

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 09:36:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618650.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR618650 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618650.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 09:36:37 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618650.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	68,781,667
Mapped reads	64,108,771 / 93.21%
Unmapped reads	4,672,896 / 6.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	135,912 / 0.2%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	41,506,614 / 60.35%
Duplication rate	39.52%
Clipped reads	12,741,786 / 18.52%

2.2. ACGT Content

Number/percentage of A's	1,566,427,145 / 25.64%
Number/percentage of C's	1,488,999,230 / 24.37%
Number/percentage of T's	1,791,463,261 / 29.32%
Number/percentage of G's	1,261,081,521 / 20.64%
Number/percentage of N's	2,498,884 / 0.04%
GC Percentage	45.01%

2.3. Coverage

Mean	1.9751

Standard Deviation	54.0016
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2.4. Mapping Quality

Mean Mapping Quality	49.51
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2.5. Mismatches and indels

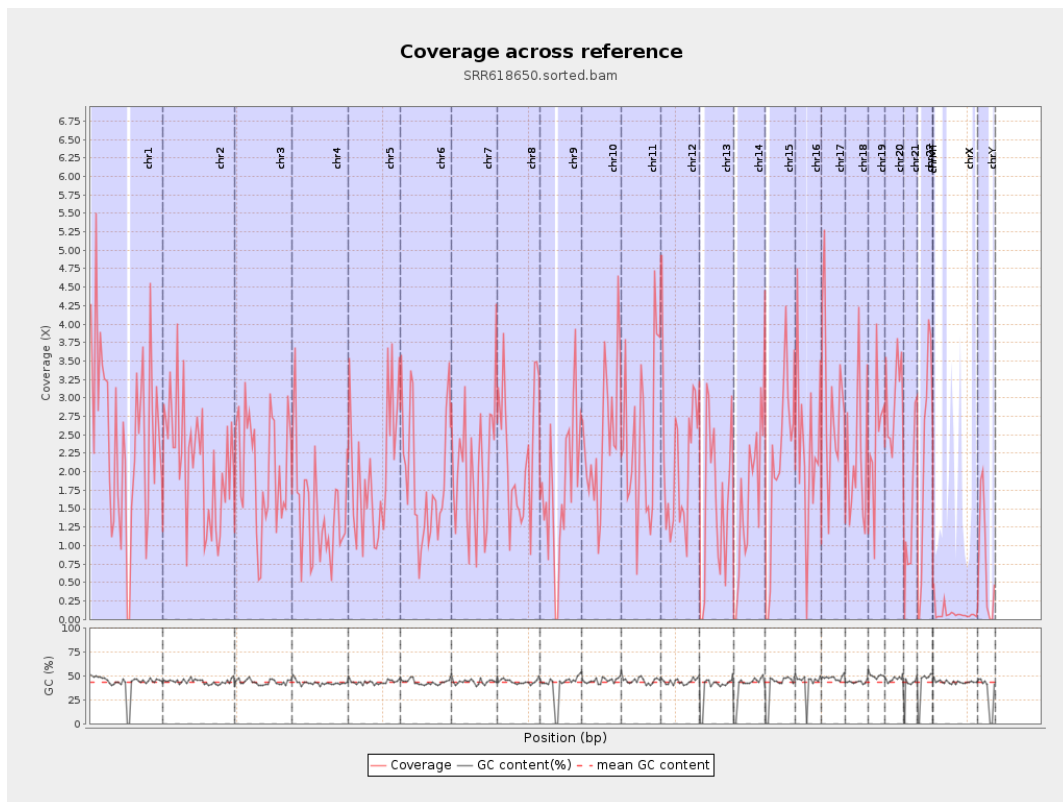
General error rate	1.28%
Mismatches	76,373,124
Insertions	1,150,009
Mapped reads with at least one insertion	1.77%
Deletions	2,717,696
Mapped reads with at least one deletion	4.14%
Homopolymer indels	50.29%

2.6. Chromosome stats

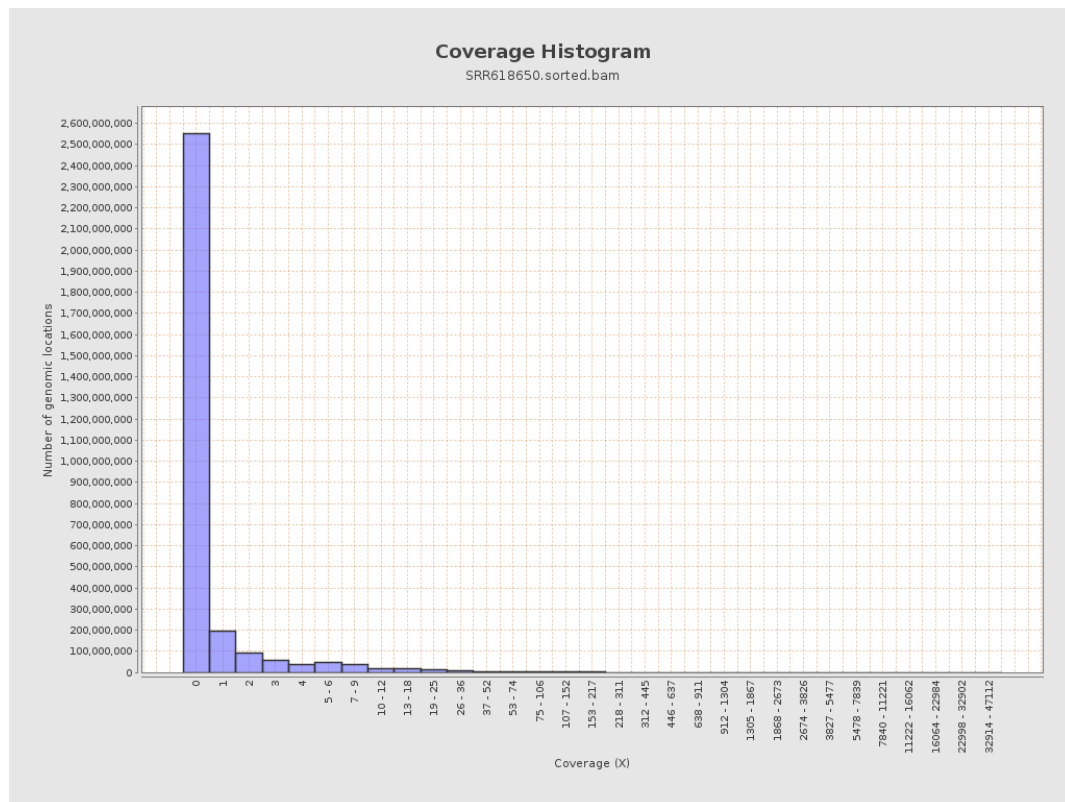
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	610801900	2.4506	67.7021
chr2	243199373	516985222	2.1258	64.3482
chr3	198022430	398858701	2.0142	48.3901
chr4	191154276	280126148	1.4654	34.1225
chr5	180915260	368013983	2.0342	56.4149
chr6	171115067	316989203	1.8525	36.4293
chr7	159138663	328981260	2.0673	65.9004

chr8	146364022	327084147	2.2347	58.9647
chr9	141213431	252116307	1.7854	41.218
chr10	135534747	328393959	2.423	55.6754
chr11	135006516	328882716	2.4361	60.928
chr12	133851895	289703899	2.1644	57.7253
chr13	115169878	182452453	1.5842	59.2114
chr14	107349540	172140783	1.6036	37.0547
chr15	102531392	217007703	2.1165	56.9211
chr16	90354753	208872260	2.3117	58.0153
chr17	81195210	242652554	2.9885	73.6126
chr18	78077248	164823296	2.111	49.8313
chr19	59128983	142186627	2.4047	56.8867
chr20	63025520	188833116	2.9961	66.6829
chr21	48129895	72670951	1.5099	44.1135
chr22	51304566	114300989	2.2279	46.335
chrMT	16571	7182	0.4334	1.5833
chrX	155270560	12775585	0.0823	11.2665
chrY	59373566	48681381	0.8199	32.8905

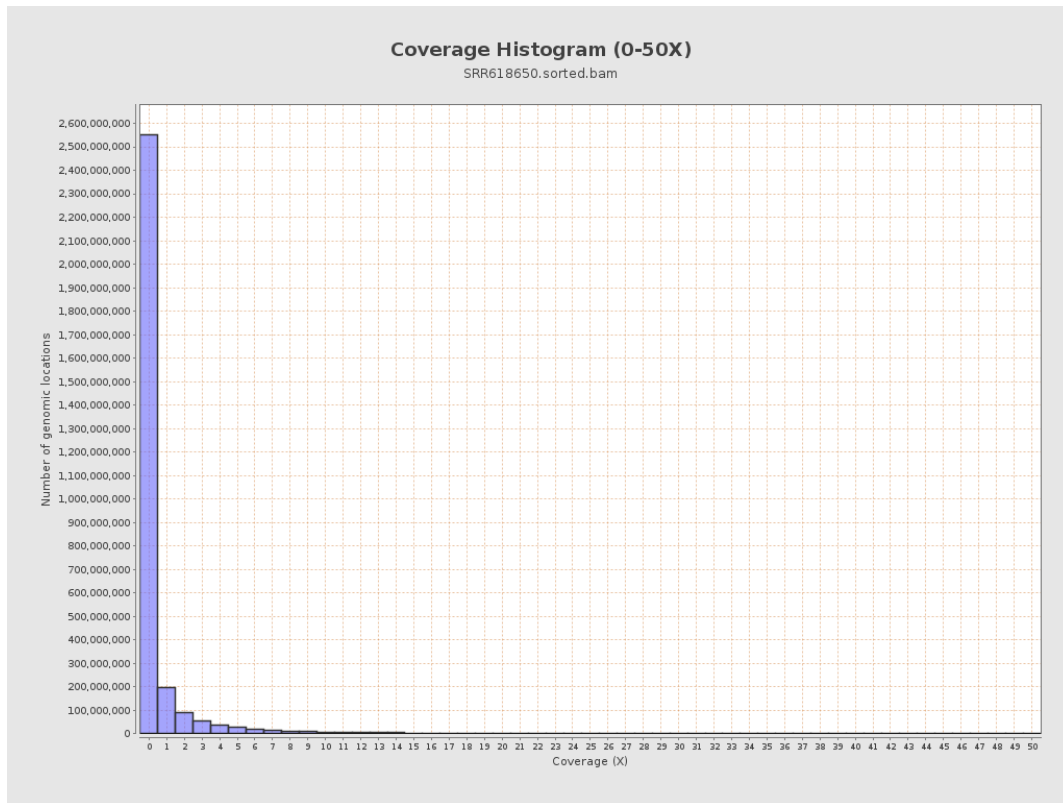
3. Results : Coverage across reference



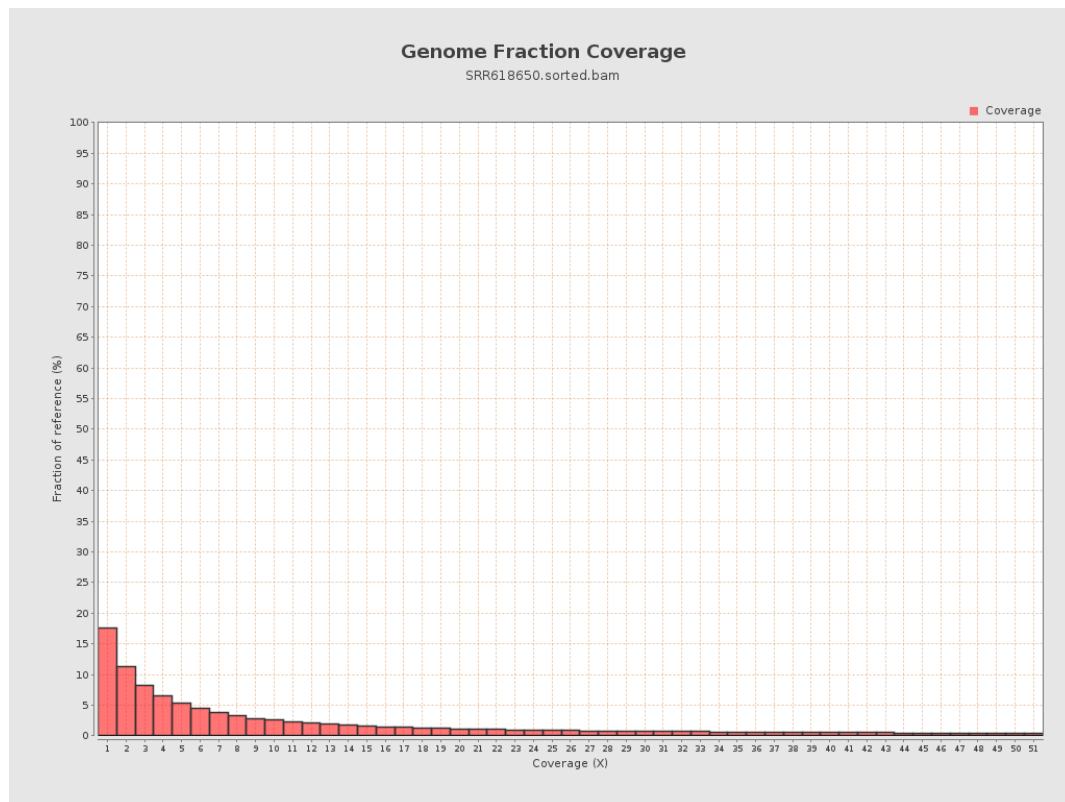
4. Results : Coverage Histogram



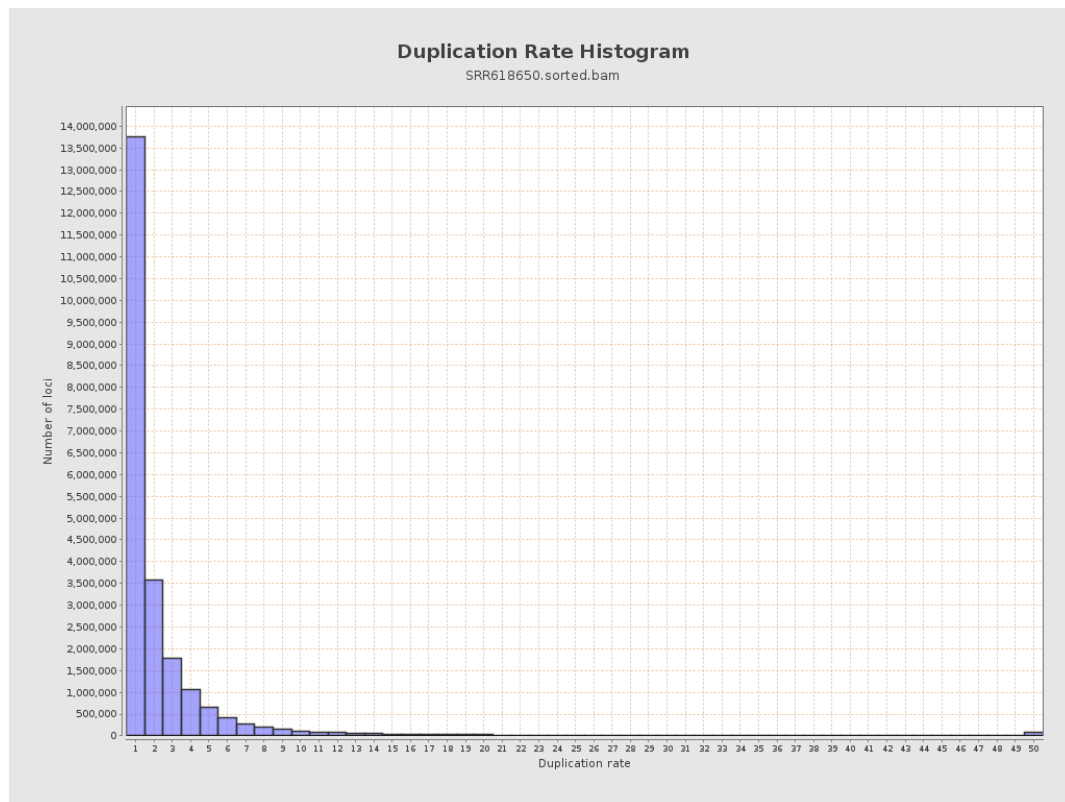
5. Results : Coverage Histogram (0-50X)



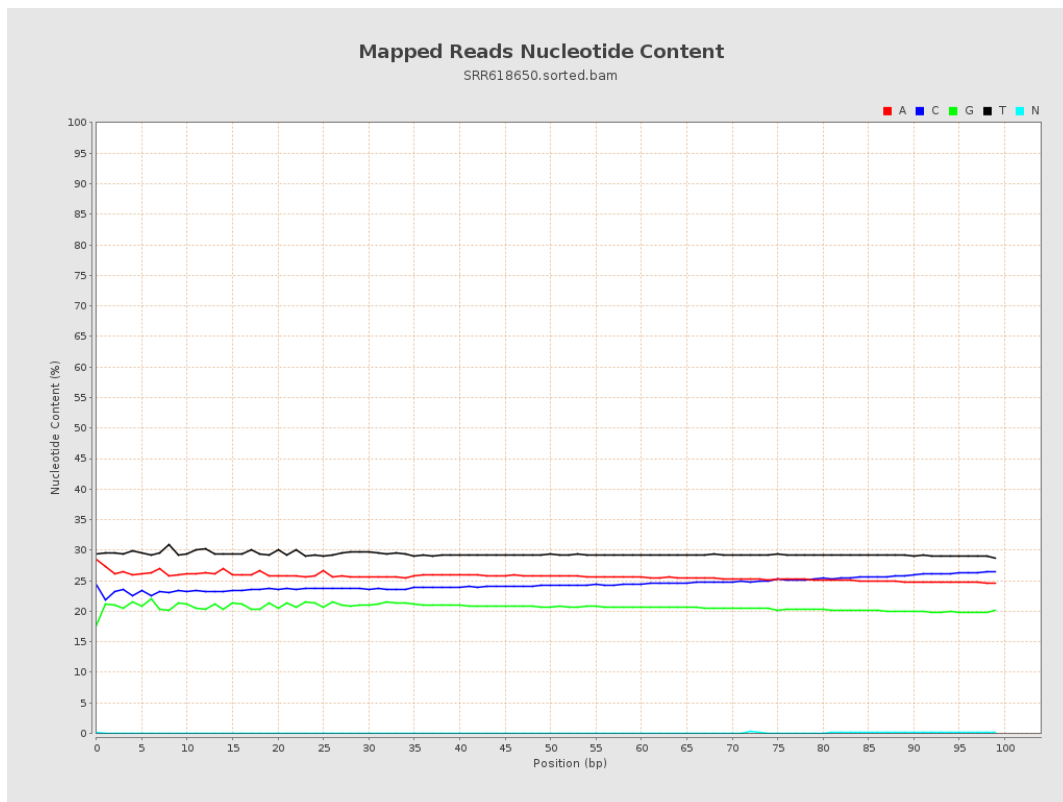
6. Results : Genome Fraction Coverage



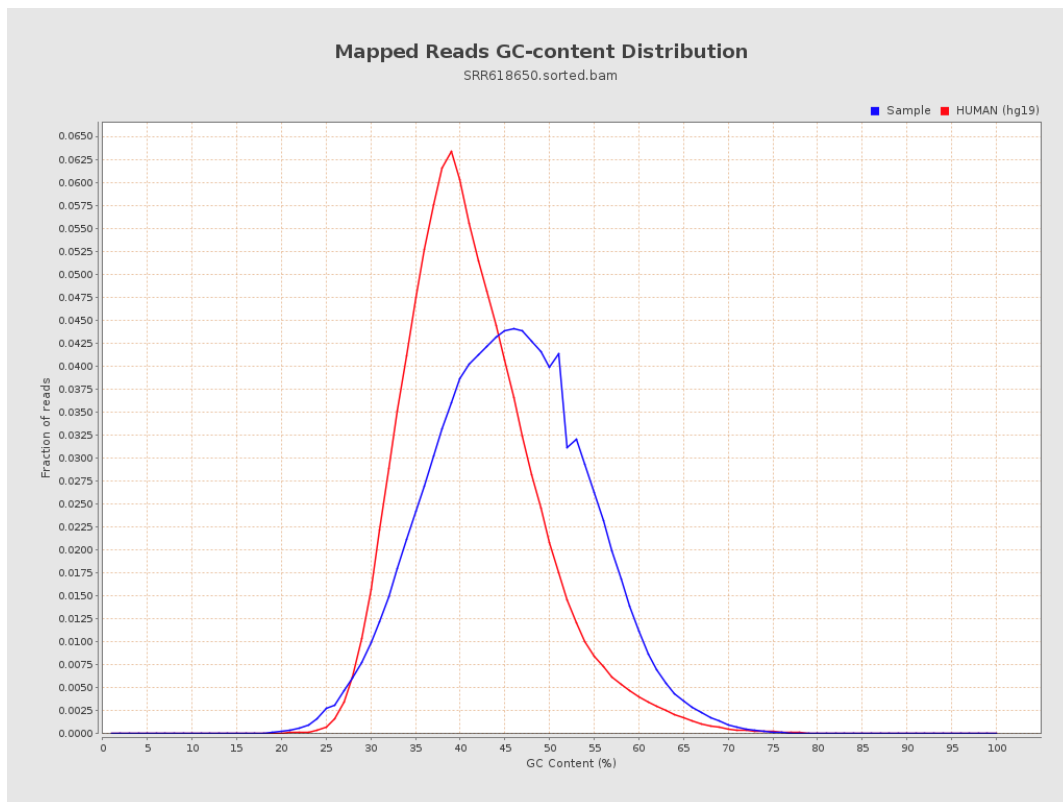
7. Results : Duplication Rate Histogram



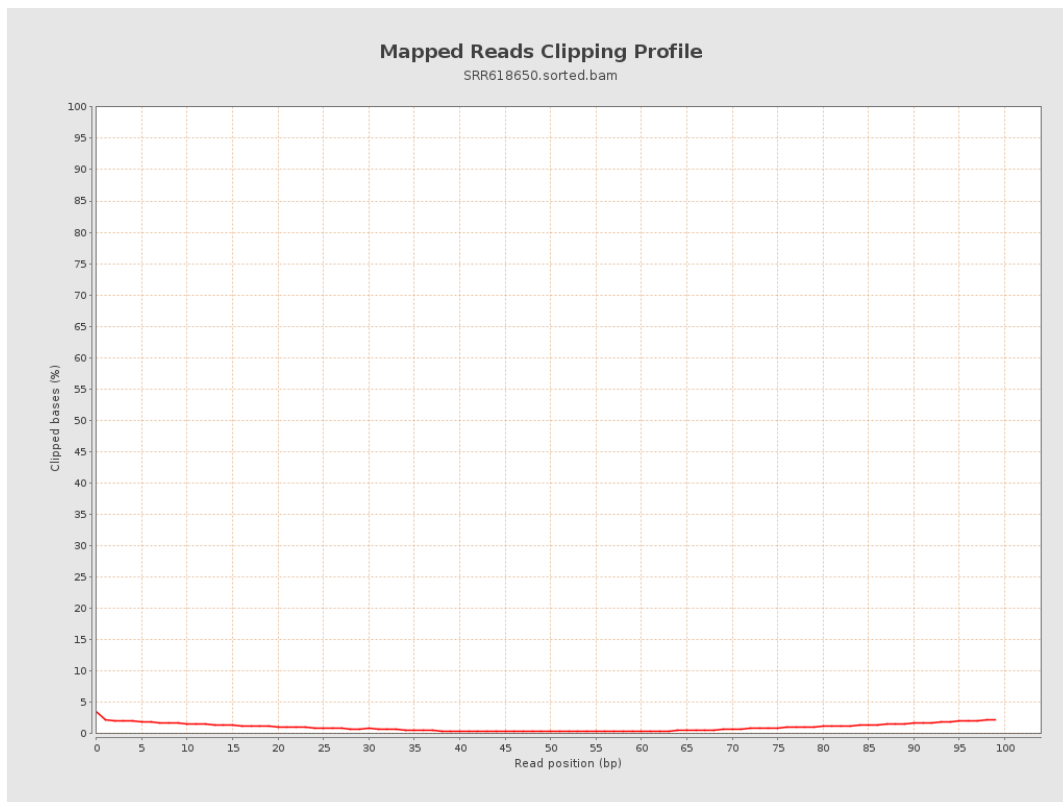
8. Results : Mapped Reads Nucleotide Content



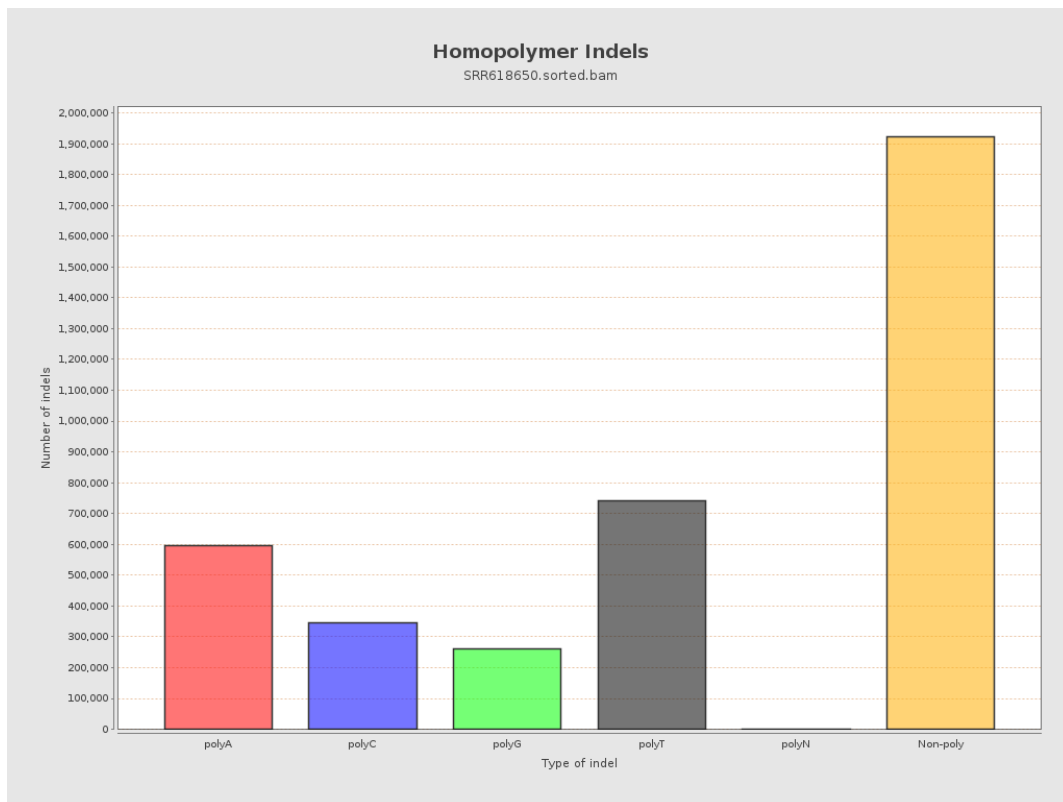
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

