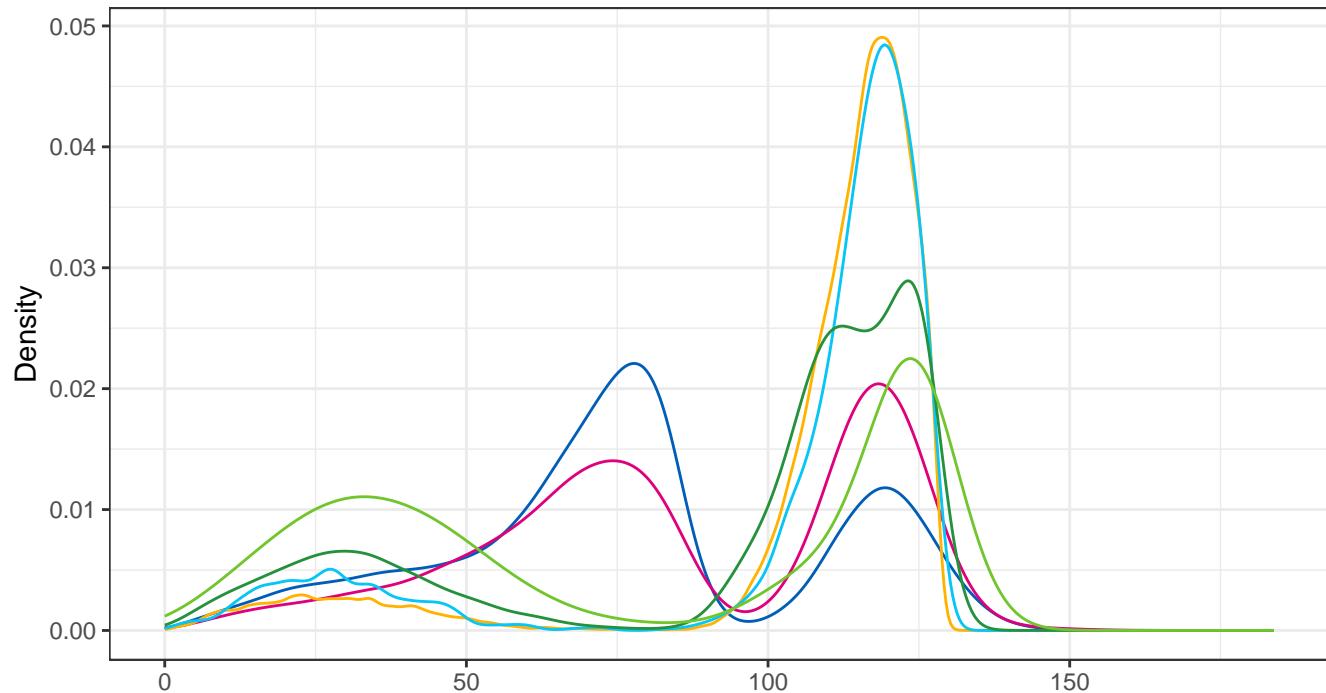
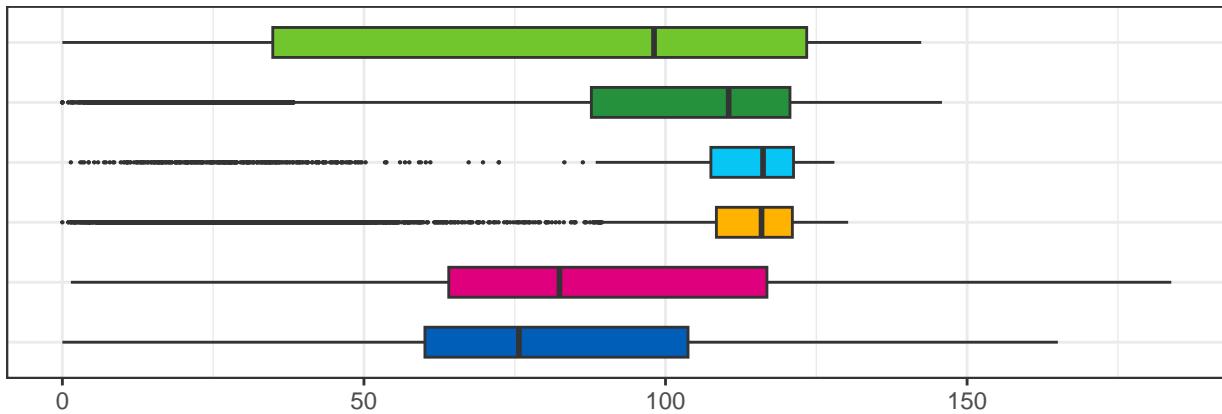
Programme Type

MP100K Rare Disease	GMS Rare Disease	COVID Mild
MP100K Cancer	GMS Cancer	COVID Severe

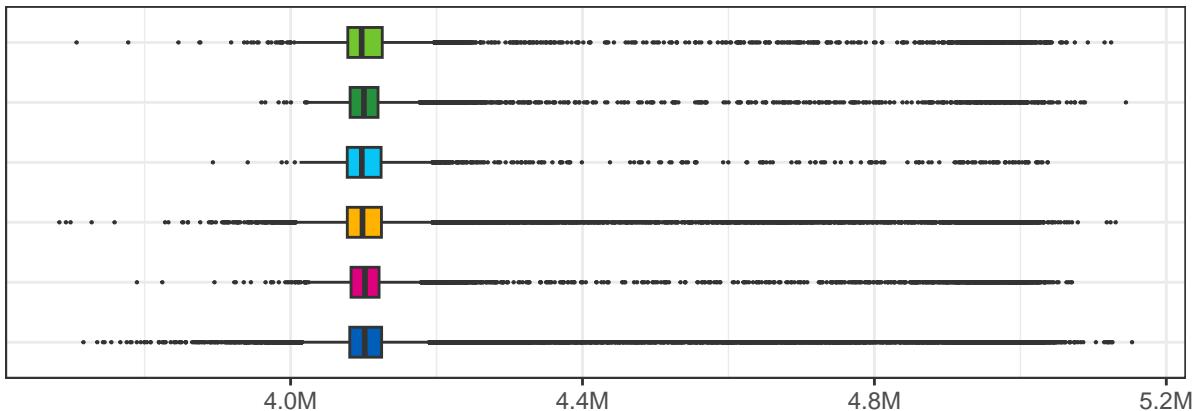
Mean Insert Length



Insert Length Standard Deviation



SNPs



4.0M

4.4M

4.8M

5.2M

1.5e-05

Density

1.0e-05

0.0e+00

4.0M

4.4M

4.8M

5.2M

Programme Type



MP100K Rare Disease



GMS Rare Disease



GMS Cancer

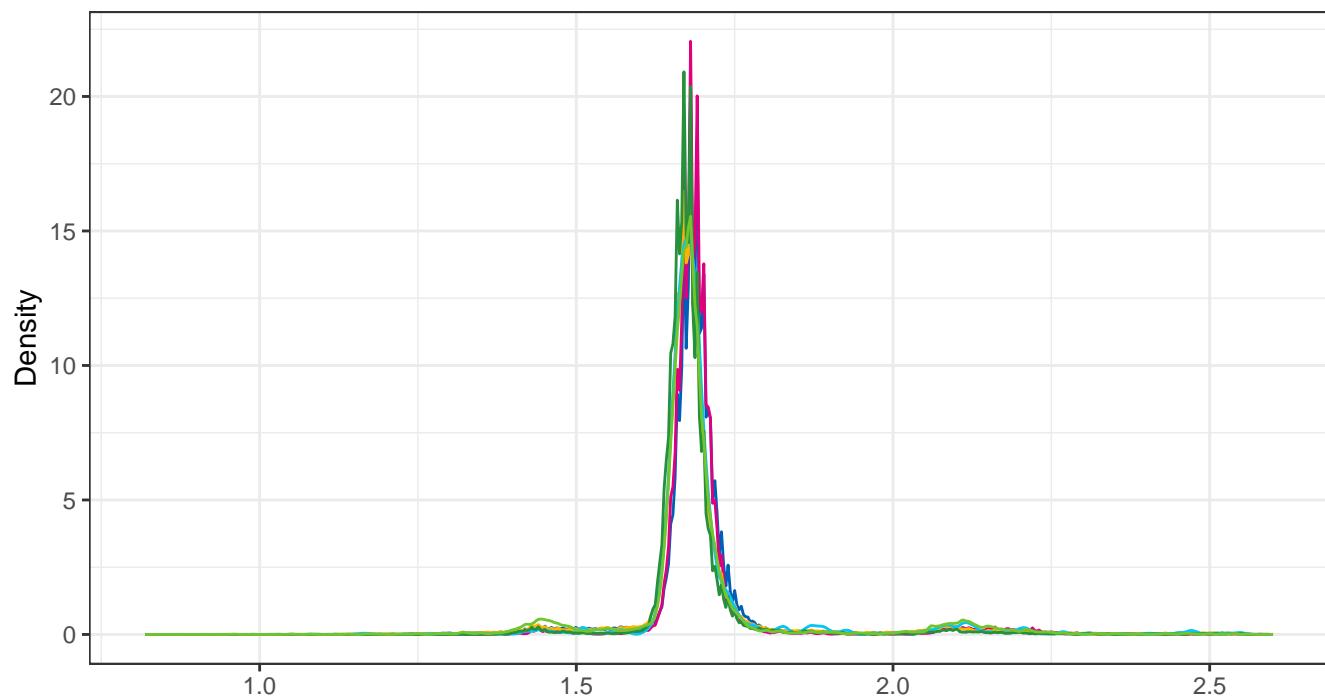
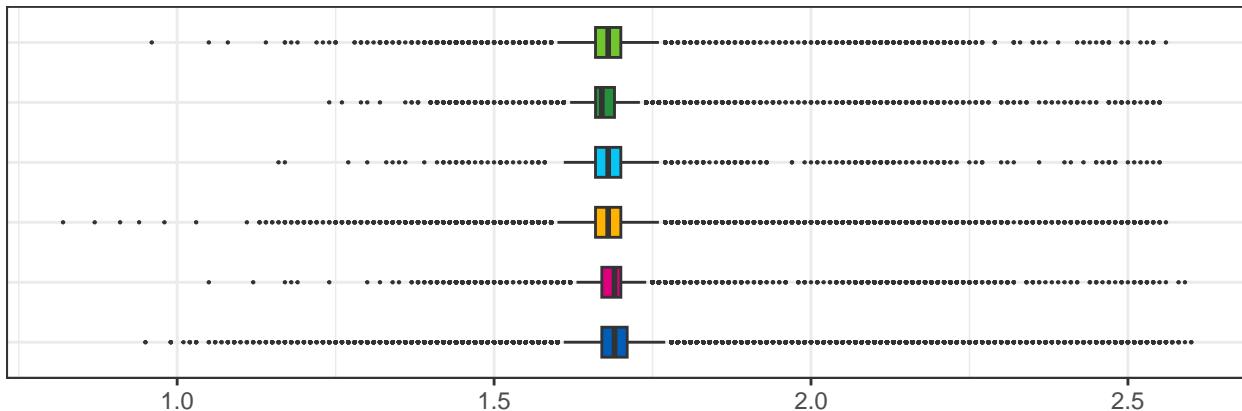


COVID Mild



COVID Severe

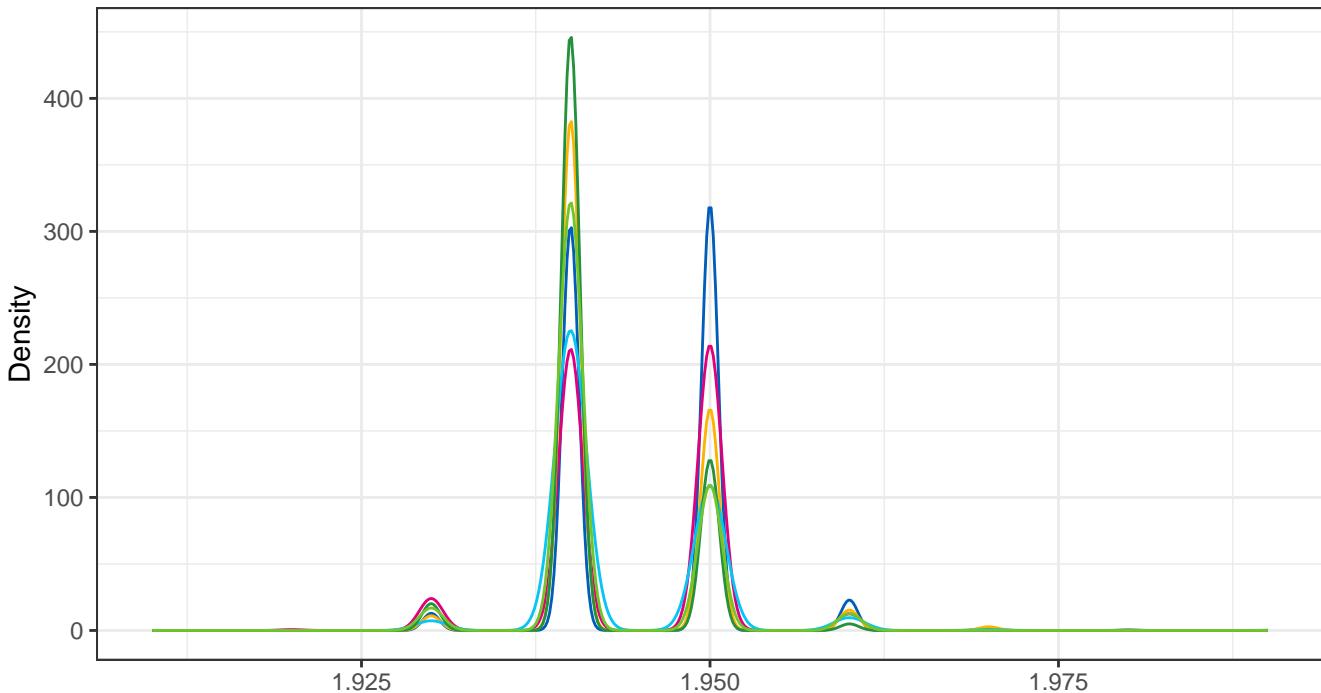
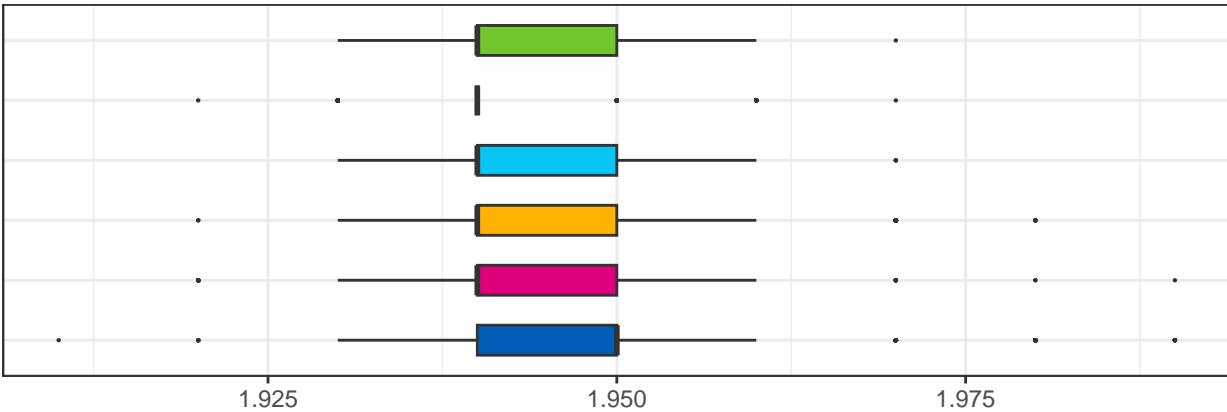
Hetrozygous/Homozygous Ratio



Programme Type

 MP100K Rare Disease	 GMS Rare Disease	 COVID Mild
 MP100K Cancer	 GMS Cancer	 COVID Severe

Transitions/Transversions Ratio



Programme Type

 MP100K Rare Disease	 GMS Rare Disease	 COVID Mild
 MP100K Cancer	 GMS Cancer	 COVID Severe