Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 07:36:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212679.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_SRR3212679 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212679.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 07:36:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212679.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,737,889
Mapped reads	2,566,653 / 93.75%
Unmapped reads	171,236 / 6.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,122 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	117,776 / 4.3%
Duplication rate	3.86%
Clipped reads	936,171 / 34.19%

2.2. ACGT Content

Number/percentage of A's	50,100,217 / 28.42%
Number/percentage of C's	33,356,985 / 18.92%
Number/percentage of T's	55,315,088 / 31.38%
Number/percentage of G's	37,491,166 / 21.27%
Number/percentage of N's	2,012 / 0%
GC Percentage	40.19%

2.3. Coverage

Mean	0.057

Standard Deviation	0.3847

2.4. Mapping Quality

Mean Mapping Quality	47.56

2.5. Mismatches and indels

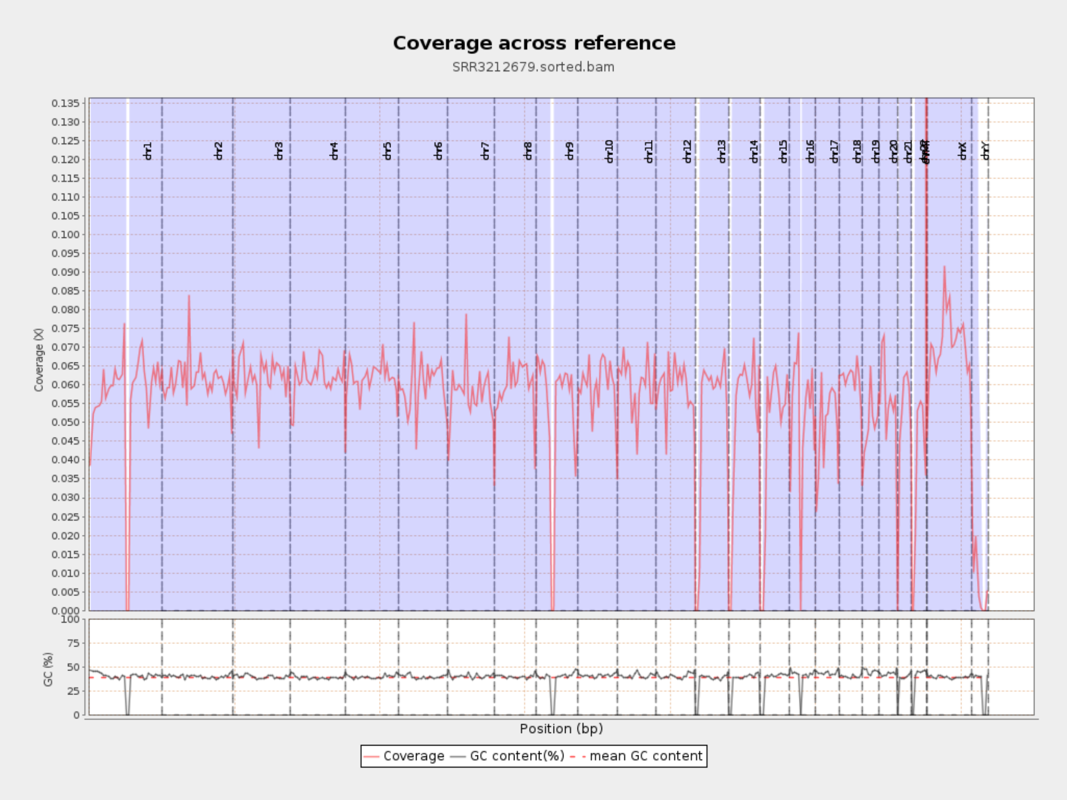
General error rate	0.83%
Mismatches	1,440,513
Insertions	12,574
Mapped reads with at least one insertion	0.49%
Deletions	36,939
Mapped reads with at least one deletion	1.42%
Homopolymer indels	48.99%

2.6. Chromosome stats

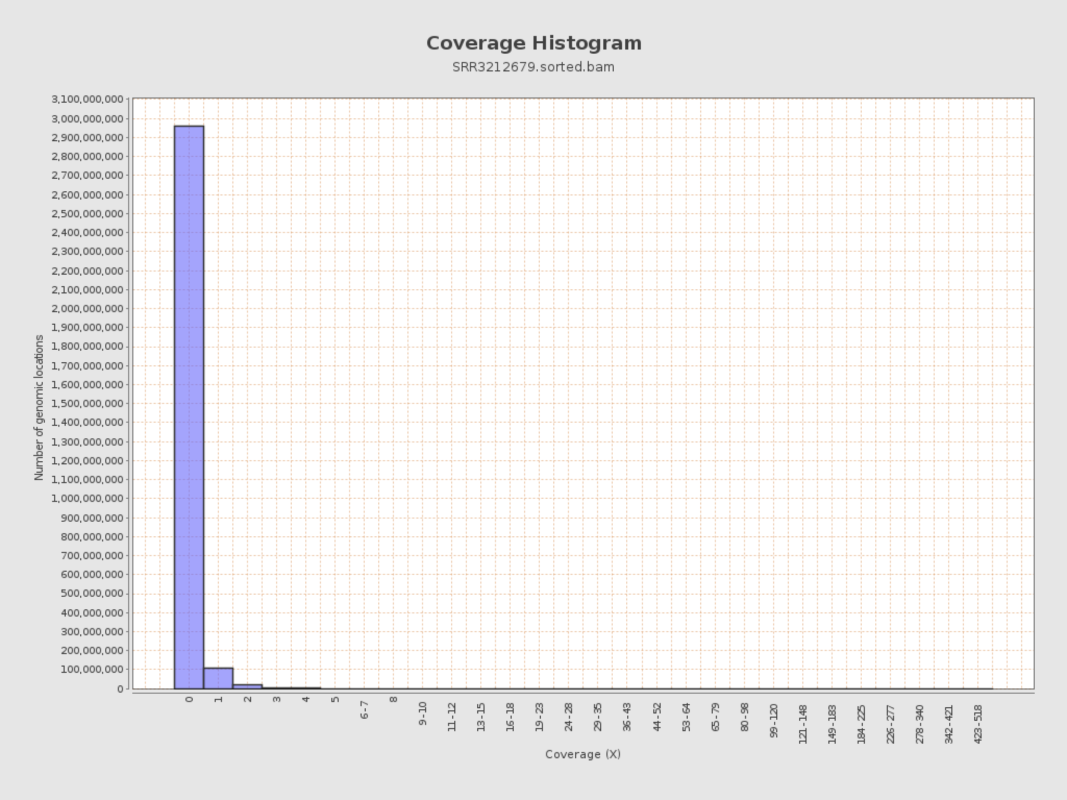
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14077308	0.0565	0.5377
chr2	243199373	14998396	0.0617	0.421
chr3	198022430	12377892	0.0625	0.3065
chr4	191154276	11813985	0.0618	0.321
chr5	180915260	11236412	0.0621	0.3085
chr6	171115067	10295481	0.0602	0.3662
chr7	159138663	9267509	0.0582	0.4924

chr8	146364022	8796511	0.0601	0.4538
chr9	141213431	7423362	0.0526	0.38
chr10	135534747	8200412	0.0605	0.3622
chr11	135006516	8118842	0.0601	0.3777
chr12	133851895	7945543	0.0594	0.3017
chr13	115169878	5879015	0.051	0.2794
chr14	107349540	5416323	0.0505	0.2968
chr15	102531392	4804303	0.0469	0.2727
chr16	90354753	4705097	0.0521	0.3019
chr17	81195210	3921853	0.0483	0.3112
chr18	78077248	4848025	0.0621	0.7
chr19	59128983	2940161	0.0497	0.4274
chr20	63025520	3580295	0.0568	0.3009
chr21	48129895	2406654	0.05	0.2972
chr22	51304566	1810429	0.0353	0.2277
chrMT	16571	93536	5.6446	4.1005
chrX	155270560	10959482	0.0706	0.3584
chrY	59373566	413741	0.007	0.1472

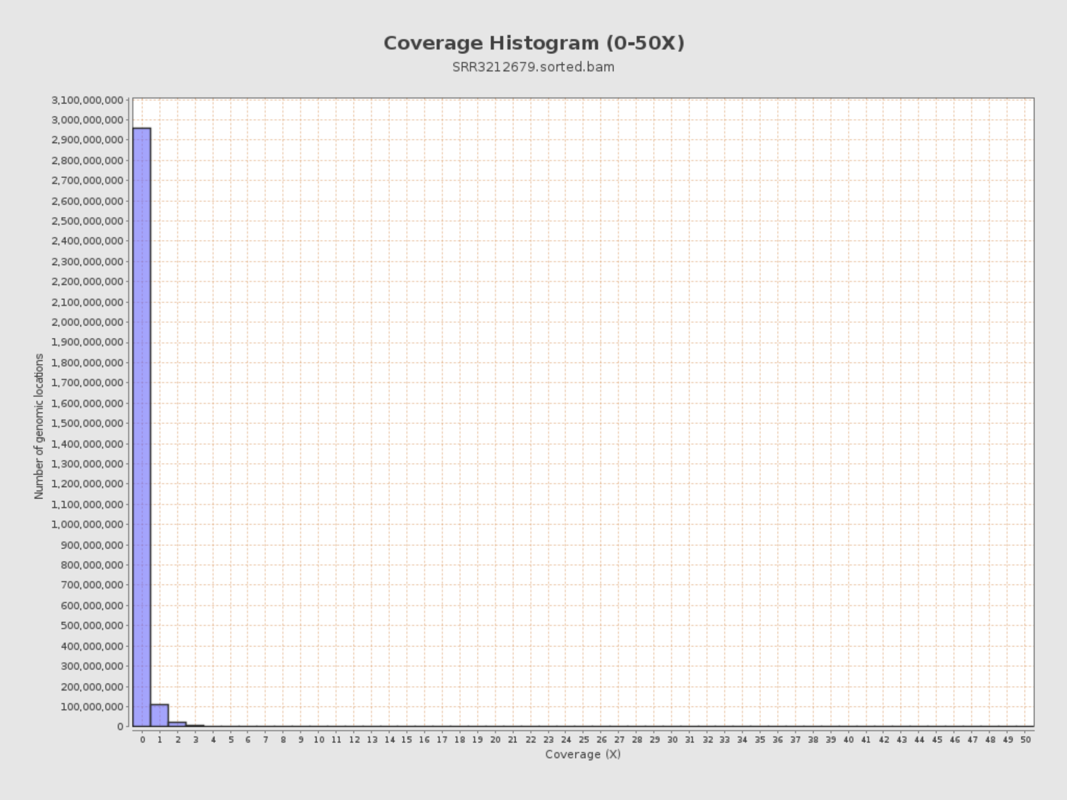
3. Results : Coverage across reference



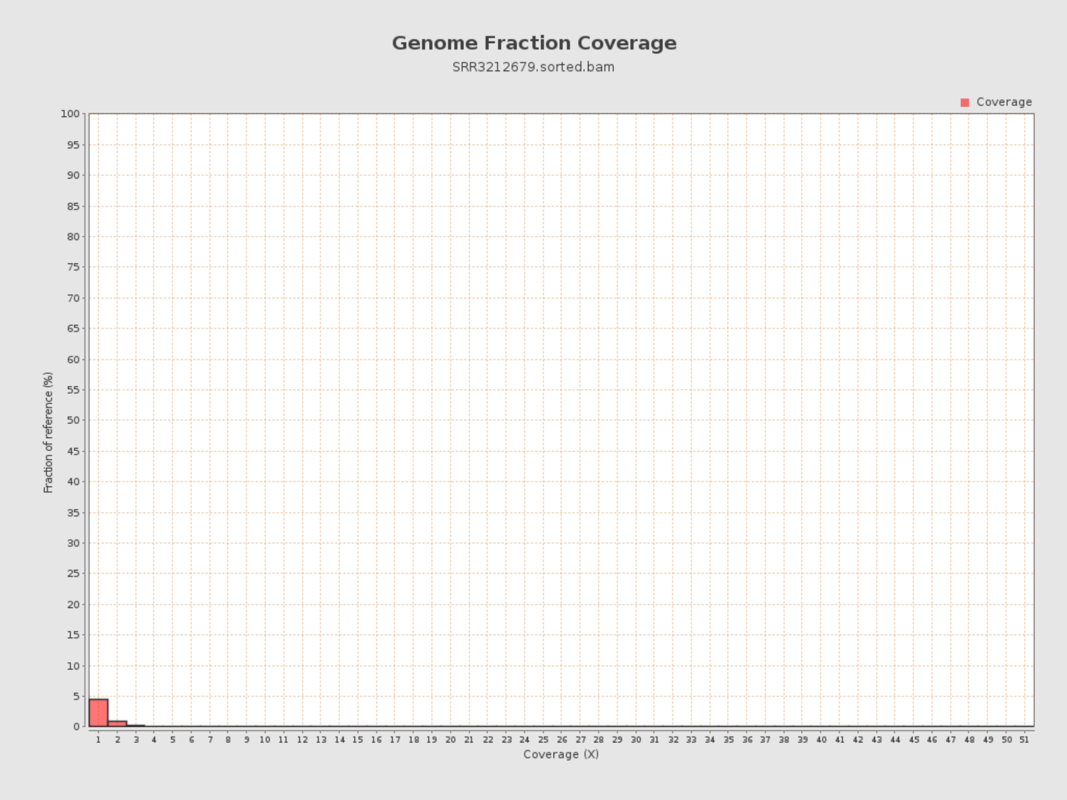
4. Results : Coverage Histogram



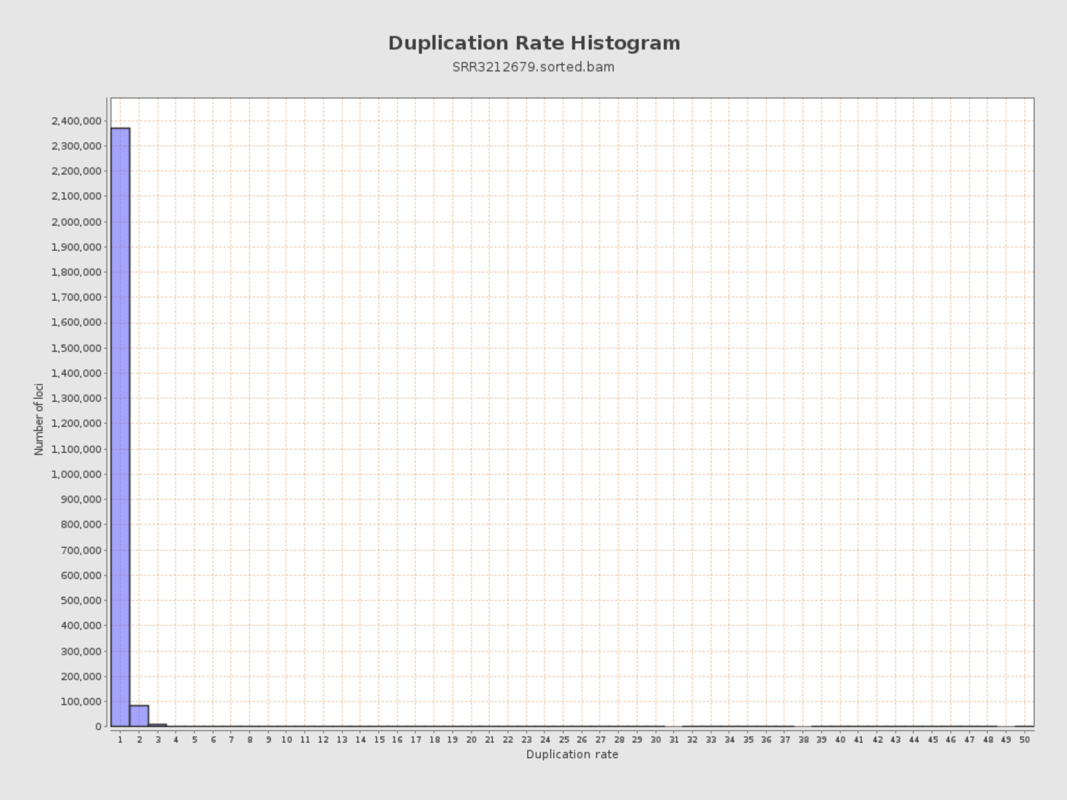
5. Results : Coverage Histogram (0-50X)



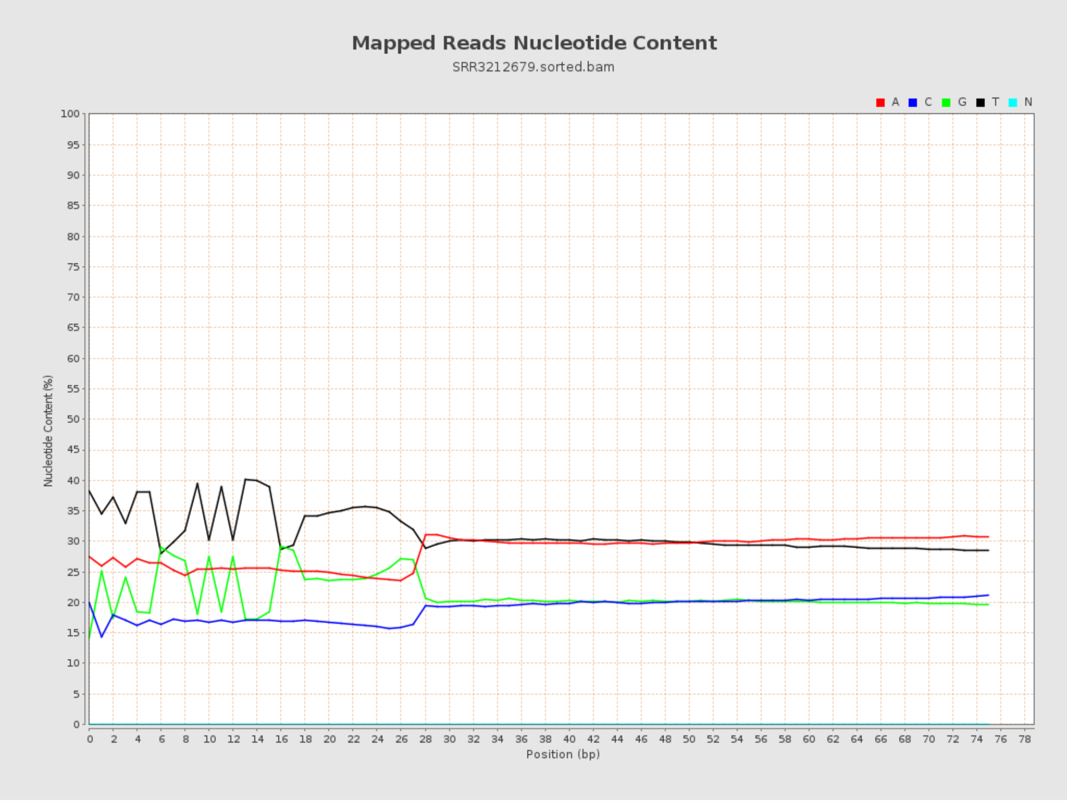
6. Results : Genome Fraction Coverage



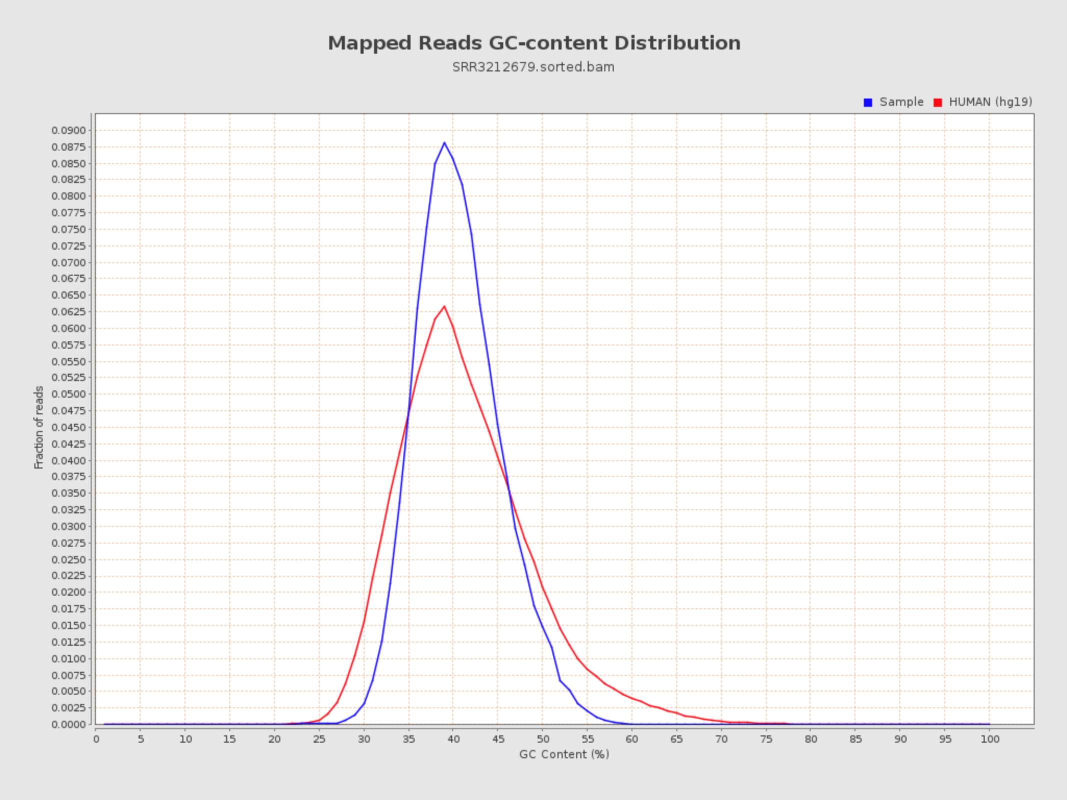
7. Results : Duplication Rate Histogram



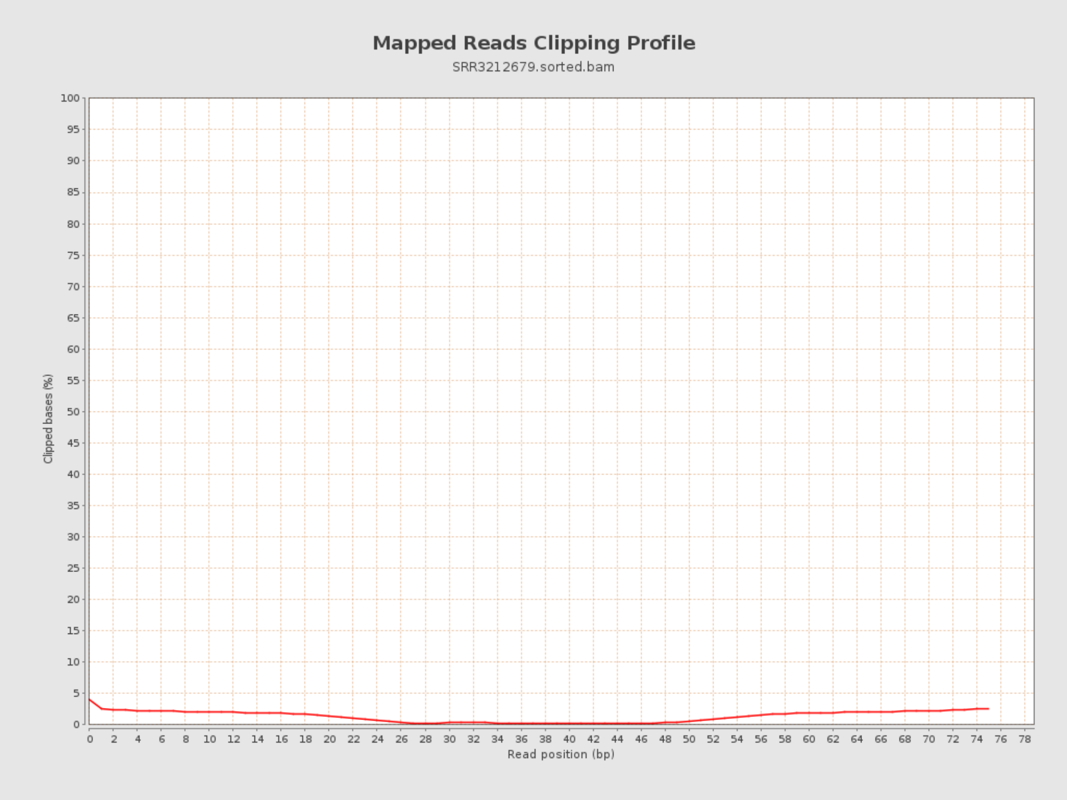
8. Results : Mapped Reads Nucleotide Content



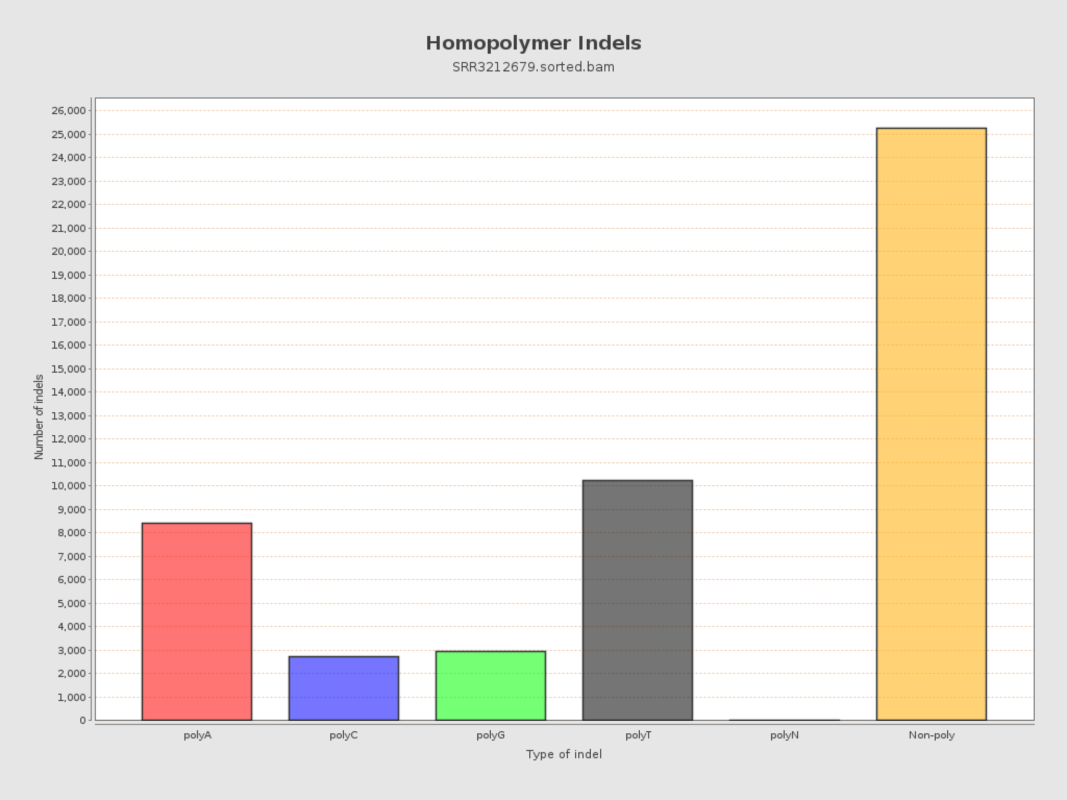
9. Results : Mapped Reads GC-content Distribution



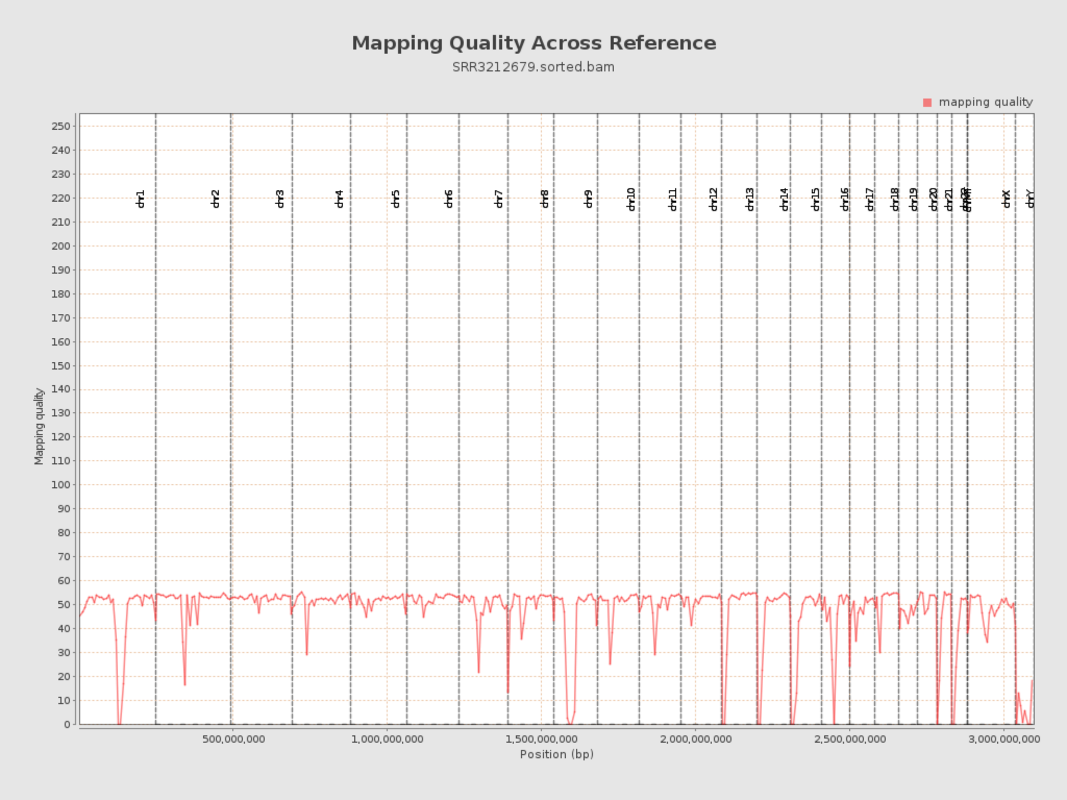
10. Results : Mapped Reads Clipping Profile



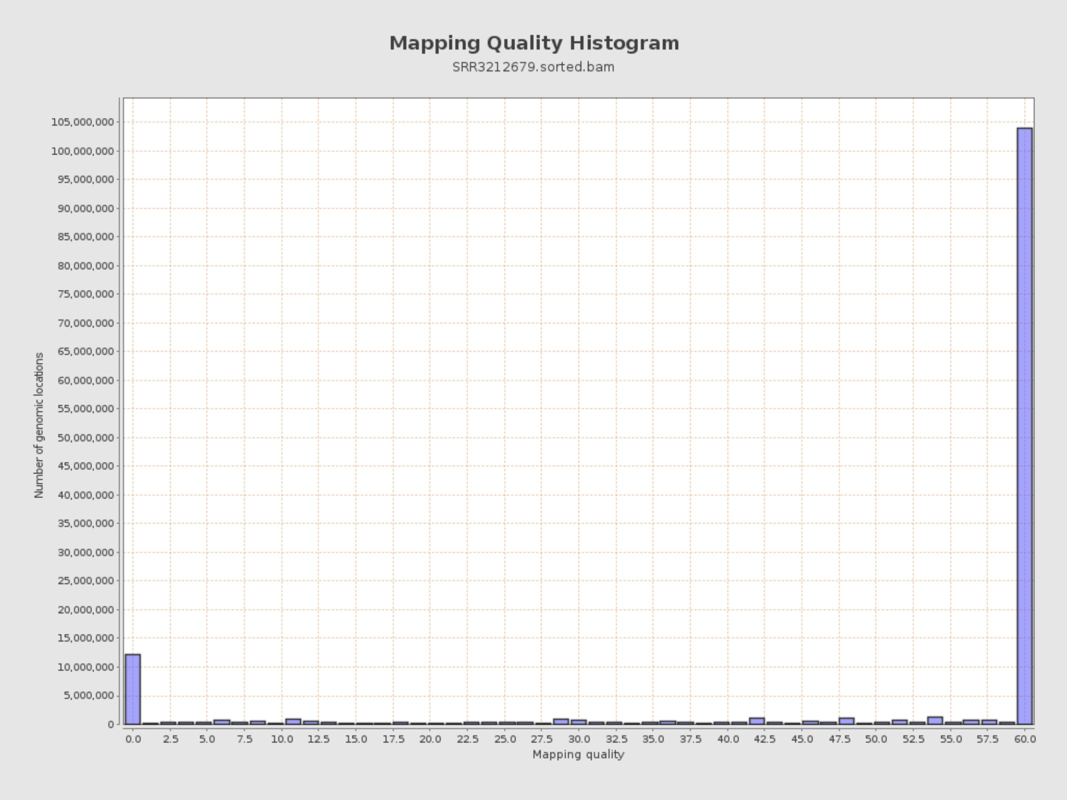
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



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