Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:29:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063560.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_SRR6063560 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063560.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:29:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063560.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,542,475
Mapped reads	2,304,673 / 90.65%
Unmapped reads	237,802 / 9.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,974 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	137,927 / 5.42%
Duplication rate	4.78%
Clipped reads	1,088,428 / 42.81%

2.2. ACGT Content

Number/percentage of A's	42,840,187 / 28.07%
Number/percentage of C's	27,956,766 / 18.32%
Number/percentage of T's	48,652,120 / 31.88%
Number/percentage of G's	33,152,588 / 21.72%
Number/percentage of N's	4,494 / 0%
GC Percentage	40.04%

2.3. Coverage

Mean	0.0493

Standard Deviation	0.4465

2.4. Mapping Quality

Mean Mapping Quality	43.8

2.5. Mismatches and indels

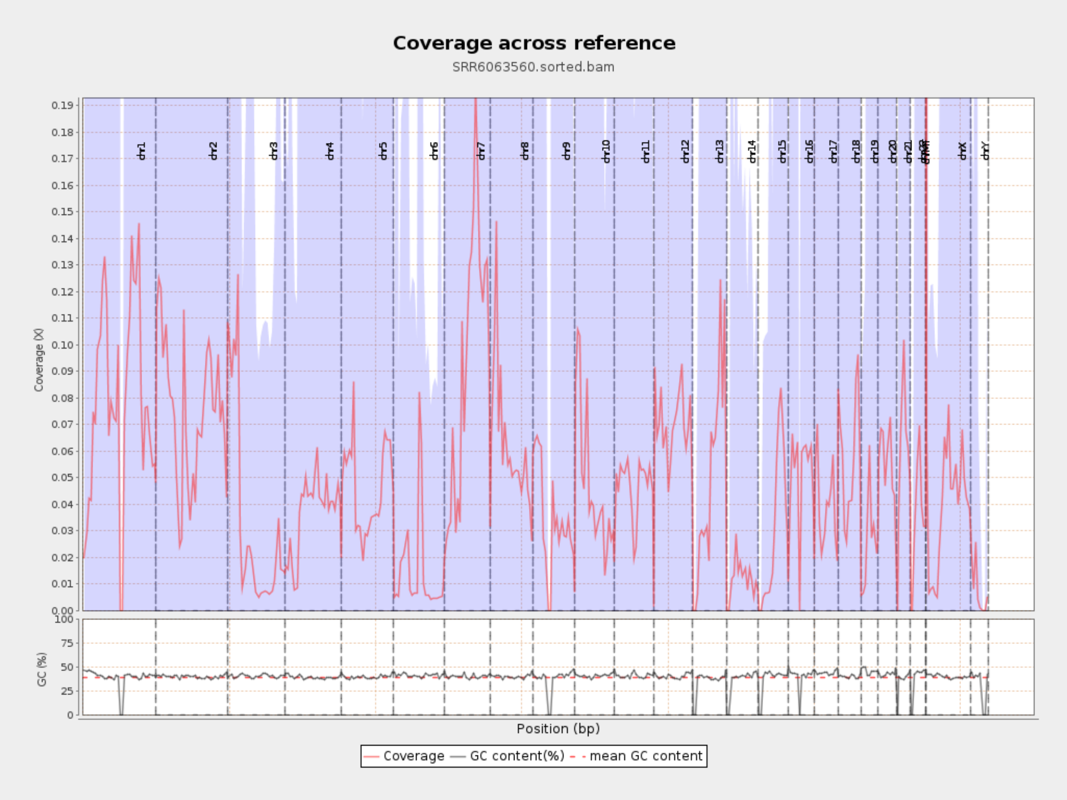
General error rate	0.82%
Mismatches	1,229,728
Insertions	11,823
Mapped reads with at least one insertion	0.51%
Deletions	41,759
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.15%

2.6. Chromosome stats

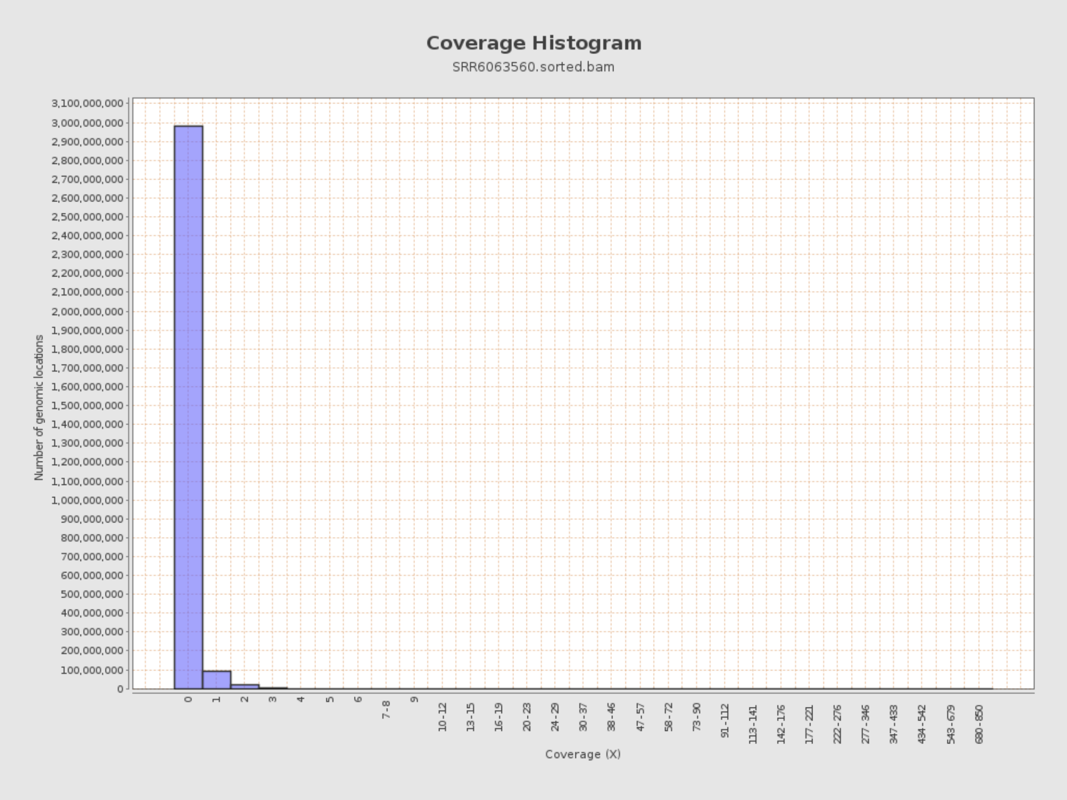
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19580013	0.0786	0.7458
chr2	243199373	18446185	0.0758	0.6013
chr3	198022430	6574146	0.0332	0.2384
chr4	191154276	7160491	0.0375	0.2539
chr5	180915260	8309946	0.0459	0.2643
chr6	171115067	2600418	0.0152	0.1832
chr7	159138663	14864446	0.0934	0.8348

chr8	146364022	9170683	0.0627	0.6075
chr9	141213431	4826140	0.0342	0.3635
chr10	135534747	6479205	0.0478	0.463
chr11	135006516	6265165	0.0464	0.3664
chr12	133851895	9457178	0.0707	0.3342
chr13	115169878	5846271	0.0508	0.285
chr14	107349540	1295987	0.0121	0.1651
chr15	102531392	3086009	0.0301	0.2237
chr16	90354753	4465376	0.0494	0.3014
chr17	81195210	3321390	0.0409	0.2742
chr18	78077248	4502108	0.0577	0.5525
chr19	59128983	1576496	0.0267	0.5423
chr20	63025520	3539330	0.0562	0.3018
chr21	48129895	2827157	0.0587	0.3112
chr22	51304566	1804755	0.0352	0.2285
chrMT	16571	108422	6.5429	4.7059
chrX	155270560	6118929	0.0394	0.2769
chrY	59373566	448716	0.0076	0.2041

