Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 13:07:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234062.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_SRR6234062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 13:07:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,690,941
Mapped reads	5,357,554 / 94.14%
Unmapped reads	333,387 / 5.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	54,182 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	794,141 / 13.95%
Duplication rate	6.02%
Clipped reads	1,941,583 / 34.12%

2.2. ACGT Content

Number/percentage of A's	94,453,397 / 25.66%
Number/percentage of C's	64,876,369 / 17.63%
Number/percentage of T's	102,407,755 / 27.82%
Number/percentage of G's	106,267,814 / 28.87%
Number/percentage of N's	79,209 / 0.02%
GC Percentage	46.5%

2.3. Coverage

Mean	0.1189

Standard Deviation	65.9341

2.4. Mapping Quality

Mean Mapping Quality	41.34

2.5. Mismatches and indels

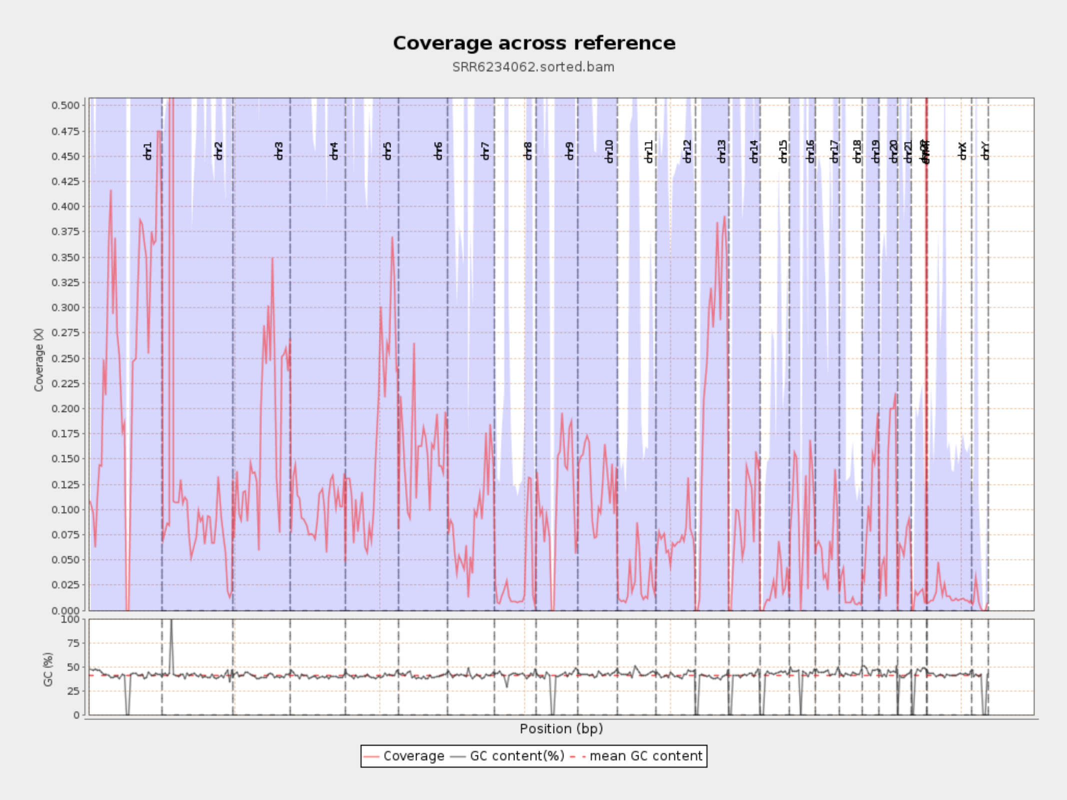
General error rate	0.59%
Mismatches	2,119,696
Insertions	23,700
Mapped reads with at least one insertion	0.44%
Deletions	75,761
Mapped reads with at least one deletion	1.4%
Homopolymer indels	47.3%

2.6. Chromosome stats

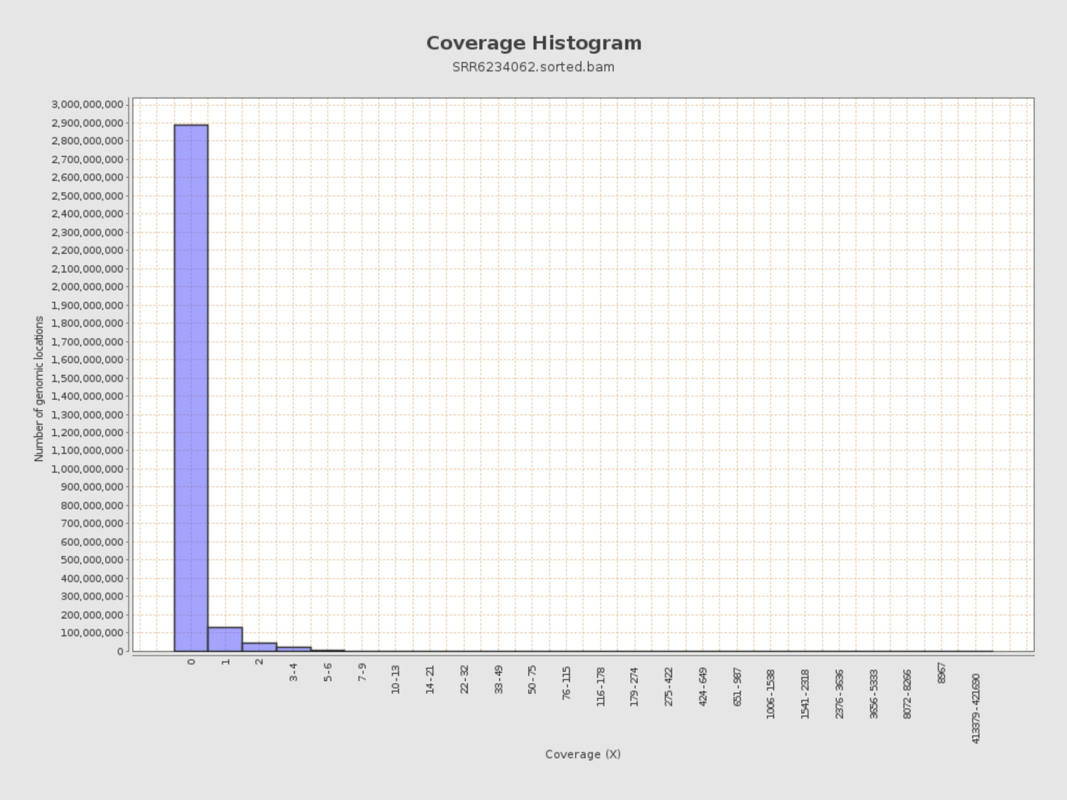
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	64082196	0.2571	1.8318
chr2	243199373	52943047	0.2177	235.223
chr3	198022430	35057717	0.177	0.6327
chr4	191154276	19627928	0.1027	0.5027
chr5	180915260	30045688	0.1661	0.6127
chr6	171115067	26921076	0.1573	0.7575
chr7	159138663	13621686	0.0856	0.552

chr8	146364022	4347836	0.0297	0.7654
chr9	141213431	15499537	0.1098	0.5384
chr10	135534747	17282261	0.1275	0.75
chr11	135006516	3612362	0.0268	0.3738
chr12	133851895	9584755	0.0716	0.3919
chr13	115169878	28322102	0.2459	0.7592
chr14	107349540	9455082	0.0881	0.5737
chr15	102531392	2264765	0.0221	0.2132
chr16	90354753	9186158	0.1017	0.4941
chr17	81195210	5130037	0.0632	0.38
chr18	78077248	1129933	0.0145	0.7674
chr19	59128983	6412330	0.1084	1.0588
chr20	63025520	7188574	0.1141	0.5202
chr21	48129895	3007756	0.0625	0.3951
chr22	51304566	658305	0.0128	0.1541
chrMT	16571	63161	3.8115	3.2852
chrX	155270560	2290057	0.0147	0.2122
chrY	59373566	475367	0.008	0.2336

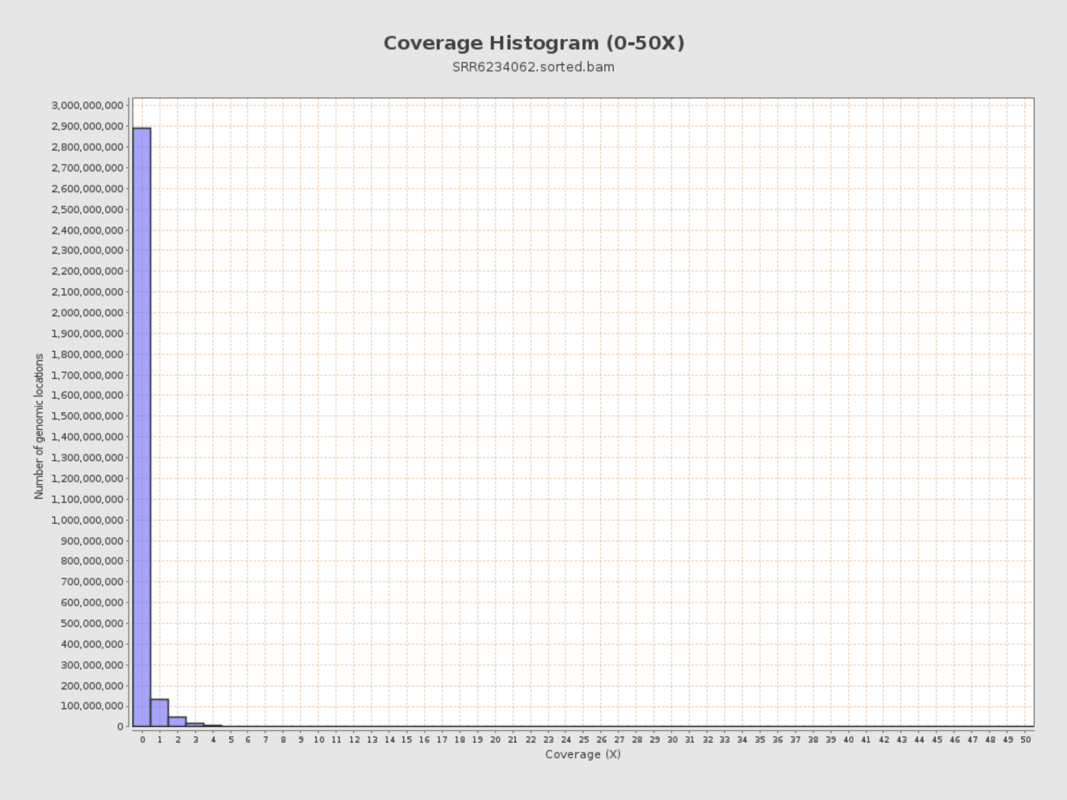
3. Results : Coverage across reference



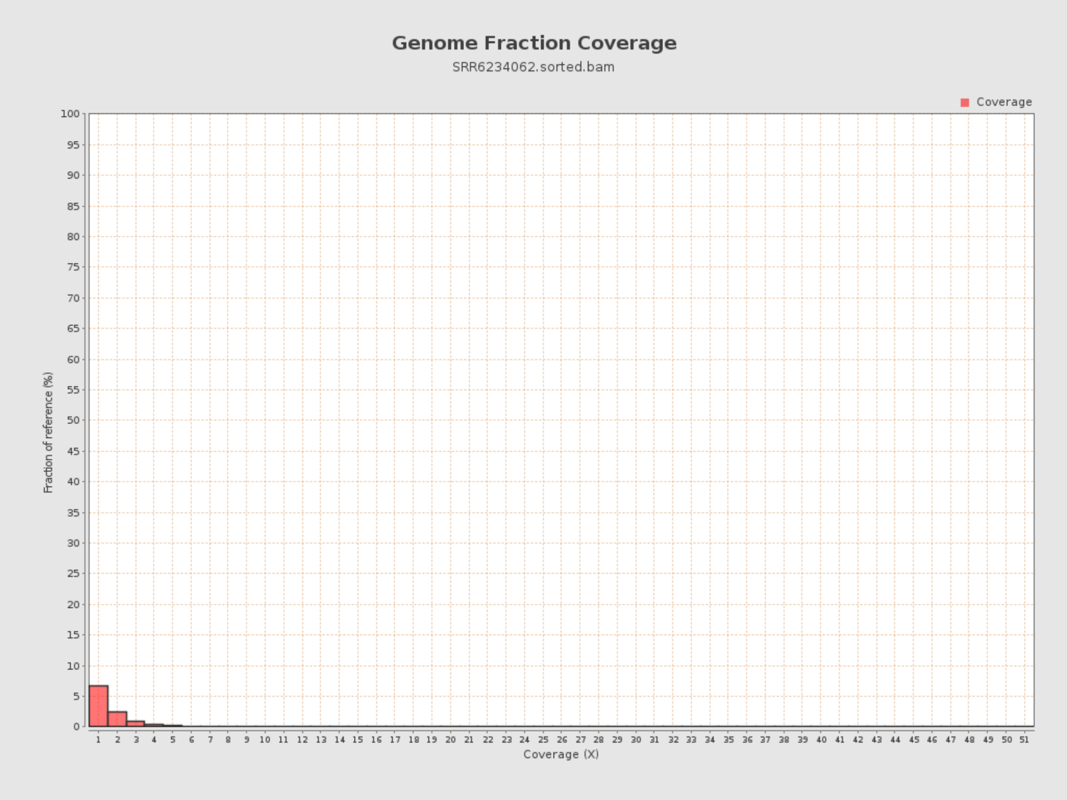
4. Results : Coverage Histogram



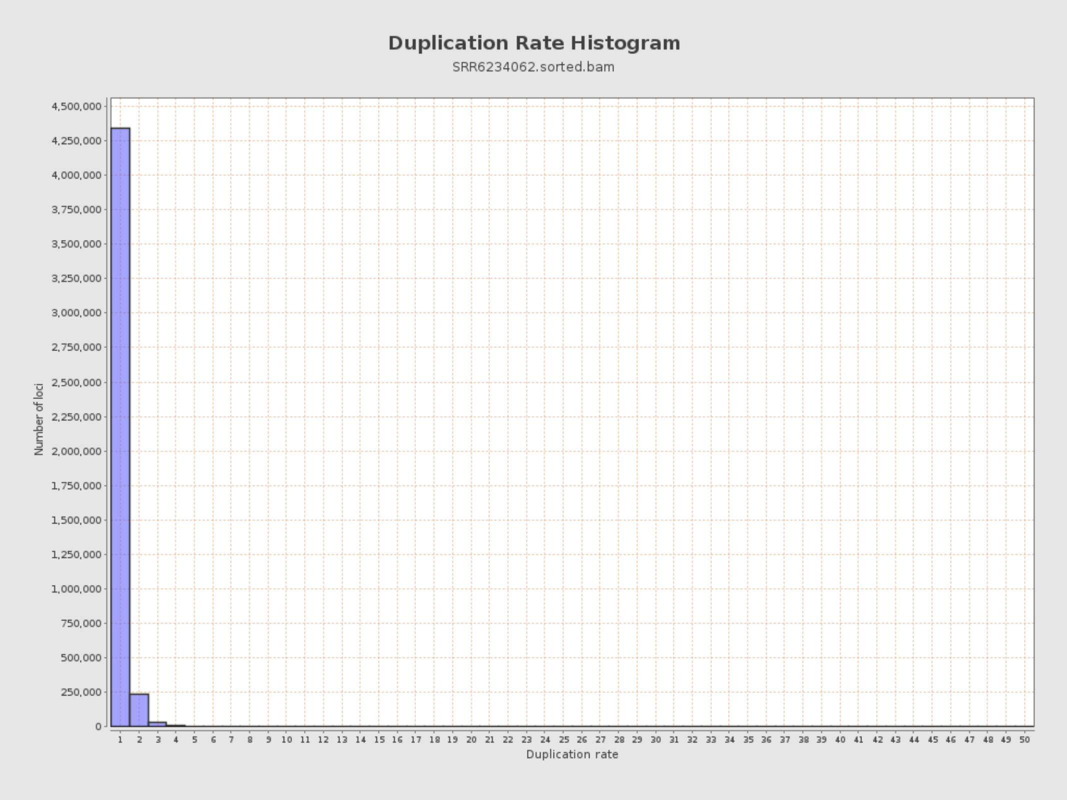
5. Results : Coverage Histogram (0-50X)



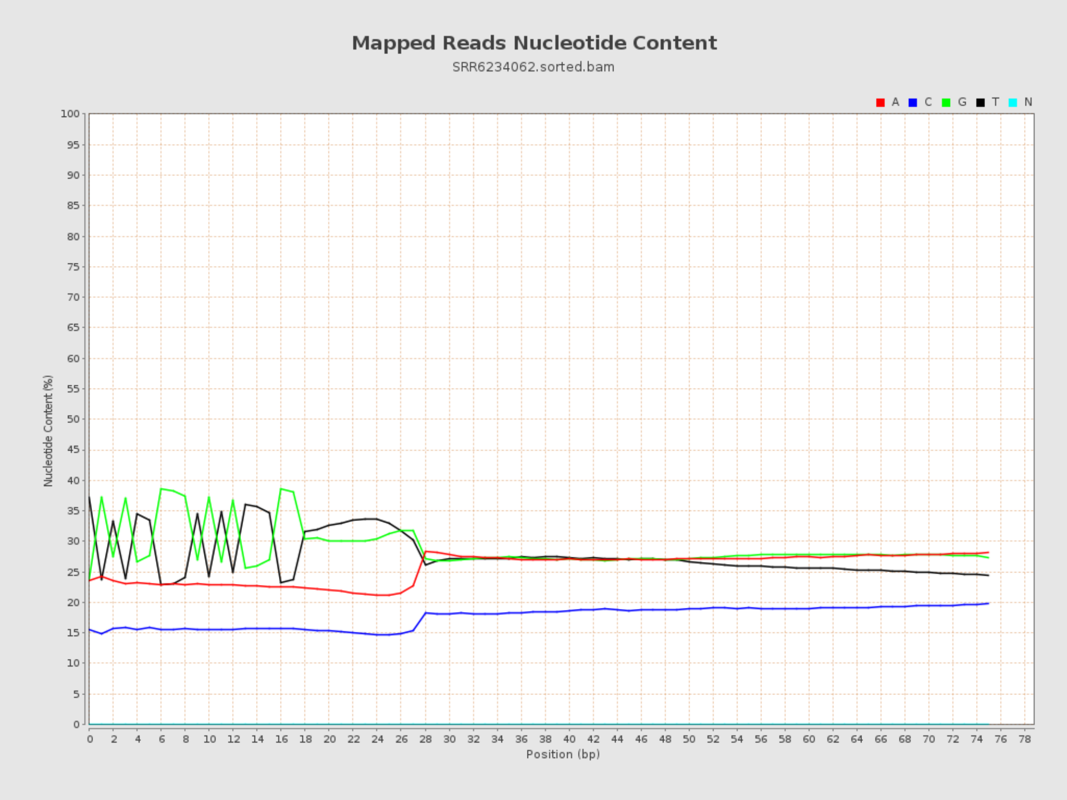
6. Results : Genome Fraction Coverage



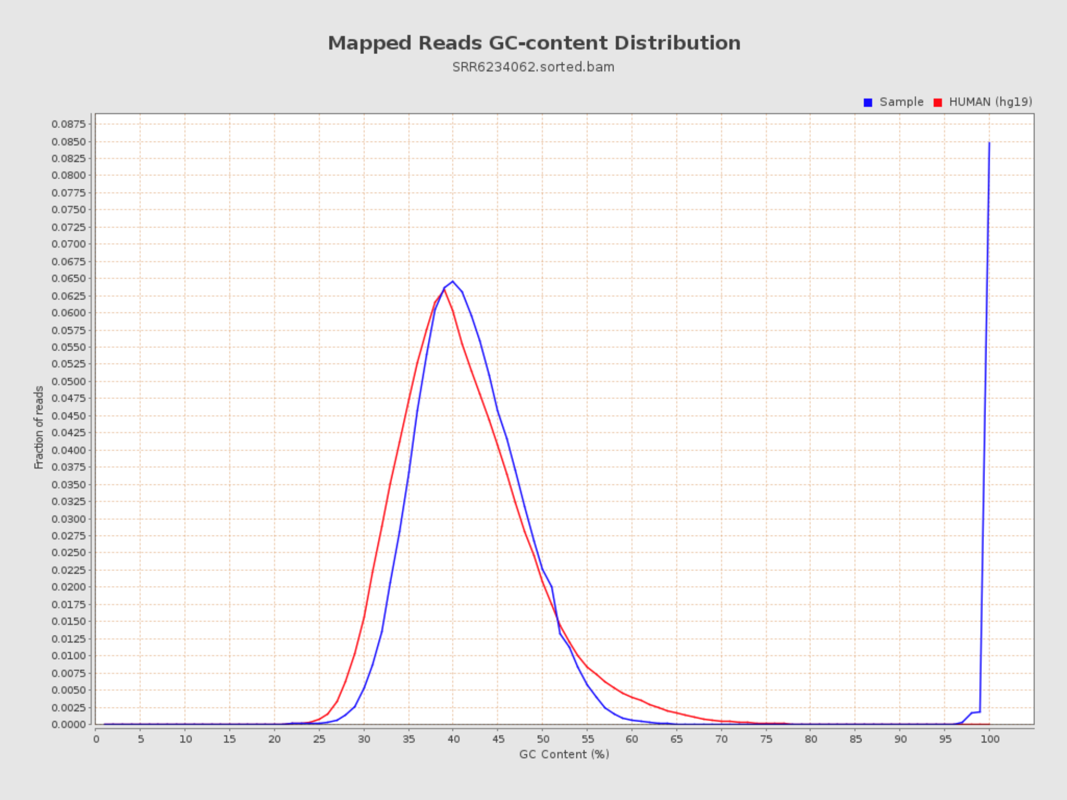
7. Results : Duplication Rate Histogram



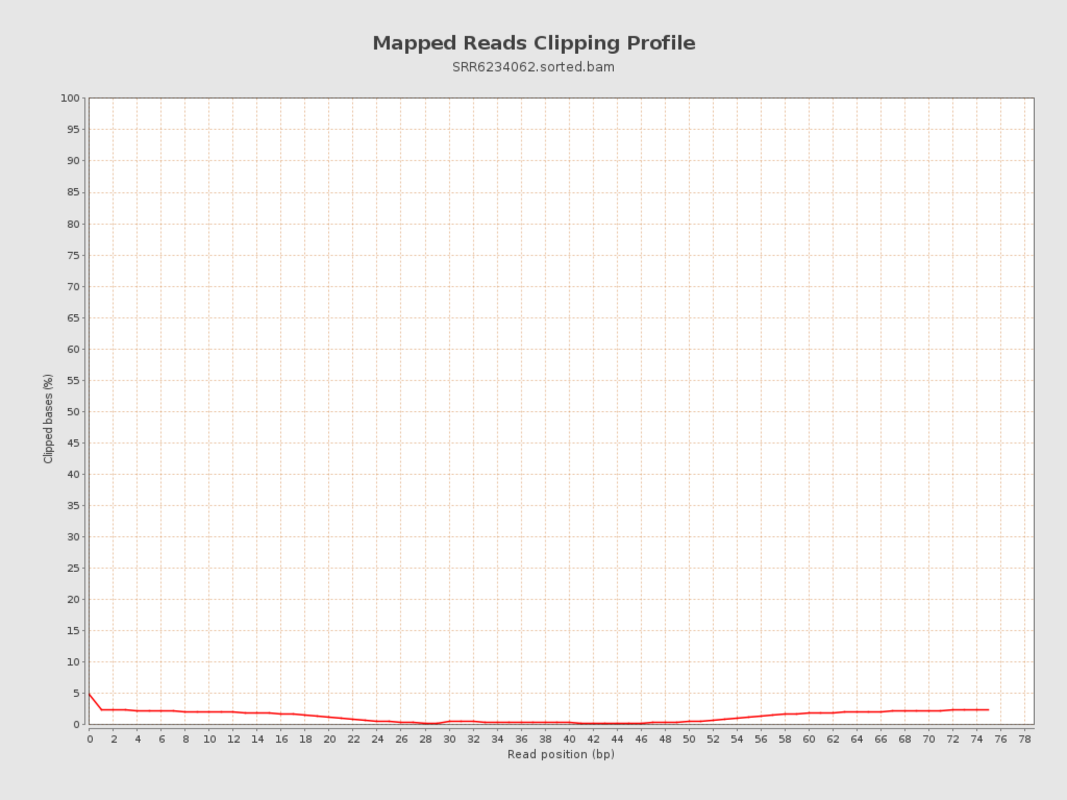
8. Results : Mapped Reads Nucleotide Content



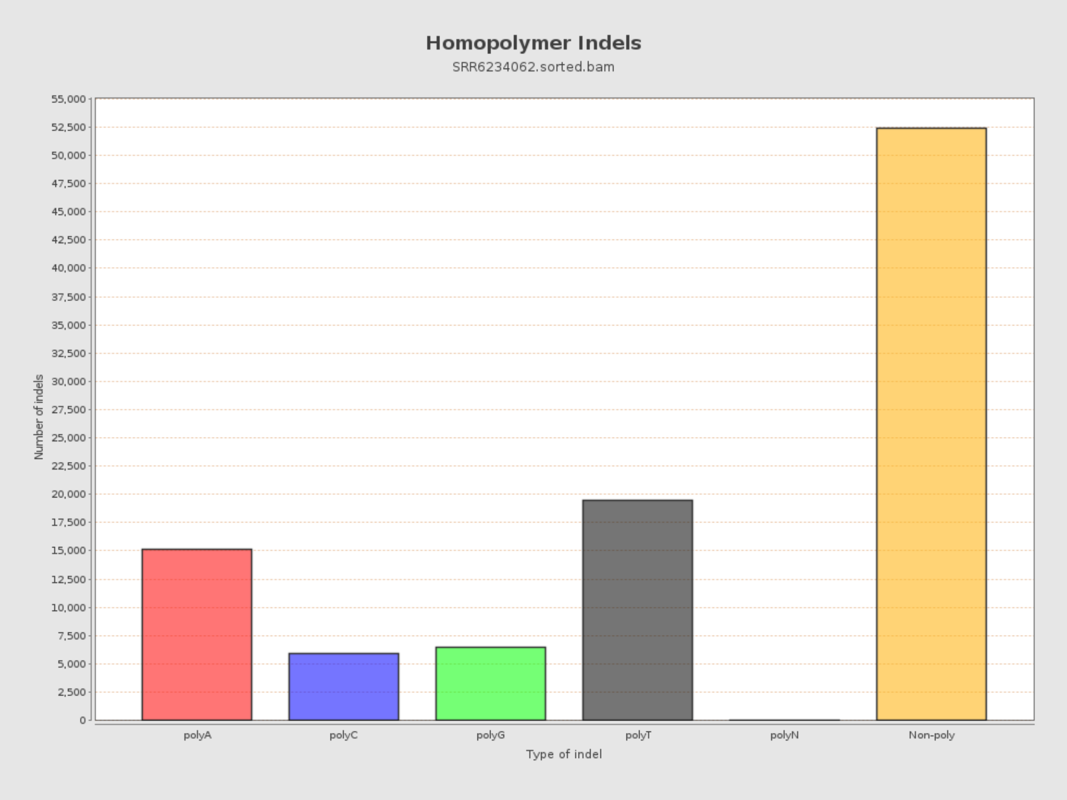
9. Results : Mapped Reads GC-content Distribution



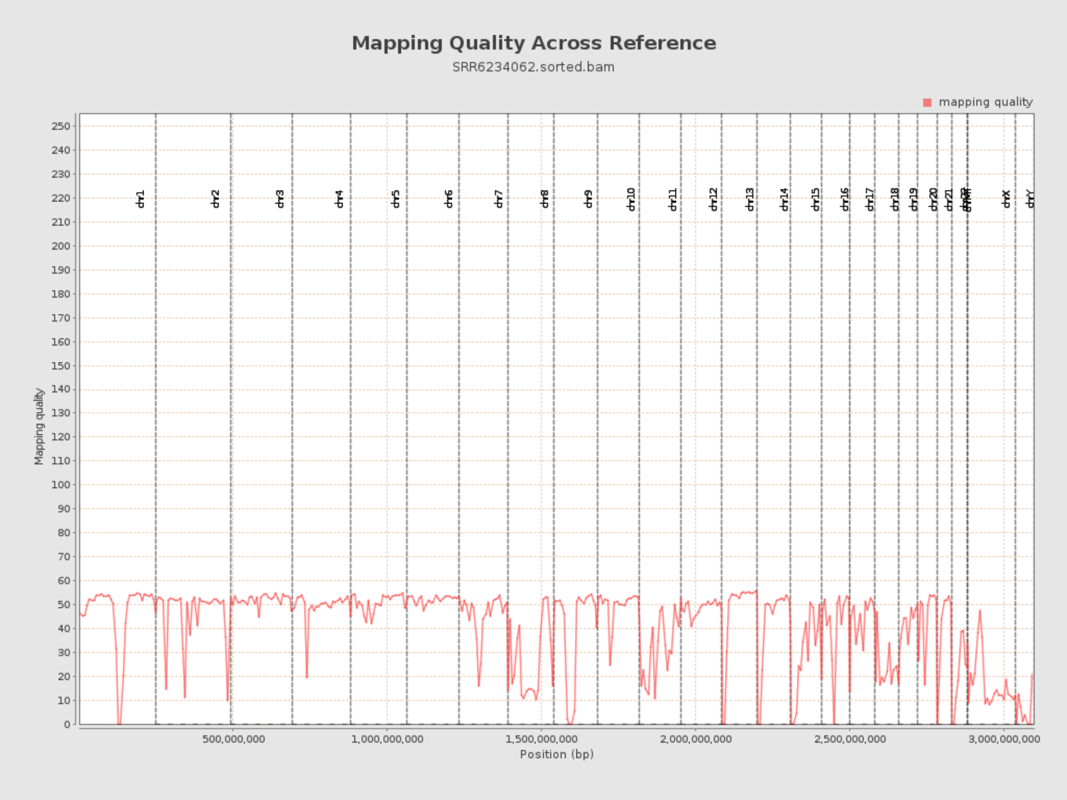
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram