Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 08:07:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618648.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_SRR618648 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618648.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 08:07:15 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618648.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	66,294,719
Mapped reads	64,674,658 / 97.56%
Unmapped reads	1,620,061 / 2.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	91,602 / 0.14%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	51,750,482 / 78.06%
Duplication rate	50.2%
Clipped reads	6,320,378 / 9.53%

2.2. ACGT Content

Number/percentage of A's	1,718,240,046 / 27.16%
Number/percentage of C's	1,452,270,795 / 22.96%
Number/percentage of T's	1,876,300,390 / 29.66%
Number/percentage of G's	1,278,186,990 / 20.2%
Number/percentage of N's	1,536,804 / 0.02%
GC Percentage	43.16%

2.3. Coverage

Mean	2.0449

Standard Deviation	49.3723

2.4. Mapping Quality

Mean Mapping Quality	50.13

2.5. Mismatches and indels

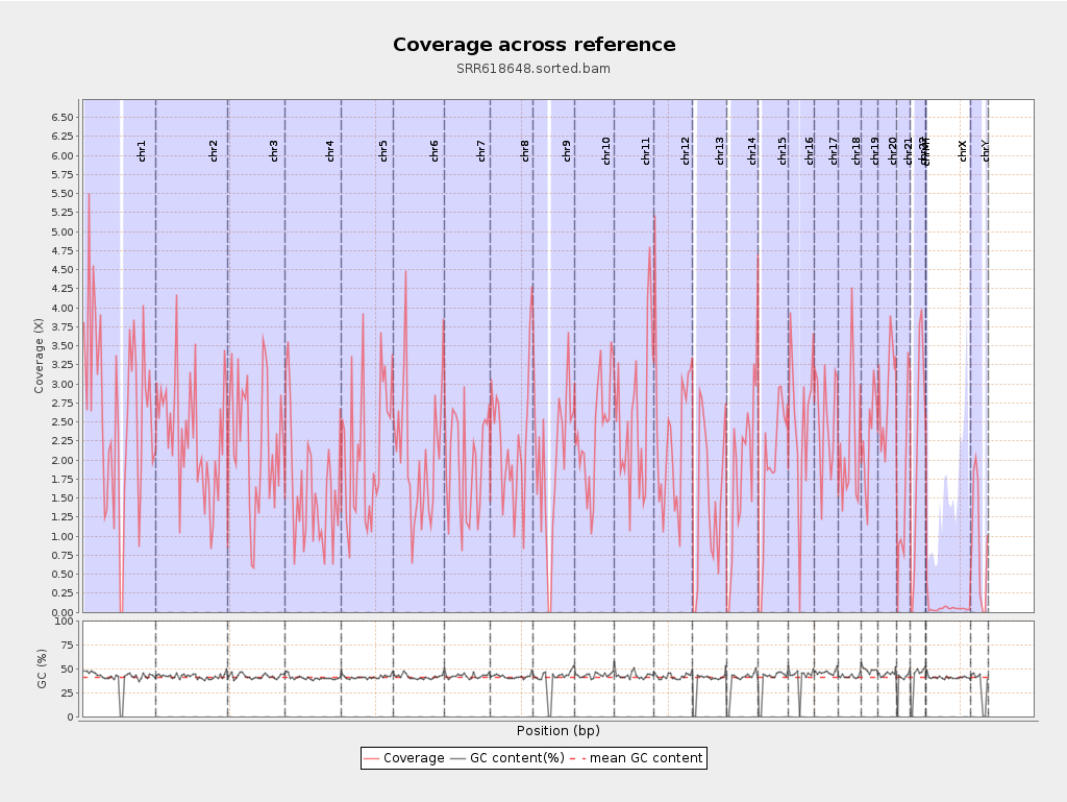
General error rate	0.8%
Mismatches	48,932,960
Insertions	1,011,028
Mapped reads with at least one insertion	1.54%
Deletions	2,610,799
Mapped reads with at least one deletion	3.95%
Homopolymer indels	52.25%

2.6. Chromosome stats

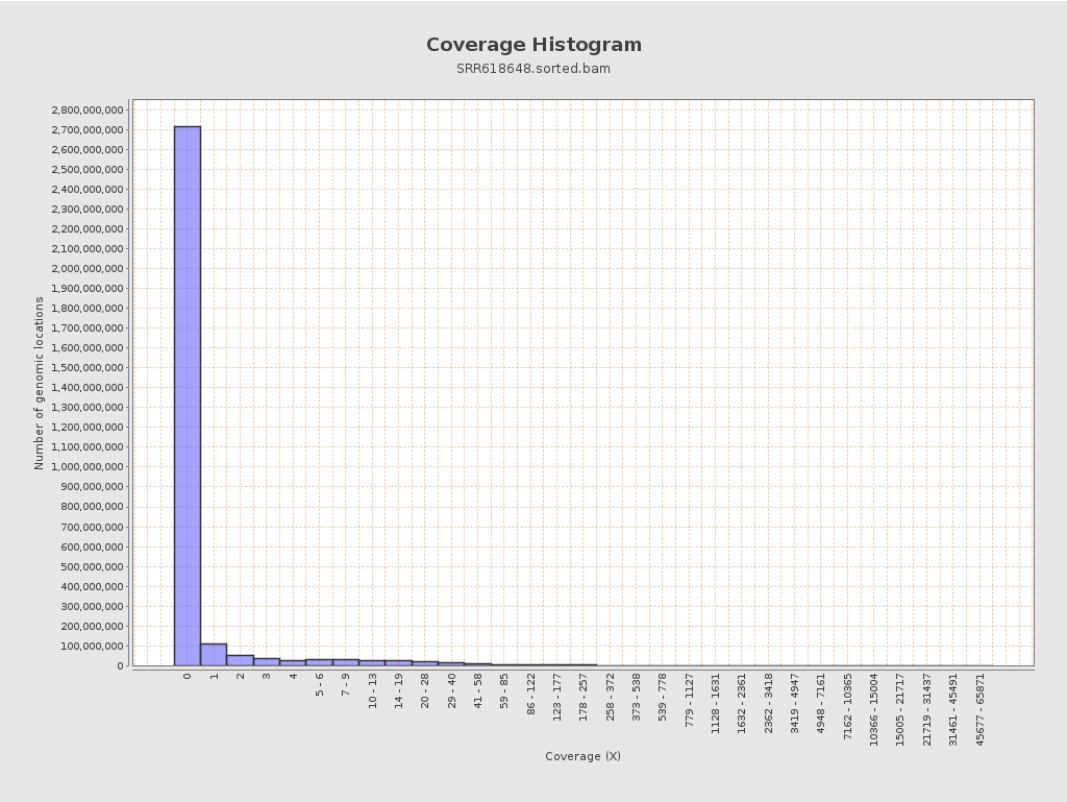
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	655457306	2.6297	76.9514
chr2	243199373	560258971	2.3037	56.0194
chr3	198022430	438238719	2.2131	53.9343
chr4	191154276	310128865	1.6224	37.5015
chr5	180915260	388817345	2.1492	63.7273
chr6	171115067	350918818	2.0508	41.112
chr7	159138663	313575573	1.9705	38.9817

chr8	146364022	328617736	2.2452	53.0916
chr9	141213431	278825240	1.9745	46.1227
chr10	135534747	314682105	2.3218	49.713
chr11	135006516	341966280	2.533	58.2954
chr12	133851895	312640345	2.3357	55.1161
chr13	115169878	171653647	1.4904	34.153
chr14	107349540	196924792	1.8344	42.9383
chr15	102531392	192355209	1.8761	31.9682
chr16	90354753	226599097	2.5079	43.0148
chr17	81195210	204615831	2.52	42.473
chr18	78077248	168863584	2.1628	44.8567
chr19	59128983	134154033	2.2688	34.9211
chr20	63025520	182396038	2.894	46.789
chr21	48129895	78813949	1.6375	29.9079
chr22	51304566	111700154	2.1772	40.8877
chrMT	16571	43107	2.6014	13.7599
chrX	155270560	10558861	0.068	4.7192
chrY	59373566	57563428	0.9695	23.1648

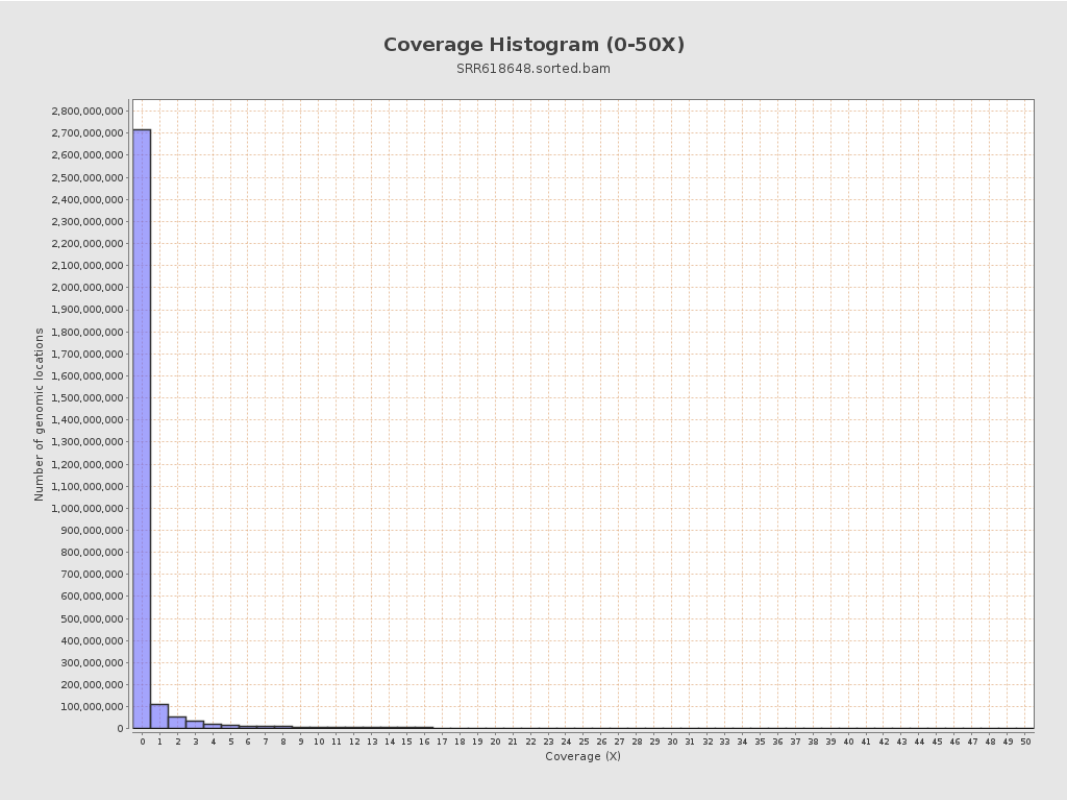
3. Results : Coverage across reference



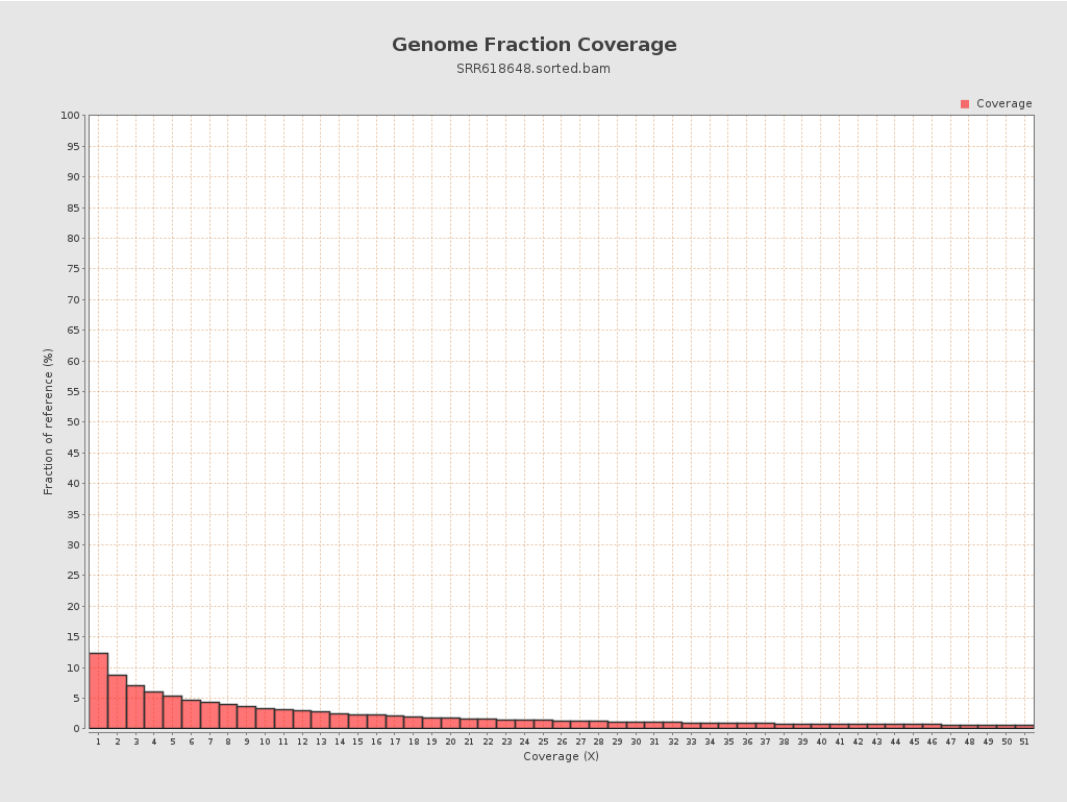
4. Results : Coverage Histogram



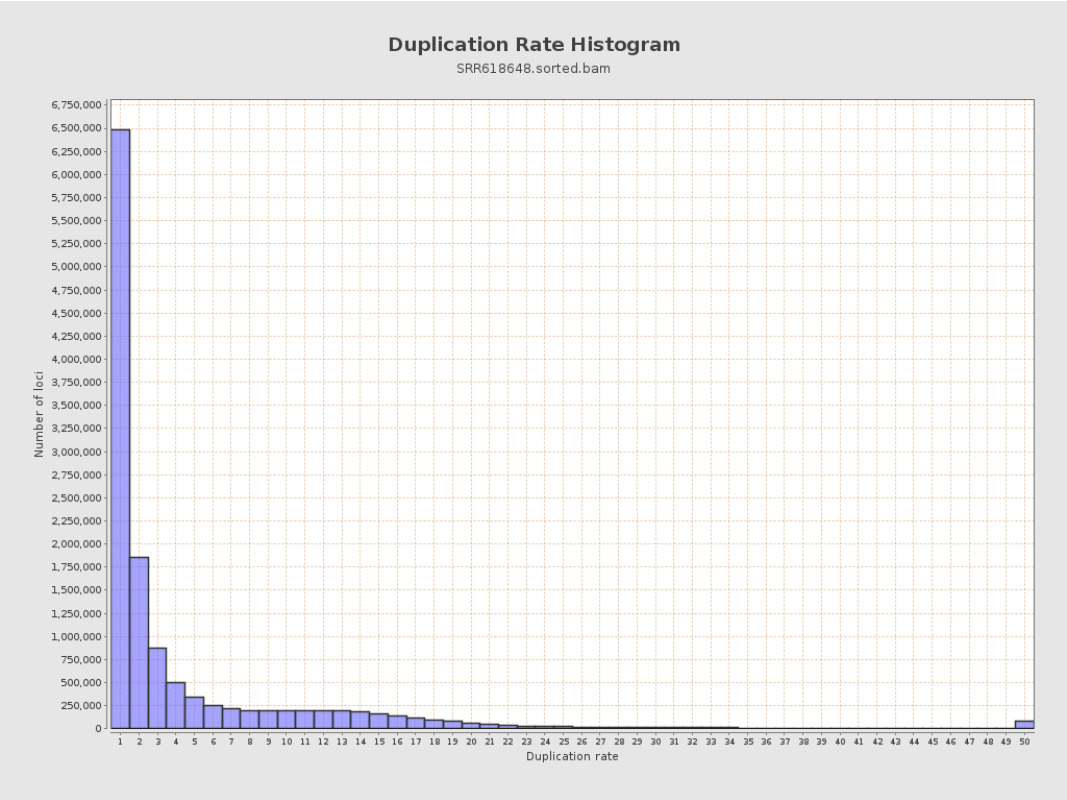
5. Results : Coverage Histogram (0-50X)



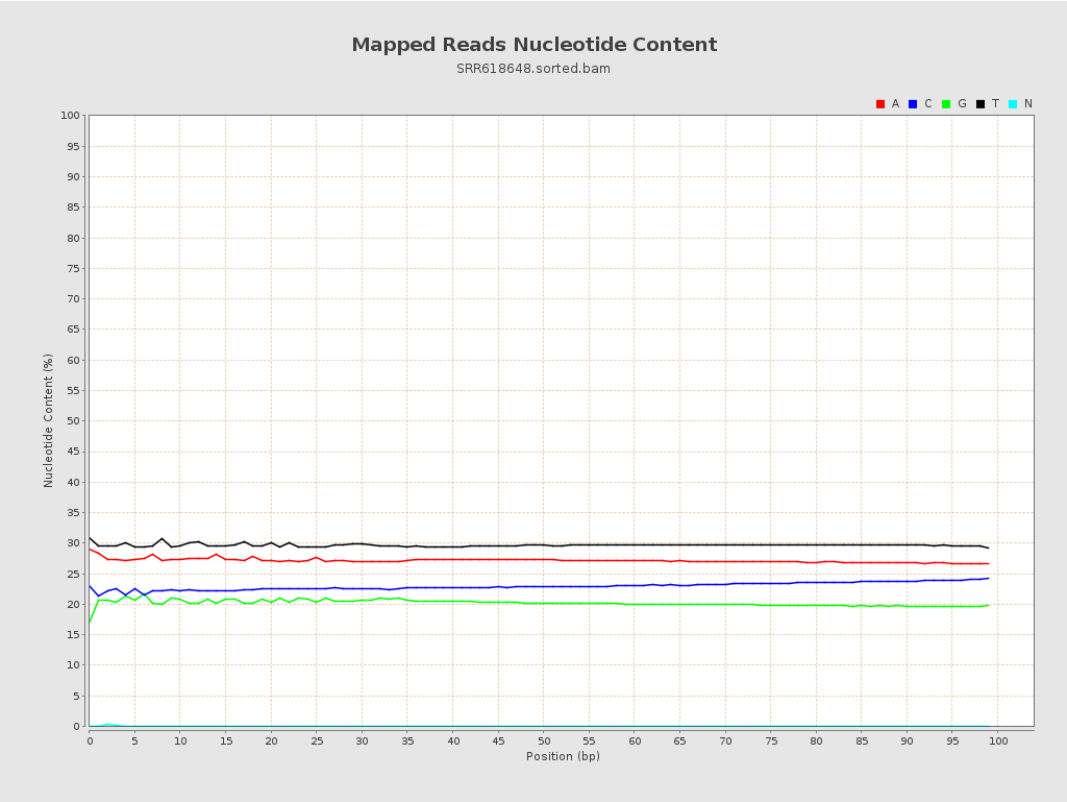
6. Results : Genome Fraction Coverage



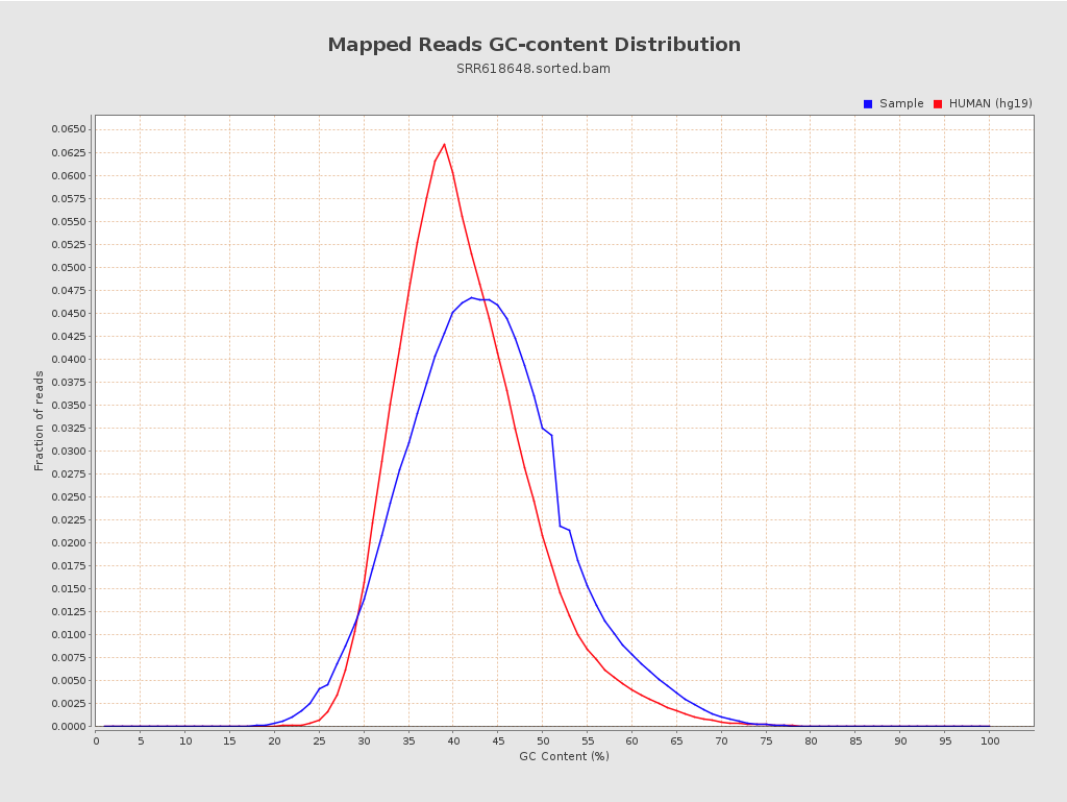
7. Results : Duplication Rate Histogram



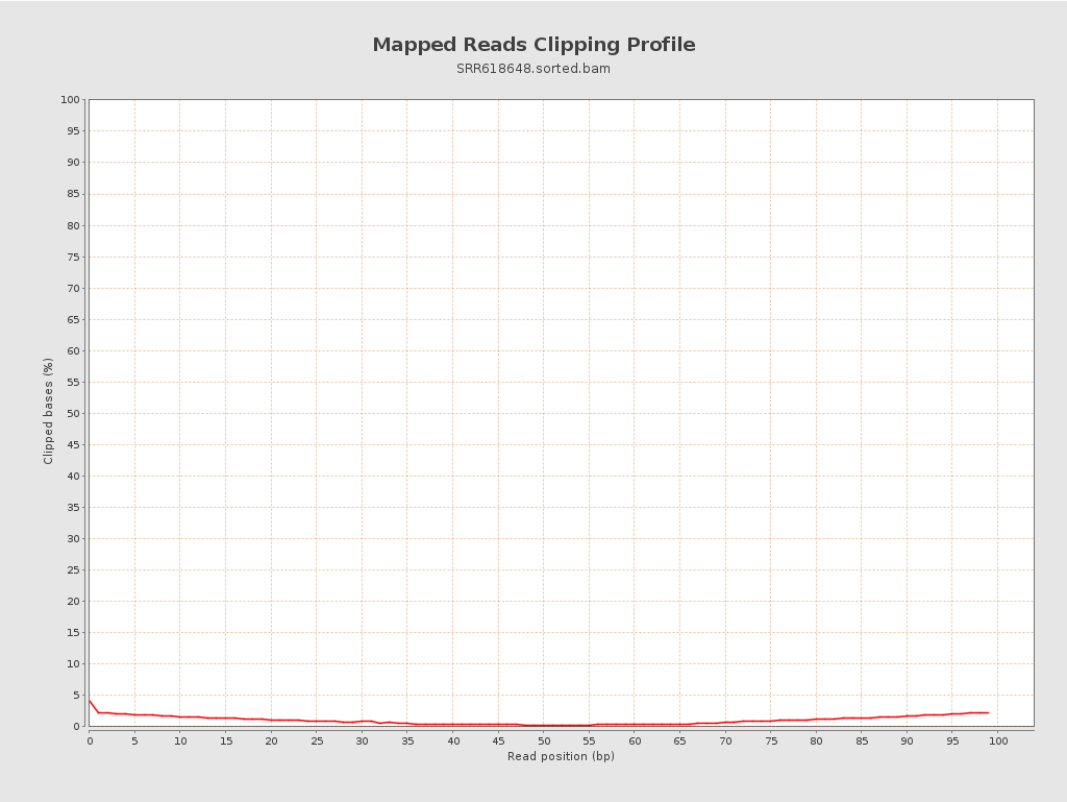
8. Results : Mapped Reads Nucleotide Content



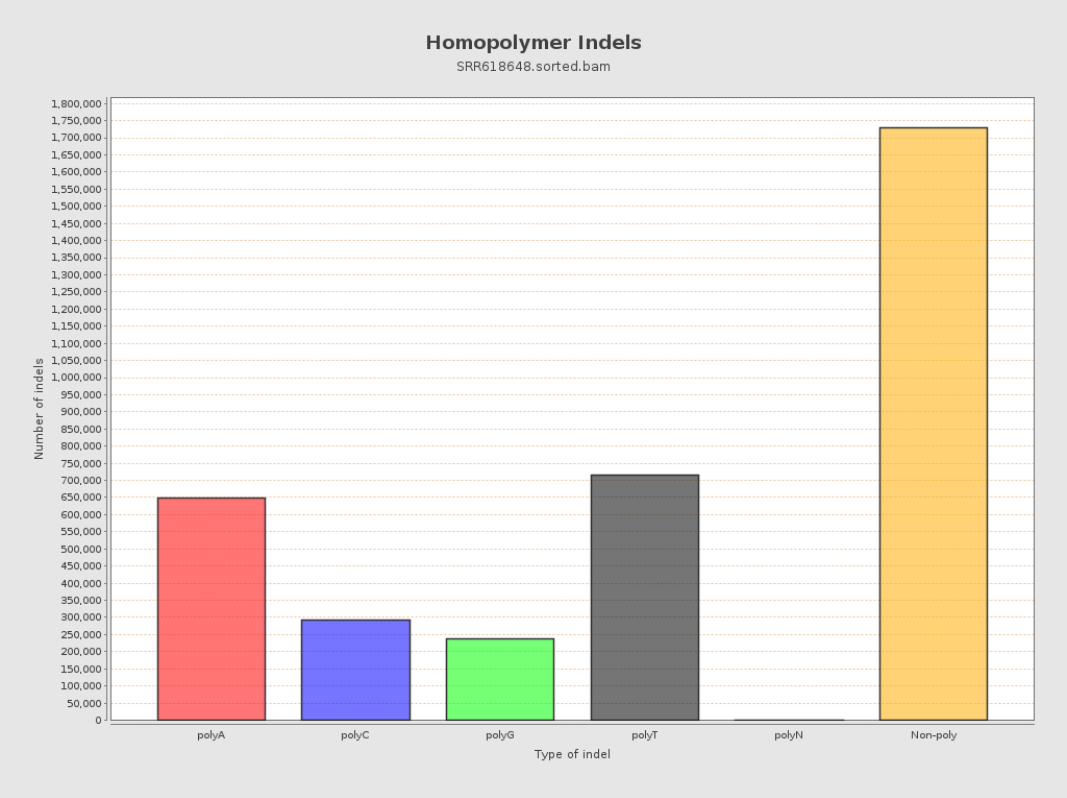
9. Results : Mapped Reads GC-content Distribution



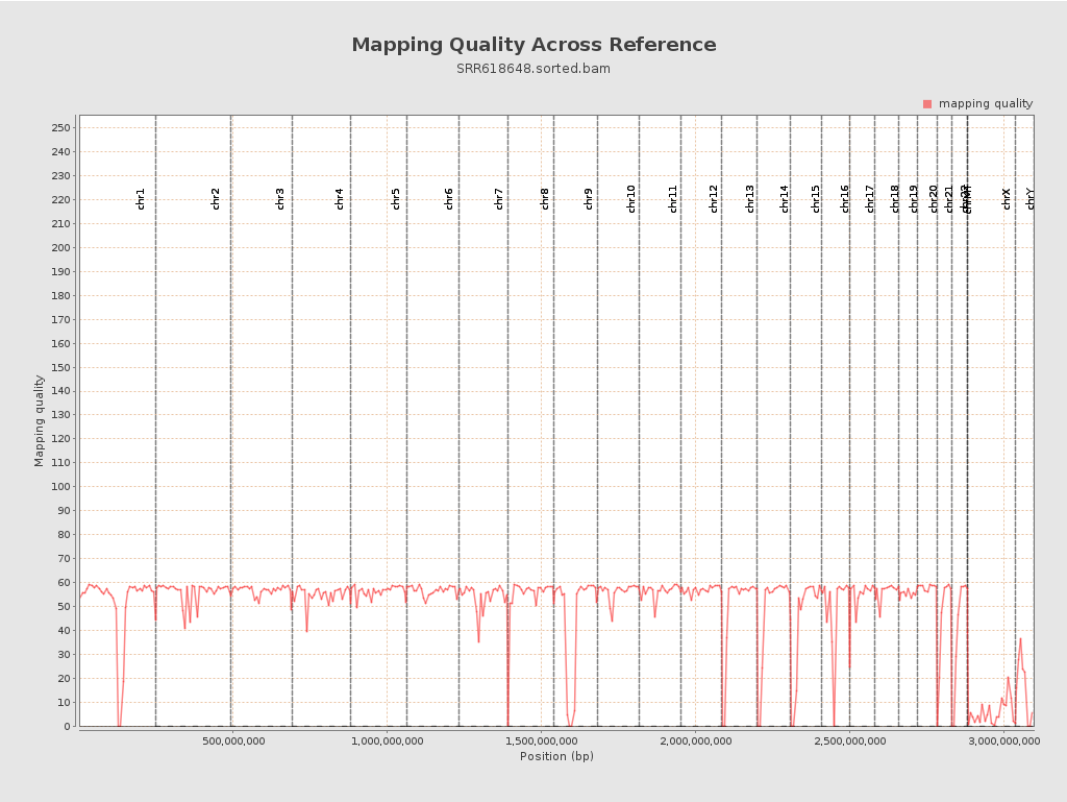
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram