Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 21:13:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238544.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_SRR6238544 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238544.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 21:13:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238544.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,231,941
Mapped reads	3,853,274 / 91.05%
Unmapped reads	378,667 / 8.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,671 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	843,605 / 19.93%
Duplication rate	17.31%
Clipped reads	2,393,015 / 56.55%

2.2. ACGT Content

Number/percentage of A's	59,983,189 / 25.04%
Number/percentage of C's	42,723,307 / 17.84%
Number/percentage of T's	79,604,269 / 33.23%
Number/percentage of G's	57,206,282 / 23.88%
Number/percentage of N's	16,930 / 0.01%
GC Percentage	41.72%

2.3. Coverage

Mean	0.0774

Standard Deviation	0.9826

2.4. Mapping Quality

Mean Mapping Quality	43.22

2.5. Mismatches and indels

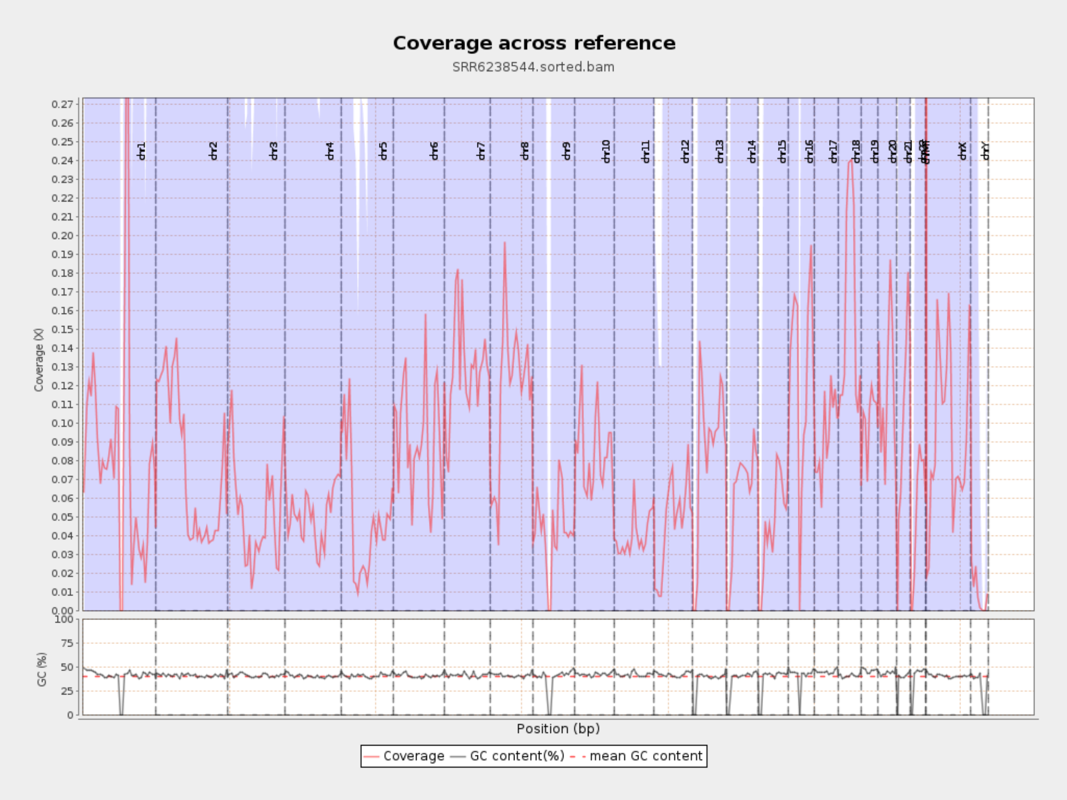
General error rate	0.61%
Mismatches	1,423,518
Insertions	15,480
Mapped reads with at least one insertion	0.4%
Deletions	79,991
Mapped reads with at least one deletion	2.05%
Homopolymer indels	40.93%

2.6. Chromosome stats

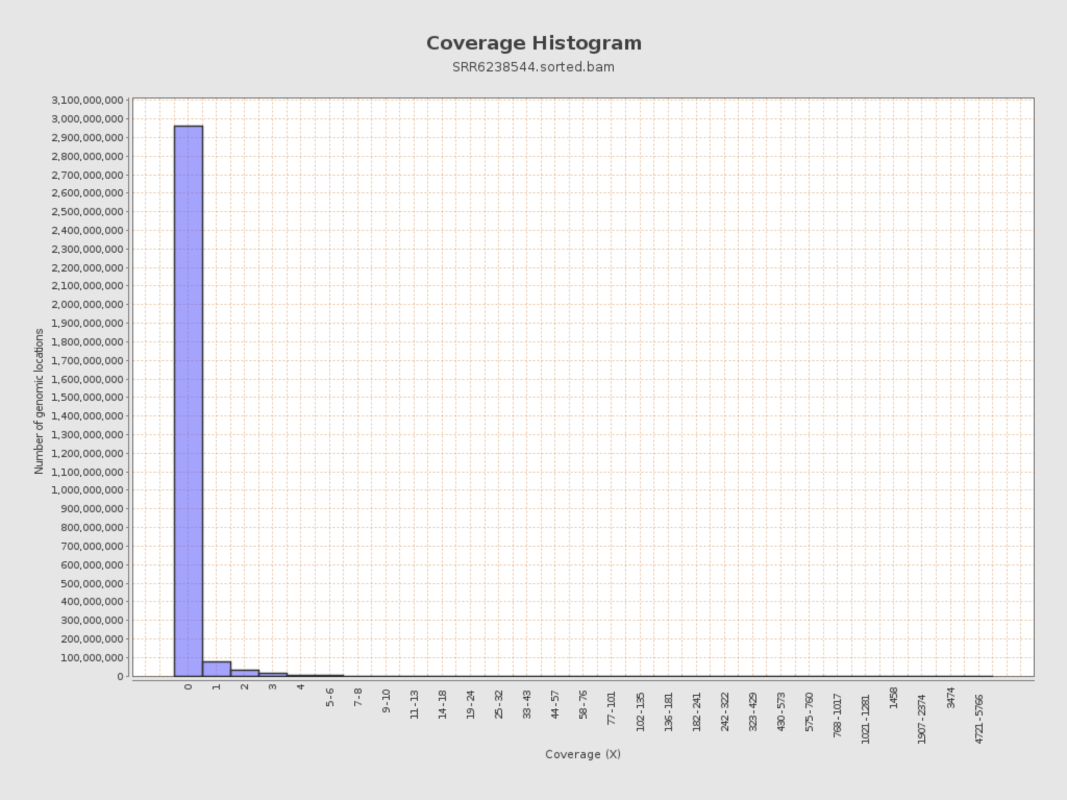
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20430594	0.082	0.822
chr2	243199373	19003831	0.0781	2.5339
chr3	198022430	10383663	0.0524	0.3948
chr4	191154276	9743151	0.051	0.3733
chr5	180915260	8714581	0.0482	0.3741
chr6	171115067	15554562	0.0909	0.9193
chr7	159138663	20518186	0.1289	1.3099

chr8	146364022	17195604	0.1175	0.8798
chr9	141213431	6027988	0.0427	0.448
chr10	135534747	11555415	0.0853	0.5116
chr11	135006516	5363219	0.0397	0.343
chr12	133851895	6267005	0.0468	0.3655
chr13	115169878	10042704	0.0872	0.6749
chr14	107349540	6675163	0.0622	0.4232
chr15	102531392	4637191	0.0452	0.6002
chr16	90354753	11060211	0.1224	0.6234
chr17	81195210	7557867	0.0931	0.5044
chr18	78077248	12478652	0.1598	1.8076
chr19	59128983	6025086	0.1019	0.7121
chr20	63025520	7364070	0.1168	0.5858
chr21	48129895	4927555	0.1024	0.5445
chr22	51304566	2743700	0.0535	0.3722
chrMT	16571	40748	2.459	3.0657
chrX	155270560	14806802	0.0954	0.538
chrY	59373566	551588	0.0093	0.3469

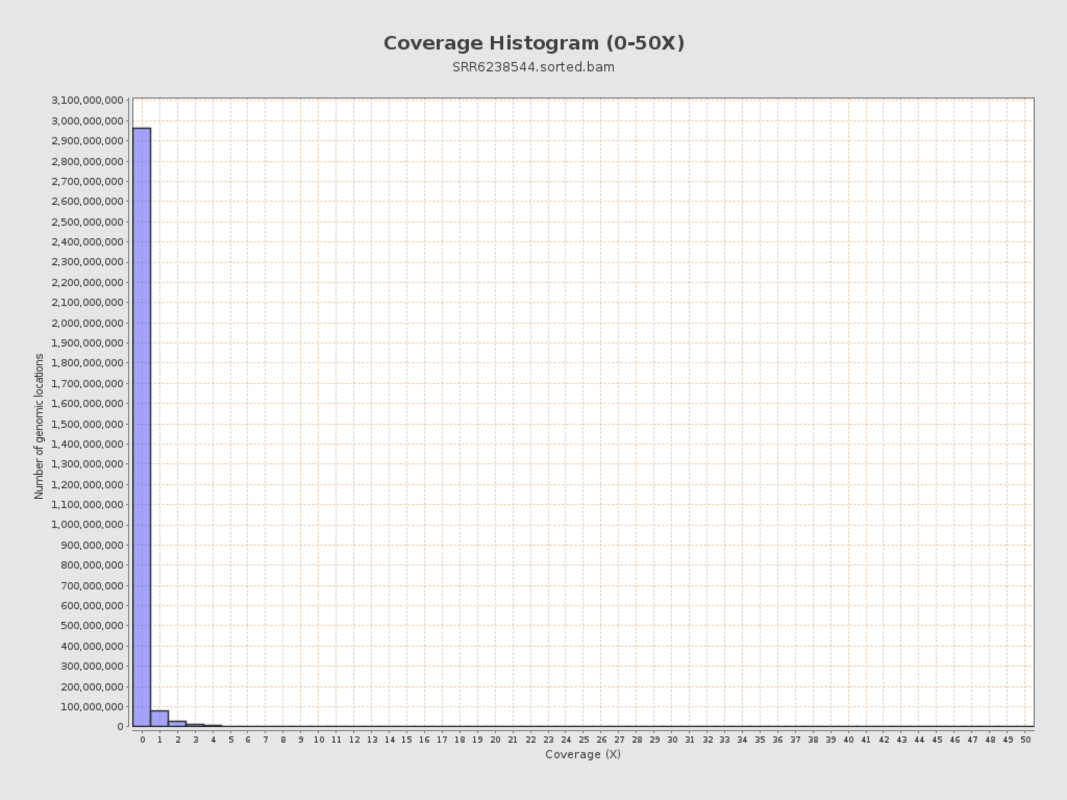
3. Results : Coverage across reference



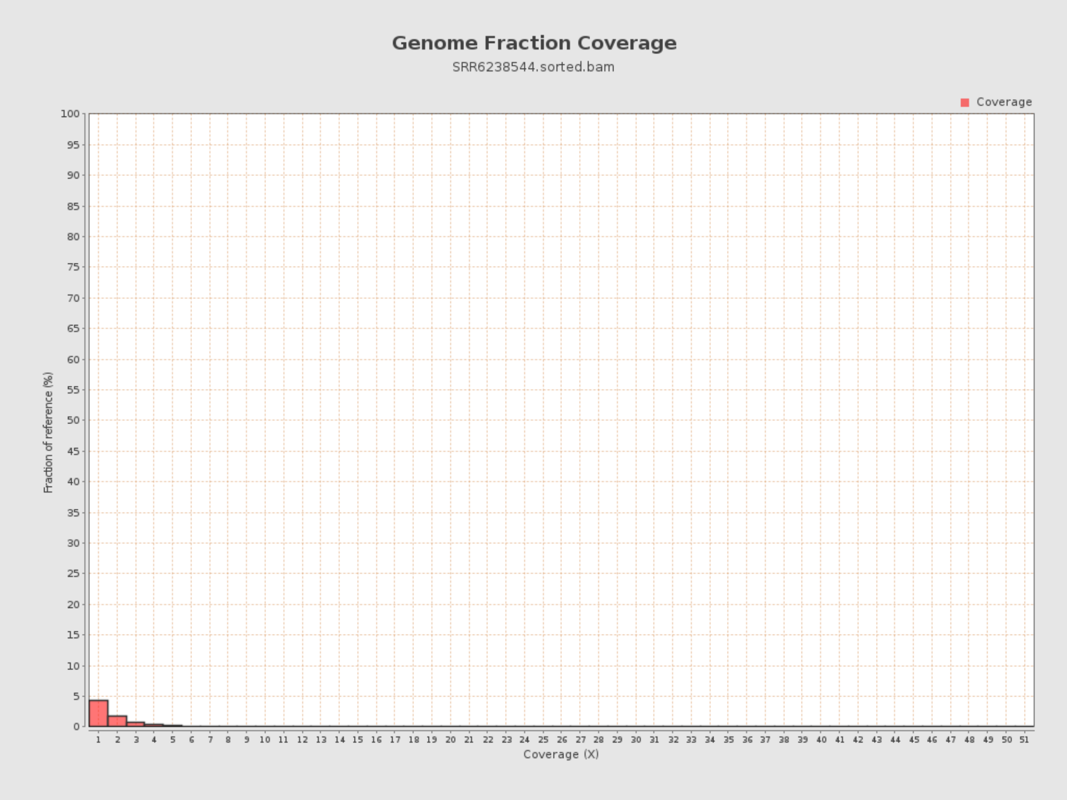
4. Results : Coverage Histogram



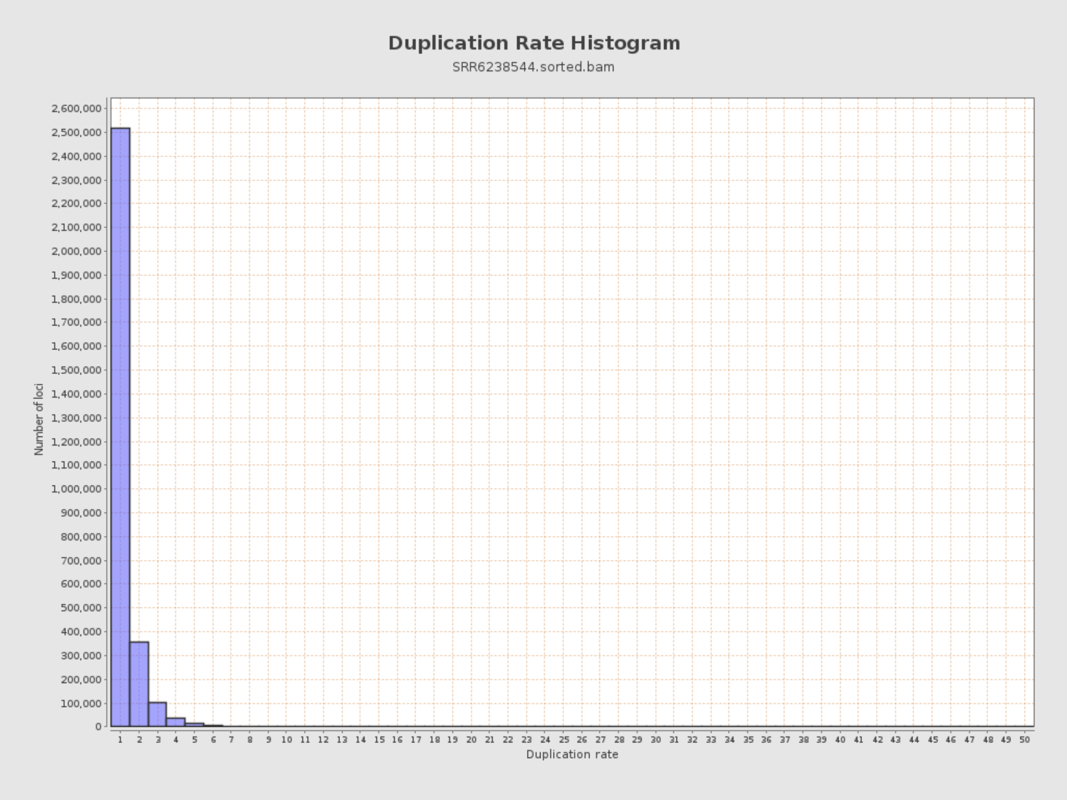
5. Results : Coverage Histogram (0-50X)



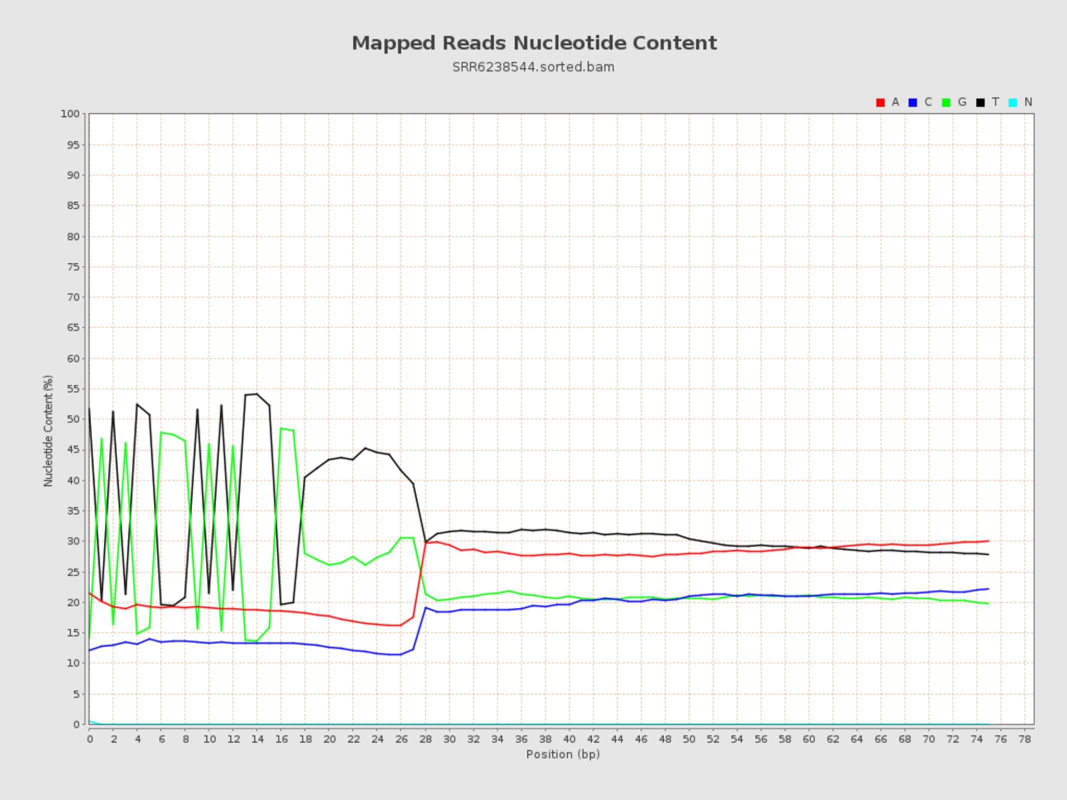
6. Results : Genome Fraction Coverage



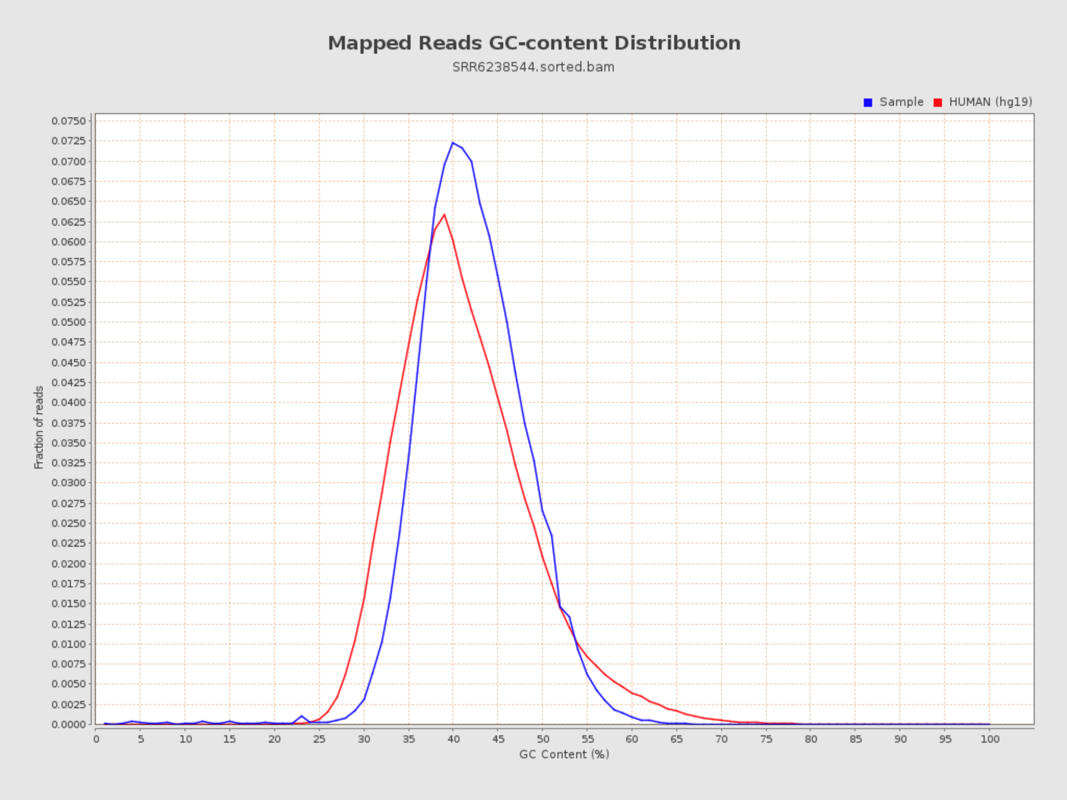
7. Results : Duplication Rate Histogram



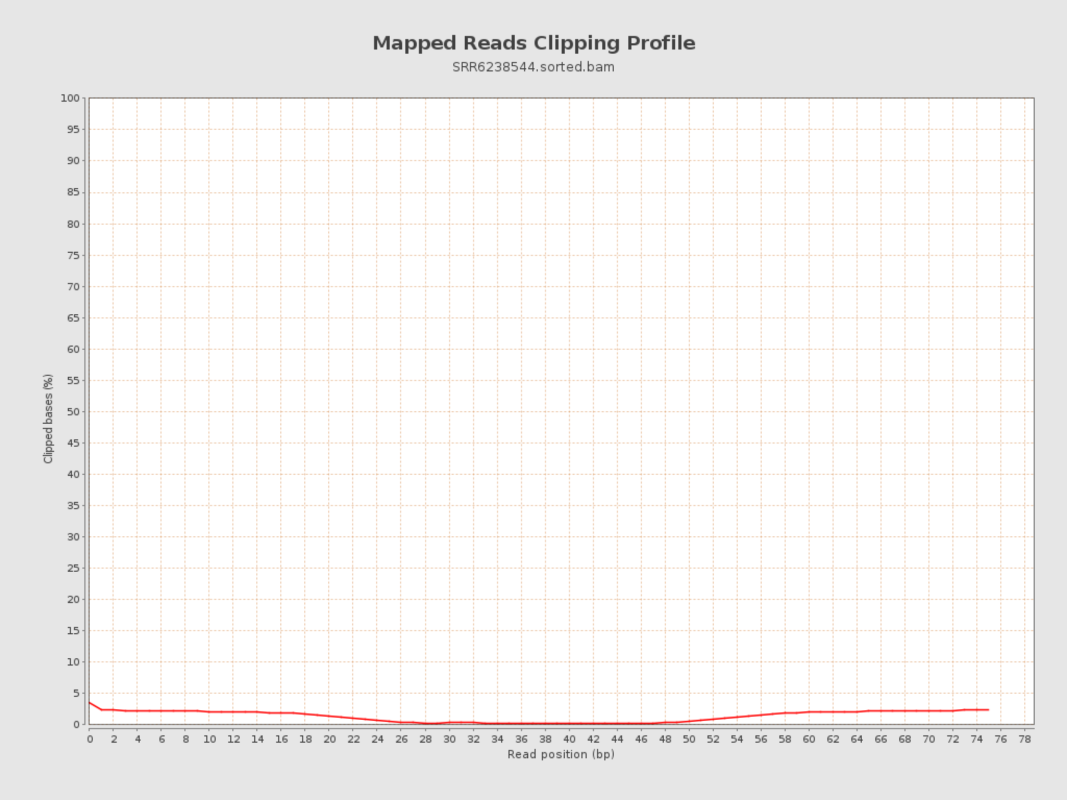
8. Results : Mapped Reads Nucleotide Content



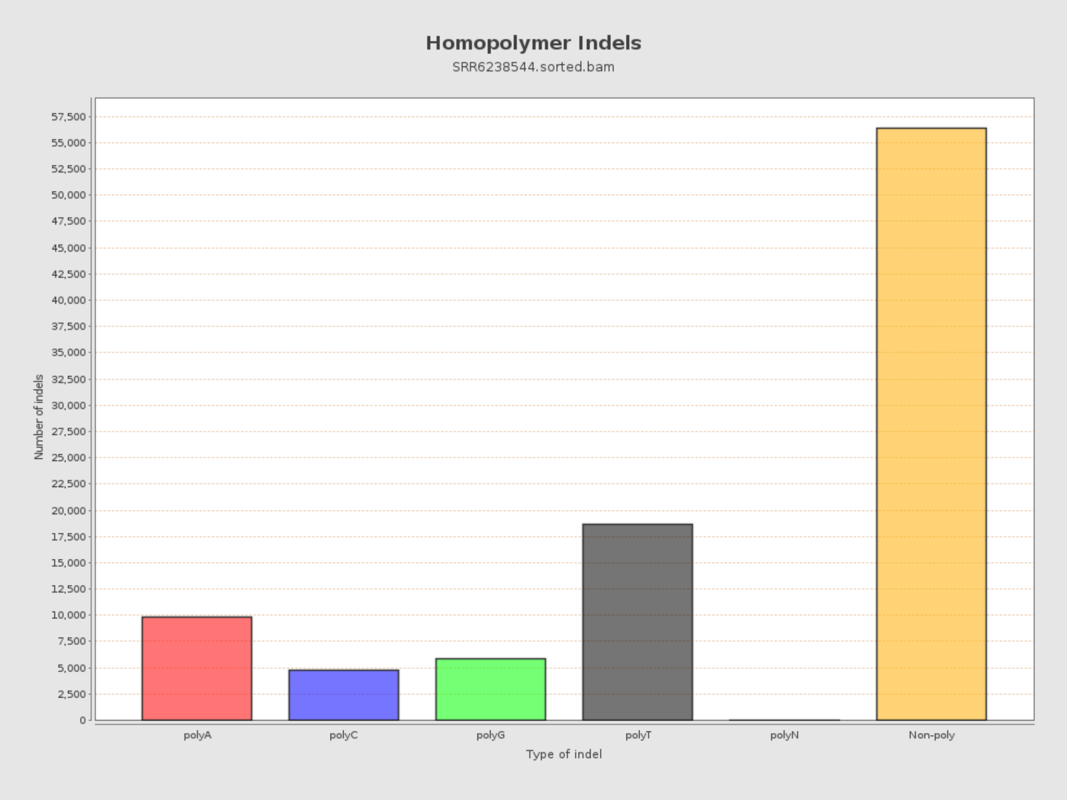
9. Results : Mapped Reads GC-content Distribution



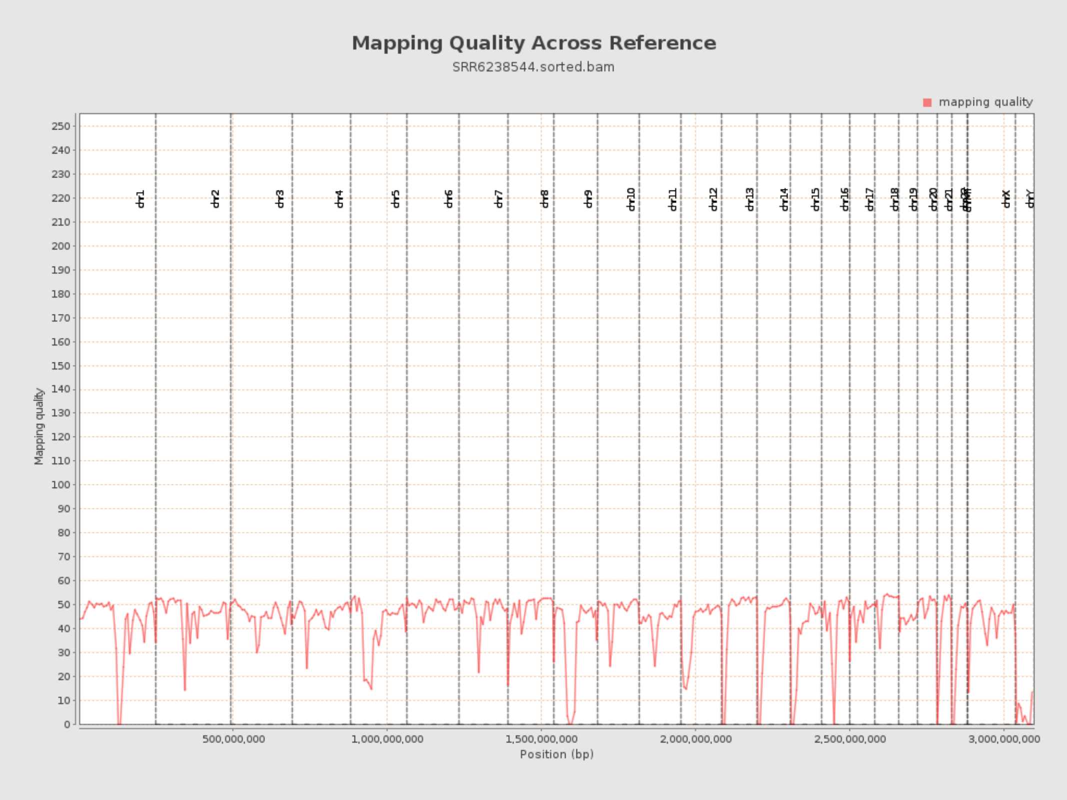
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram