Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:18:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063527.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_SRR6063527 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063527.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:18:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063527.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,884,984
Mapped reads	2,567,291 / 88.99%
Unmapped reads	317,693 / 11.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,637 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	579,407 / 20.08%
Duplication rate	17.24%
Clipped reads	1,640,819 / 56.87%

2.2. ACGT Content

Number/percentage of A's	40,004,770 / 25.33%
Number/percentage of C's	27,048,302 / 17.13%
Number/percentage of T's	53,316,066 / 33.76%
Number/percentage of G's	37,560,868 / 23.78%
Number/percentage of N's	15,835 / 0.01%
GC Percentage	40.91%

2.3. Coverage

Mean	0.051

Standard Deviation	0.7035

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

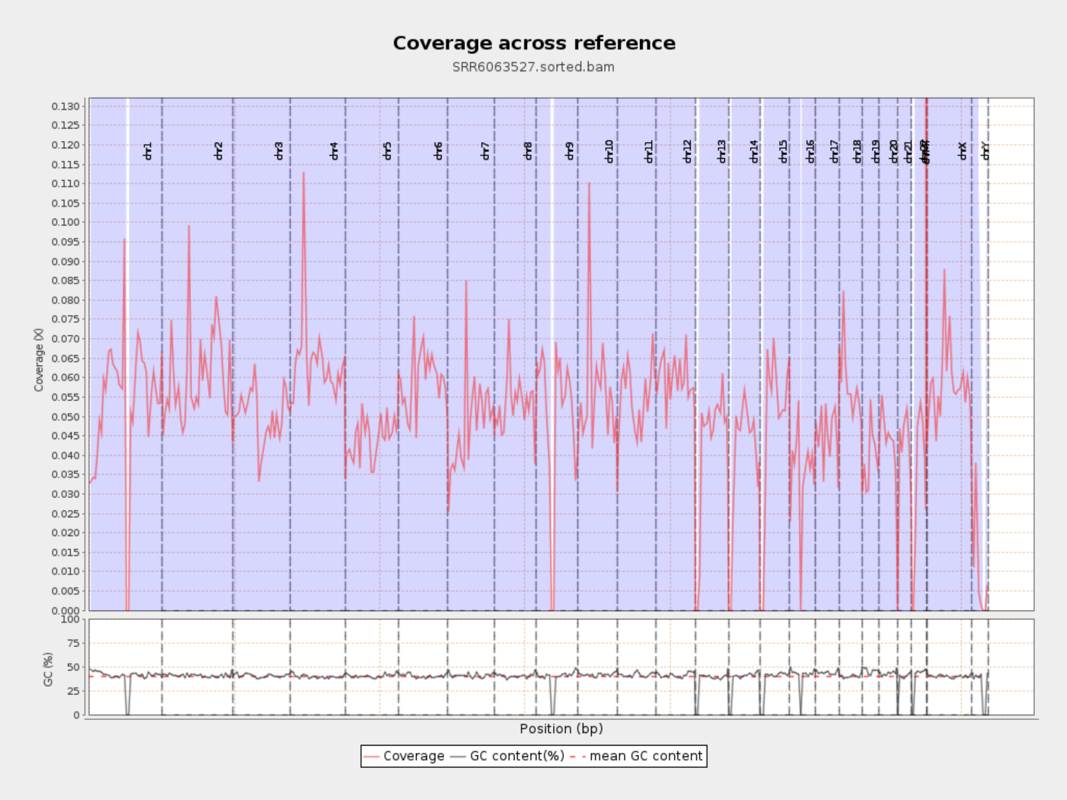
General error rate	0.66%
Mismatches	1,020,934
Insertions	11,049
Mapped reads with at least one insertion	0.43%
Deletions	46,408
Mapped reads with at least one deletion	1.79%
Homopolymer indels	41.68%

2.6. Chromosome stats

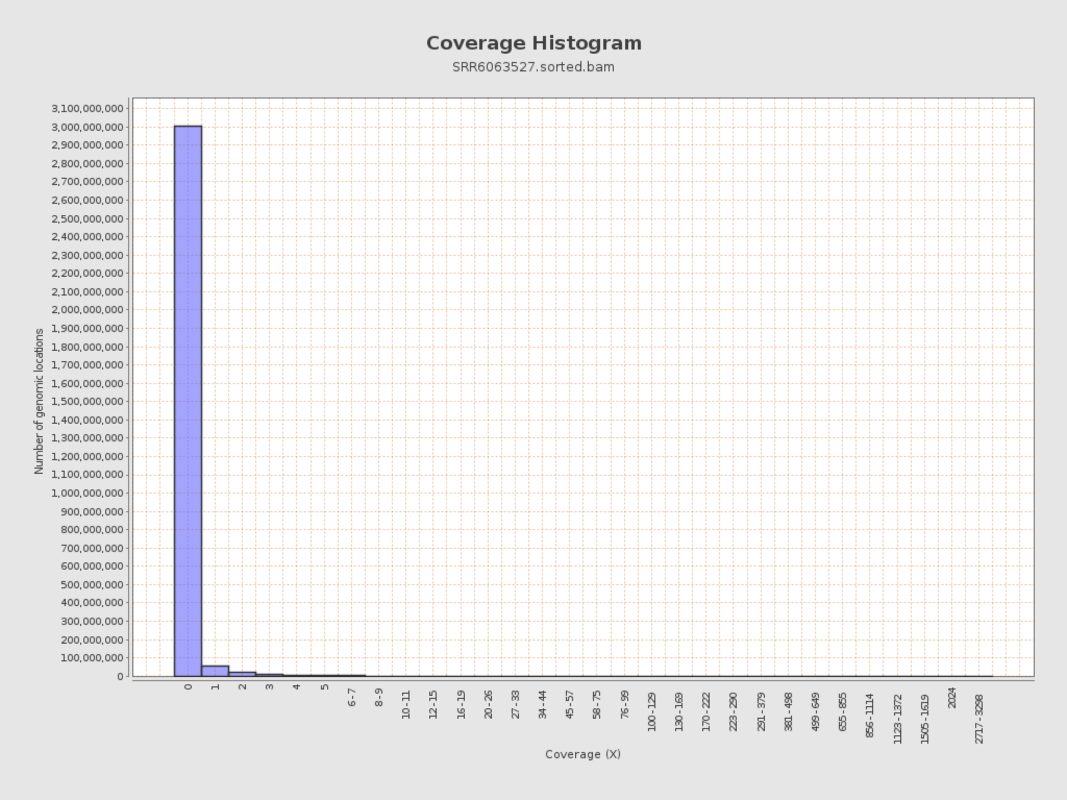
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13315124	0.0534	0.9267
chr2	243199373	14717194	0.0605	1.5786
chr3	198022430	9951973	0.0503	0.364
chr4	191154276	12245013	0.0641	0.4833
chr5	180915260	8033753	0.0444	0.3444
chr6	171115067	10218793	0.0597	0.6338
chr7	159138663	7714410	0.0485	0.6072

chr8	146364022	7808127	0.0533	0.6444
chr9	141213431	7090291	0.0502	0.5447
chr10	135534747	7645477	0.0564	0.6024
chr11	135006516	7404540	0.0548	0.4976
chr12	133851895	7994297	0.0597	0.4229
chr13	115169878	4816551	0.0418	0.3919
chr14	107349540	4238403	0.0395	0.3521
chr15	102531392	4907339	0.0479	0.3901
chr16	90354753	3196644	0.0354	0.358
chr17	81195210	3658292	0.0451	0.3786
chr18	78077248	4584735	0.0587	1.3237
chr19	59128983	2327101	0.0394	0.5718
chr20	63025520	2796234	0.0444	0.3693
chr21	48129895	1929285	0.0401	0.3702
chr22	51304566	1662223	0.0324	0.287
chrMT	16571	87784	5.2974	4.3661
chrX	155270560	9096115	0.0586	0.4282
chrY	59373566	586246	0.0099	0.3694

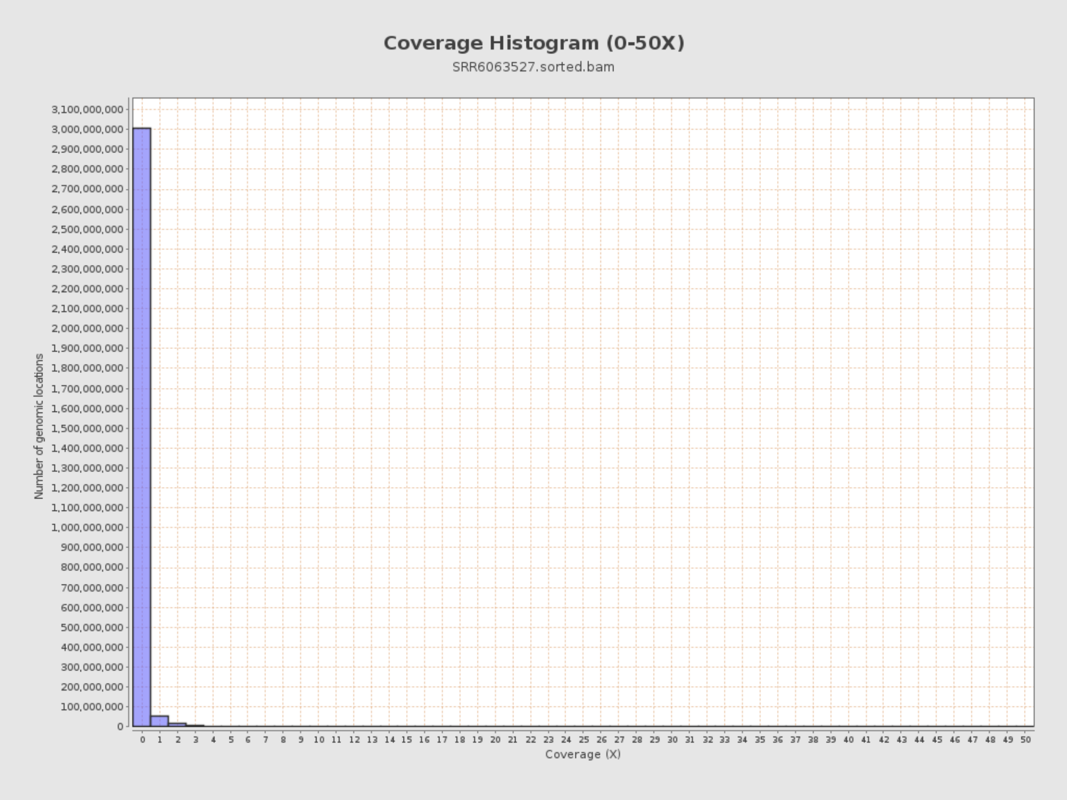
3. Results : Coverage across reference



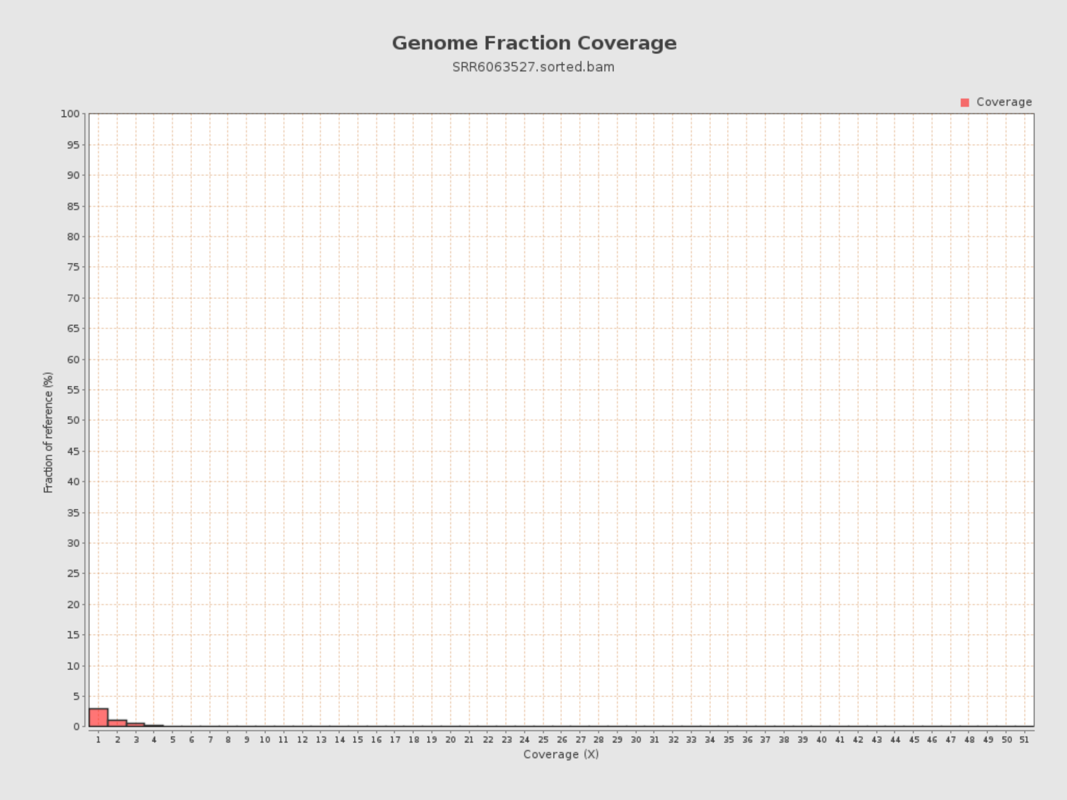
4. Results : Coverage Histogram



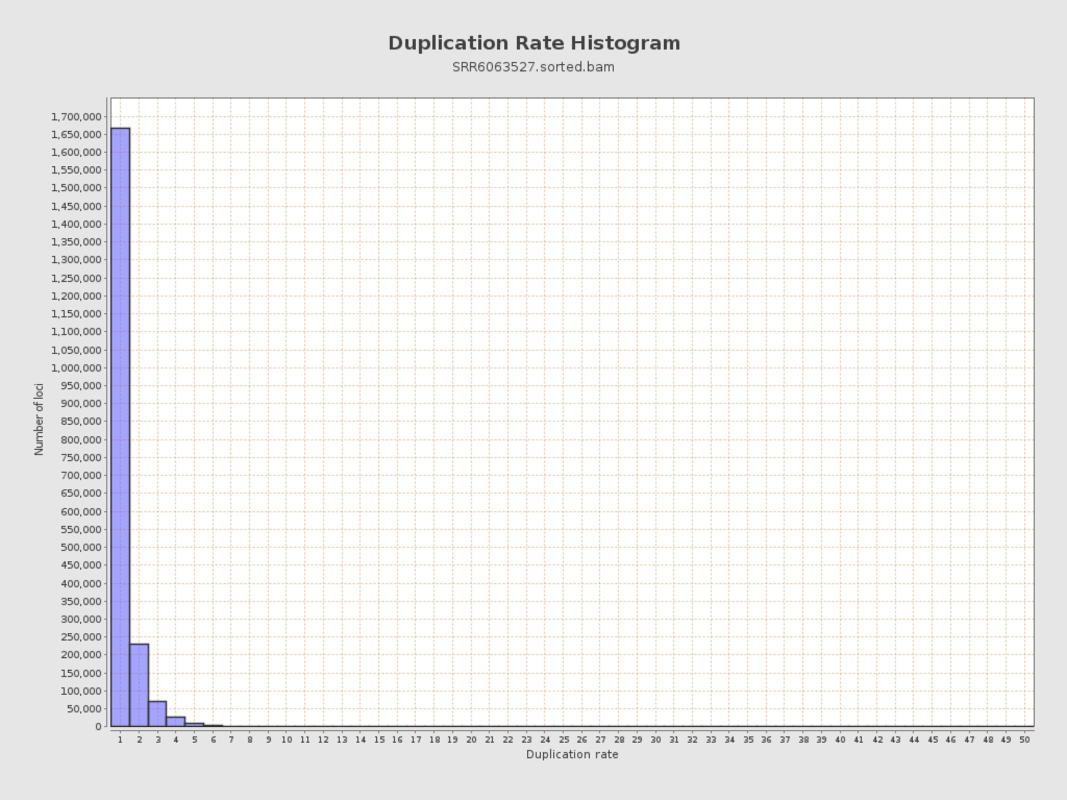
5. Results : Coverage Histogram (0-50X)



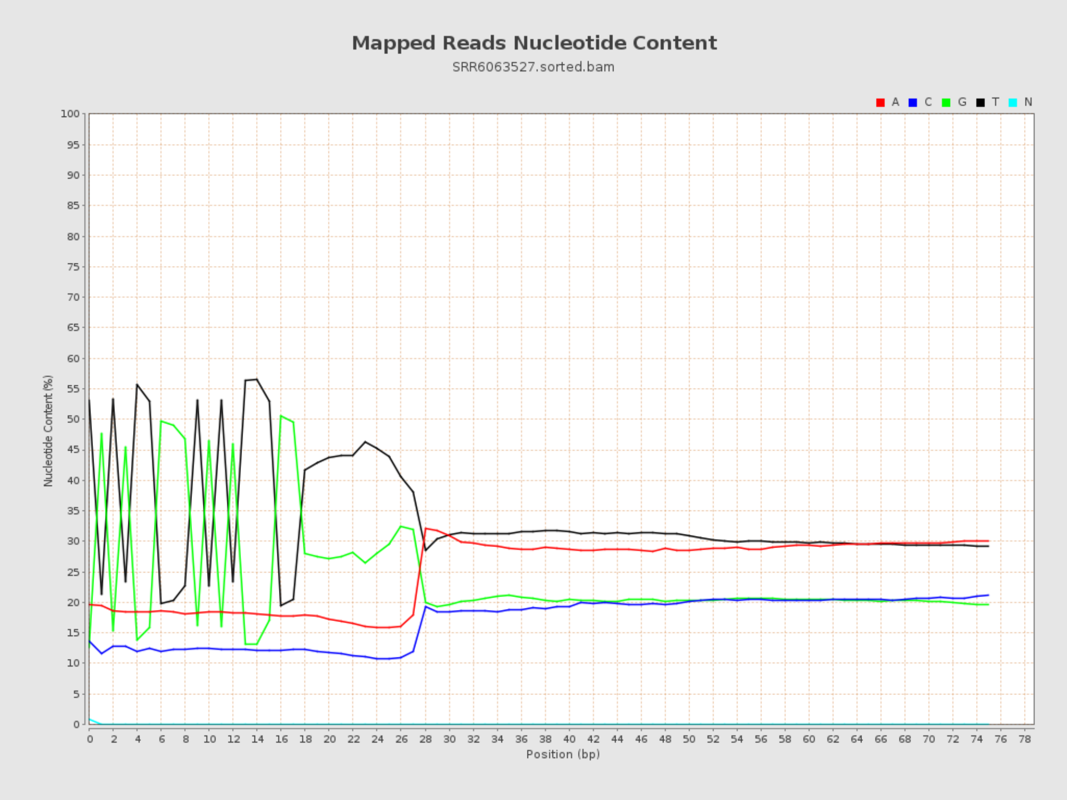
6. Results : Genome Fraction Coverage



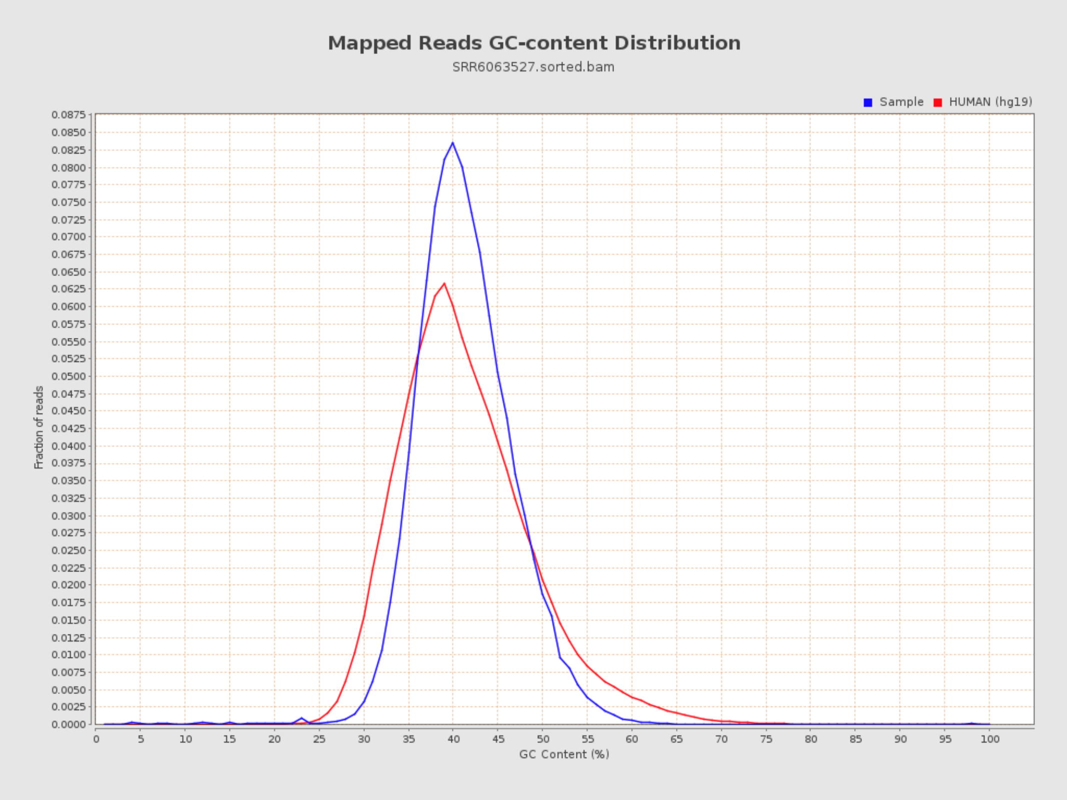
7. Results : Duplication Rate Histogram



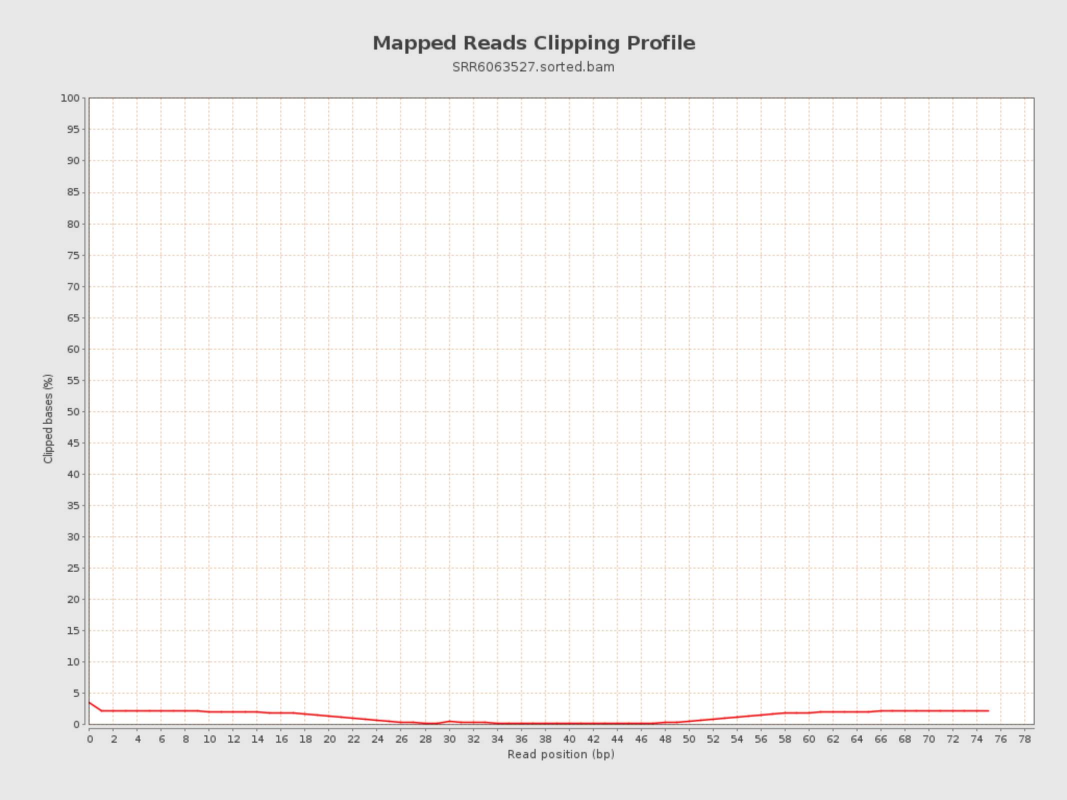
8. Results : Mapped Reads Nucleotide Content



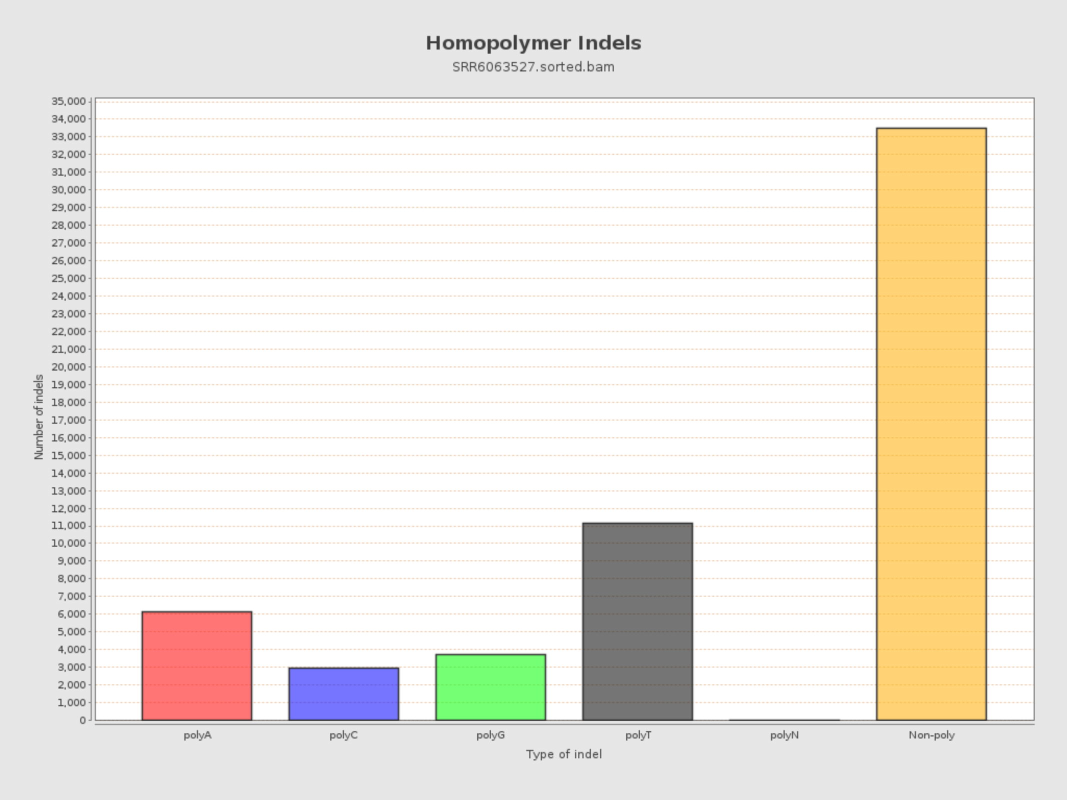
9. Results : Mapped Reads GC-content Distribution



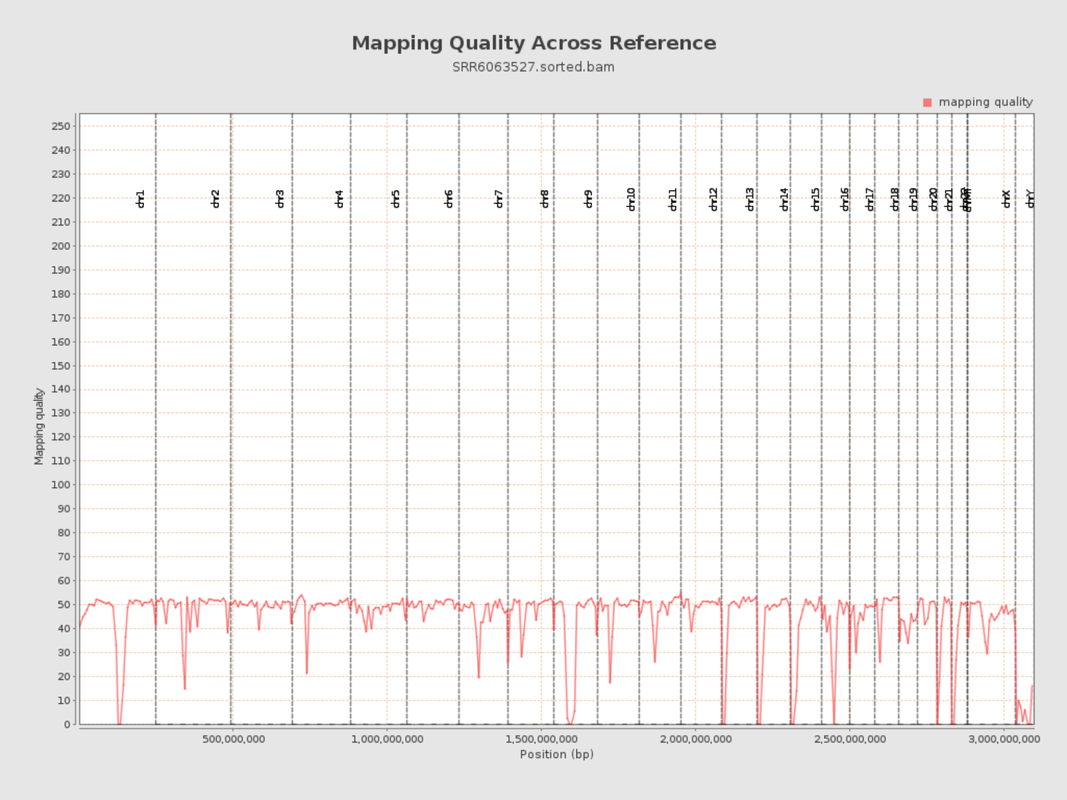
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram