Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:07:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082419.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_SRR3082419 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082419.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:07:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082419.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,958,556
Mapped reads	2,670,320 / 90.26%
Unmapped reads	288,236 / 9.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,060 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	111,603 / 3.77%
Duplication rate	2.97%
Clipped reads	1,184,114 / 40.02%

2.2. ACGT Content

Number/percentage of A's	50,170,152 / 28.02%
Number/percentage of C's	33,657,801 / 18.8%
Number/percentage of T's	55,283,412 / 30.88%
Number/percentage of G's	39,928,772 / 22.3%
Number/percentage of N's	3,558 / 0%
GC Percentage	41.1%

2.3. Coverage

Mean	0.0579

Standard Deviation	0.5283

2.4. Mapping Quality

Mean Mapping Quality	44.99

2.5. Mismatches and indels

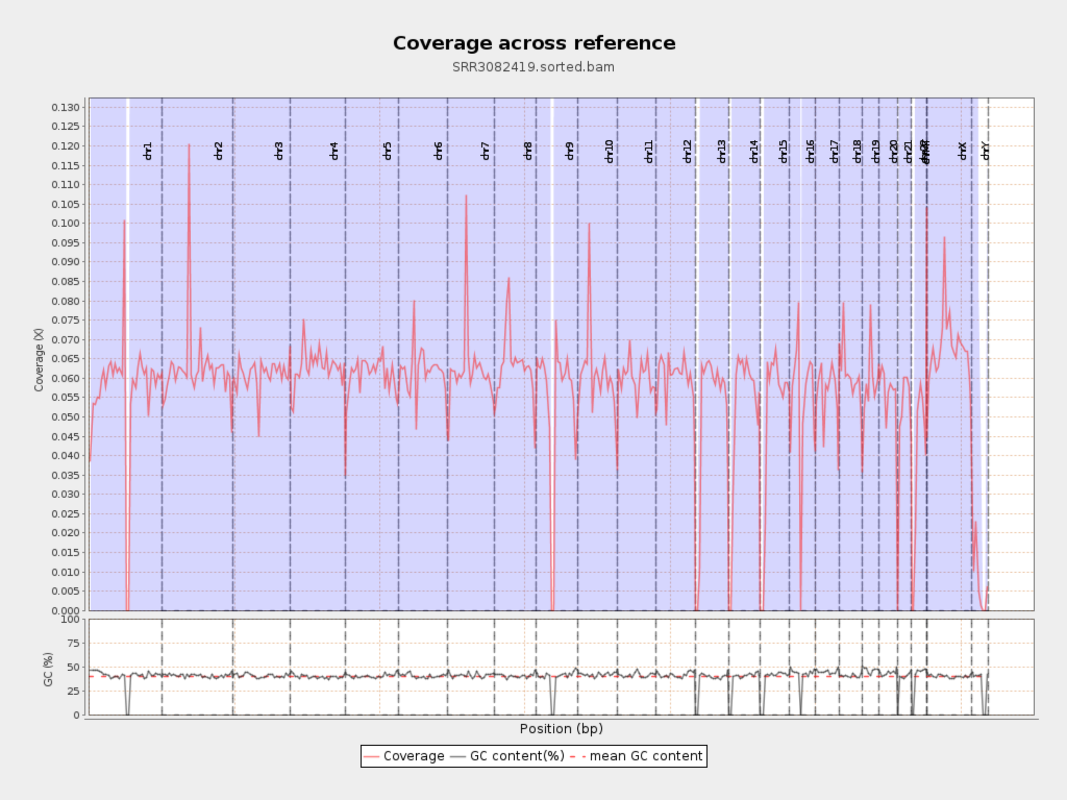
General error rate	0.86%
Mismatches	1,514,486
Insertions	14,925
Mapped reads with at least one insertion	0.55%
Deletions	40,870
Mapped reads with at least one deletion	1.51%
Homopolymer indels	46.78%

2.6. Chromosome stats

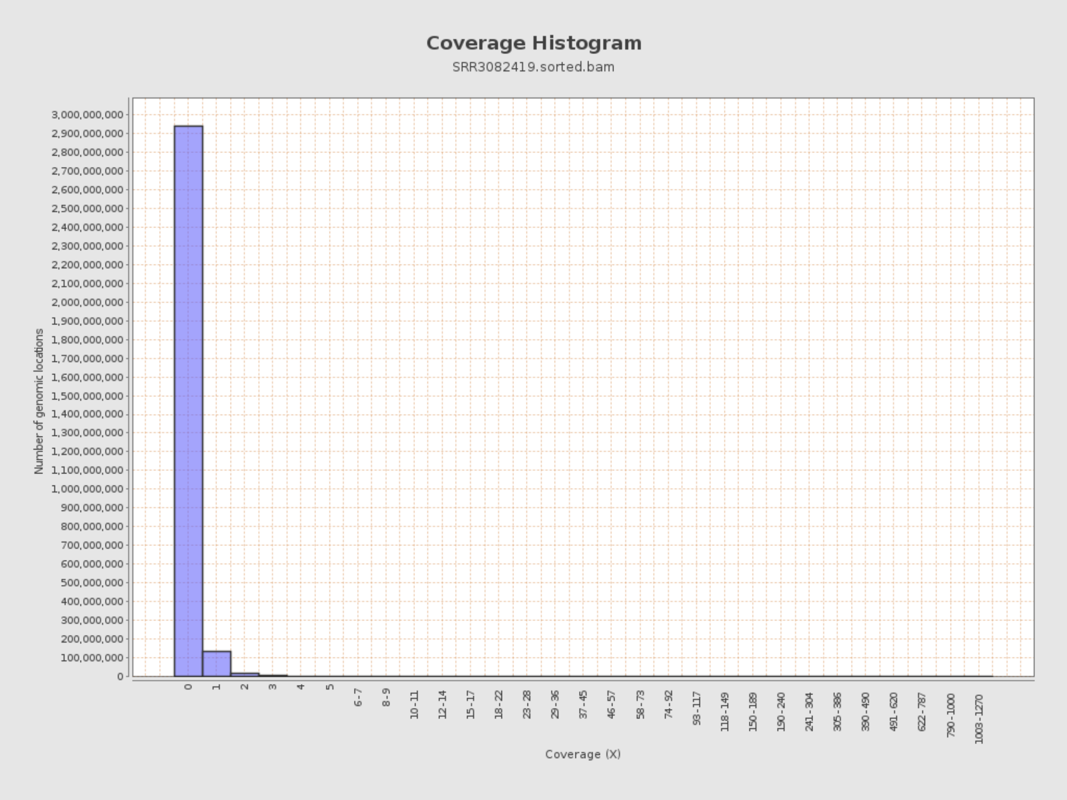
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14136028	0.0567	0.949
chr2	243199373	15303464	0.0629	0.6886
chr3	198022430	12045165	0.0608	0.2793
chr4	191154276	12006273	0.0628	0.3008
chr5	180915260	11056140	0.0611	0.2838
chr6	171115067	10564117	0.0617	0.3719
chr7	159138663	10008780	0.0629	0.7134

chr8	146364022	9234077	0.0631	0.8238
chr9	141213431	7560656	0.0535	0.4785
chr10	135534747	8319068	0.0614	0.4815
chr11	135006516	8096250	0.06	0.4272
chr12	133851895	8092430	0.0605	0.2858
chr13	115169878	5768505	0.0501	0.2524
chr14	107349540	5414003	0.0504	0.2971
chr15	102531392	5034881	0.0491	0.2565
chr16	90354753	4921202	0.0545	0.3178
chr17	81195210	4542079	0.0559	0.3138
chr18	78077248	4796649	0.0614	0.9371
chr19	59128983	3480535	0.0589	0.7398
chr20	63025520	3543910	0.0562	0.2798
chr21	48129895	2351865	0.0489	0.2757
chr22	51304566	1870437	0.0365	0.2135
chrMT	16571	1726	0.1042	0.3391
chrX	155270560	10490493	0.0676	0.3511
chrY	59373566	471259	0.0079	0.1696

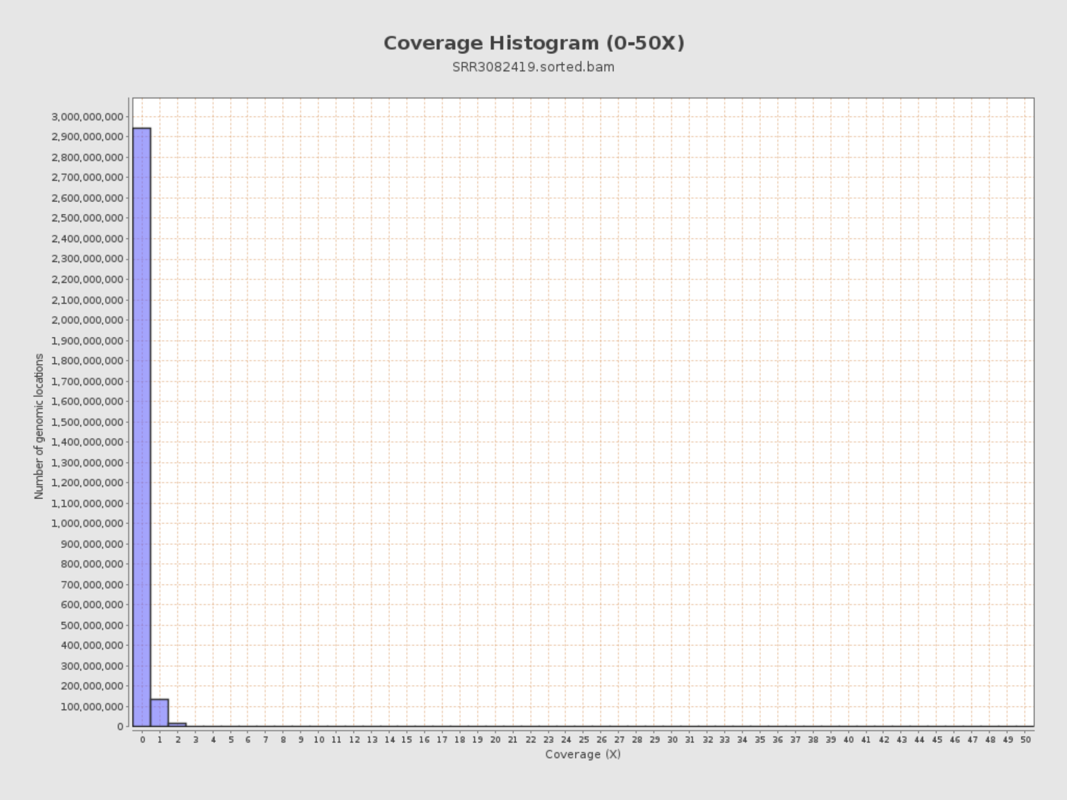
3. Results : Coverage across reference



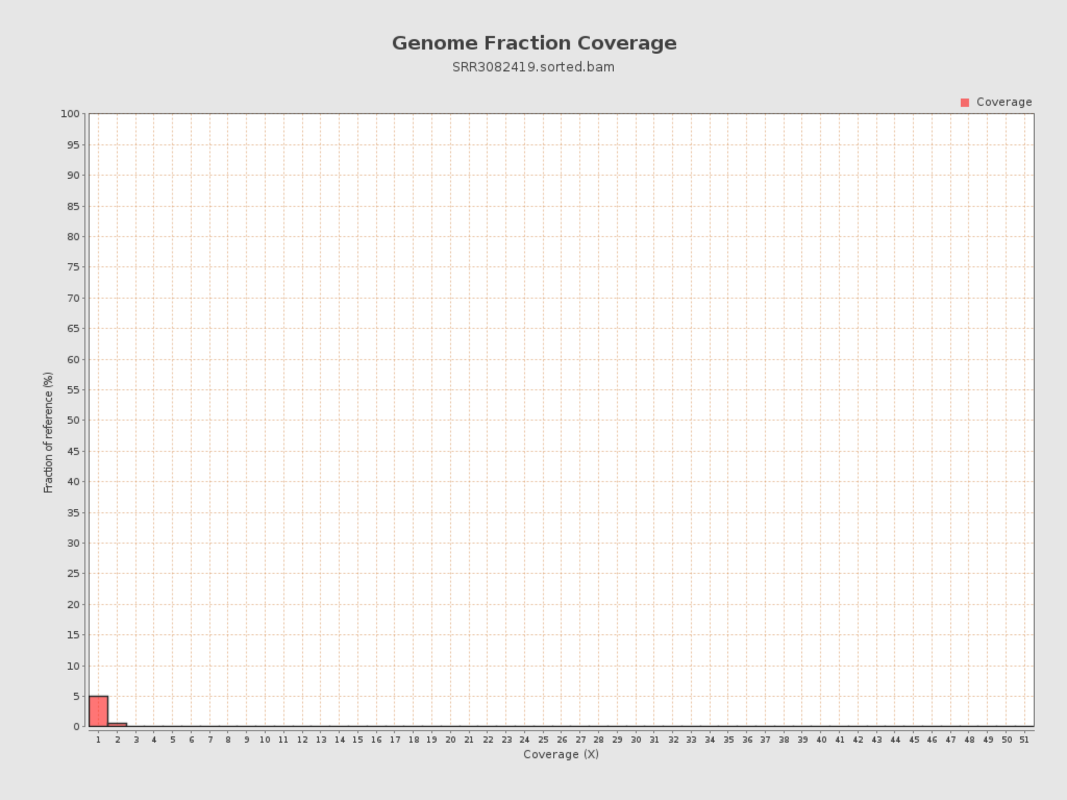
4. Results : Coverage Histogram



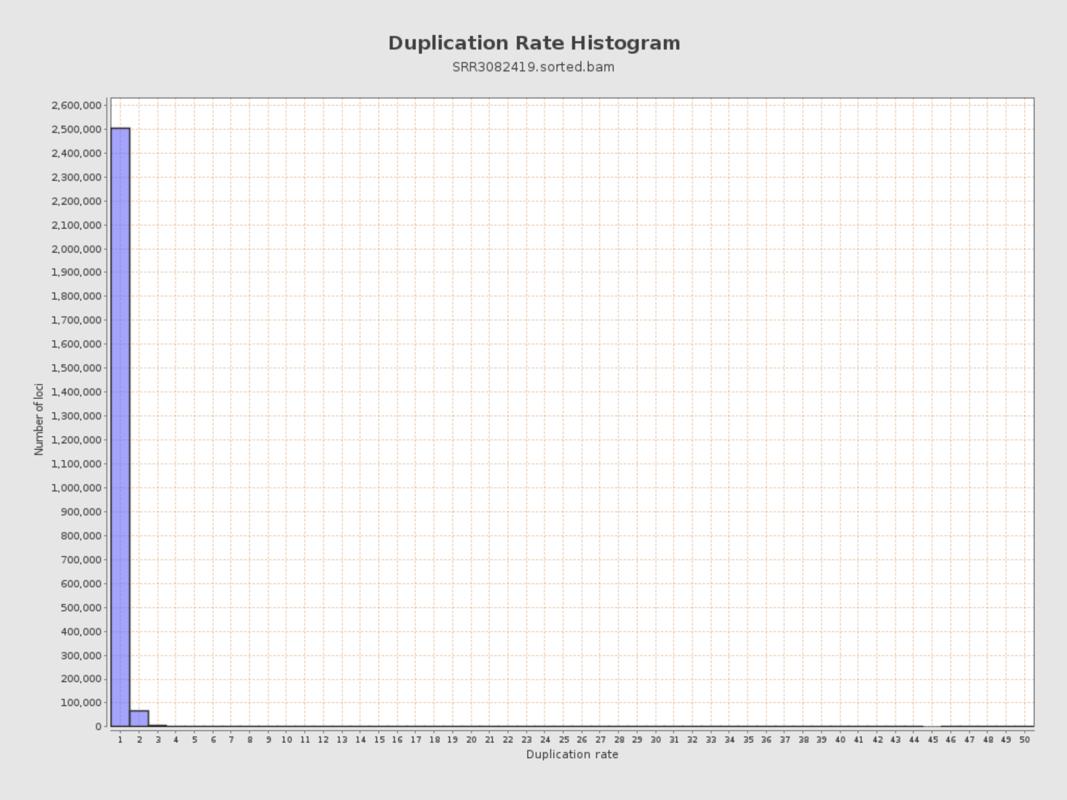
5. Results : Coverage Histogram (0-50X)



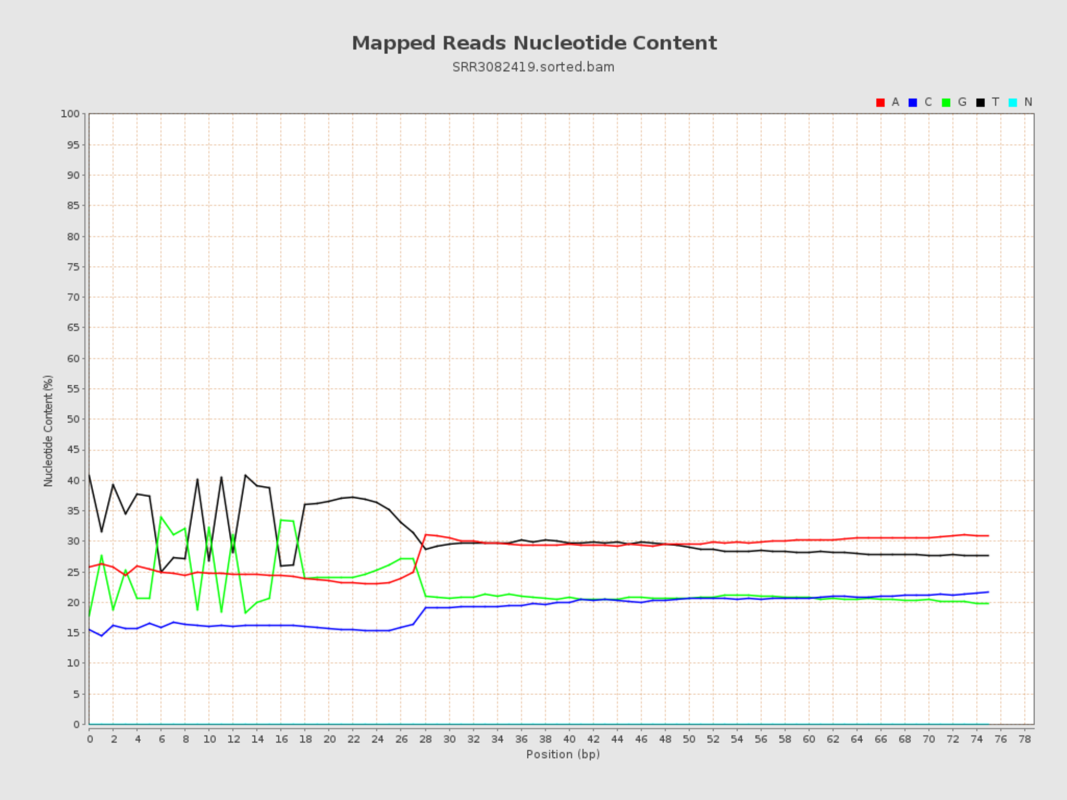
6. Results : Genome Fraction Coverage



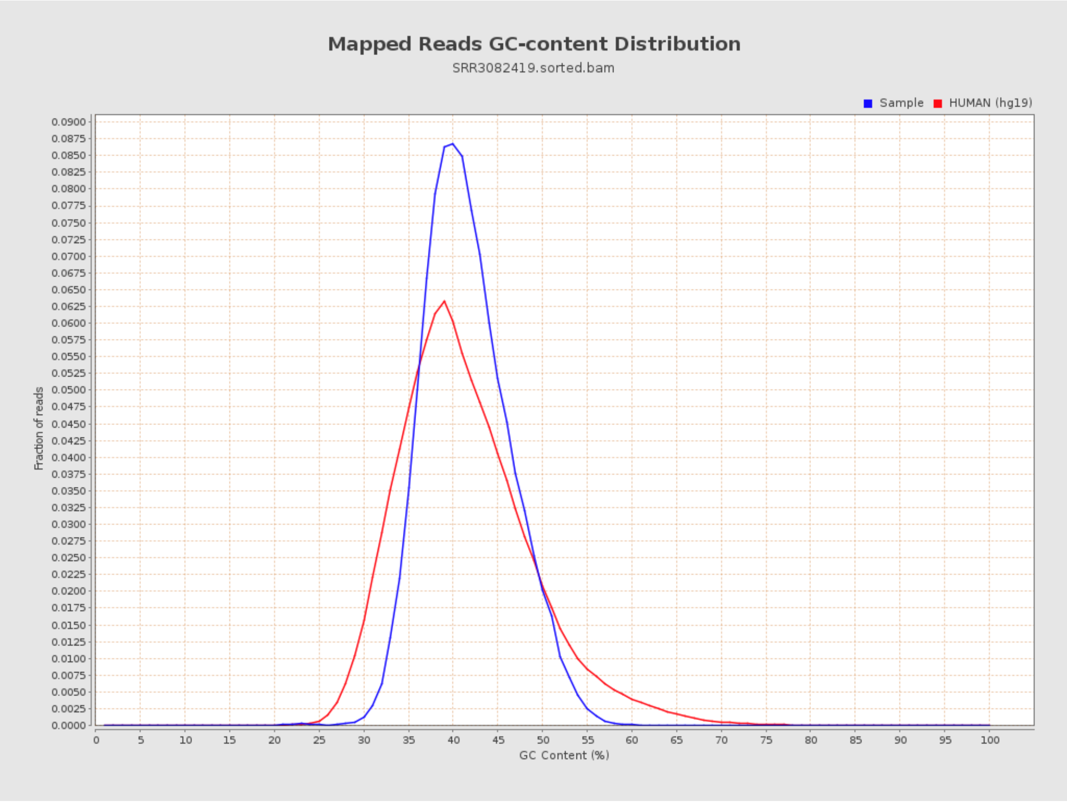
7. Results : Duplication Rate Histogram



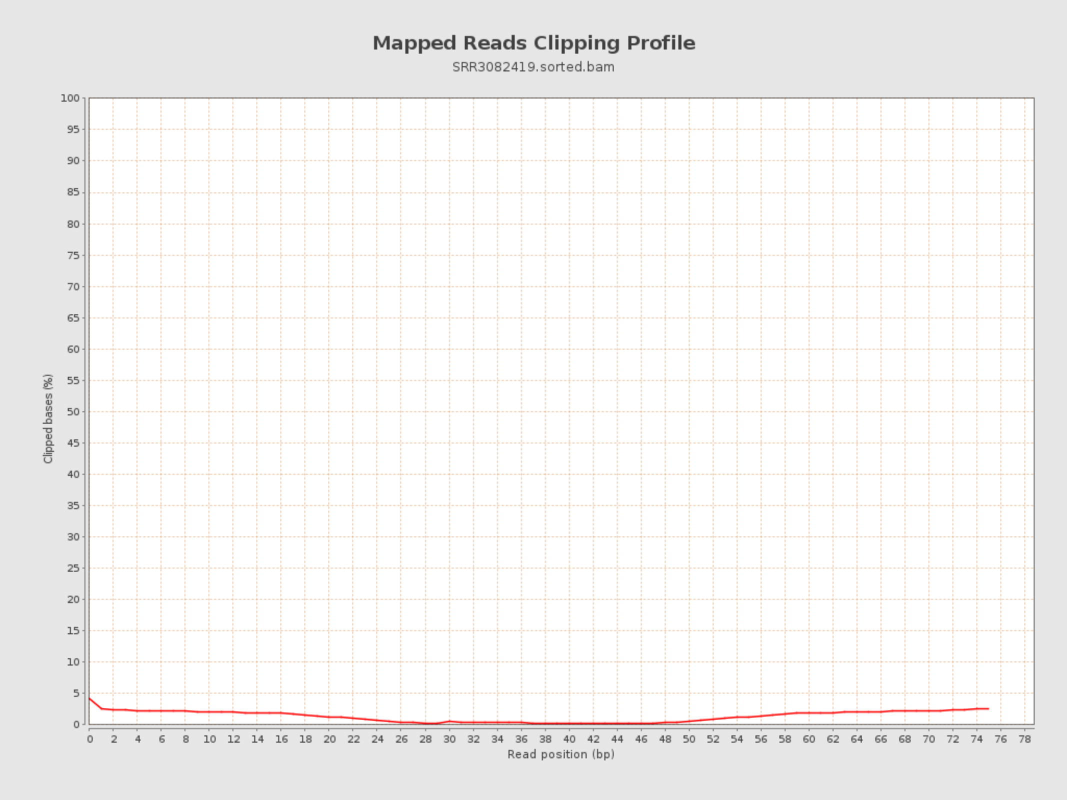
8. Results : Mapped Reads Nucleotide Content



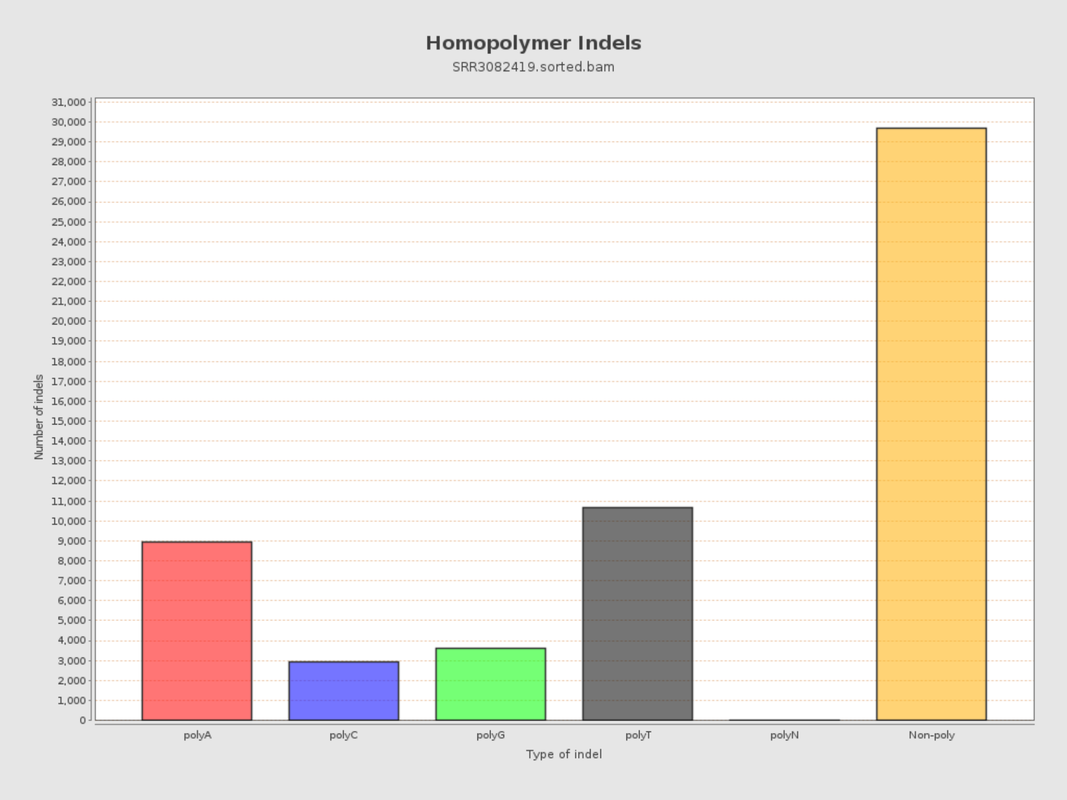
9. Results : Mapped Reads GC-content Distribution



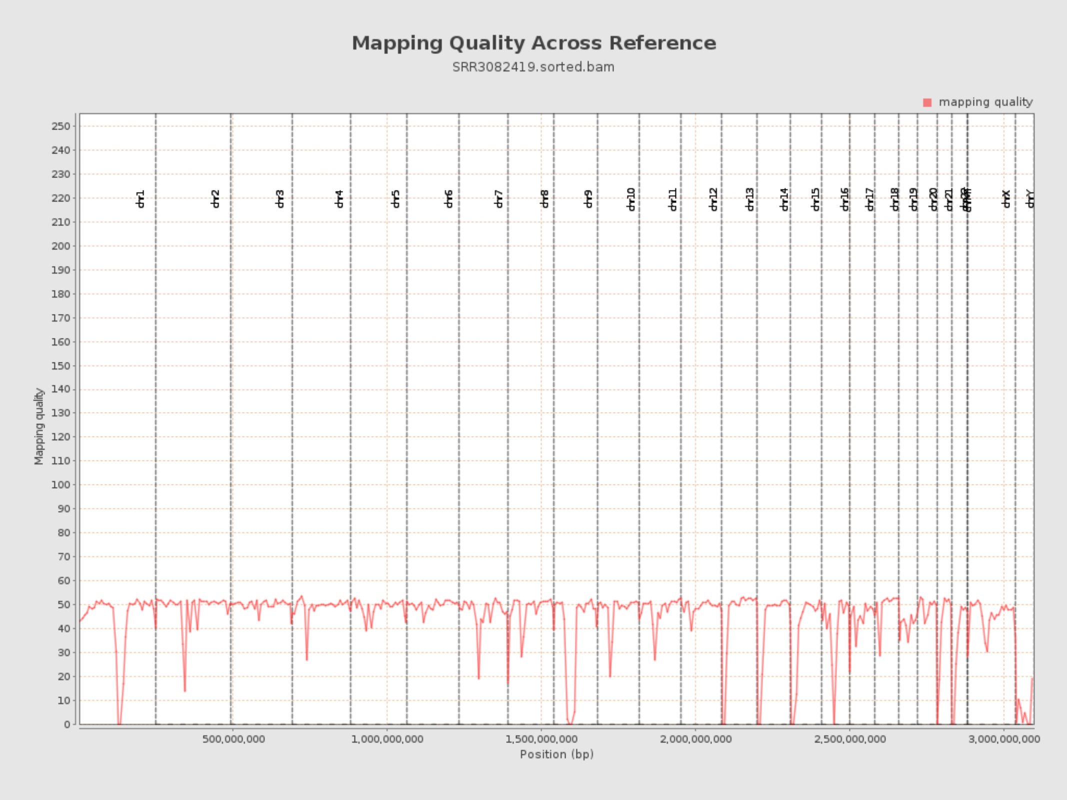
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram