Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:23:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063528.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_SRR6063528 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063528.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:23:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063528.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,536,827
Mapped reads	5,252,569 / 94.87%
Unmapped reads	284,258 / 5.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,817 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	662,894 / 11.97%
Duplication rate	10.57%
Clipped reads	2,733,877 / 49.38%

2.2. ACGT Content

Number/percentage of A's	86,666,012 / 25.64%
Number/percentage of C's	61,282,899 / 18.13%
Number/percentage of T's	109,543,286 / 32.41%
Number/percentage of G's	80,469,297 / 23.81%
Number/percentage of N's	37,567 / 0.01%
GC Percentage	41.94%

2.3. Coverage

Mean	0.1092

Standard Deviation	1.3461

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

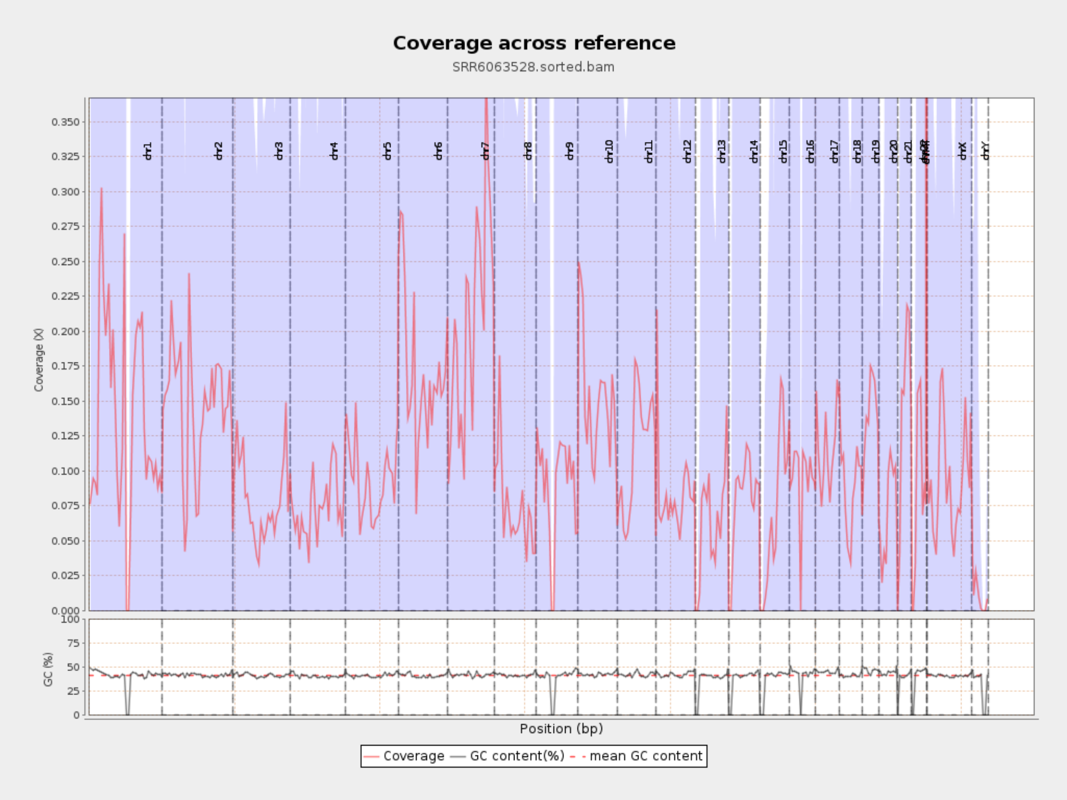
General error rate	0.54%
Mismatches	1,779,649
Insertions	20,234
Mapped reads with at least one insertion	0.38%
Deletions	82,558
Mapped reads with at least one deletion	1.56%
Homopolymer indels	44.61%

2.6. Chromosome stats

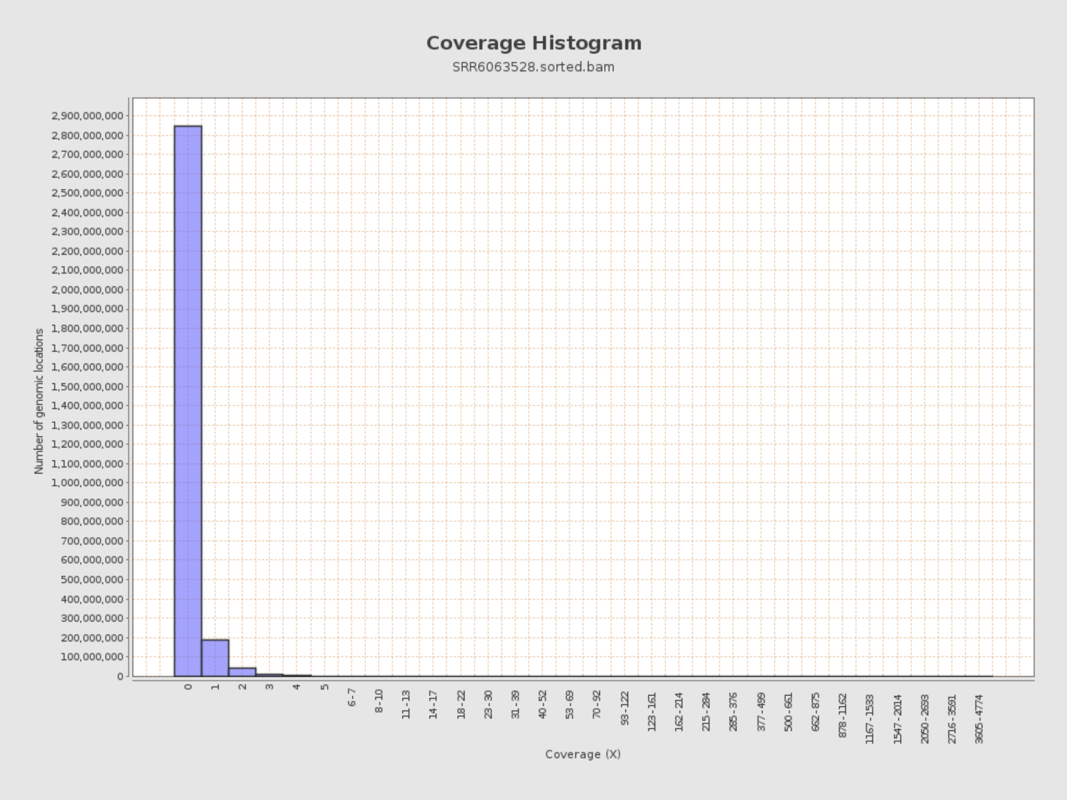
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34828443	0.1397	3.6558
chr2	243199373	35895407	0.1476	1.7964
chr3	198022430	15609884	0.0788	0.3713
chr4	191154276	14089282	0.0737	0.3766
chr5	180915260	16890981	0.0934	0.4084
chr6	171115067	29356283	0.1716	0.8443
chr7	159138663	33458573	0.2102	1.5392

chr8	146364022	10837597	0.074	0.6278
chr9	141213431	12687200	0.0898	0.7477
chr10	135534747	20835488	0.1537	0.7701
chr11	135006516	15371881	0.1139	0.5833
chr12	133851895	11268940	0.0842	0.4311
chr13	115169878	7333087	0.0637	0.3927
chr14	107349540	8428568	0.0785	0.4404
chr15	102531392	7203202	0.0703	0.4132
chr16	90354753	8469542	0.0937	0.4672
chr17	81195210	9556530	0.1177	0.4928
chr18	78077248	6960194	0.0891	1.4787
chr19	59128983	8287677	0.1402	2.1371
chr20	63025520	4478111	0.0711	0.4134
chr21	48129895	6793868	0.1412	0.5084
chr22	51304566	4130367	0.0805	0.364
chrMT	16571	125167	7.5534	5.1355
chrX	155270560	14613089	0.0941	0.5424
chrY	59373566	634383	0.0107	0.238

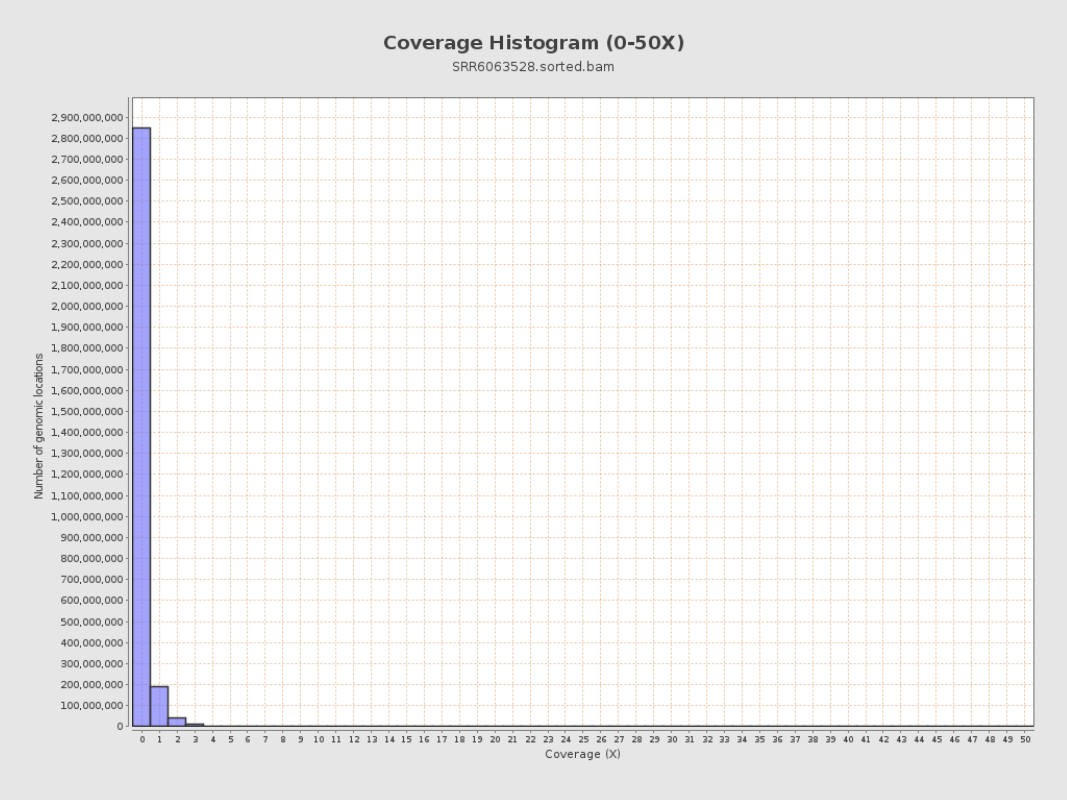
3. Results : Coverage across reference



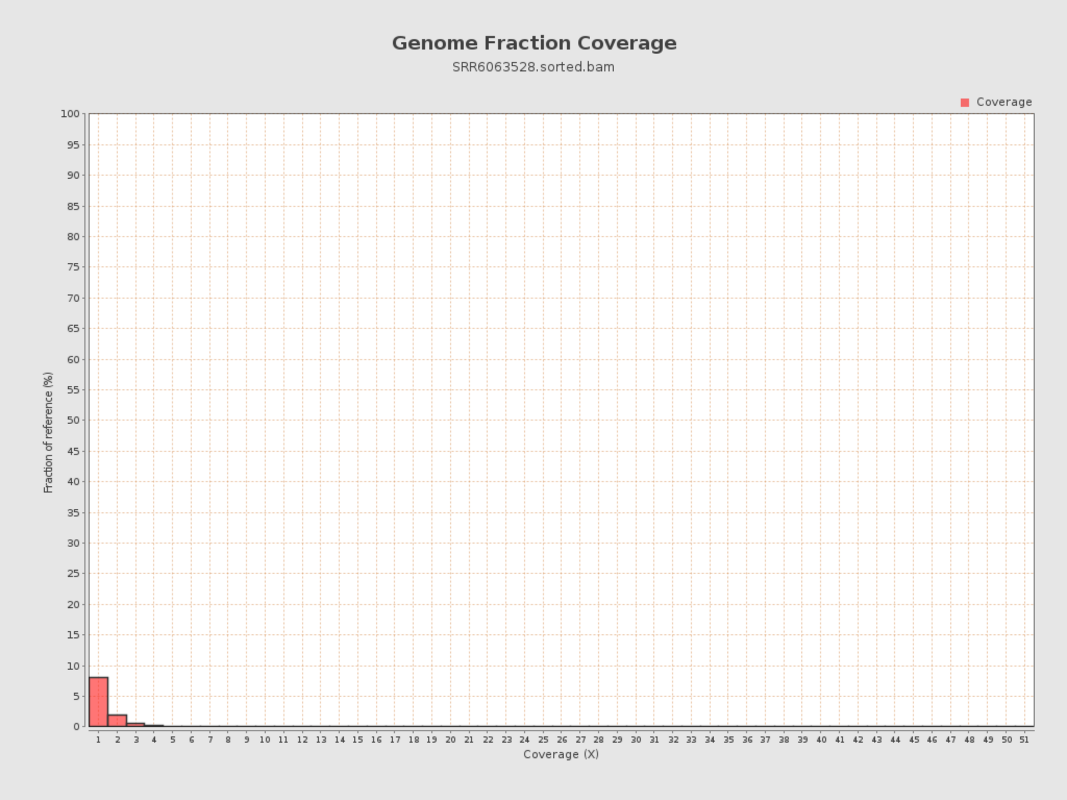
4. Results : Coverage Histogram



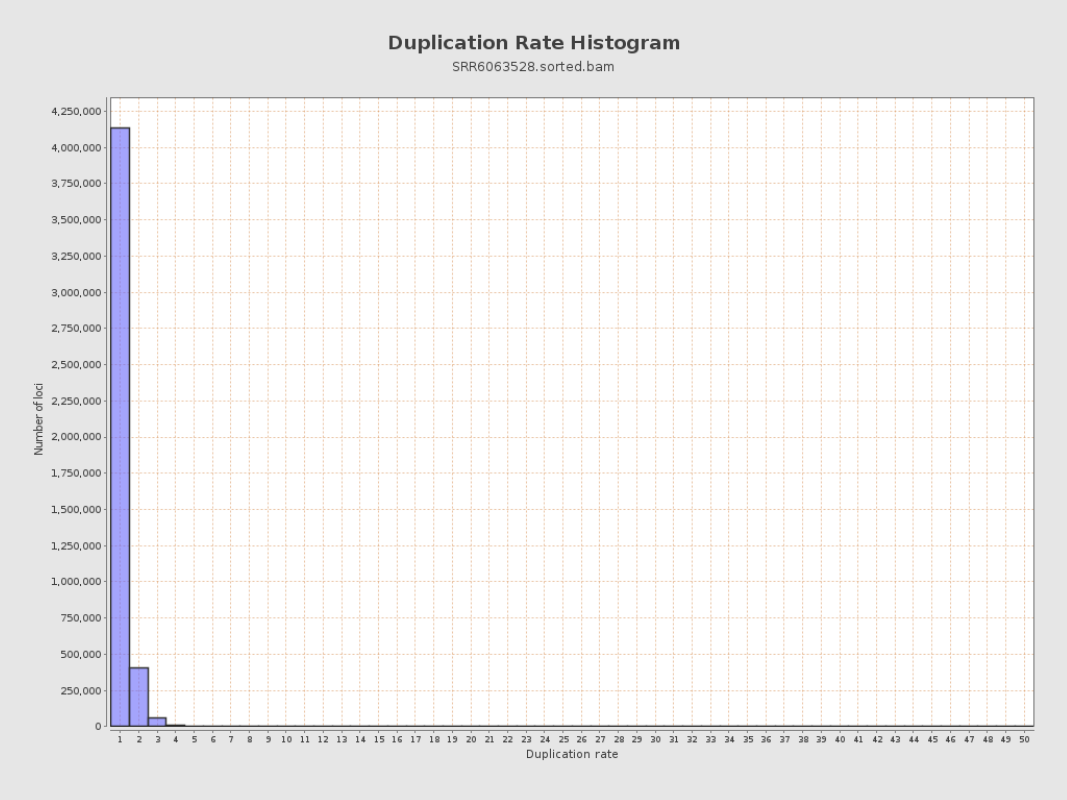
5. Results : Coverage Histogram (0-50X)



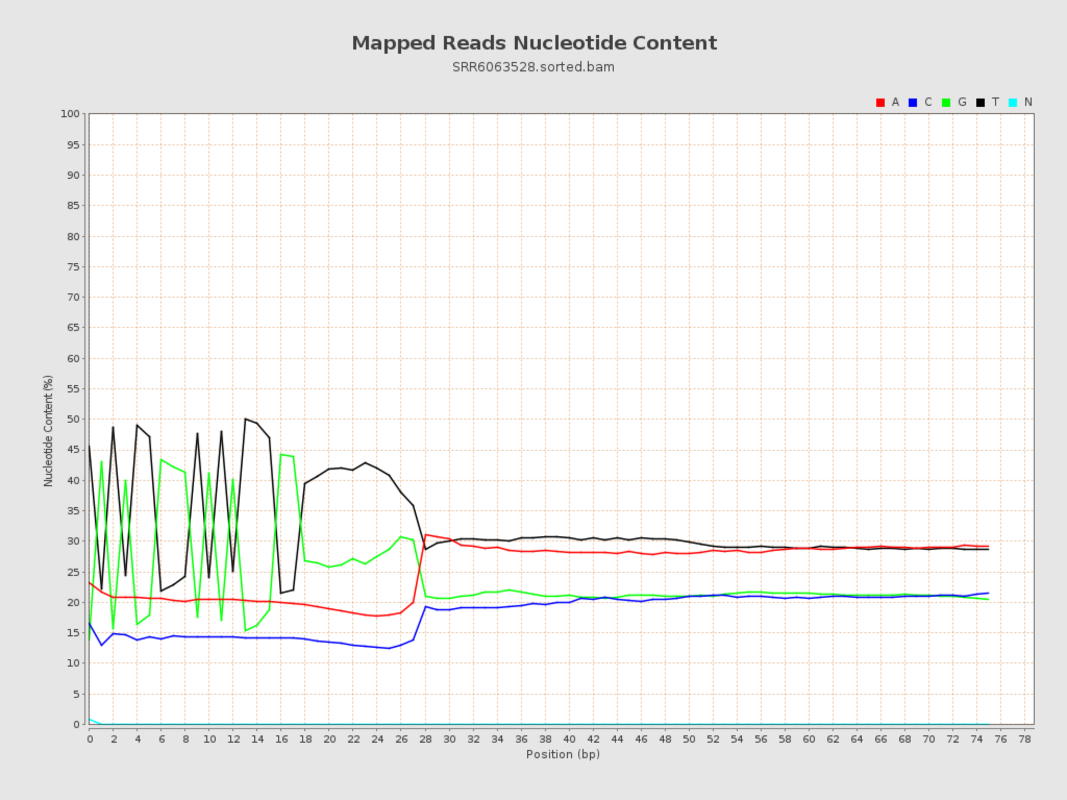
6. Results : Genome Fraction Coverage



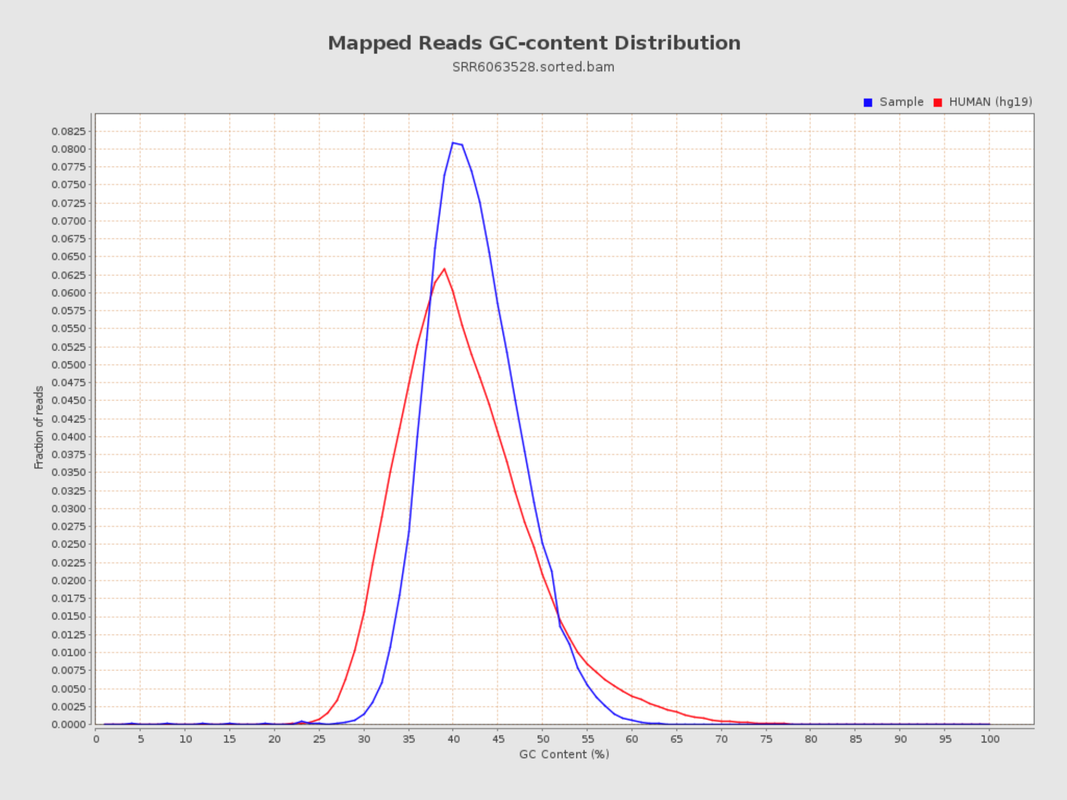
7. Results : Duplication Rate Histogram



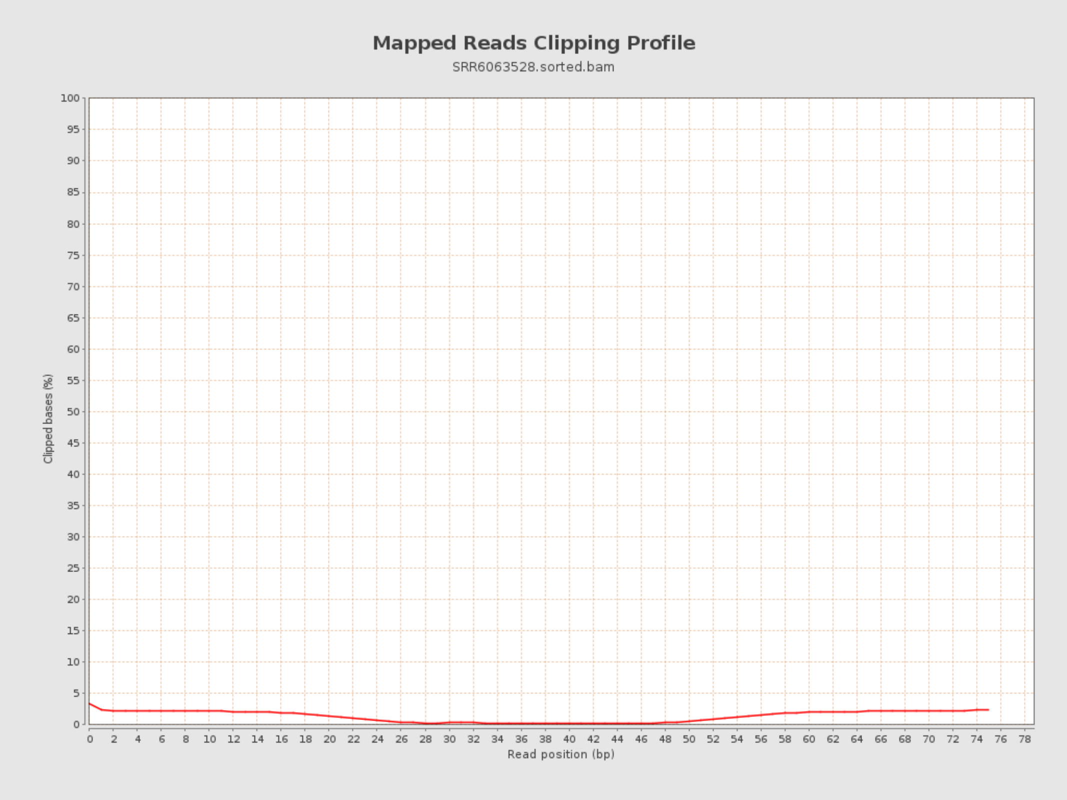
8. Results : Mapped Reads Nucleotide Content



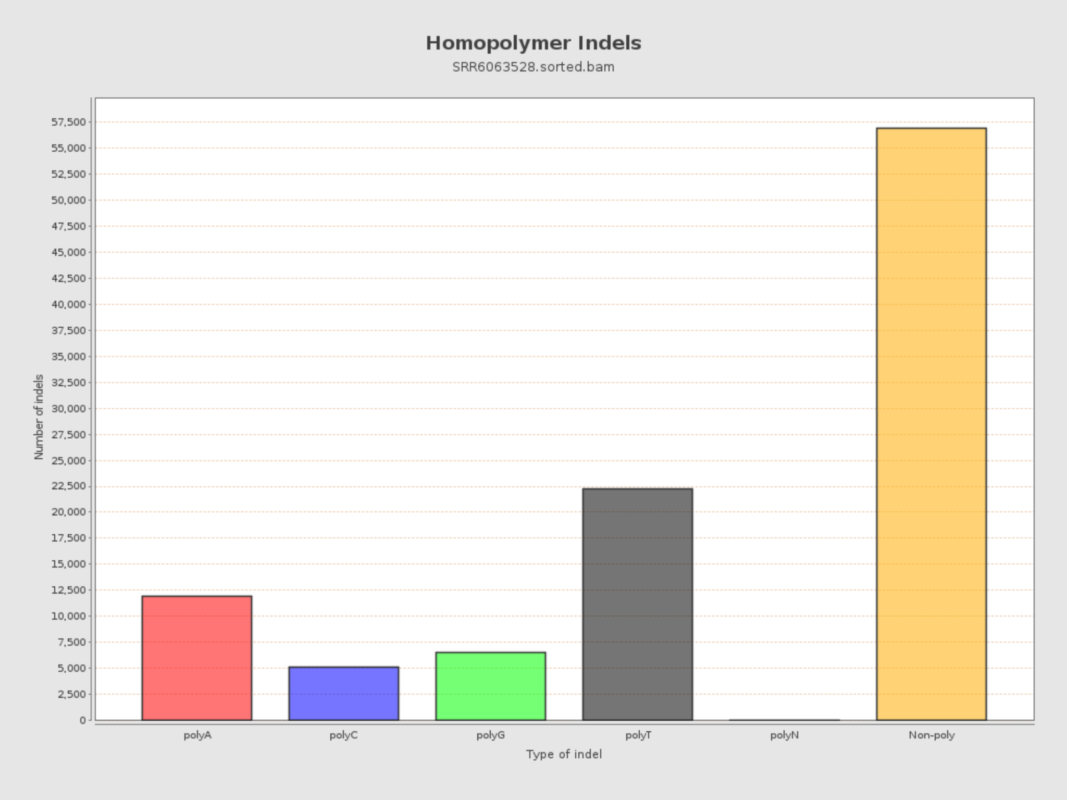
9. Results : Mapped Reads GC-content Distribution



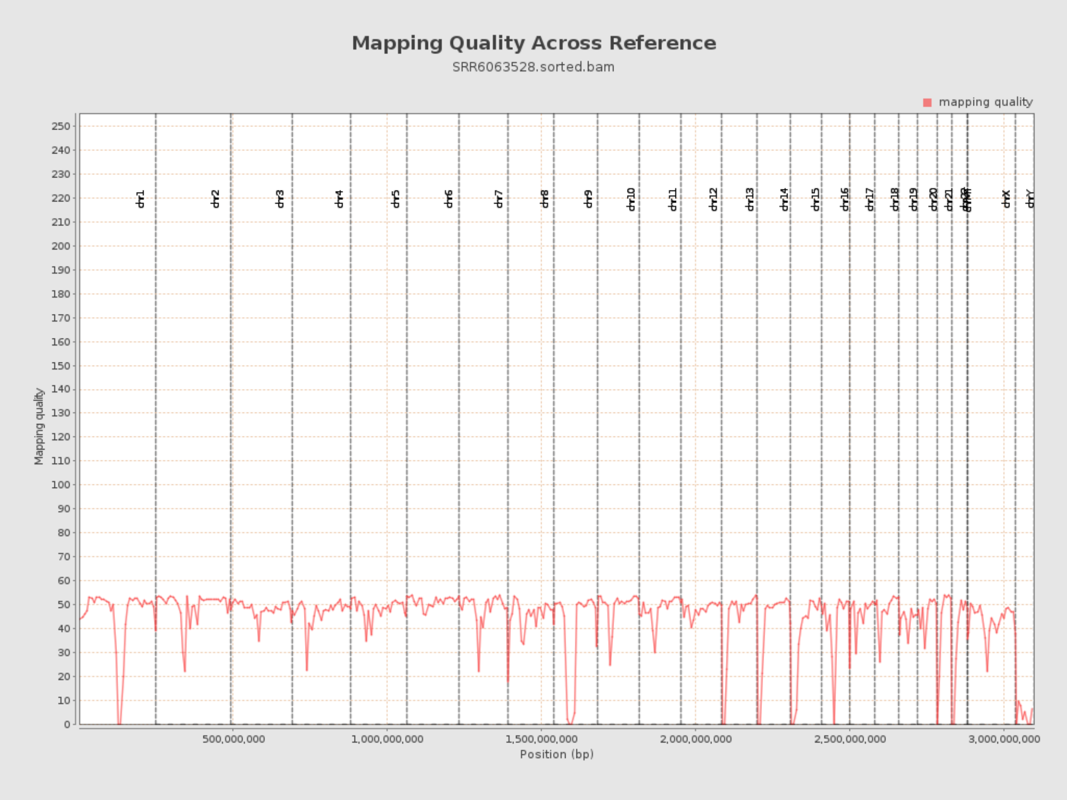
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram