

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 08:50:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618649.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_SRR618649 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618649.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 08:50:48 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618649.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	66,652,853
Mapped reads	63,993,189 / 96.01%
Unmapped reads	2,659,664 / 3.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	337,845 / 0.51%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	39,966,278 / 59.96%
Duplication rate	48.75%
Clipped reads	9,307,508 / 13.96%

2.2. ACGT Content

Number/percentage of A's	1,632,029,657 / 26.39%
Number/percentage of C's	1,439,360,862 / 23.27%
Number/percentage of T's	1,941,682,950 / 31.39%
Number/percentage of G's	1,171,639,972 / 18.94%
Number/percentage of N's	429,098 / 0.01%
GC Percentage	42.21%

2.3. Coverage

Mean	1.9997

Standard Deviation	44.5192
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2.4. Mapping Quality

Mean Mapping Quality	51.5
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2.5. Mismatches and indels

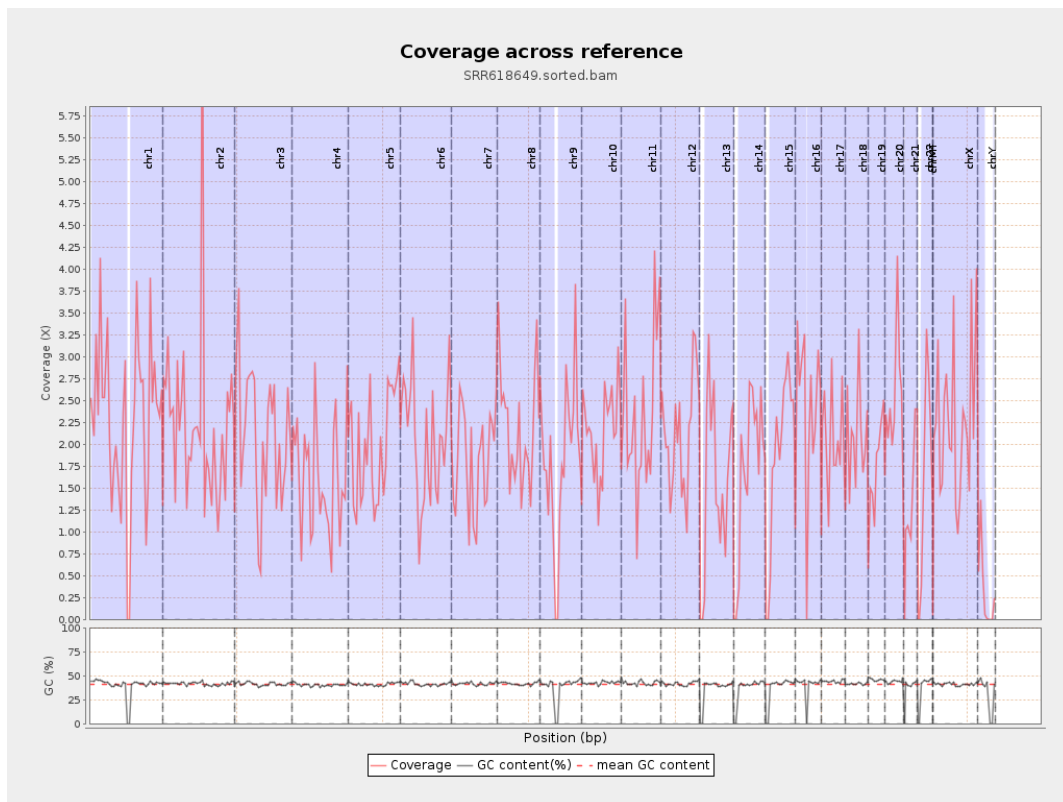
General error rate	0.92%
Mismatches	54,117,913
Insertions	1,320,089
Mapped reads with at least one insertion	1.99%
Deletions	3,028,655
Mapped reads with at least one deletion	4.6%
Homopolymer indels	48.32%

2.6. Chromosome stats

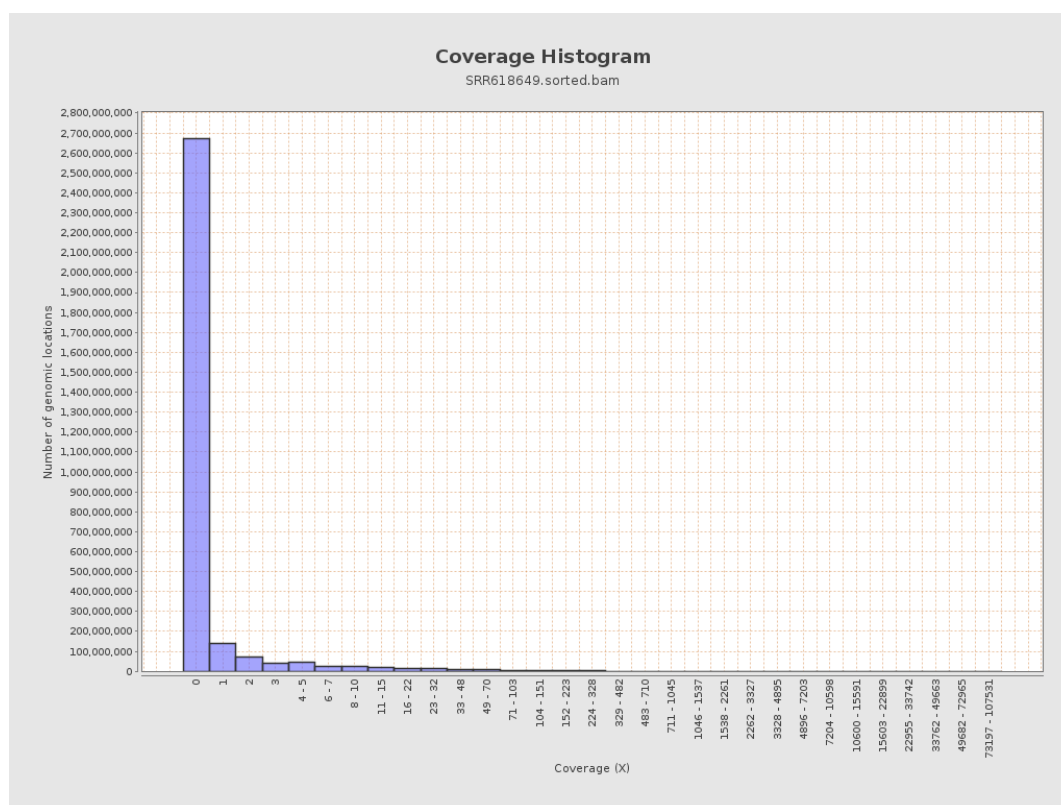
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	570988042	2.2908	44.9954
chr2	243199373	548075468	2.2536	92.7127
chr3	198022430	407989525	2.0603	35.7613
chr4	191154276	310734133	1.6256	37.727
chr5	180915260	361907574	2.0004	33.5922
chr6	171115067	351026737	2.0514	31.3706
chr7	159138663	289679067	1.8203	29.0337

chr8	146364022	317359877	2.1683	37.2856
chr9	141213431	252199161	1.7859	36.623
chr10	135534747	294259465	2.1711	39.9948
chr11	135006516	315330332	2.3357	38.7247
chr12	133851895	288561220	2.1558	36.3873
chr13	115169878	177901808	1.5447	32.056
chr14	107349540	184309668	1.7169	30.8927
chr15	102531392	189873209	1.8519	29.0027
chr16	90354753	212750167	2.3546	62.1827
chr17	81195210	167776709	2.0663	34.573
chr18	78077248	161786659	2.0721	31.1401
chr19	59128983	102413905	1.732	28.5608
chr20	63025520	161680686	2.5653	34.0514
chr21	48129895	66426652	1.3802	27.9847
chr22	51304566	85517485	1.6669	52.5494
chrMT	16571	690	0.0416	0.3873
chrX	155270560	352295257	2.2689	33.6244
chrY	59373566	19756638	0.3328	59.9359

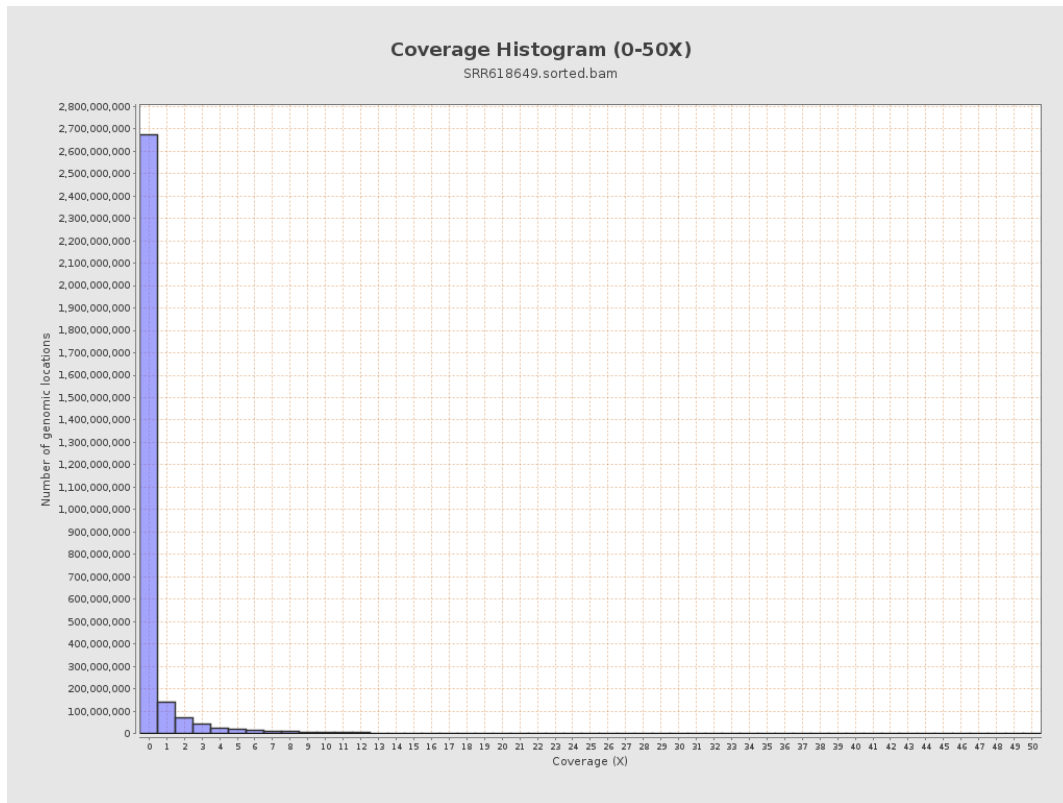
3. Results : Coverage across reference



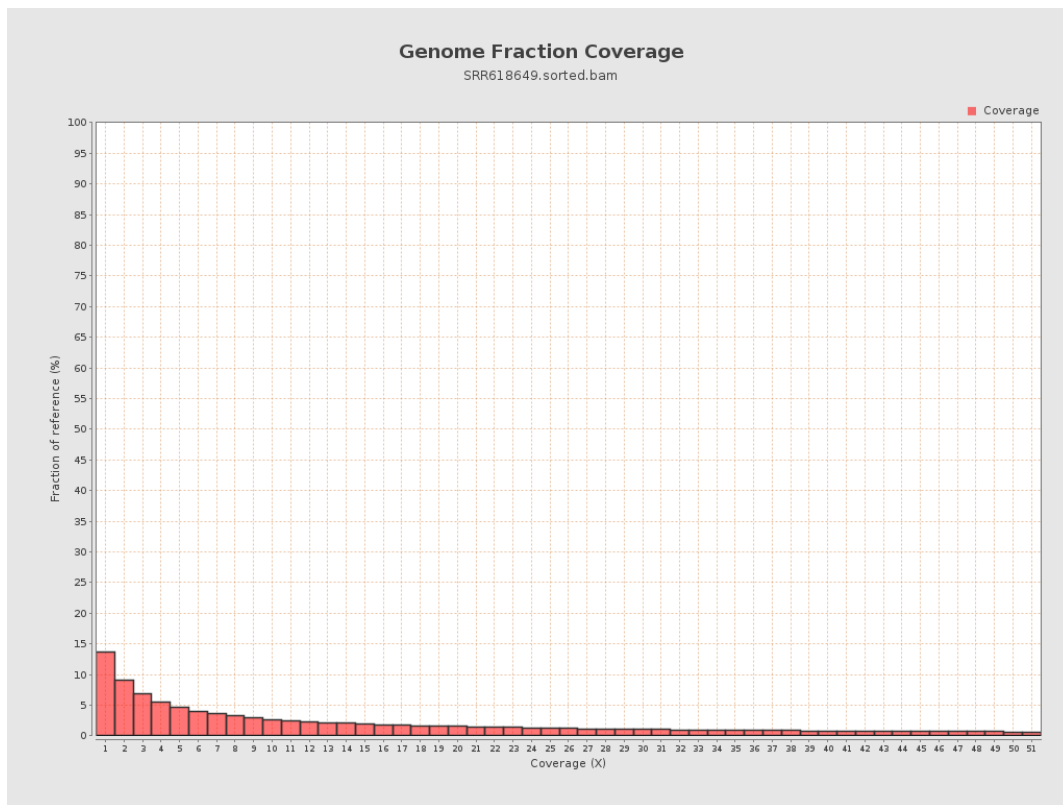
4. Results : Coverage Histogram



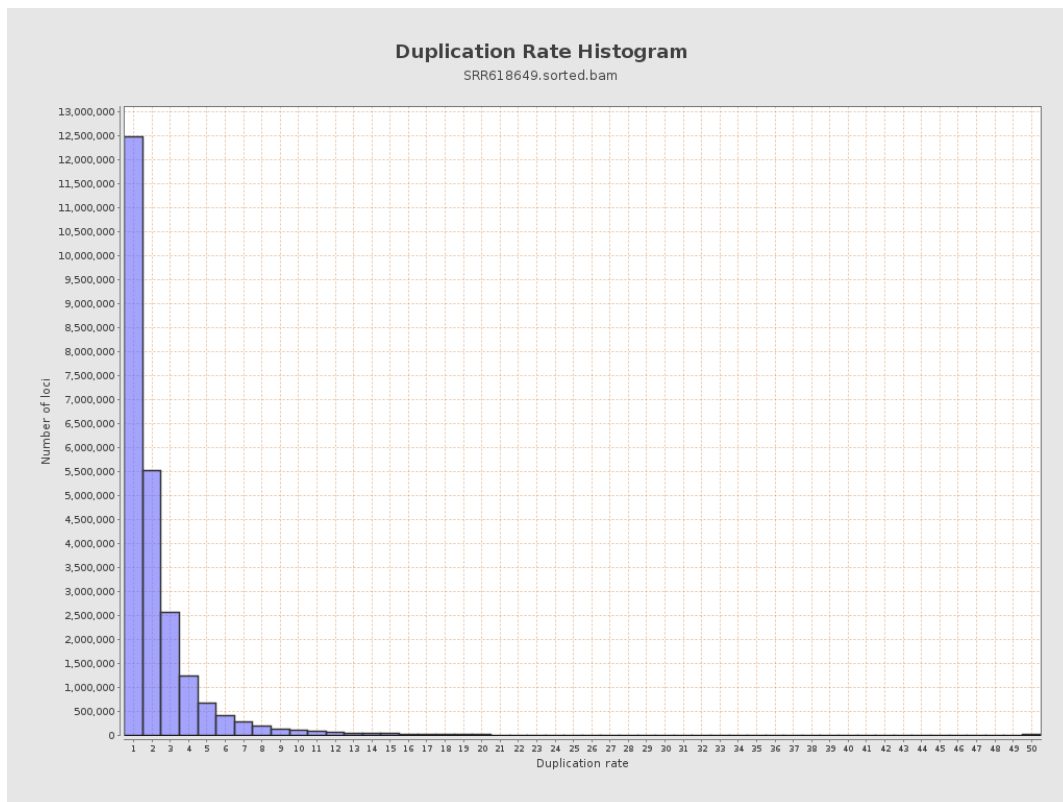
5. Results : Coverage Histogram (0-50X)



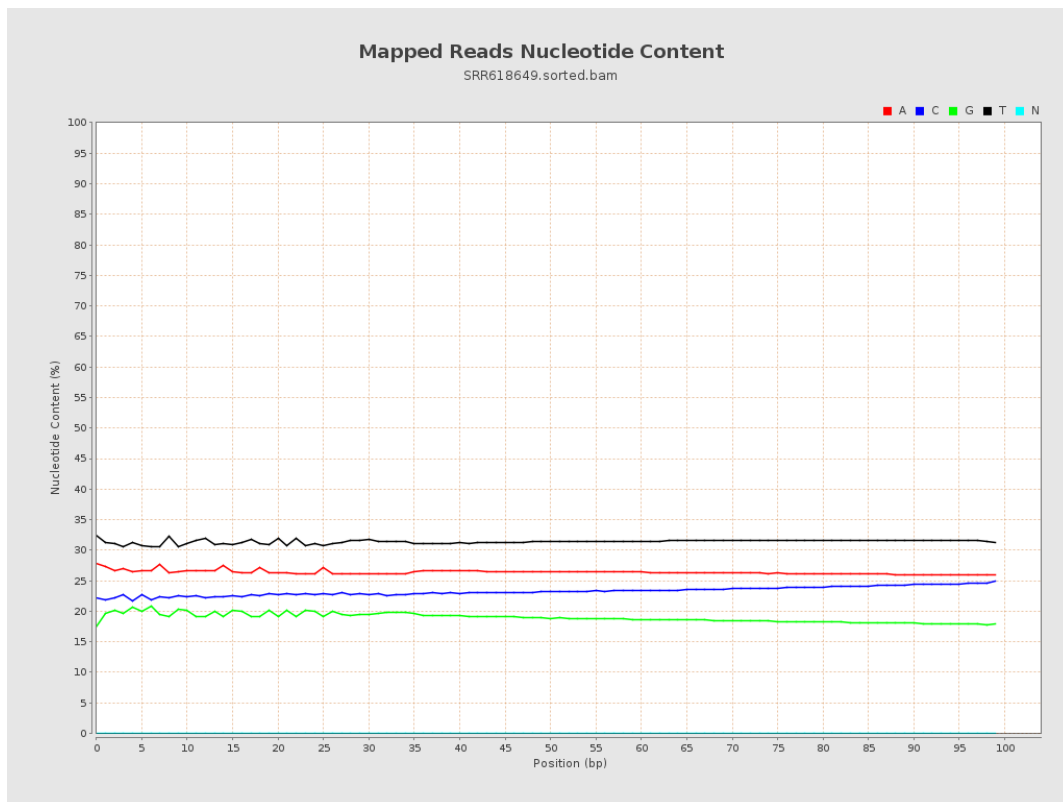
6. Results : Genome Fraction Coverage



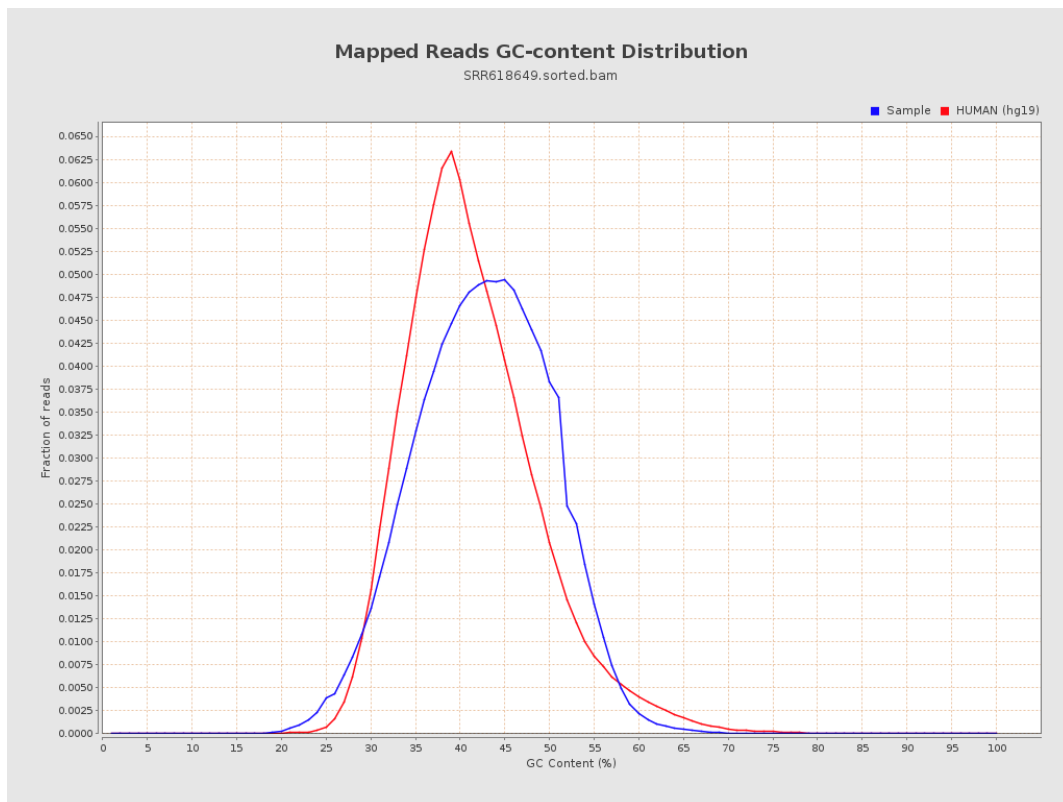
7. Results : Duplication Rate Histogram



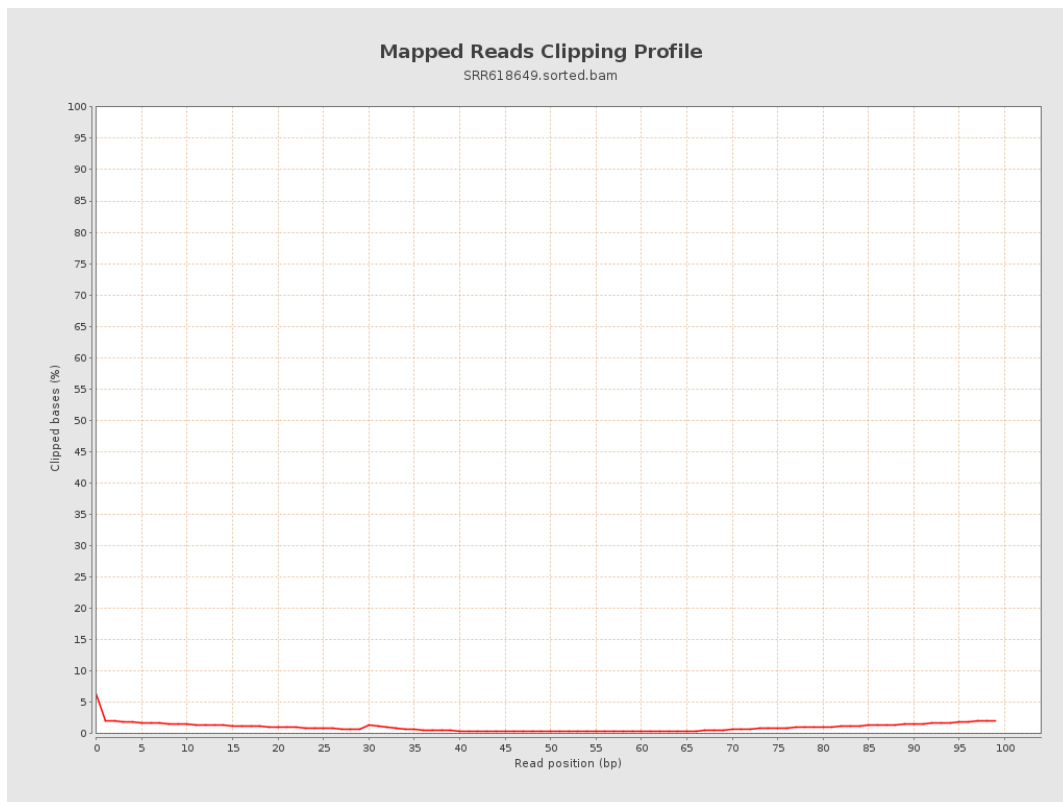
8. Results : Mapped Reads Nucleotide Content



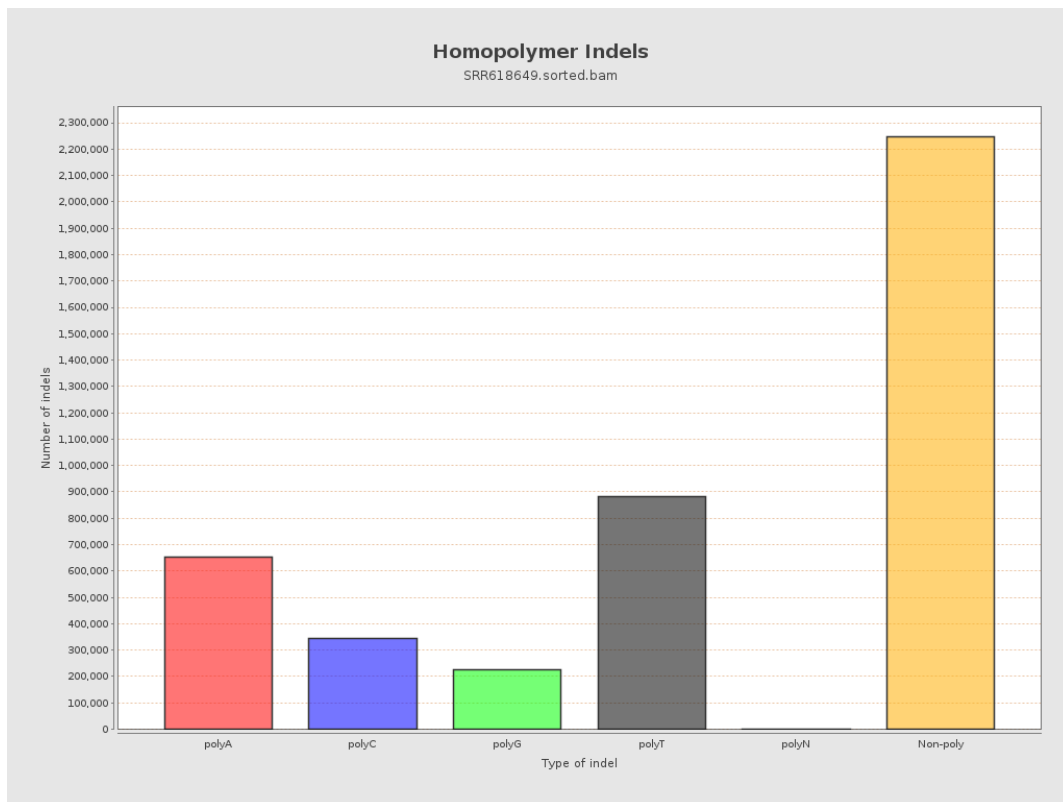
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