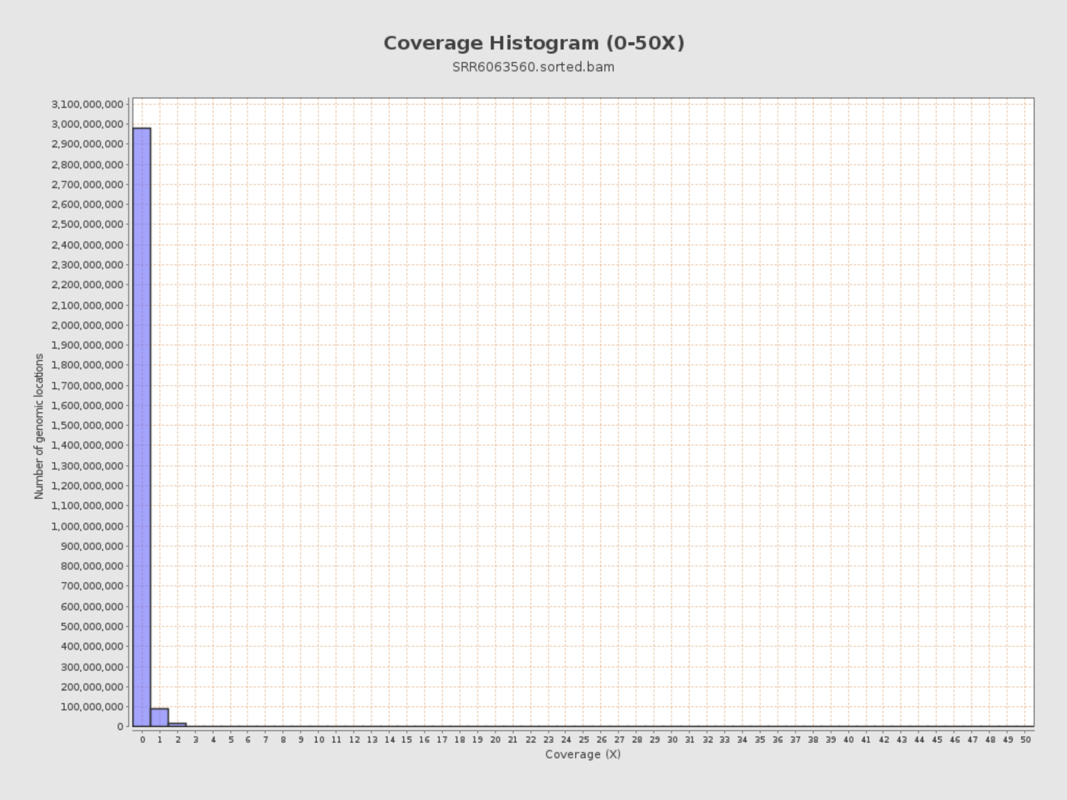
3. Results : Coverage across reference



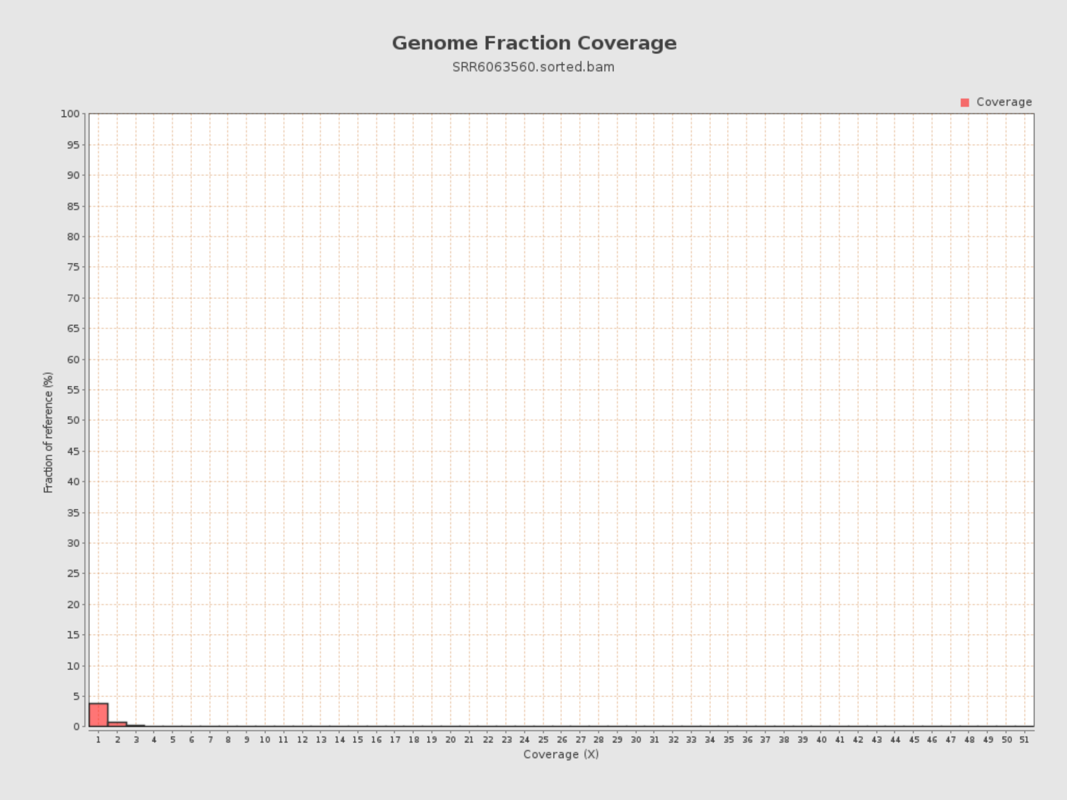
4. Results : Coverage Histogram



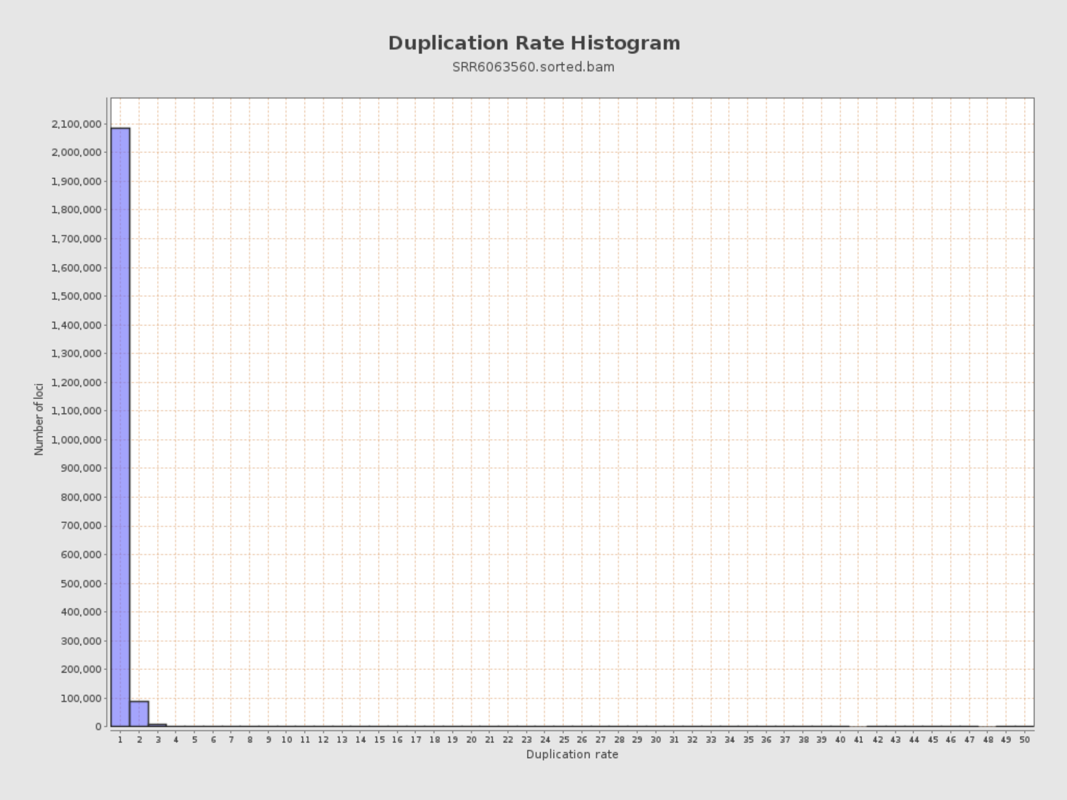
5. Results : Coverage Histogram (0-50X)



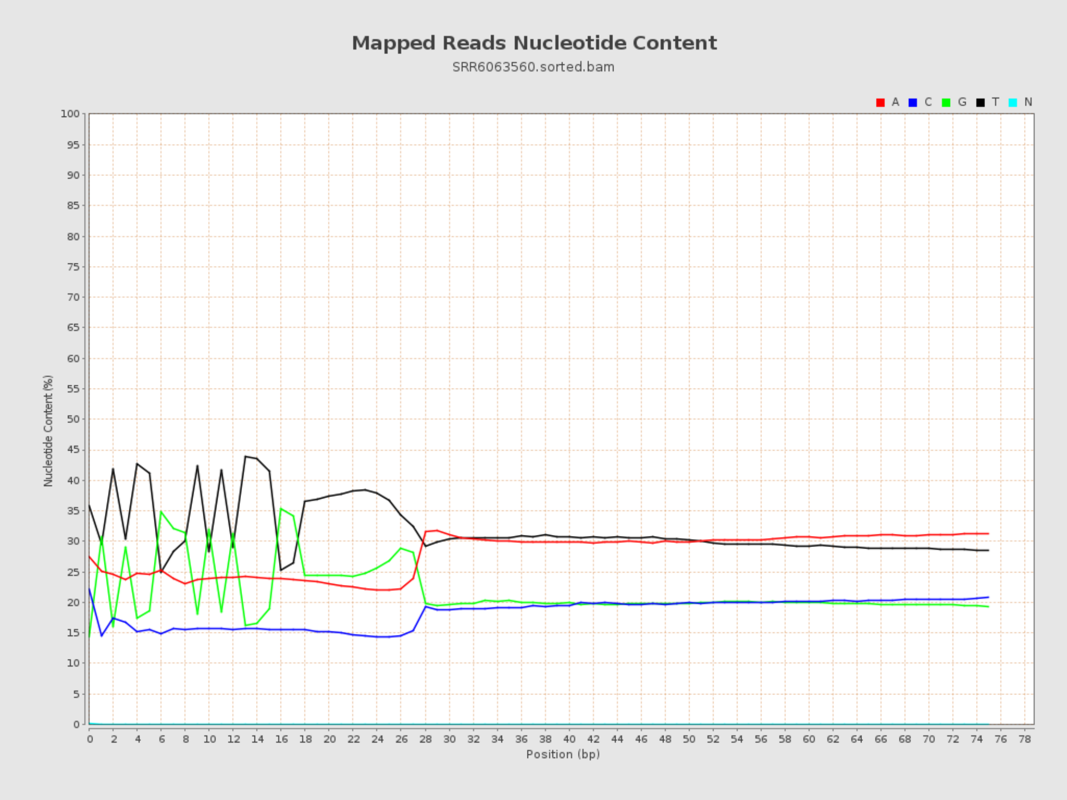
6. Results : Genome Fraction Coverage



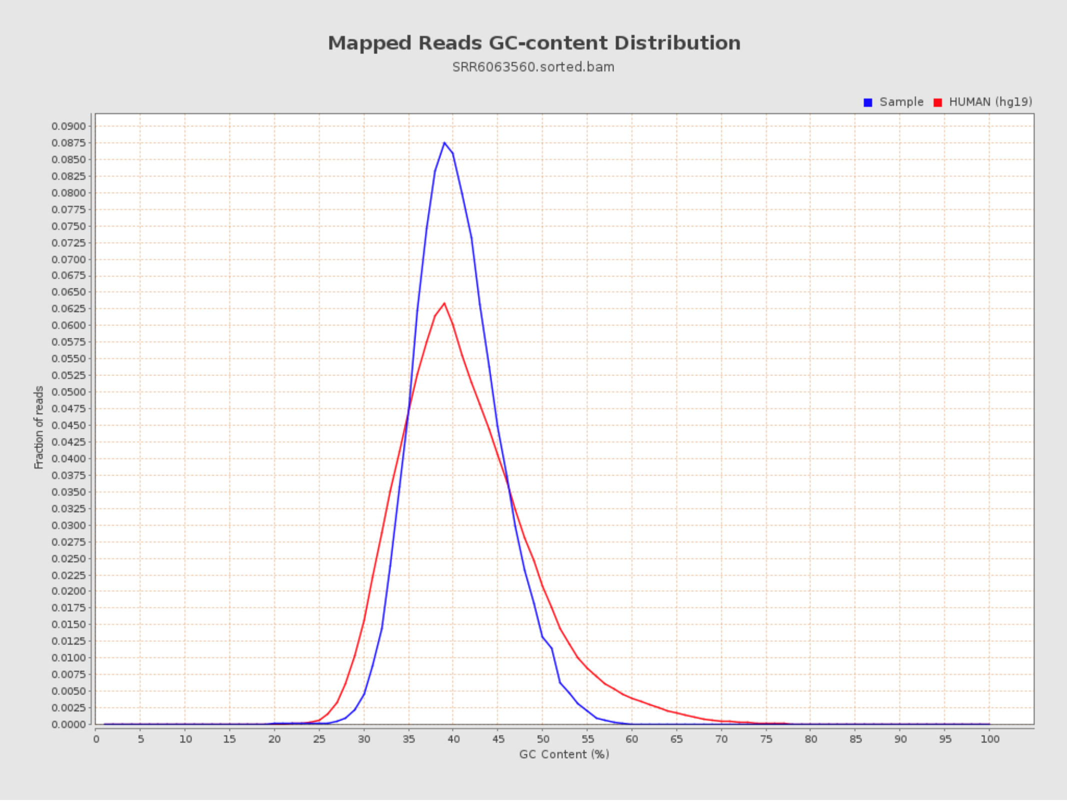
7. Results : Duplication Rate Histogram



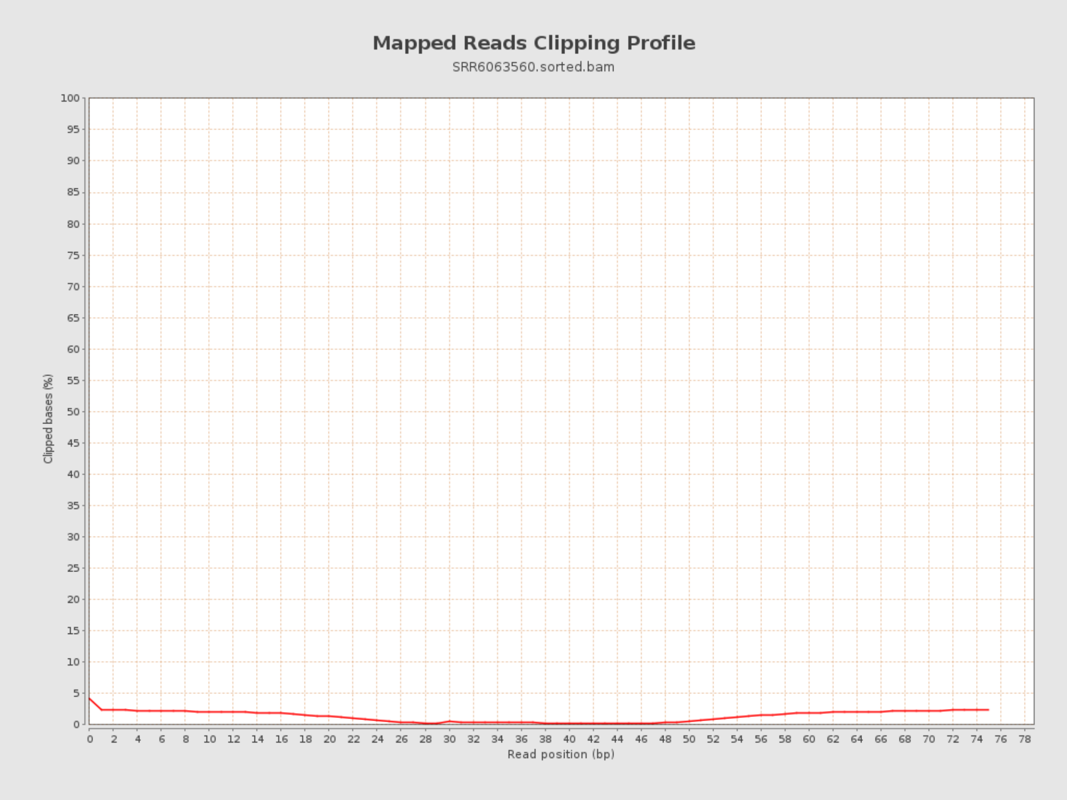
8. Results : Mapped Reads Nucleotide Content



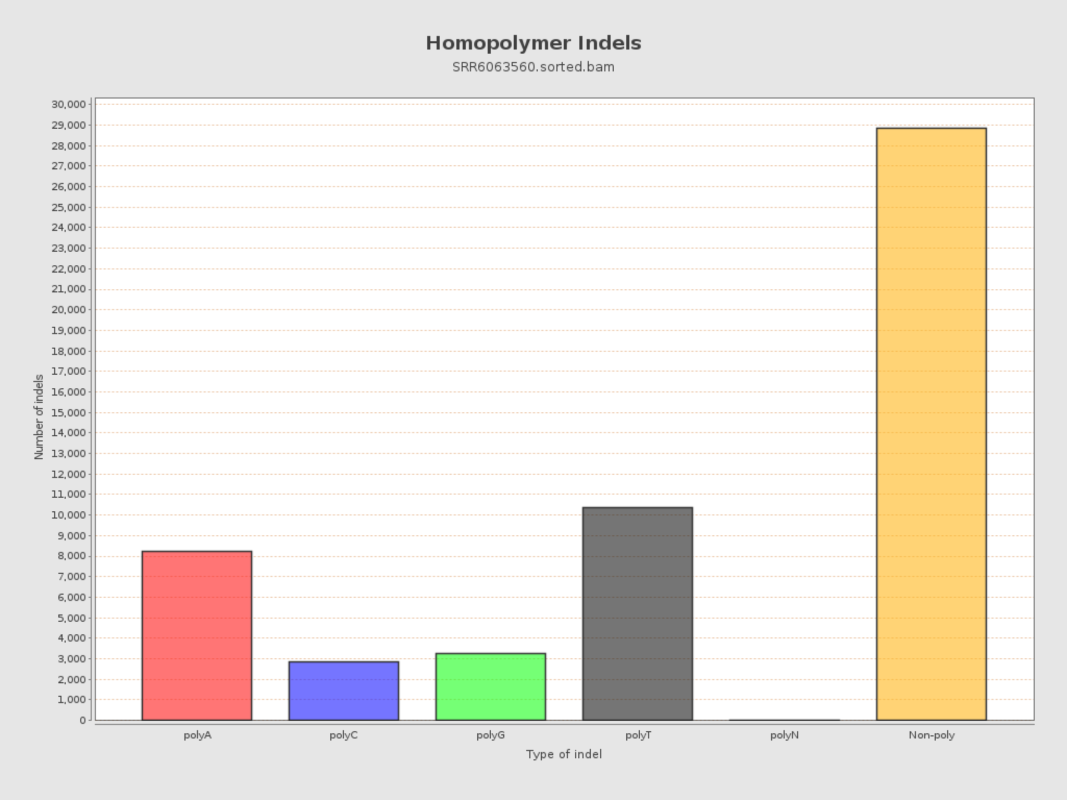
9. Results : Mapped Reads GC-content Distribution



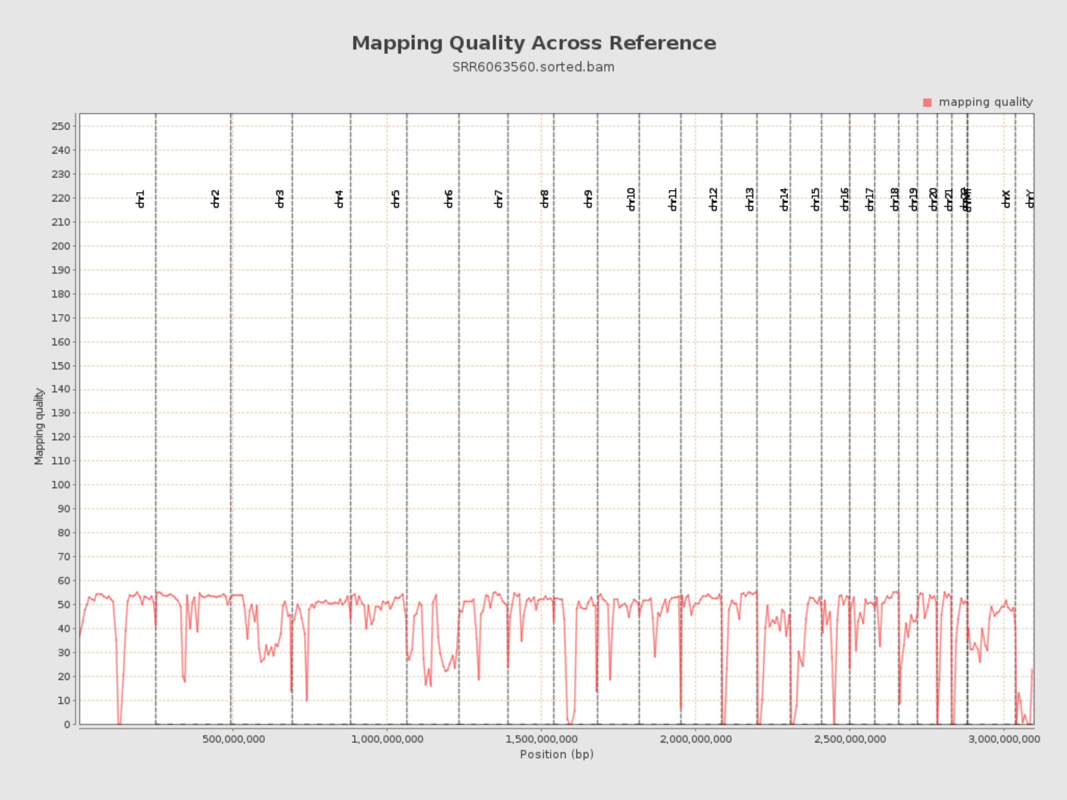
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram