Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:47:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063548.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_SRR6063548 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063548.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:47:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063548.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,242,127
Mapped reads	2,006,601 / 89.5%
Unmapped reads	235,526 / 10.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,186 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	134,618 / 6%
Duplication rate	5.4%
Clipped reads	1,020,144 / 45.5%

2.2. ACGT Content

Number/percentage of A's	36,337,245 / 27.69%
Number/percentage of C's	23,678,441 / 18.04%
Number/percentage of T's	42,272,757 / 32.21%
Number/percentage of G's	28,939,135 / 22.05%
Number/percentage of N's	3,423 / 0%
GC Percentage	40.1%

2.3. Coverage

Mean	0.0424

Standard Deviation	0.4198

2.4. Mapping Quality

Mean Mapping Quality	43.7

2.5. Mismatches and indels

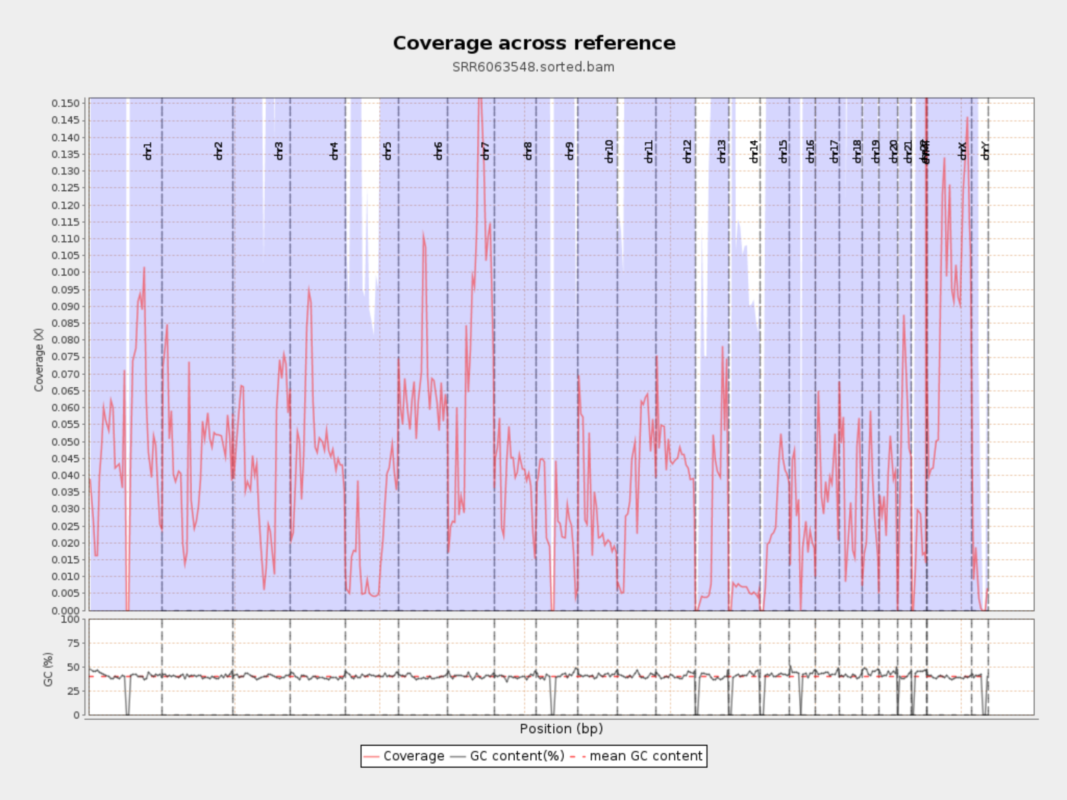
General error rate	0.83%
Mismatches	1,069,985
Insertions	9,765
Mapped reads with at least one insertion	0.48%
Deletions	35,223
Mapped reads with at least one deletion	1.73%
Homopolymer indels	46.3%

2.6. Chromosome stats

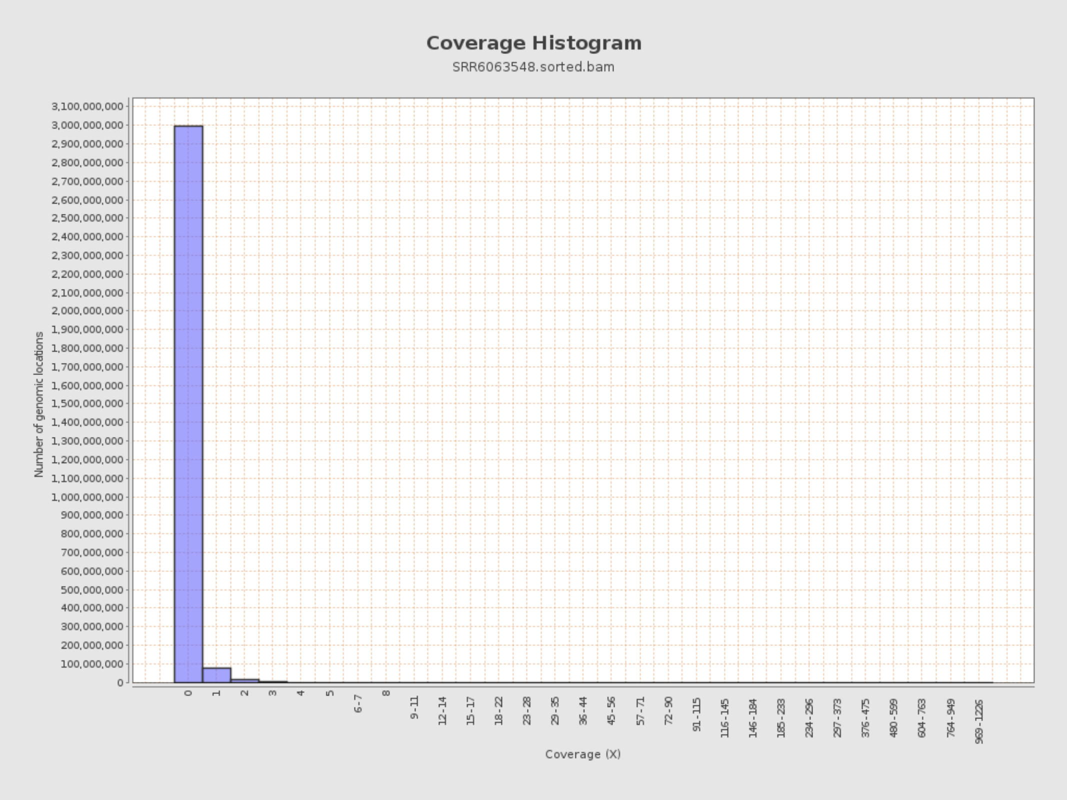
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12391222	0.0497	0.7285
chr2	243199373	11361405	0.0467	0.537
chr3	198022430	8586699	0.0434	0.2609
chr4	191154276	9535707	0.0499	0.286
chr5	180915260	3439953	0.019	0.1739
chr6	171115067	11386972	0.0665	0.3816
chr7	159138663	12528332	0.0787	0.528

chr8	146364022	5808082	0.0397	0.7416
chr9	141213431	3590455	0.0254	0.3578
chr10	135534747	4160152	0.0307	0.3168
chr11	135006516	5226139	0.0387	0.3004
chr12	133851895	6274037	0.0469	0.2852
chr13	115169878	3252100	0.0282	0.213
chr14	107349540	593404	0.0055	0.162
chr15	102531392	2735861	0.0267	0.2116
chr16	90354753	2217882	0.0245	0.2067
chr17	81195210	3161313	0.0389	0.2673
chr18	78077248	2758602	0.0353	0.5227
chr19	59128983	1709271	0.0289	0.5019
chr20	63025520	2256897	0.0358	0.2505
chr21	48129895	2460461	0.0511	0.2954
chr22	51304566	832158	0.0162	0.1536
chrMT	16571	66711	4.0258	3.6494
chrX	155270560	14502671	0.0934	0.4562
chrY	59373566	451586	0.0076	0.1905

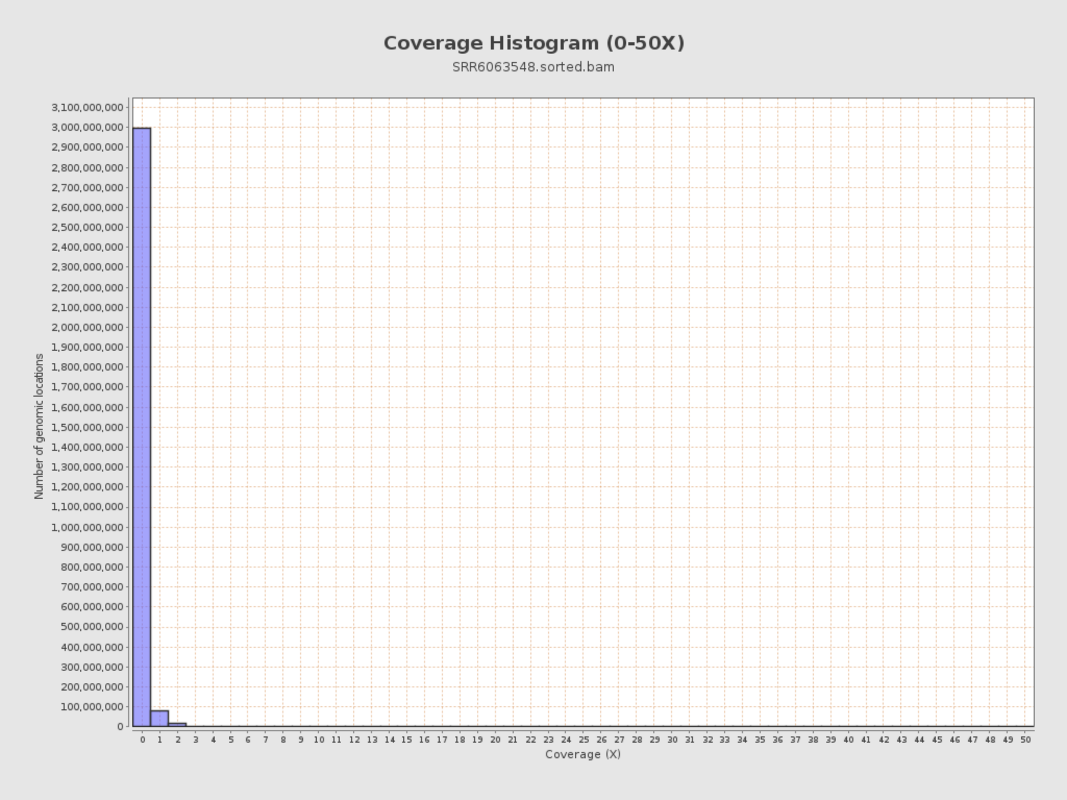
3. Results : Coverage across reference



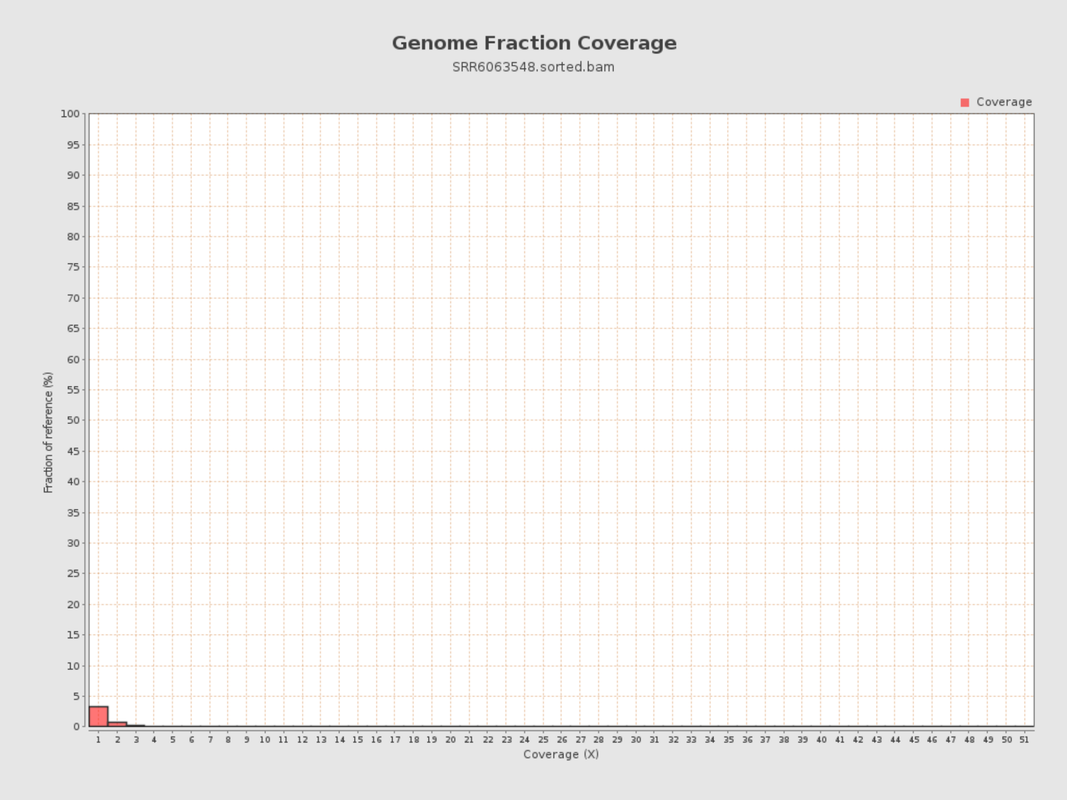
4. Results : Coverage Histogram



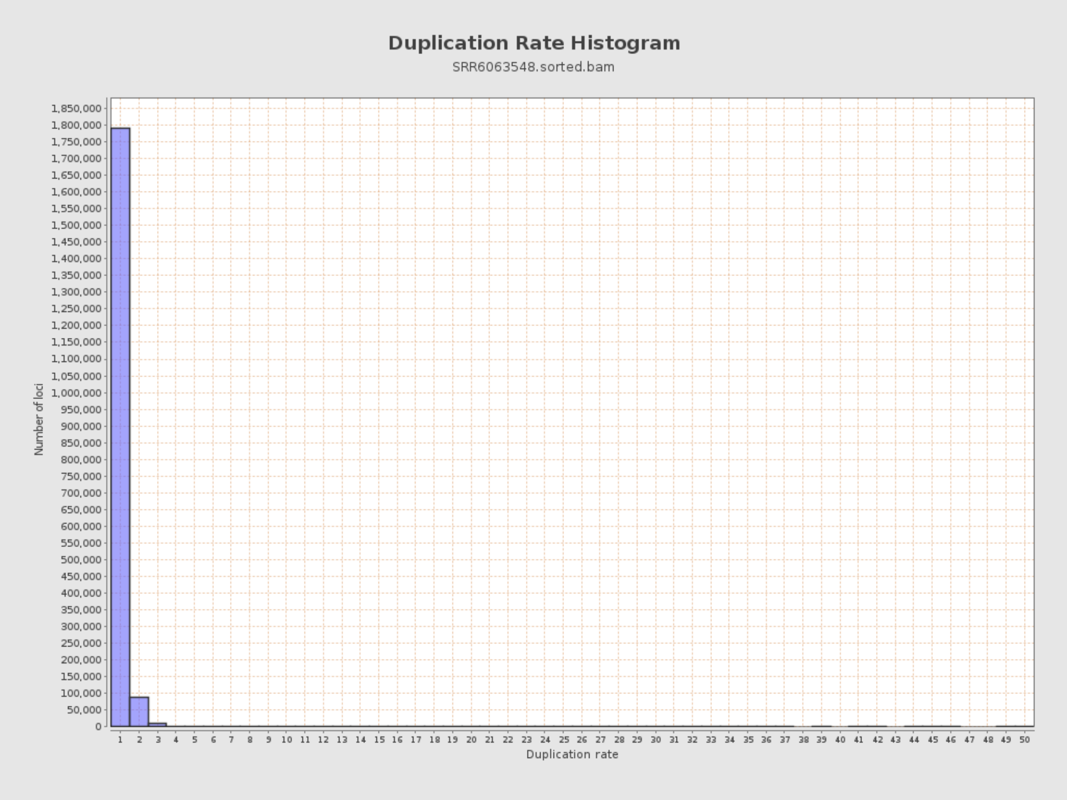
5. Results : Coverage Histogram (0-50X)



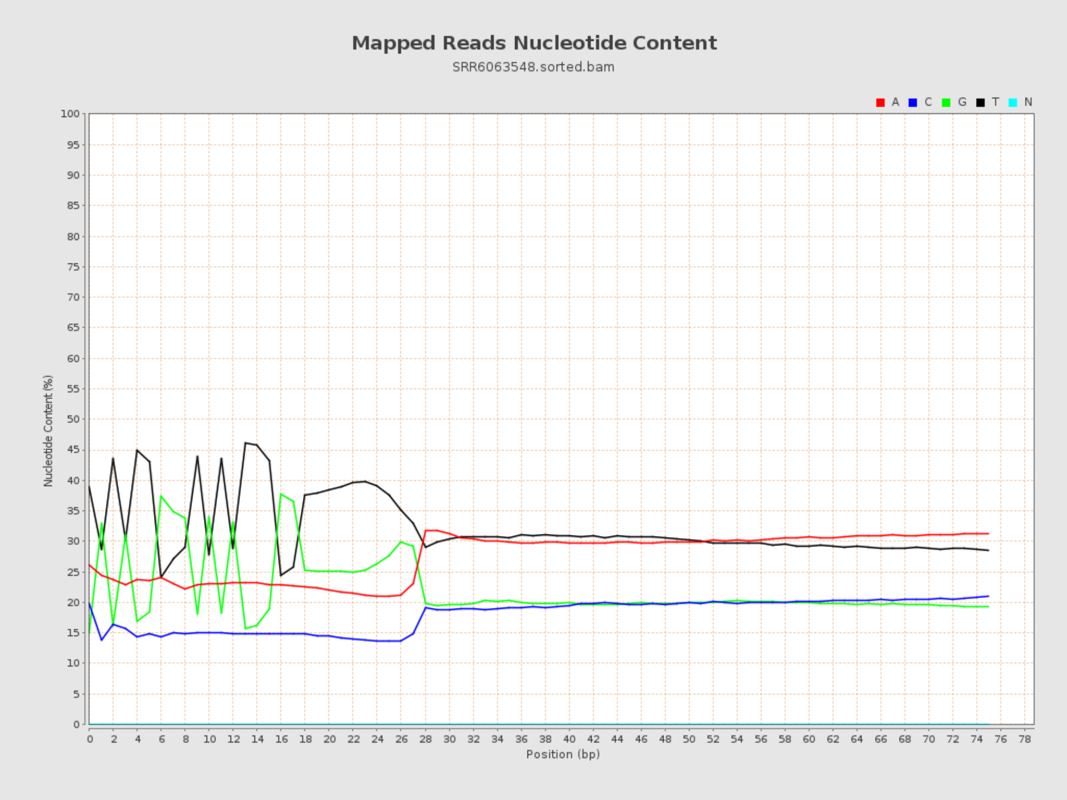
6. Results : Genome Fraction Coverage



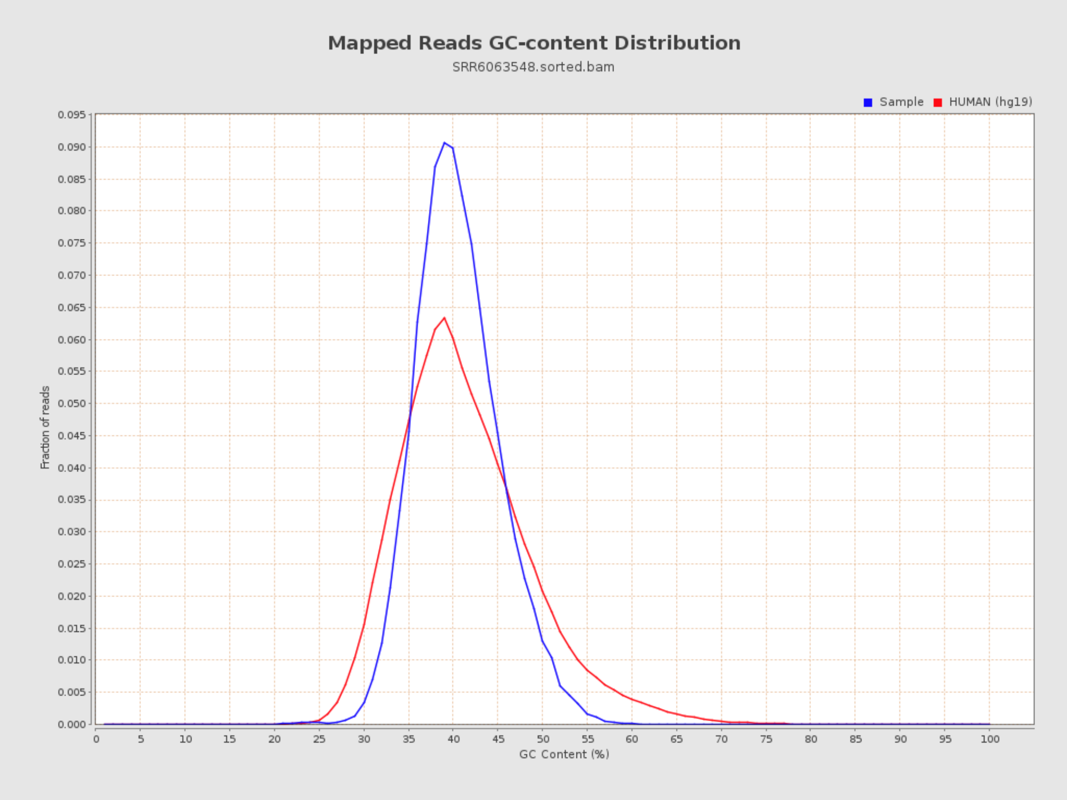
7. Results : Duplication Rate Histogram



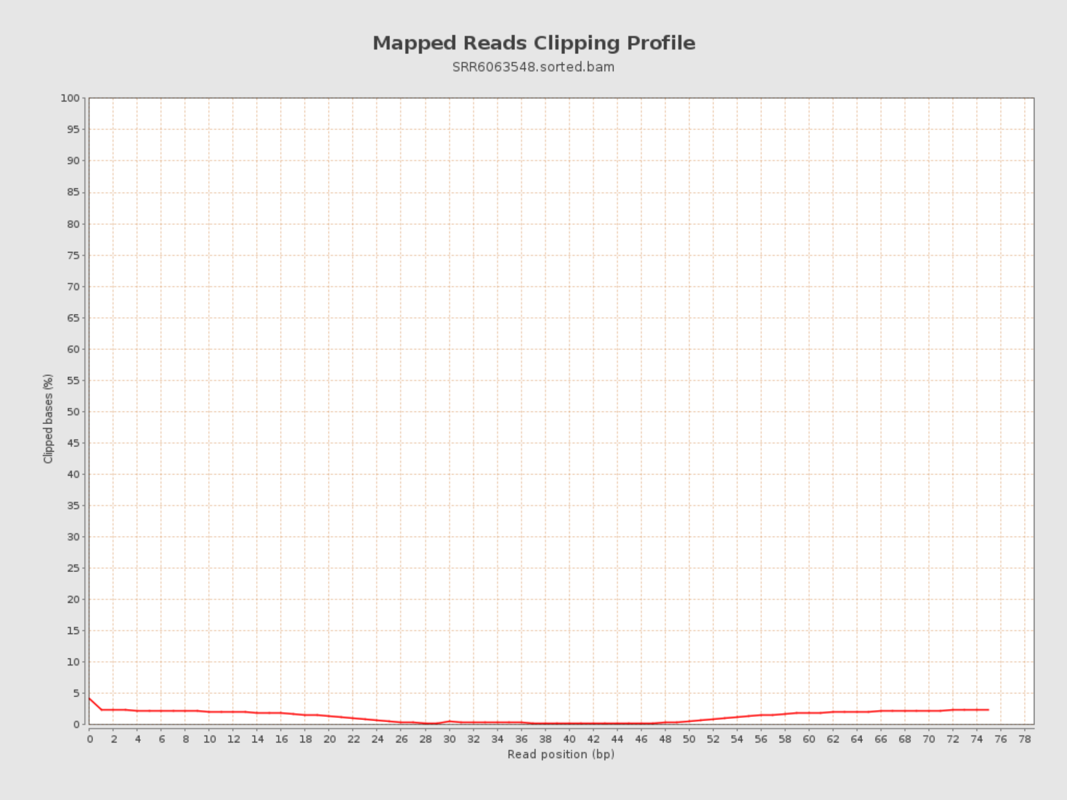
8. Results : Mapped Reads Nucleotide Content



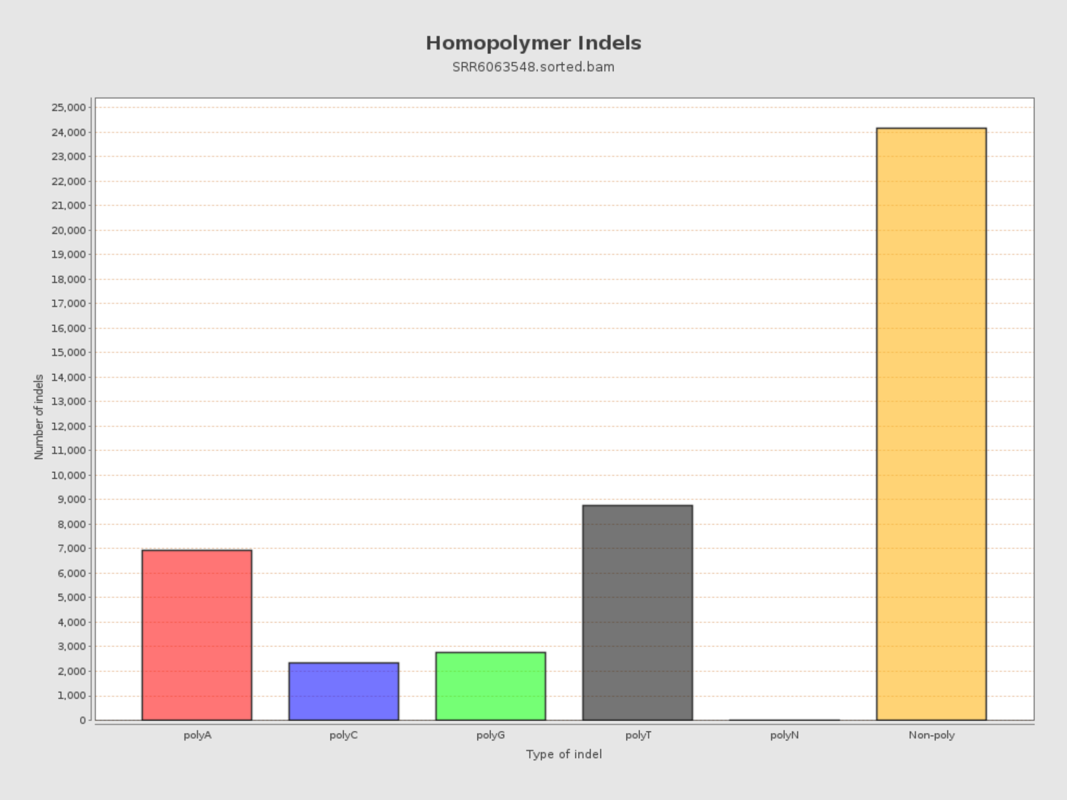
9. Results : Mapped Reads GC-content Distribution



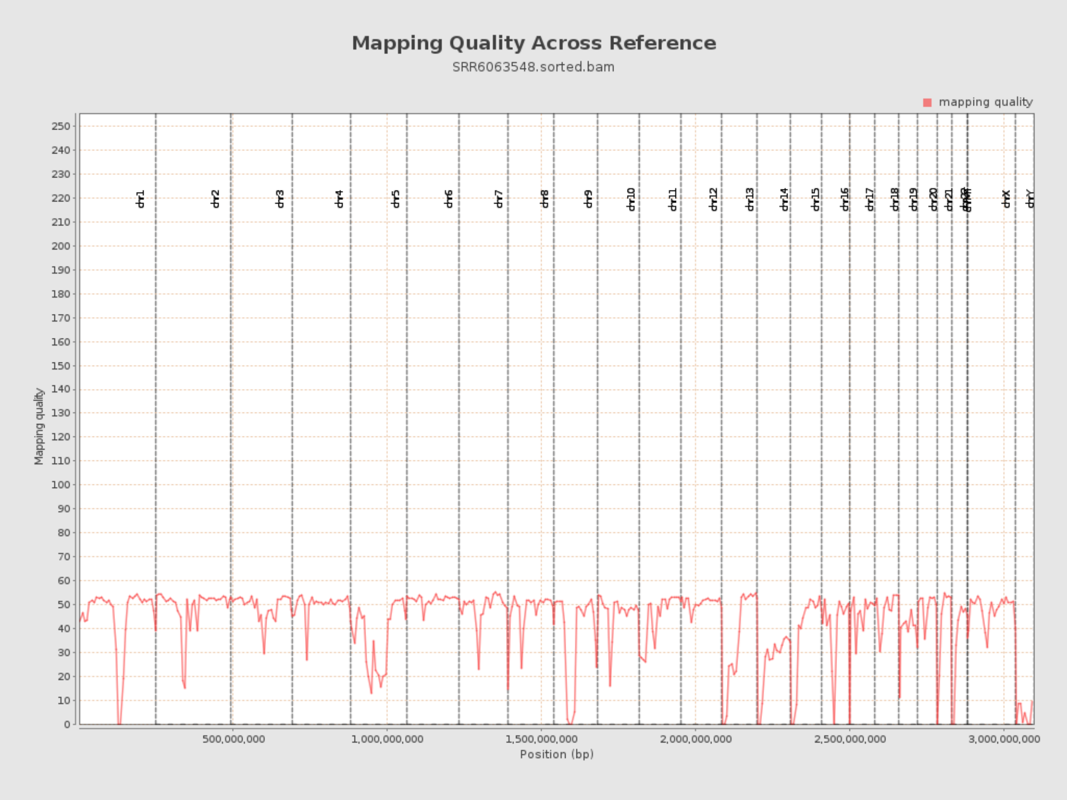
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram