

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 14:15:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618657.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_SRR618657 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618657.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 14:15:41 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618657.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	40,992,774
Mapped reads	38,957,036 / 95.03%
Unmapped reads	2,035,738 / 4.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	113,806 / 0.28%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	13,774,021 / 33.6%
Duplication rate	30.23%
Clipped reads	4,161,386 / 10.15%

2.2. ACGT Content

Number/percentage of A's	1,042,479,660 / 27.43%
Number/percentage of C's	833,692,951 / 21.93%
Number/percentage of T's	1,059,654,378 / 27.88%
Number/percentage of G's	827,566,547 / 21.77%
Number/percentage of N's	37,798,702 / 0.99%
GC Percentage	43.7%

2.3. Coverage

Mean	1.2287

Standard Deviation	4.5172
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2.4. Mapping Quality

Mean Mapping Quality	51.34
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2.5. Mismatches and indels

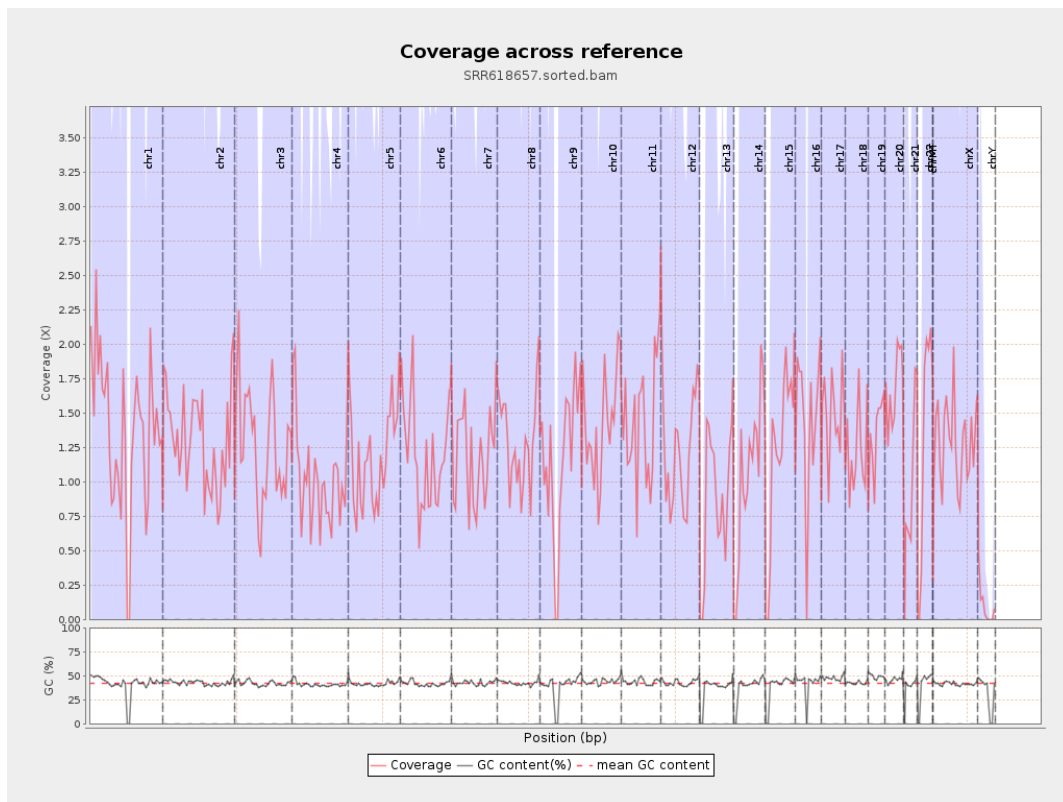
General error rate	1.97%
Mismatches	73,844,774
Insertions	685,712
Mapped reads with at least one insertion	1.74%
Deletions	1,890,984
Mapped reads with at least one deletion	4.74%
Homopolymer indels	53.36%

2.6. Chromosome stats

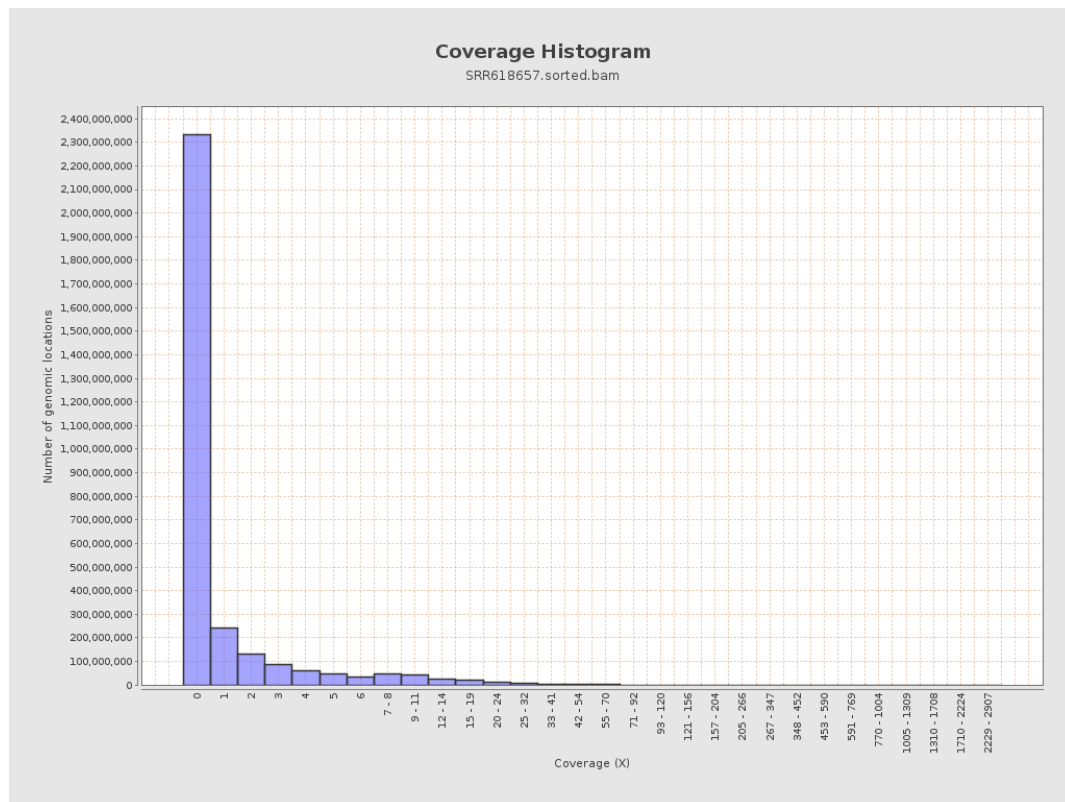
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	338833820	1.3594	5.4036
chr2	243199373	316676933	1.3021	4.8844
chr3	198022430	248579050	1.2553	3.9995
chr4	191154276	194562569	1.0178	3.8748
chr5	180915260	215359799	1.1904	3.8497
chr6	171115067	204915464	1.1975	3.9877
chr7	159138663	190933708	1.1998	4.2695

chr8	146364022	188469868	1.2877	4.2878
chr9	141213431	163581604	1.1584	4.623
chr10	135534747	192408580	1.4196	4.487
chr11	135006516	192643020	1.4269	5.3301
chr12	133851895	165843622	1.239	4.0671
chr13	115169878	101062167	0.8775	3.2135
chr14	107349540	114232497	1.0641	3.8107
chr15	102531392	124238190	1.2117	4.1807
chr16	90354753	129248209	1.4305	6.0101
chr17	81195210	121858655	1.5008	4.9843
chr18	78077248	93776537	1.2011	5.4314
chr19	59128983	78980263	1.3357	5.1069
chr20	63025520	106012982	1.6821	5.2137
chr21	48129895	47513291	0.9872	5.8999
chr22	51304566	67737683	1.3203	4.8278
chrMT	16571	4495	0.2713	1.1959
chrX	155270560	200640088	1.2922	4.1586
chrY	59373566	5678453	0.0956	1.7217

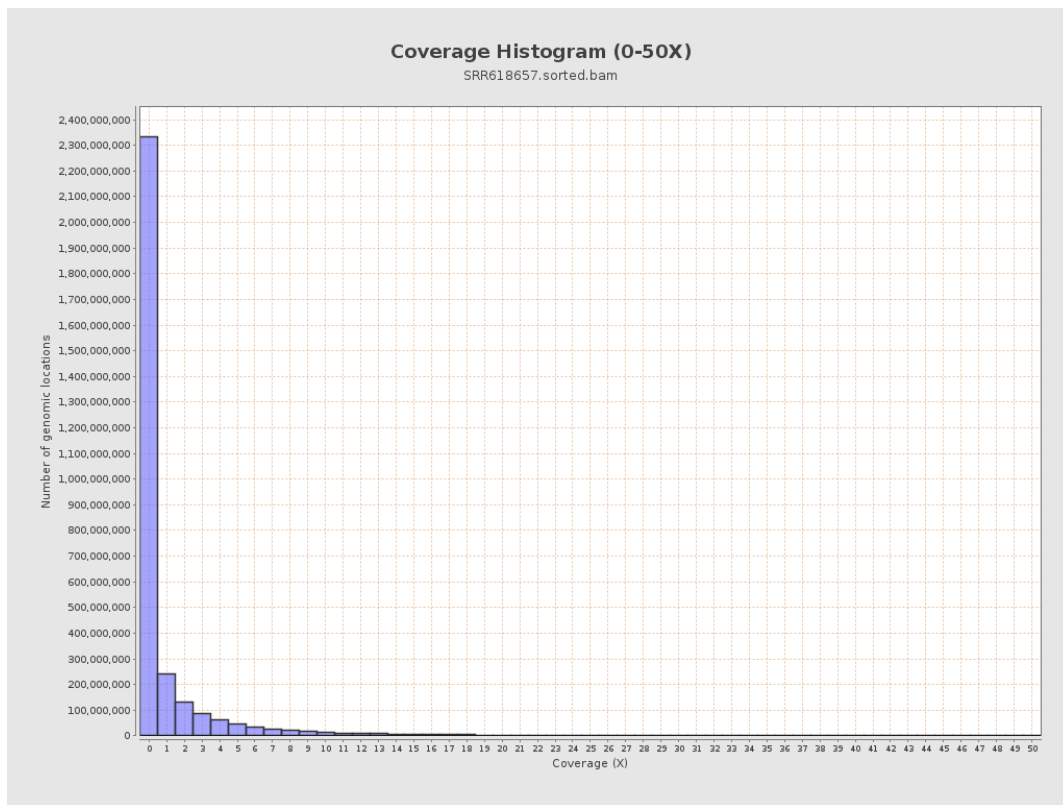
3. Results : Coverage across reference



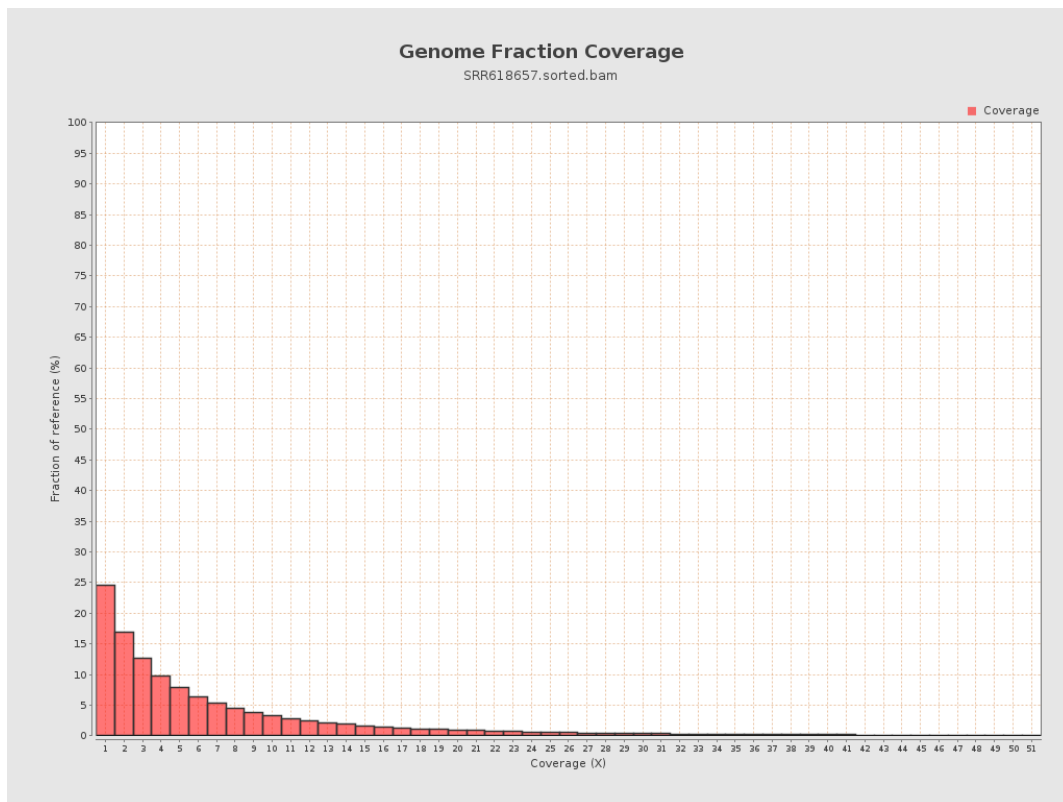
4. Results : Coverage Histogram



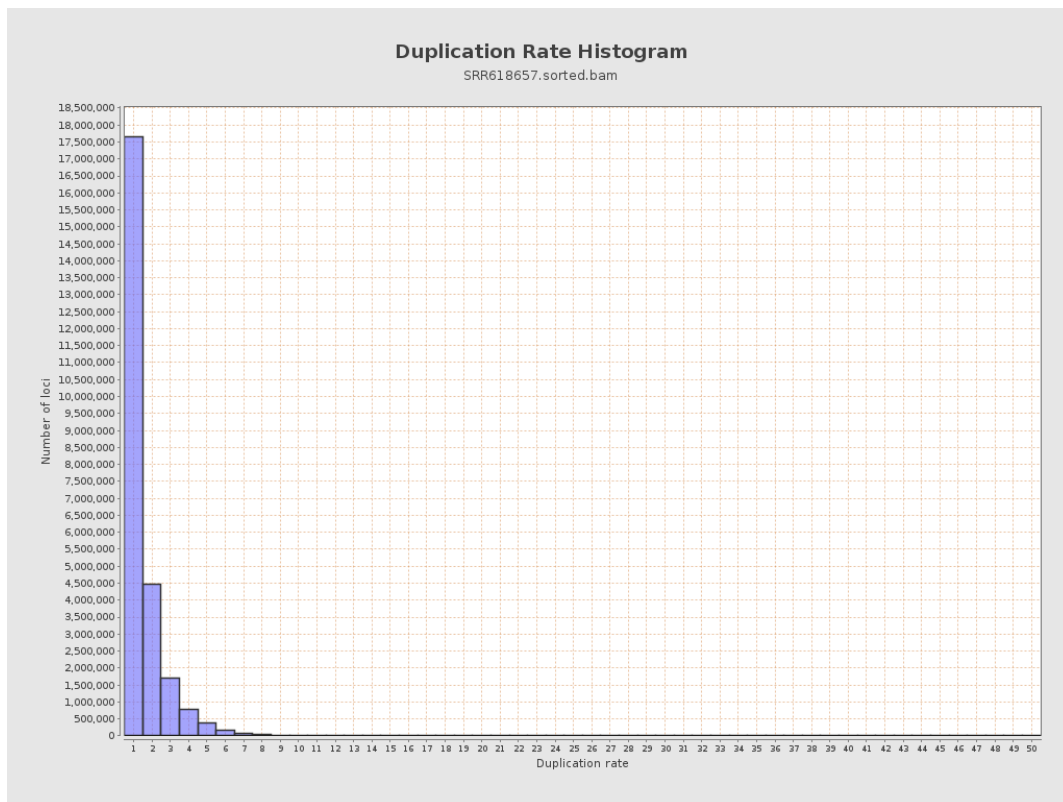
5. Results : Coverage Histogram (0-50X)



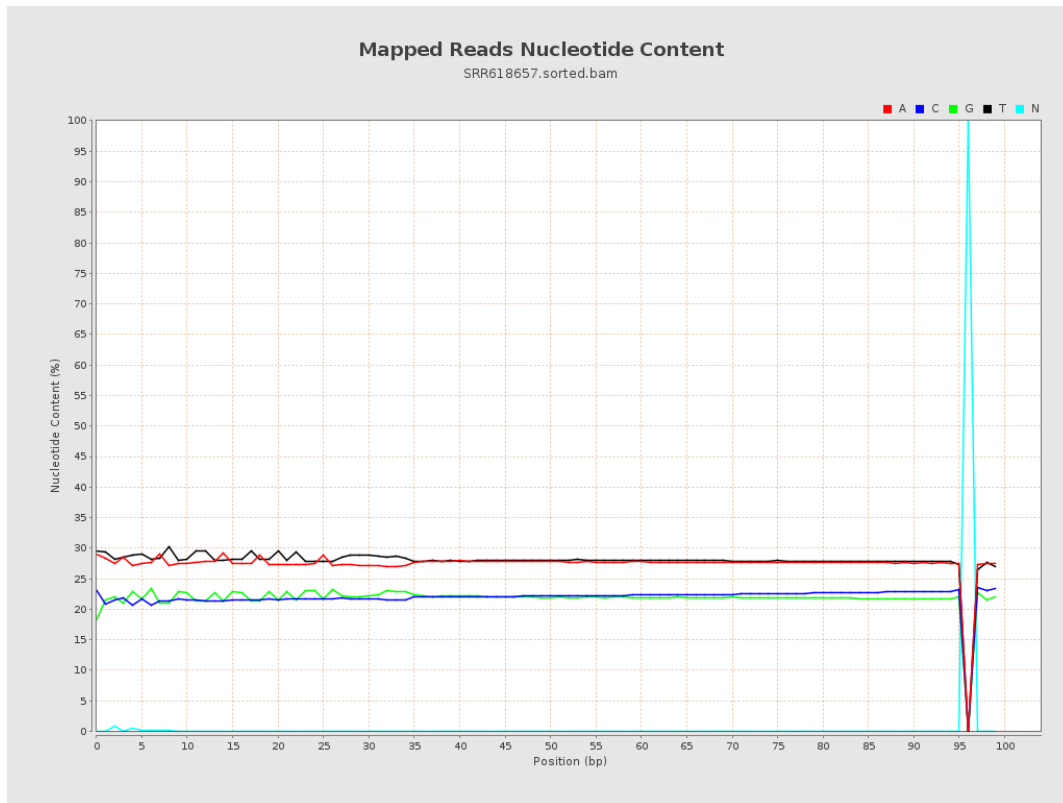
6. Results : Genome Fraction Coverage



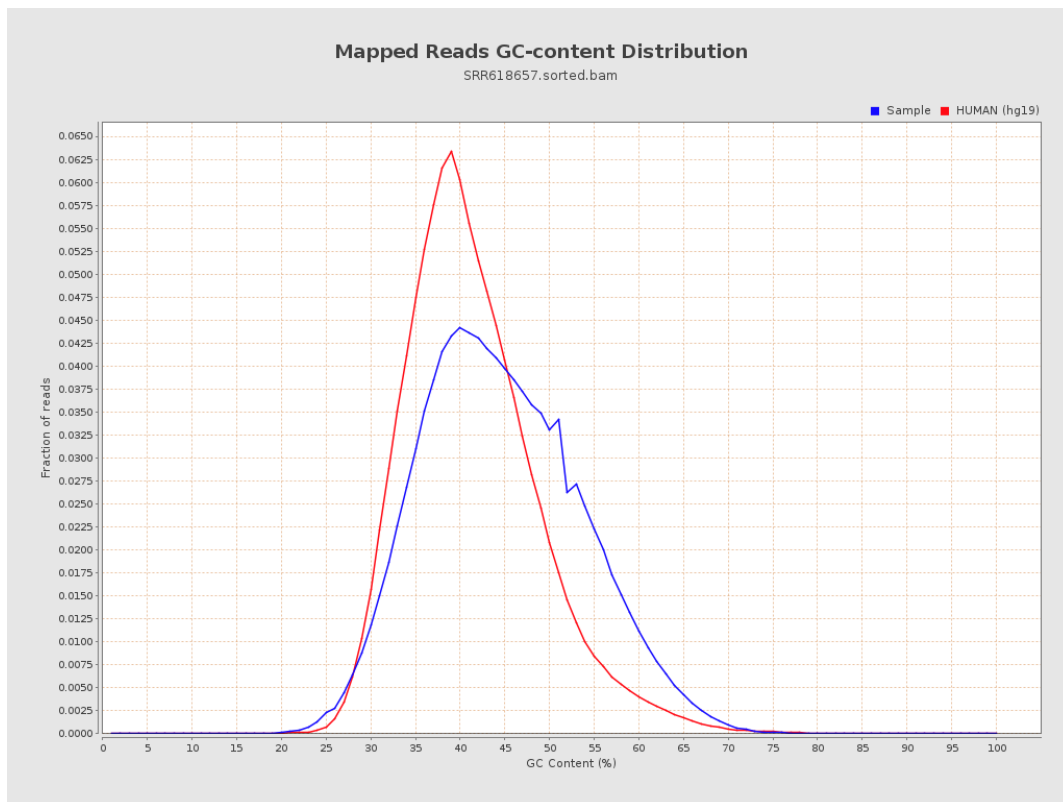
7. Results : Duplication Rate Histogram



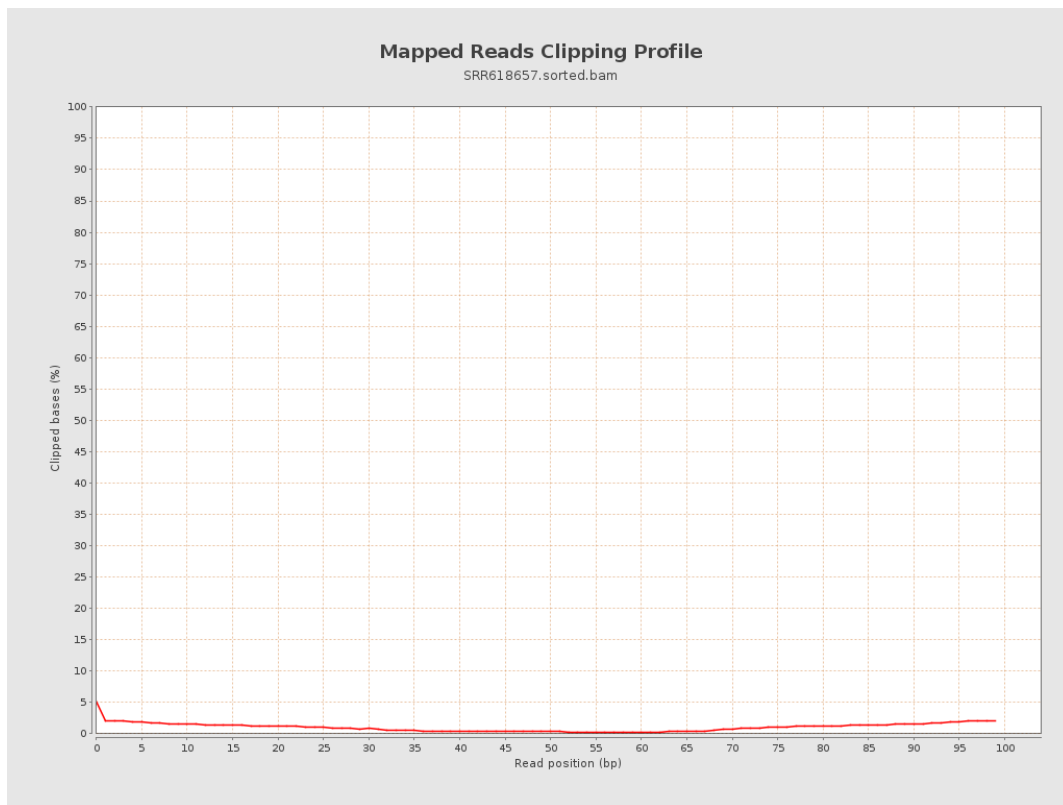
8. Results : Mapped Reads Nucleotide Content



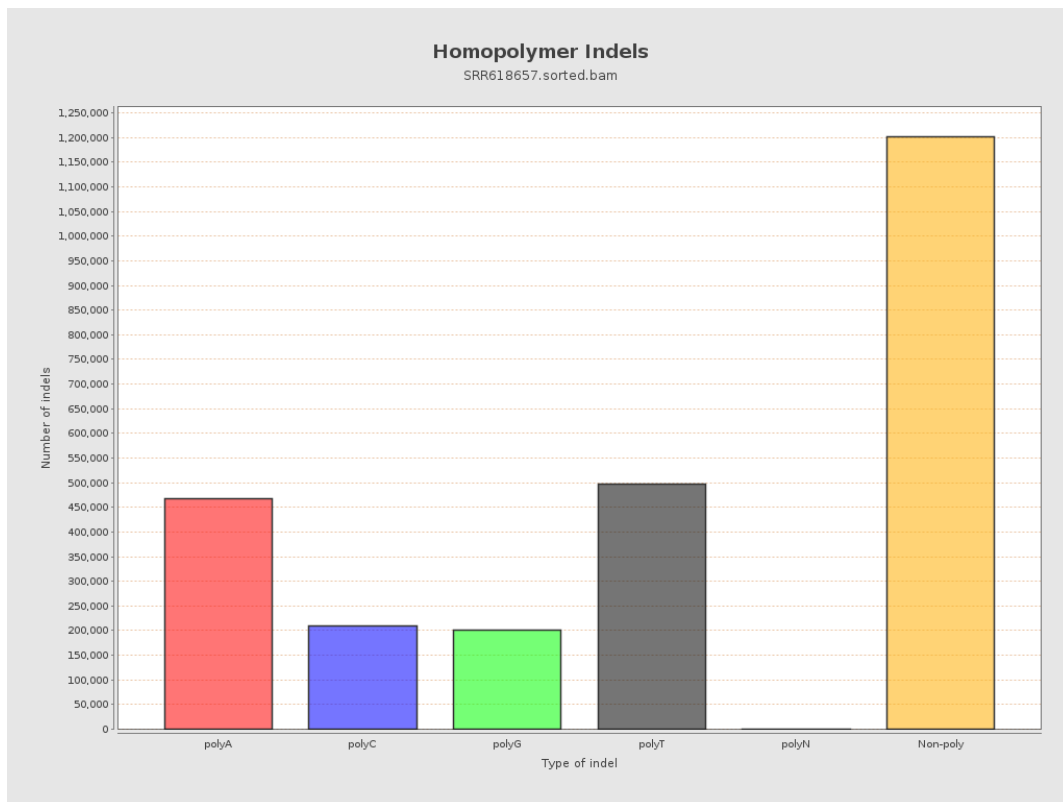
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

