



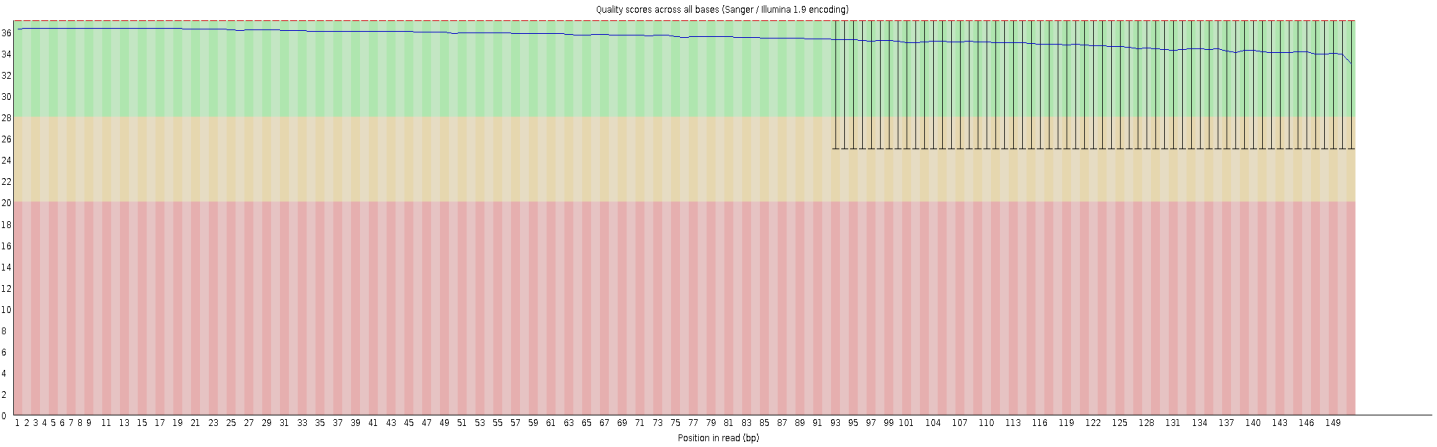
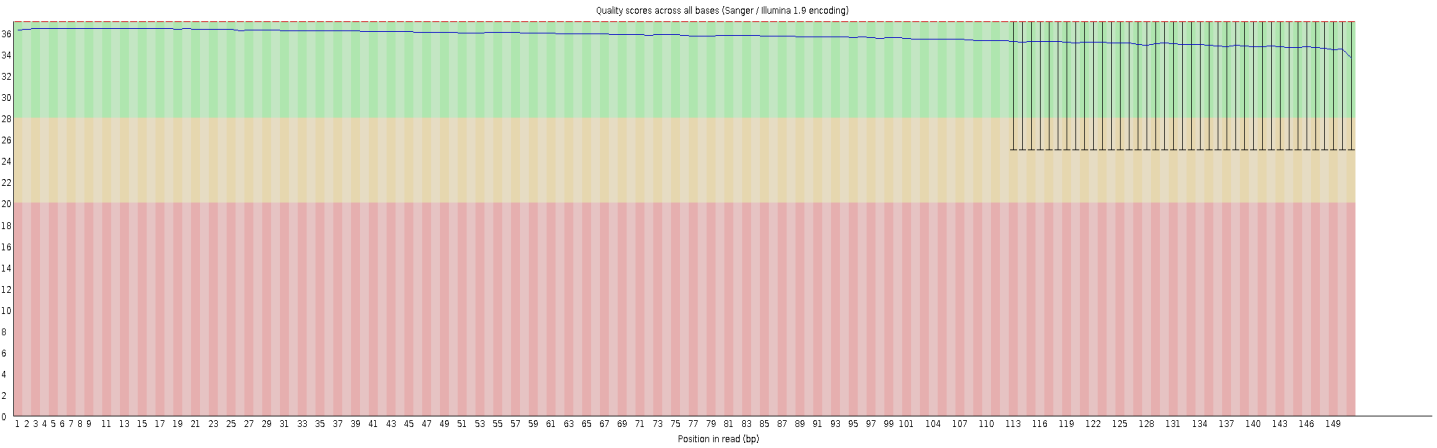
The Institute of Medical Science
The University of Tokyo

Genome Sequence Quality Report

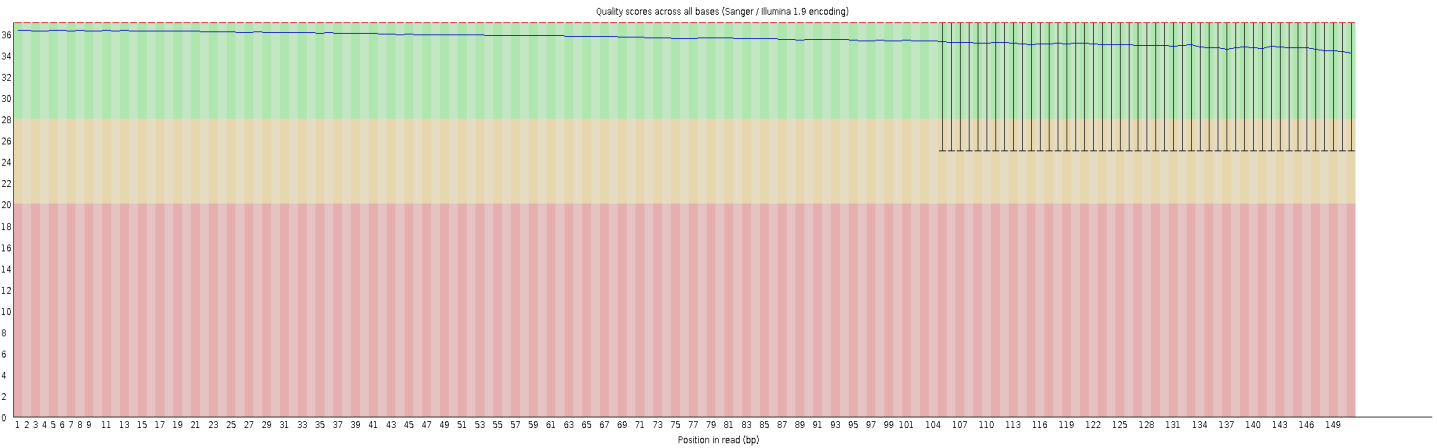
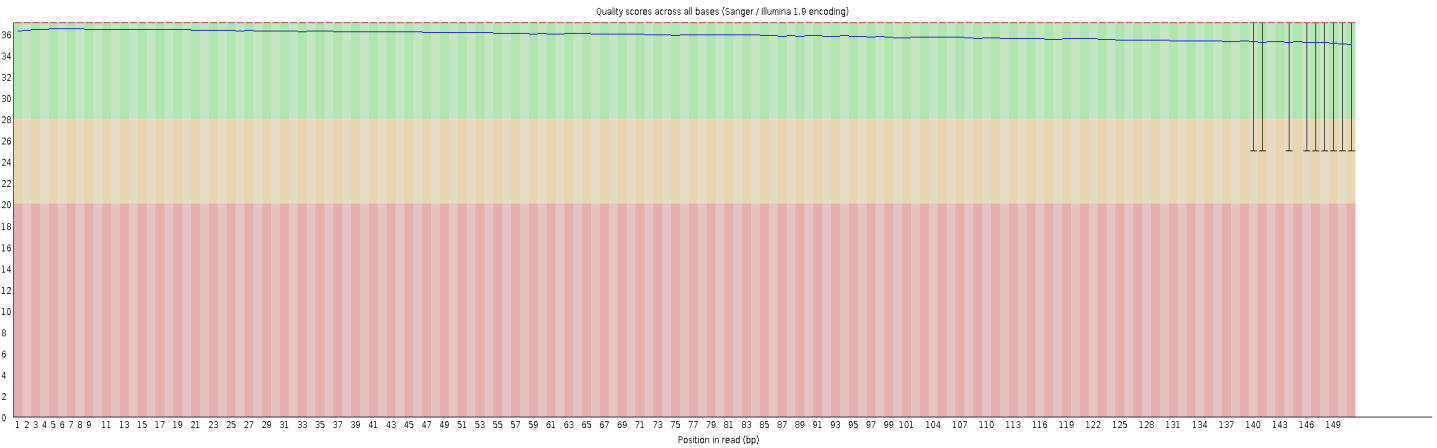
Case ID: B042-668

Sample ID	B042-668
Tumor sample name	2022-668-BM1
Normal sample name	2023-668-SW1
Tumor cellularity	NA
Normal cellularity	NA
Tumor contamination estimate	0.00341853
Normal contamination estimate	0.211021
Platform reagents/Sequencer type	B042
Platform informatics	genomon2.6.2,Parabricks v3.8.0.1
Sequencer reagent lot No.	240221_A01885_0025_BHJCCDSX7_202403081028
Sequencing date	2023/06/07
Informatics analysis date	2024/03/08
Per base sequence quality	PASS
Per sequence quality scores	PASS
%>=Q30(tumor/normal, R1&R2)	96.7% / 96.8%
%>=Q20(tumor/normal, R1&R2)	99.9% / 99.9%
Depth coverage	PASS
20x_ratio	99.0% / 98.2%
30x_ratio	98.9% / 87.8%
50x_ratio	98.5% / 6.8%
100x_ratio	58.3% / 0.2%
Average Depth (tumor/normal)	102.2 / 38.0
total_reads (tumor/normal)	2,673,459,014 / 902,804,636
Mapped_reads (tumor/normal)	2,670,120,118 / 854,281,962
Mapped_reads/total_reads (tumor/normal)	99.9% / 94.7%
Mean_insert_size (tumor/normal)	361.917 / 357.418
Sequence duplication level	PASS
Duplicate_reads (tumor/normal)	597,434,242 / 79,993,020
Duplicated read ratio (tumor/normal)	22.3% / 8.8%
Sequence length distribution	WARN
read_length_r1 (tumor/normal)	151 / 151
read_length_r2 (tumor/normal)	151 / 151

Base quality (tumor)



Base quality (normal)



Tile quality (tumor)

Tile quality (normal)