Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:35:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063562.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_SRR6063562 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063562.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:35:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063562.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,697,506
Mapped reads	2,454,272 / 90.98%
Unmapped reads	243,234 / 9.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,735 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	106,415 / 3.94%
Duplication rate	3.28%
Clipped reads	1,168,046 / 43.3%

2.2. ACGT Content

Number/percentage of A's	45,459,575 / 28.02%
Number/percentage of C's	29,946,274 / 18.46%
Number/percentage of T's	51,199,545 / 31.56%
Number/percentage of G's	35,609,769 / 21.95%
Number/percentage of N's	3,545 / 0%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0524

Standard Deviation	0.4669

2.4. Mapping Quality

Mean Mapping Quality	45.54

2.5. Mismatches and indels

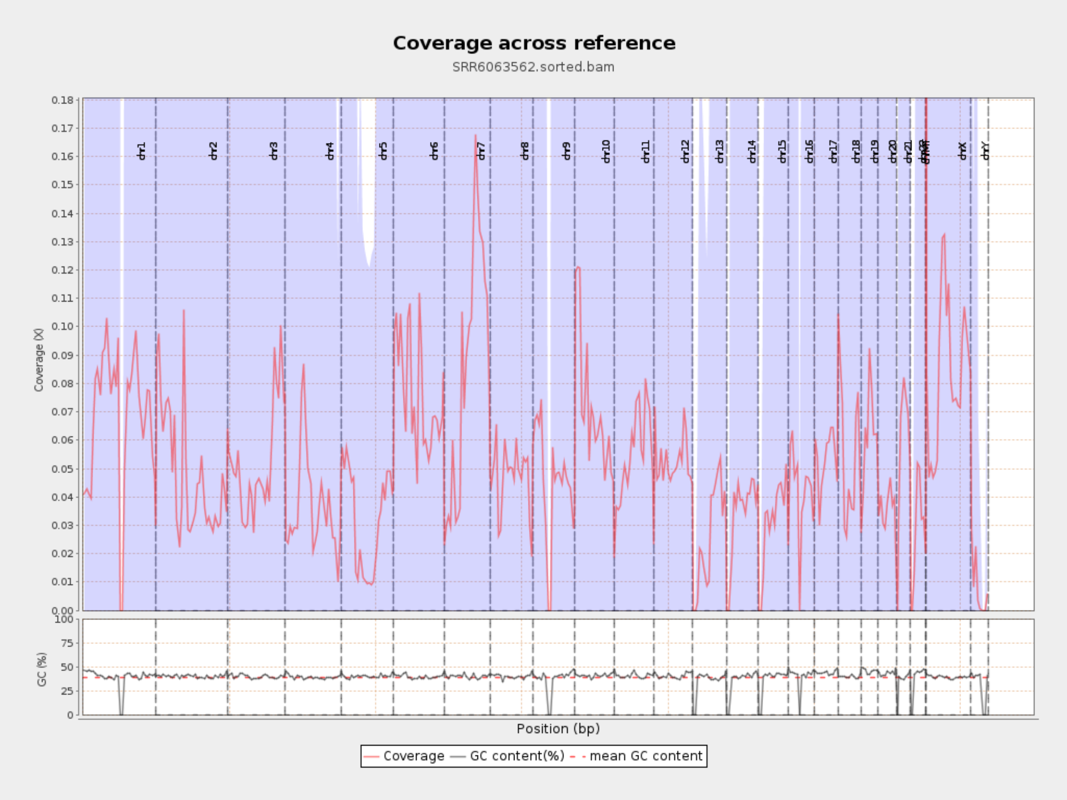
General error rate	0.79%
Mismatches	1,254,946
Insertions	12,219
Mapped reads with at least one insertion	0.49%
Deletions	42,836
Mapped reads with at least one deletion	1.73%
Homopolymer indels	46.33%

2.6. Chromosome stats

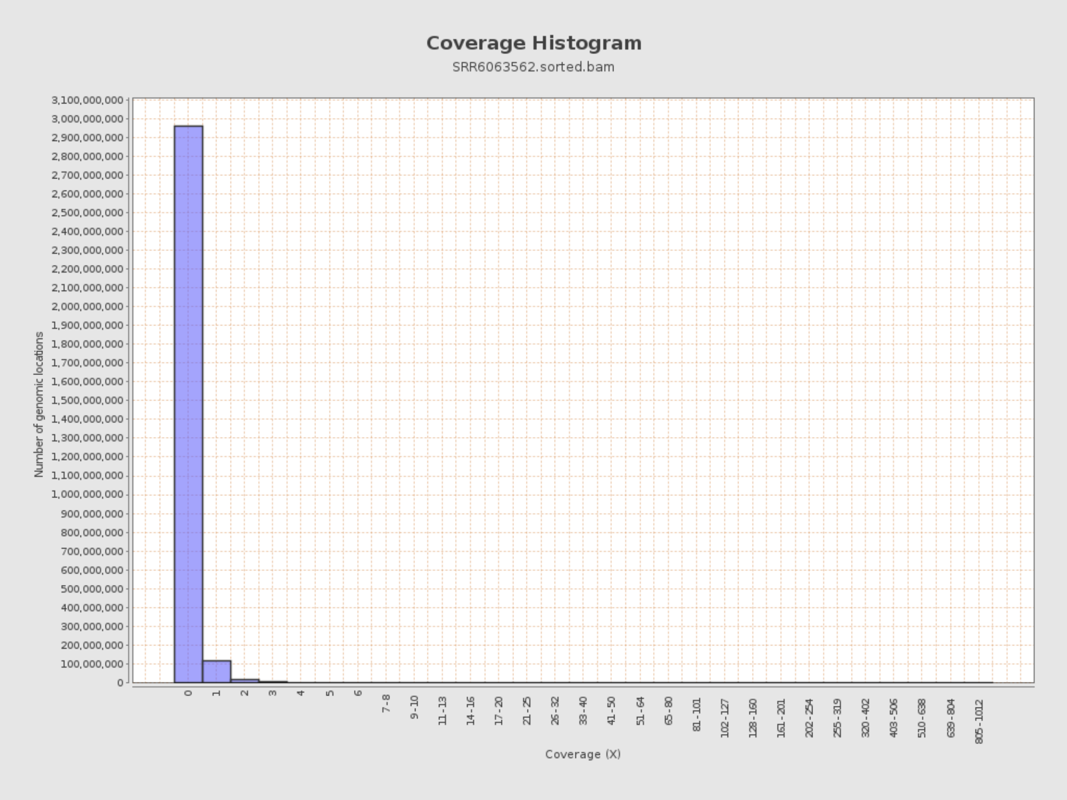
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17013604	0.0683	0.873
chr2	243199373	11788824	0.0485	0.5401
chr3	198022430	10355449	0.0523	0.2684
chr4	191154276	7076238	0.037	0.2382
chr5	180915260	5748831	0.0318	0.2104
chr6	171115067	13122148	0.0767	0.4065
chr7	159138663	13591325	0.0854	0.7205

chr8	146364022	6830170	0.0467	0.6462
chr9	141213431	6398625	0.0453	0.4191
chr10	135534747	9739385	0.0719	0.4617
chr11	135006516	7477317	0.0554	0.3917
chr12	133851895	7110022	0.0531	0.279
chr13	115169878	3052193	0.0265	0.1891
chr14	107349540	3665340	0.0341	0.264
chr15	102531392	3173077	0.0309	0.2085
chr16	90354753	3711429	0.0411	0.2678
chr17	81195210	4370779	0.0538	0.2906
chr18	78077248	4277142	0.0548	0.6748
chr19	59128983	3737343	0.0632	0.5844
chr20	63025520	2288044	0.0363	0.2314
chr21	48129895	2789645	0.058	0.3017
chr22	51304566	1444331	0.0282	0.1923
chrMT	16571	81421	4.9135	3.4939
chrX	155270560	12981129	0.0836	0.4047
chrY	59373566	464972	0.0078	0.1875

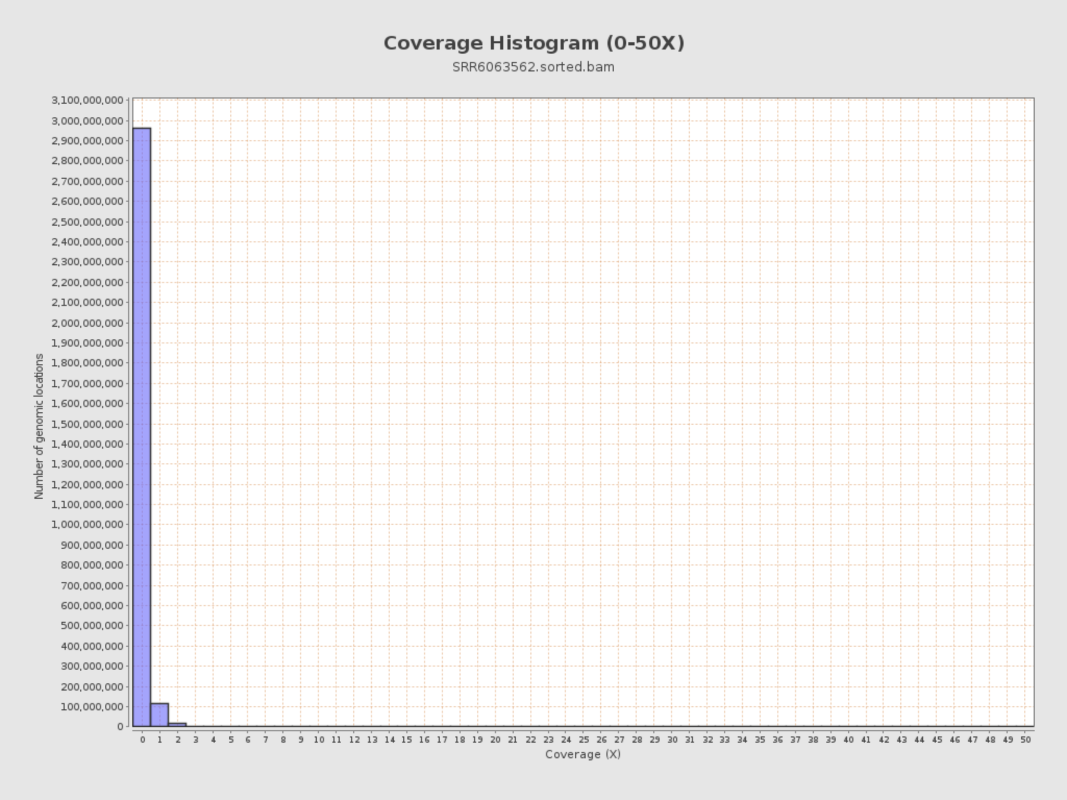
3. Results : Coverage across reference



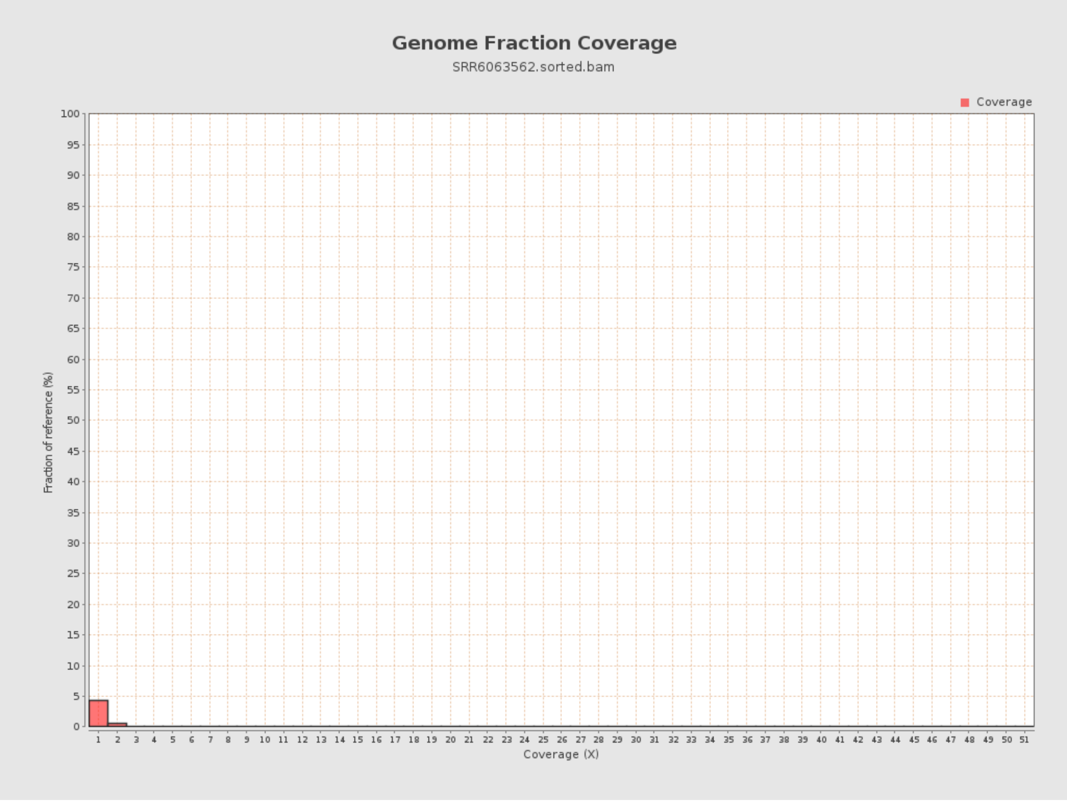
4. Results : Coverage Histogram



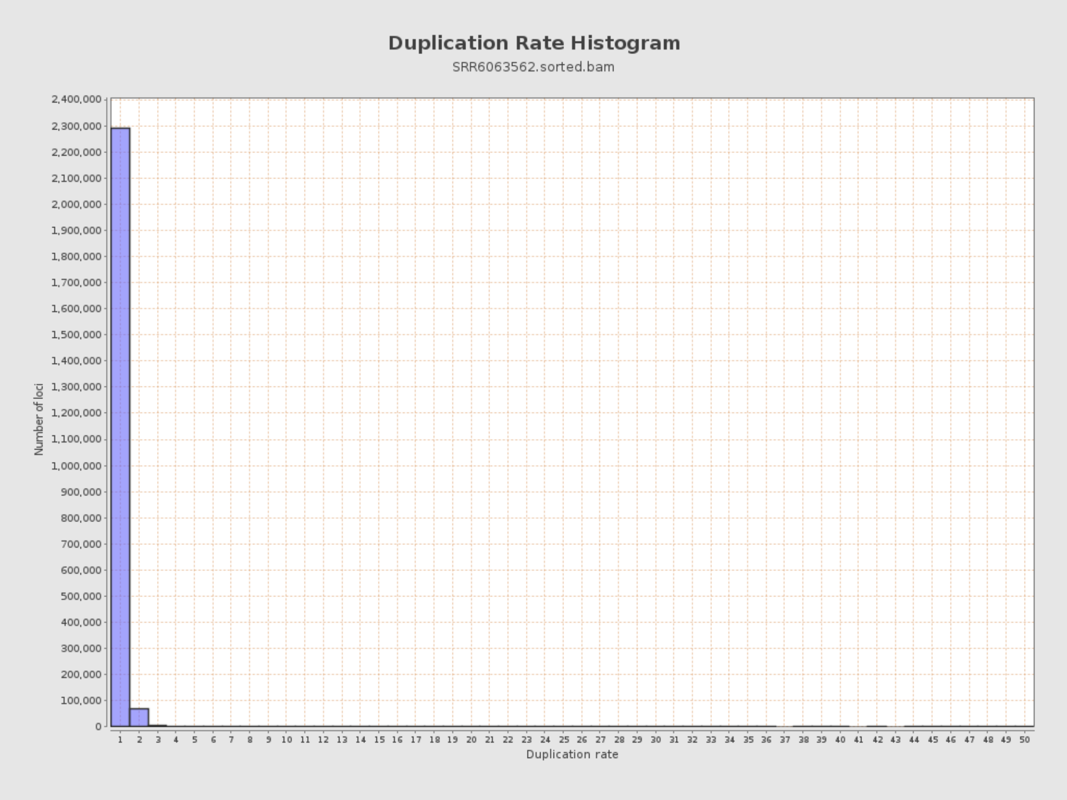
5. Results : Coverage Histogram (0-50X)



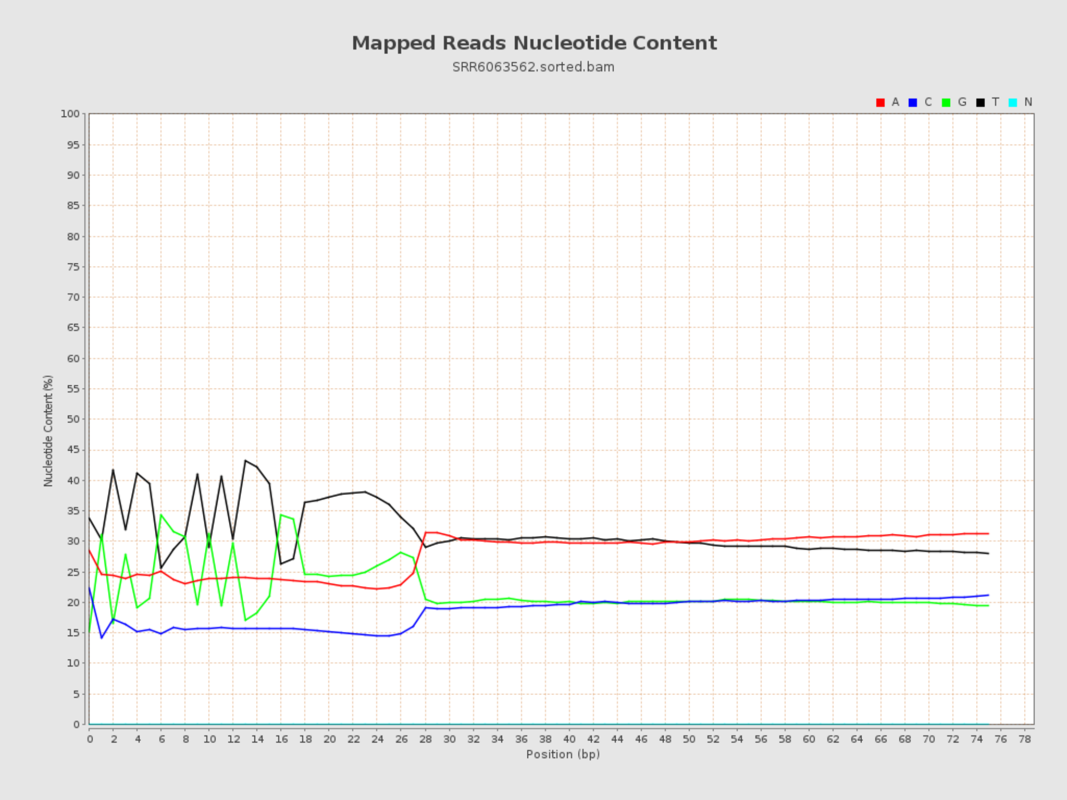
6. Results : Genome Fraction Coverage



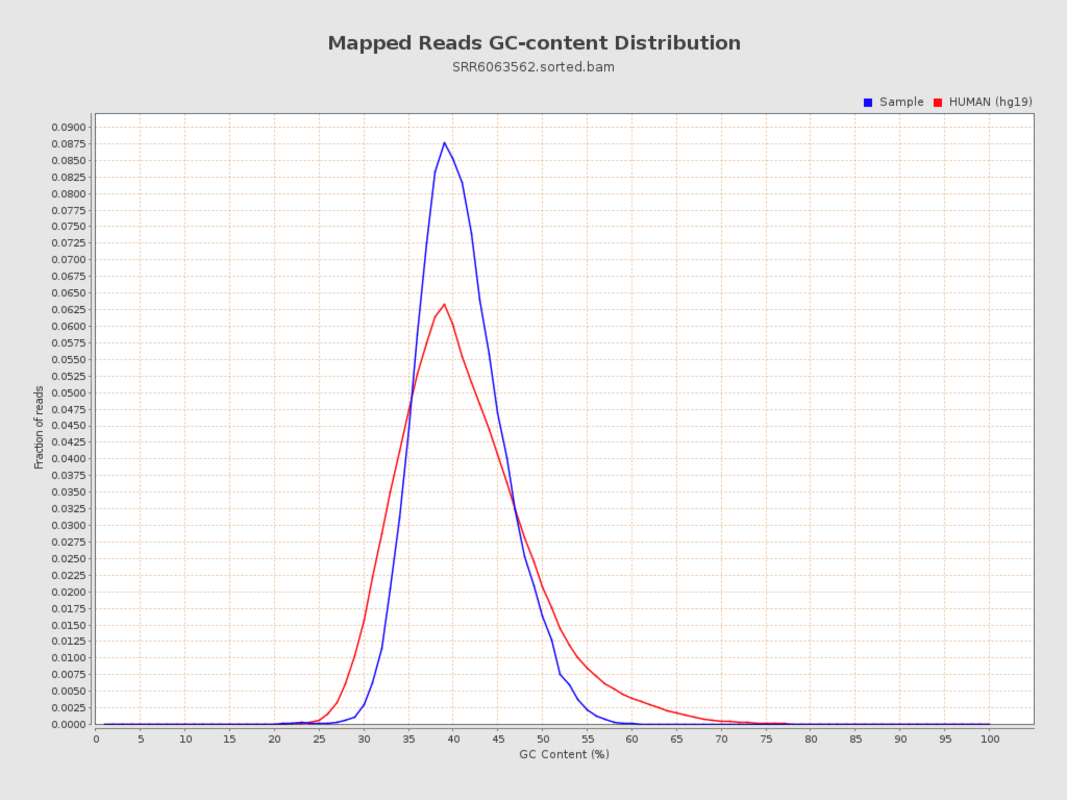
7. Results : Duplication Rate Histogram



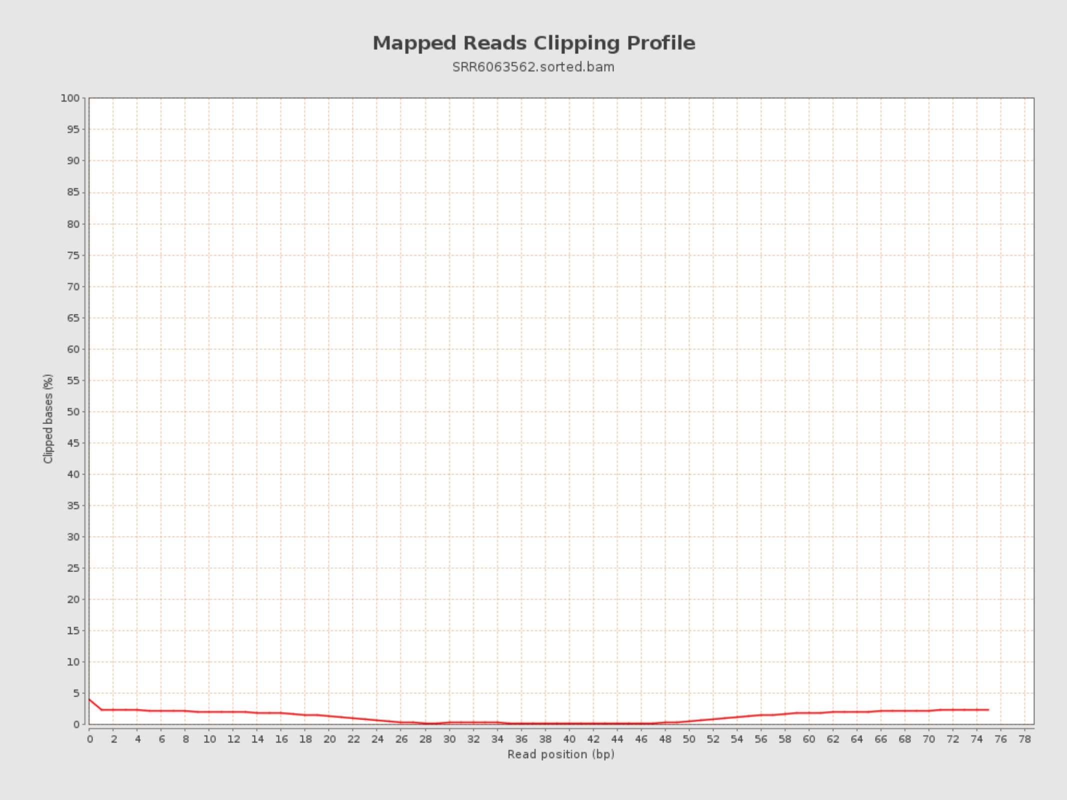
8. Results : Mapped Reads Nucleotide Content



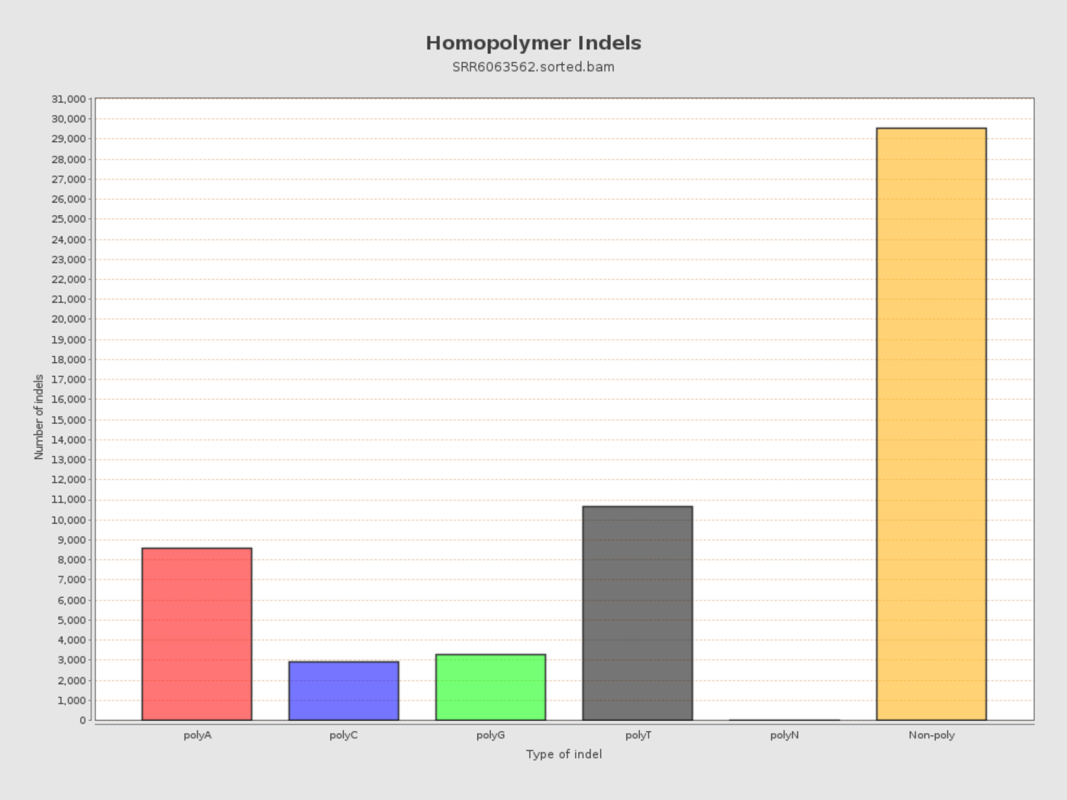
9. Results : Mapped Reads GC-content Distribution



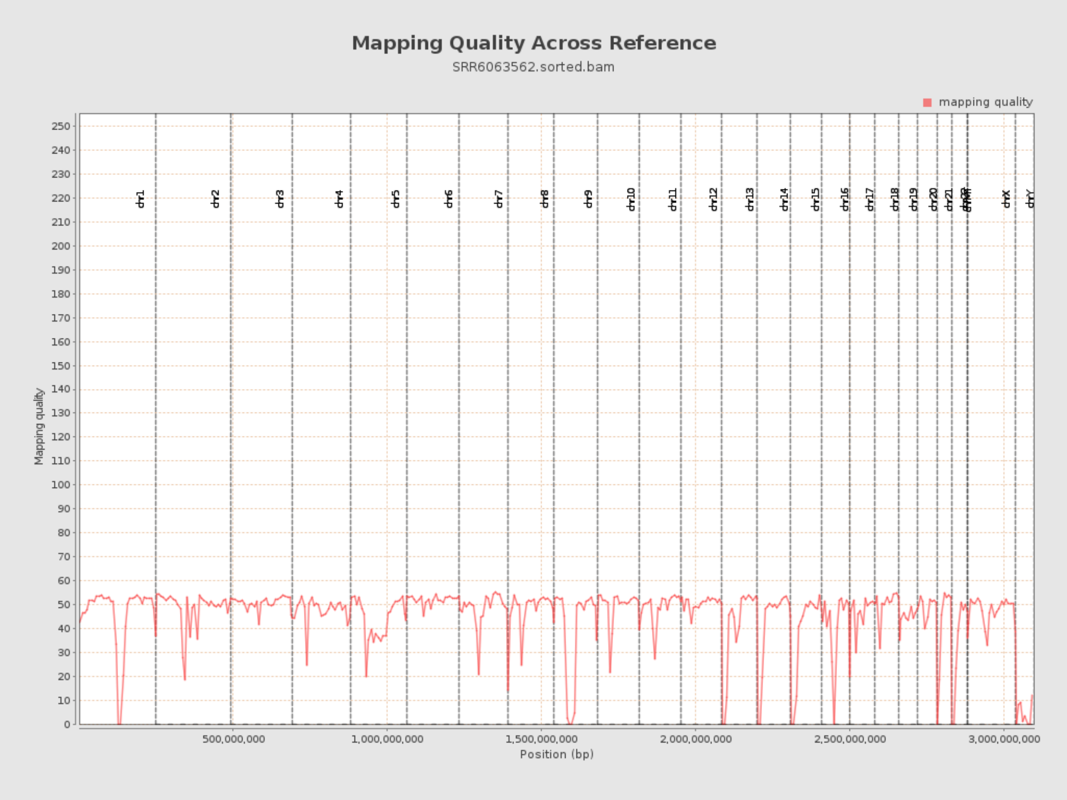
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram