Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:34:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063530.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_SRR6063530 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063530.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:34:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063530.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,410,657
Mapped reads	5,834,948 / 91.02%
Unmapped reads	575,709 / 8.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	62,793 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	1,173,603 / 18.31%
Duplication rate	15.57%
Clipped reads	3,490,376 / 54.45%

2.2. ACGT Content

Number/percentage of A's	96,404,947 / 26.13%
Number/percentage of C's	68,390,820 / 18.54%
Number/percentage of T's	117,164,582 / 31.76%
Number/percentage of G's	86,924,609 / 23.56%
Number/percentage of N's	41,831 / 0.01%
GC Percentage	42.1%

2.3. Coverage

Mean	0.1192

Standard Deviation	1.1062

2.4. Mapping Quality

Mean Mapping Quality	43.96

2.5. Mismatches and indels

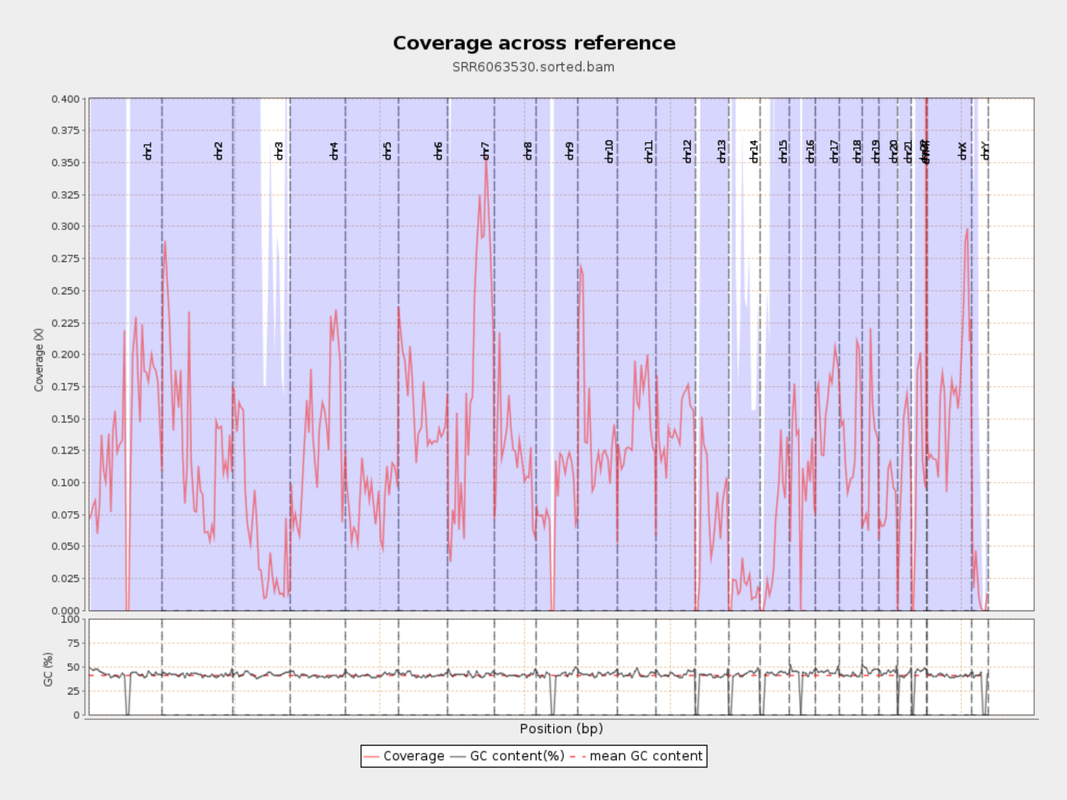
General error rate	0.55%
Mismatches	1,987,899
Insertions	23,778
Mapped reads with at least one insertion	0.4%
Deletions	80,612
Mapped reads with at least one deletion	1.37%
Homopolymer indels	43.86%

2.6. Chromosome stats

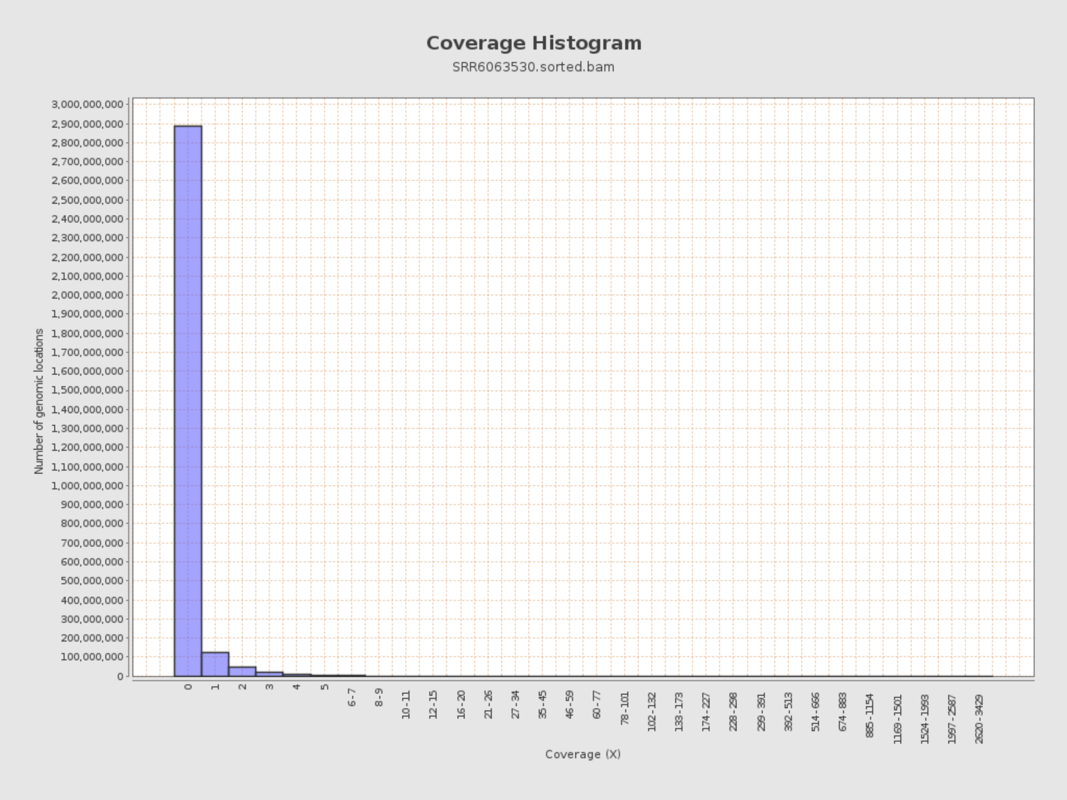
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34251679	0.1374	2.2413
chr2	243199373	32708867	0.1345	1.7696
chr3	198022430	12753173	0.0644	0.415
chr4	191154276	26086812	0.1365	0.6889
chr5	180915260	15583244	0.0861	0.4798
chr6	171115067	27200949	0.159	0.7976
chr7	159138663	29568307	0.1858	1.4156

chr8	146364022	17863297	0.122	1.0052
chr9	141213431	11952614	0.0846	0.8663
chr10	135534747	19563995	0.1443	0.8681
chr11	135006516	19691712	0.1459	0.7641
chr12	133851895	19481464	0.1455	0.6627
chr13	115169878	8596056	0.0746	0.4811
chr14	107349540	1846743	0.0172	0.4276
chr15	102531392	5970317	0.0582	0.4477
chr16	90354753	9834717	0.1088	0.586
chr17	81195210	13643727	0.168	0.7218
chr18	78077248	11001497	0.1409	1.5758
chr19	59128983	7002815	0.1184	1.4968
chr20	63025520	5439709	0.0863	0.5527
chr21	48129895	5450880	0.1133	0.5856
chr22	51304566	5320675	0.1037	0.5101
chrMT	16571	818927	49.4193	31.1376
chrX	155270560	26473351	0.1705	0.8
chrY	59373566	961978	0.0162	0.4004

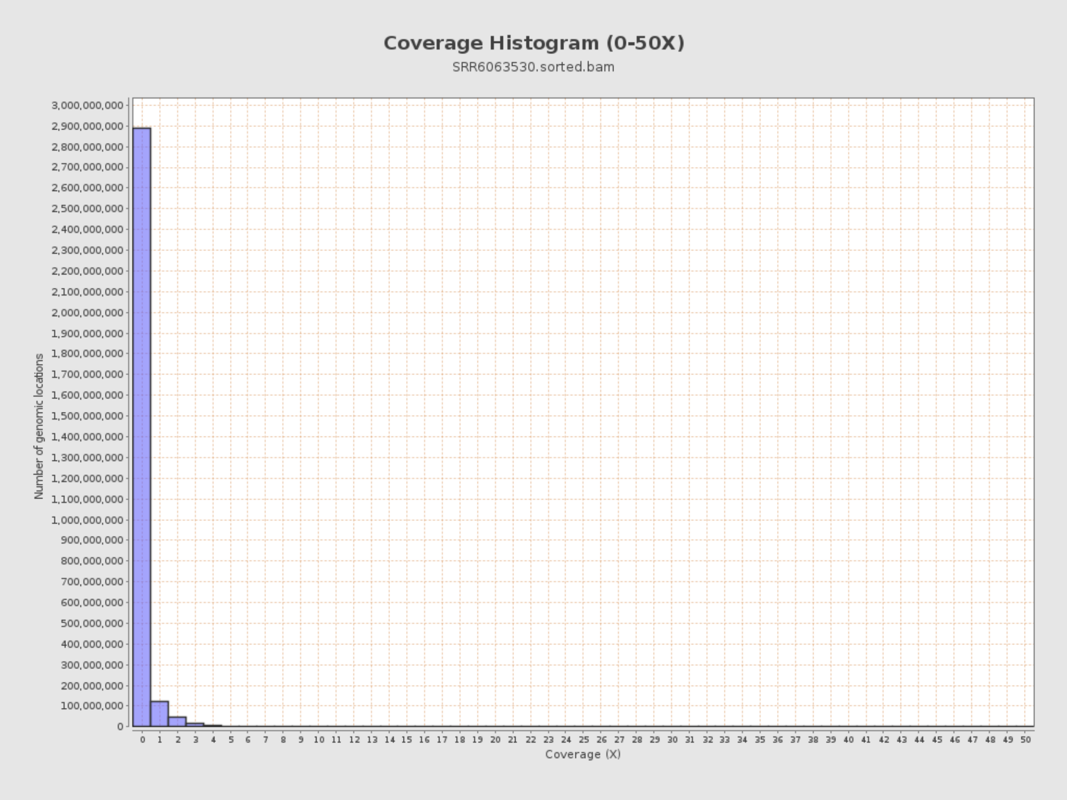
3. Results : Coverage across reference



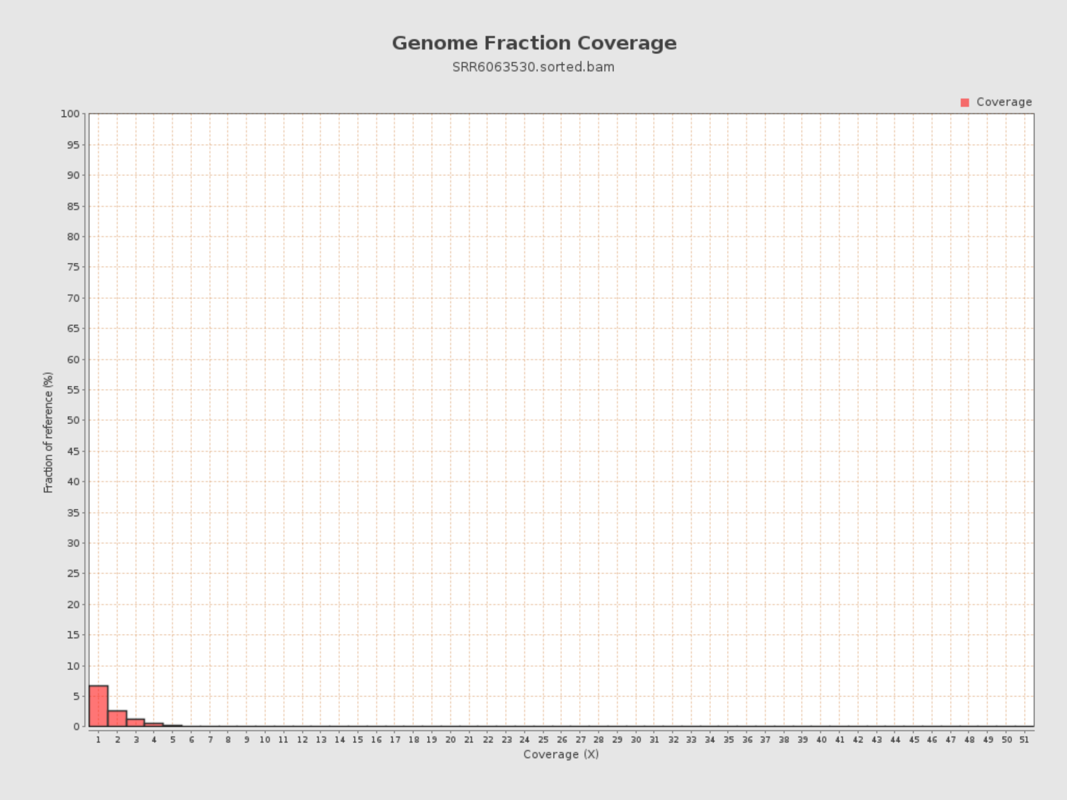
4. Results : Coverage Histogram



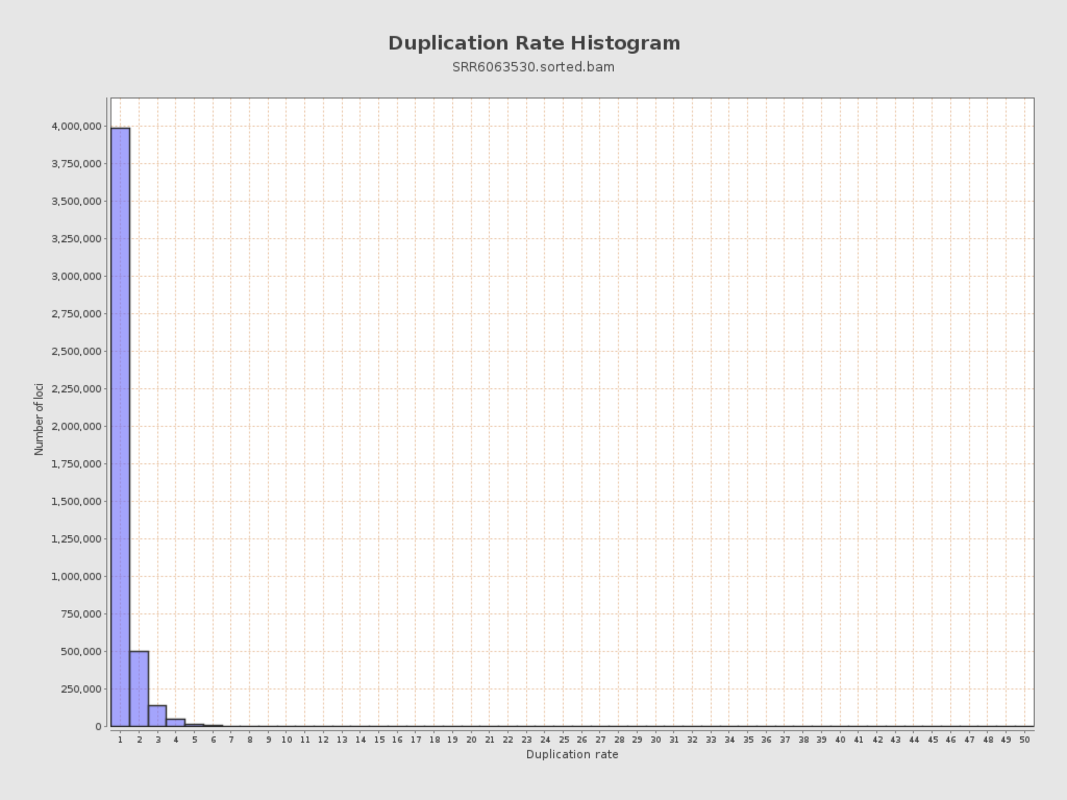
5. Results : Coverage Histogram (0-50X)



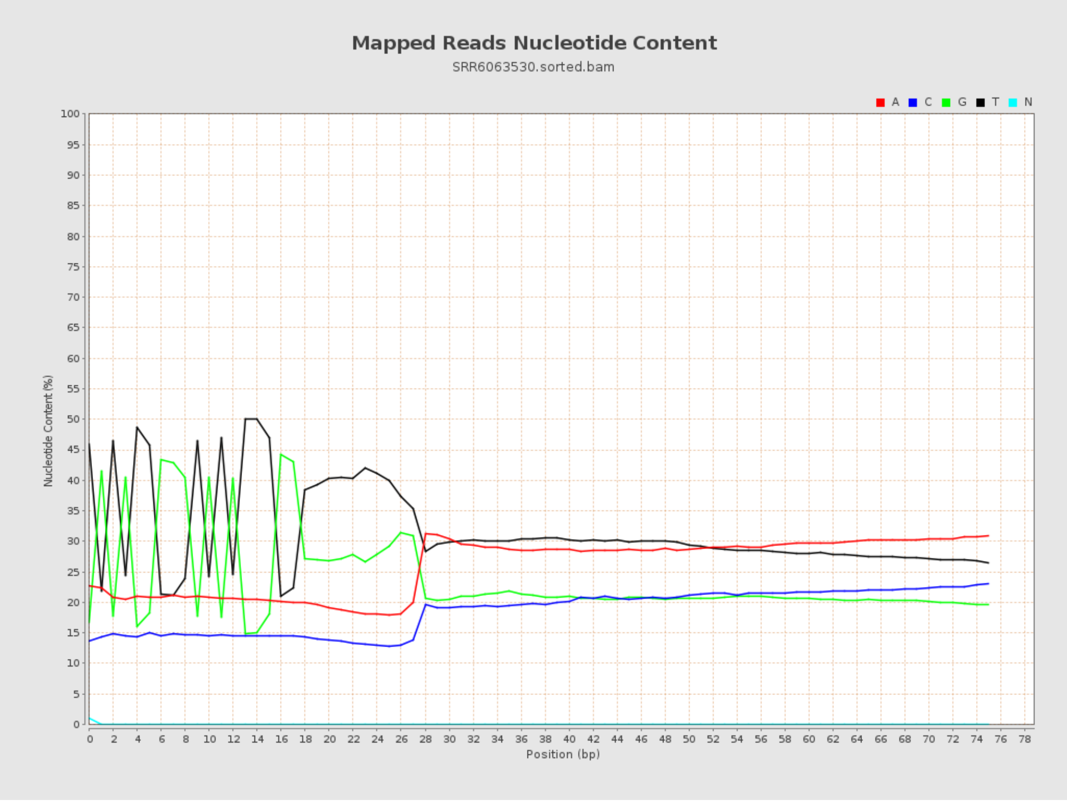
6. Results : Genome Fraction Coverage



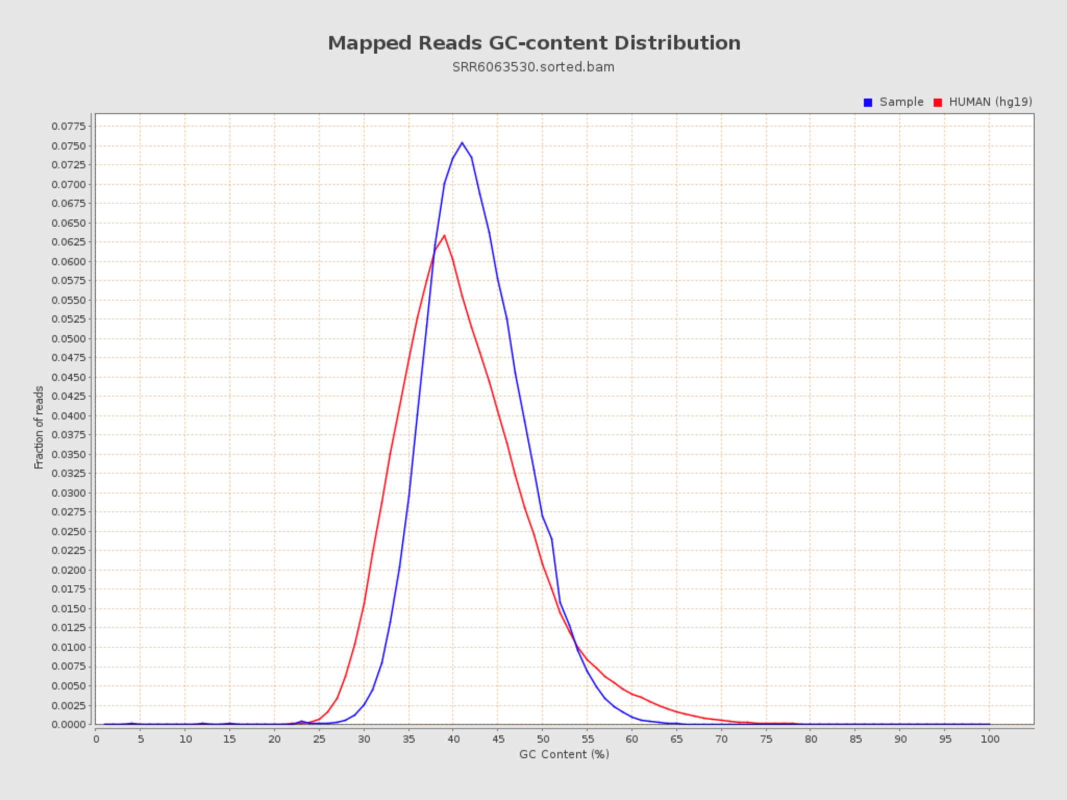
7. Results : Duplication Rate Histogram



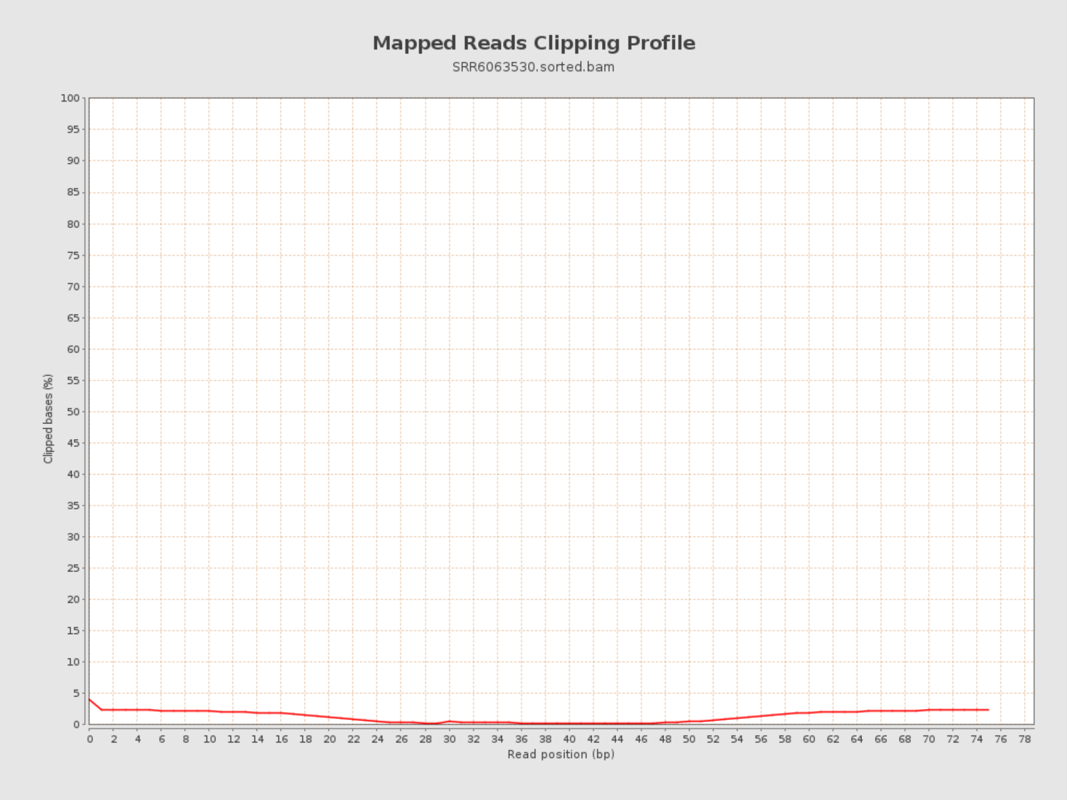
8. Results : Mapped Reads Nucleotide Content



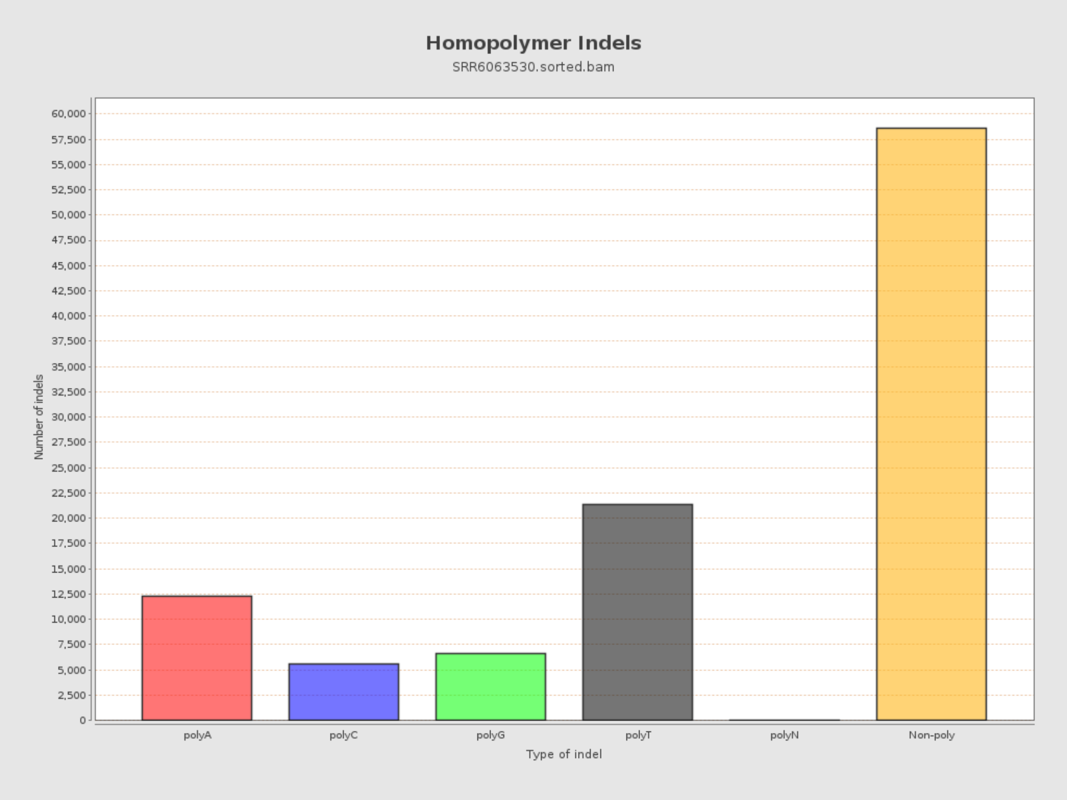
9. Results : Mapped Reads GC-content Distribution



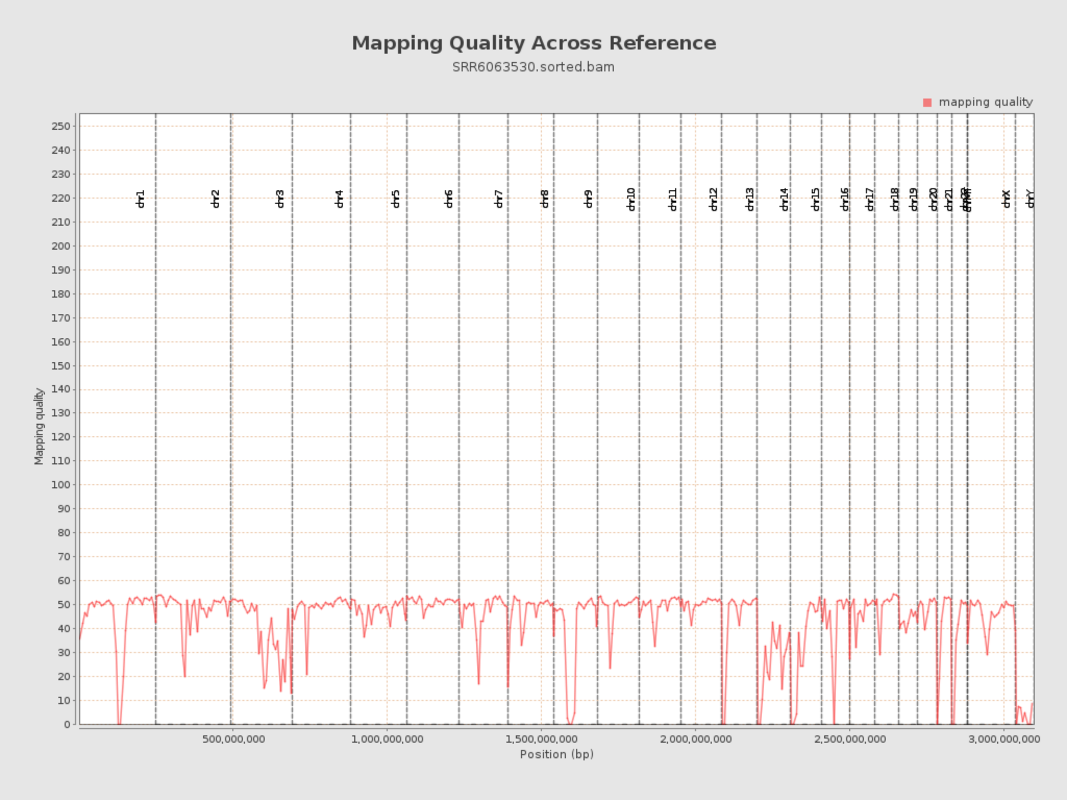
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram