Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:10:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082927.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_SRR3082927 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082927.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:10:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082927.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,008,345
Mapped reads	1,780,362 / 88.65%
Unmapped reads	227,983 / 11.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,405 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	88,876 / 4.43%
Duplication rate	4.43%
Clipped reads	817,277 / 40.69%

2.2. ACGT Content

Number/percentage of A's	31,599,356 / 26.79%
Number/percentage of C's	22,001,105 / 18.65%
Number/percentage of T's	37,175,053 / 31.52%
Number/percentage of G's	27,161,111 / 23.03%
Number/percentage of N's	5,528 / 0%
GC Percentage	41.68%

2.3. Coverage

Mean	0.0381

Standard Deviation	0.2687

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

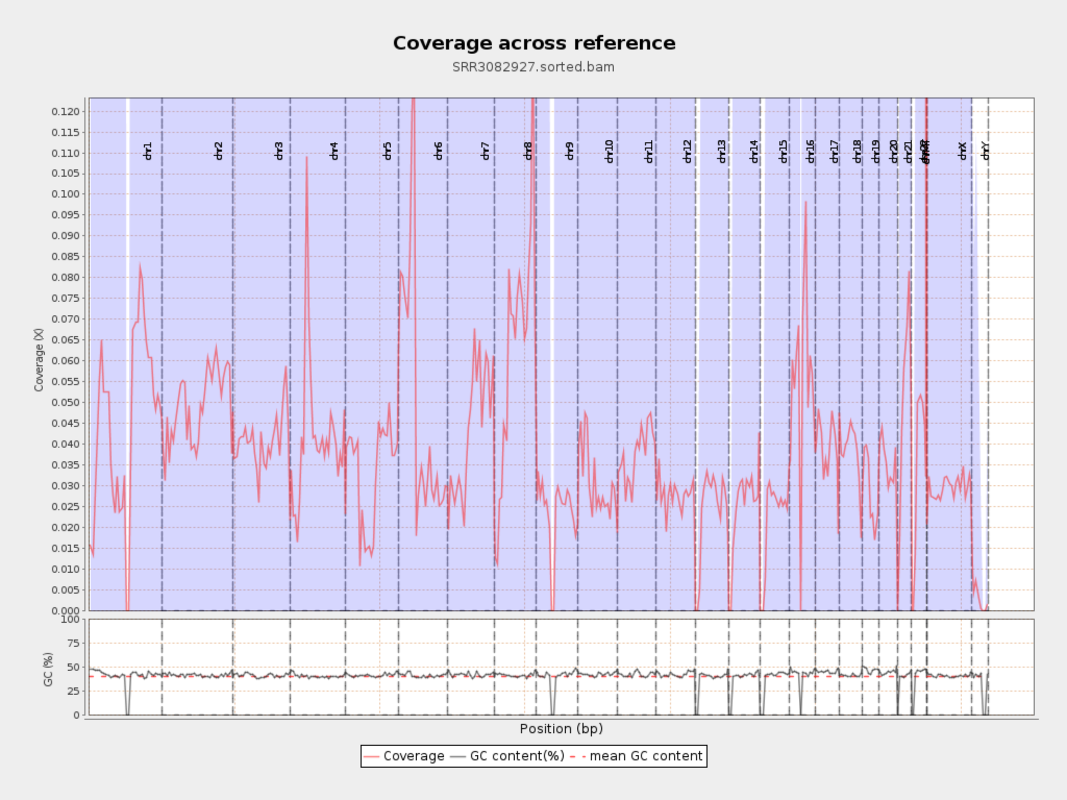
General error rate	0.73%
Mismatches	840,159
Insertions	9,095
Mapped reads with at least one insertion	0.51%
Deletions	26,836
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.33%

2.6. Chromosome stats

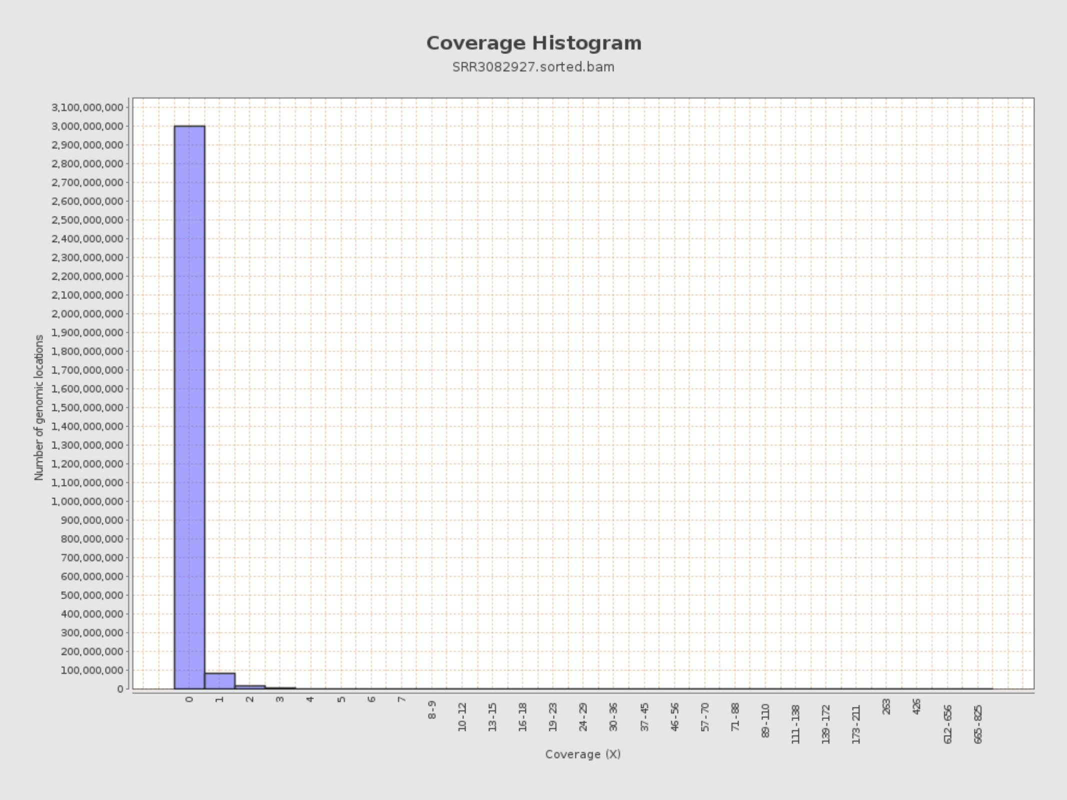
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11211887	0.045	0.2941
chr2	243199373	11984902	0.0493	0.4314
chr3	198022430	8117962	0.041	0.2387
chr4	191154276	7944346	0.0416	0.2456
chr5	180915260	5975243	0.033	0.2154
chr6	171115067	8569009	0.0501	0.3115
chr7	159138663	6990120	0.0439	0.2723

chr8	146364022	9236053	0.0631	0.3199
chr9	141213431	3306115	0.0234	0.2045
chr10	135534747	4229544	0.0312	0.2129
chr11	135006516	5031005	0.0373	0.2695
chr12	133851895	3696610	0.0276	0.1968
chr13	115169878	2750682	0.0239	0.1852
chr14	107349540	2590416	0.0241	0.1876
chr15	102531392	2266758	0.0221	0.1871
chr16	90354753	5029277	0.0557	0.2863
chr17	81195210	3142143	0.0387	0.2405
chr18	78077248	3019367	0.0387	0.3425
chr19	59128983	1715036	0.029	0.2441
chr20	63025520	2241406	0.0356	0.2252
chr21	48129895	2335012	0.0485	0.2651
chr22	51304566	1693982	0.033	0.2157
chrMT	16571	172110	10.3862	7.3403
chrX	155270560	4559541	0.0294	0.2077
chrY	59373566	177697	0.003	0.0647

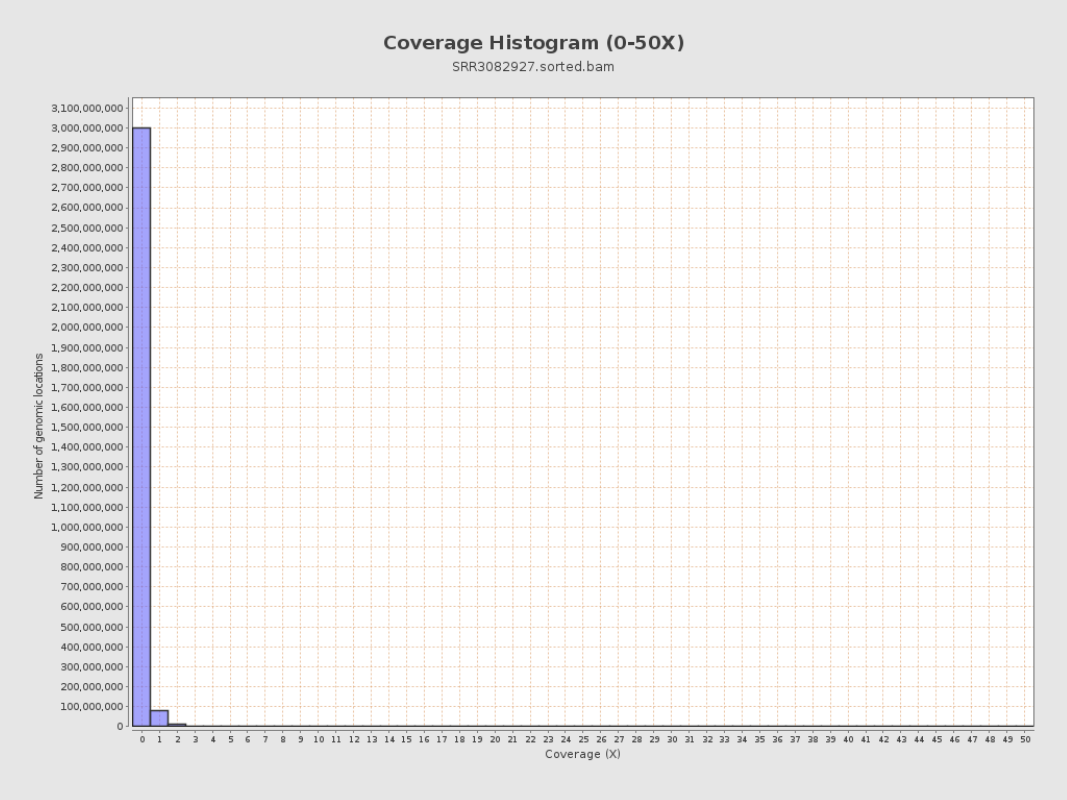
3. Results : Coverage across reference



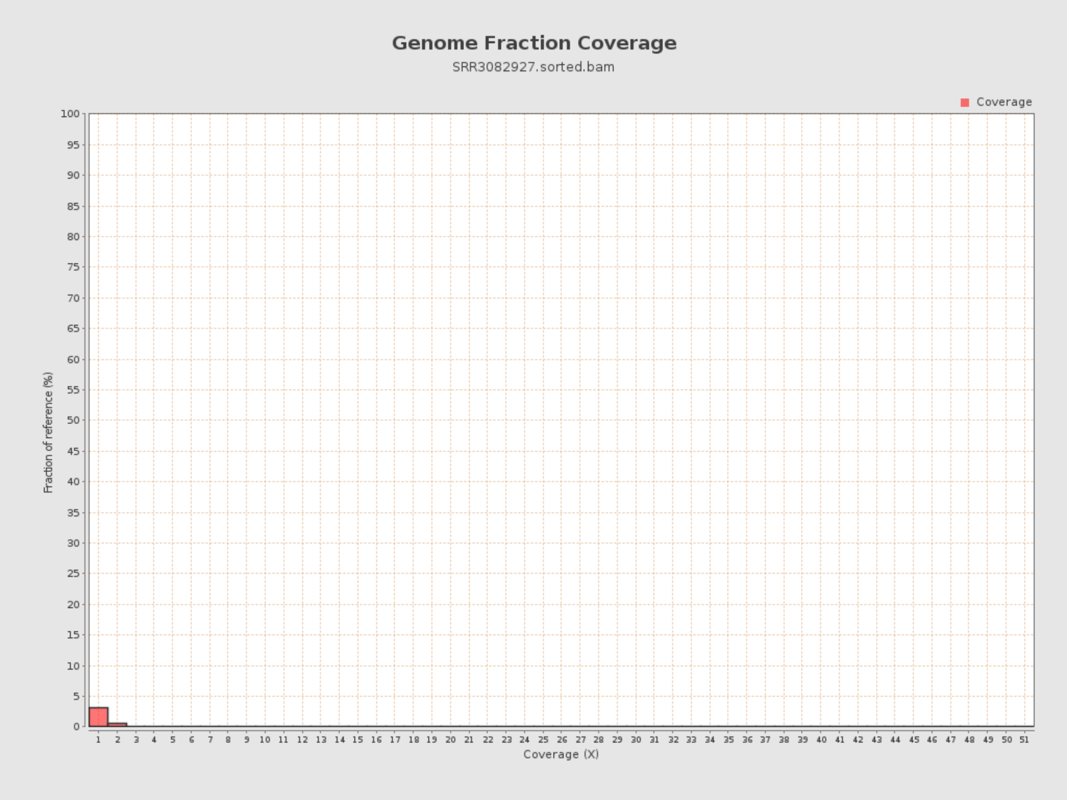
4. Results : Coverage Histogram



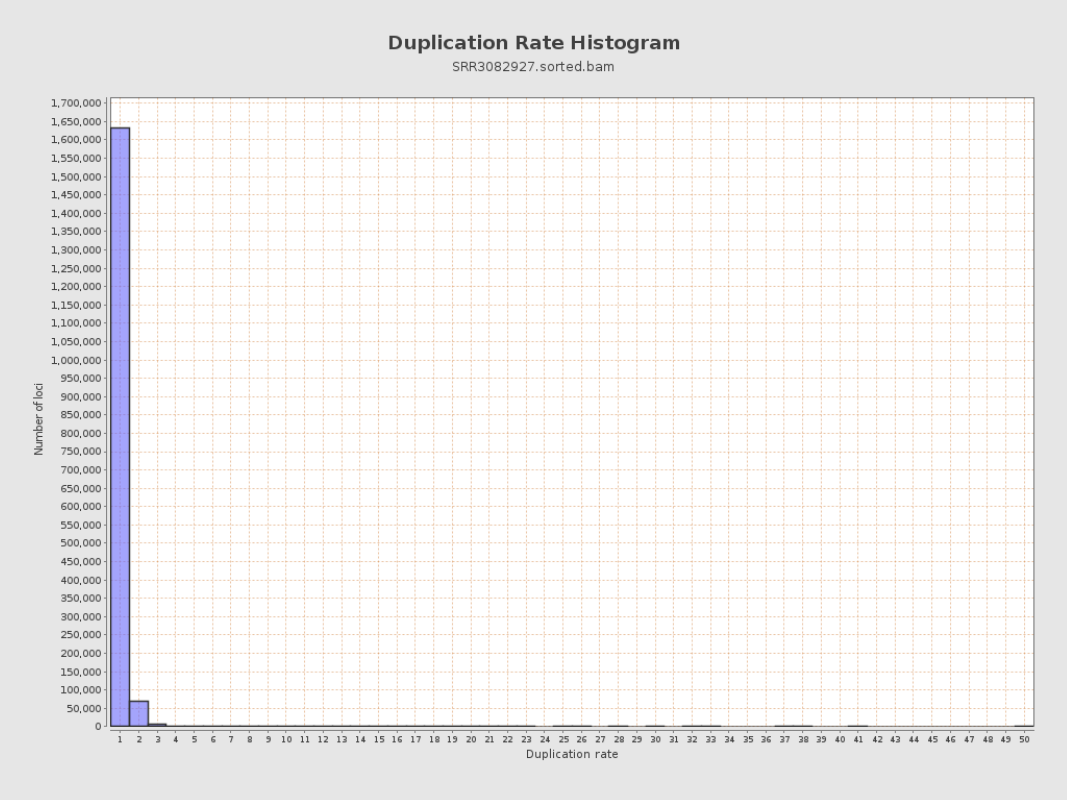
5. Results : Coverage Histogram (0-50X)



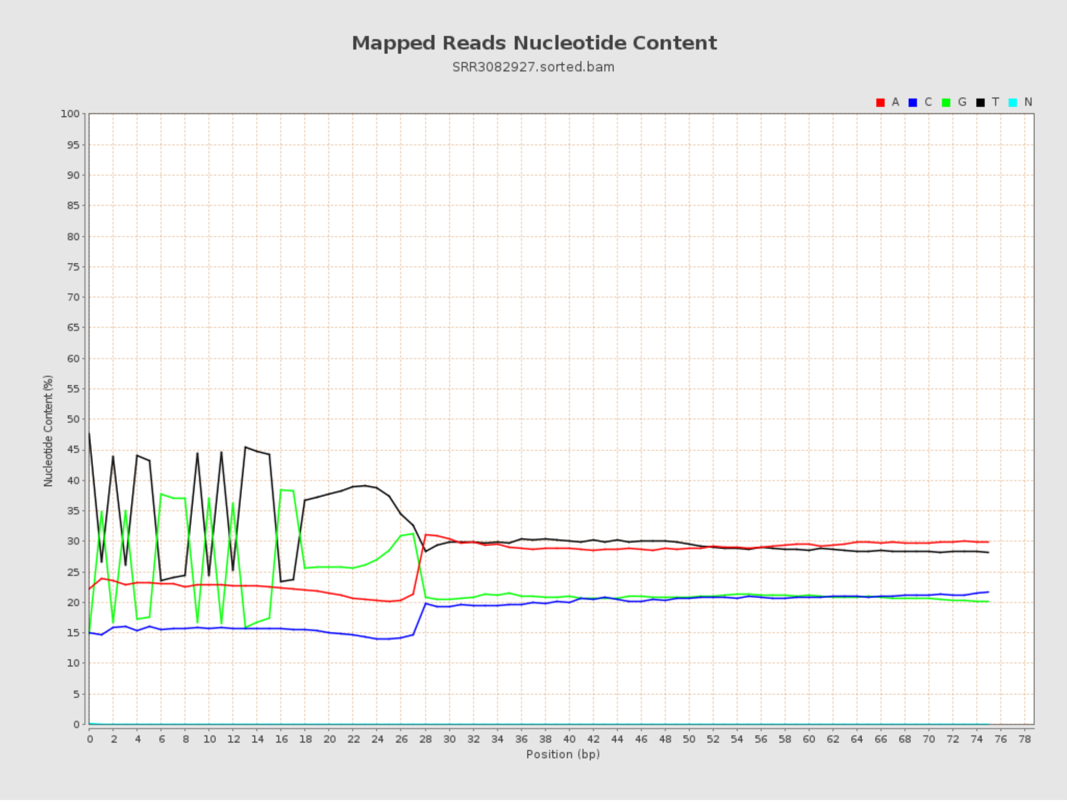
6. Results : Genome Fraction Coverage



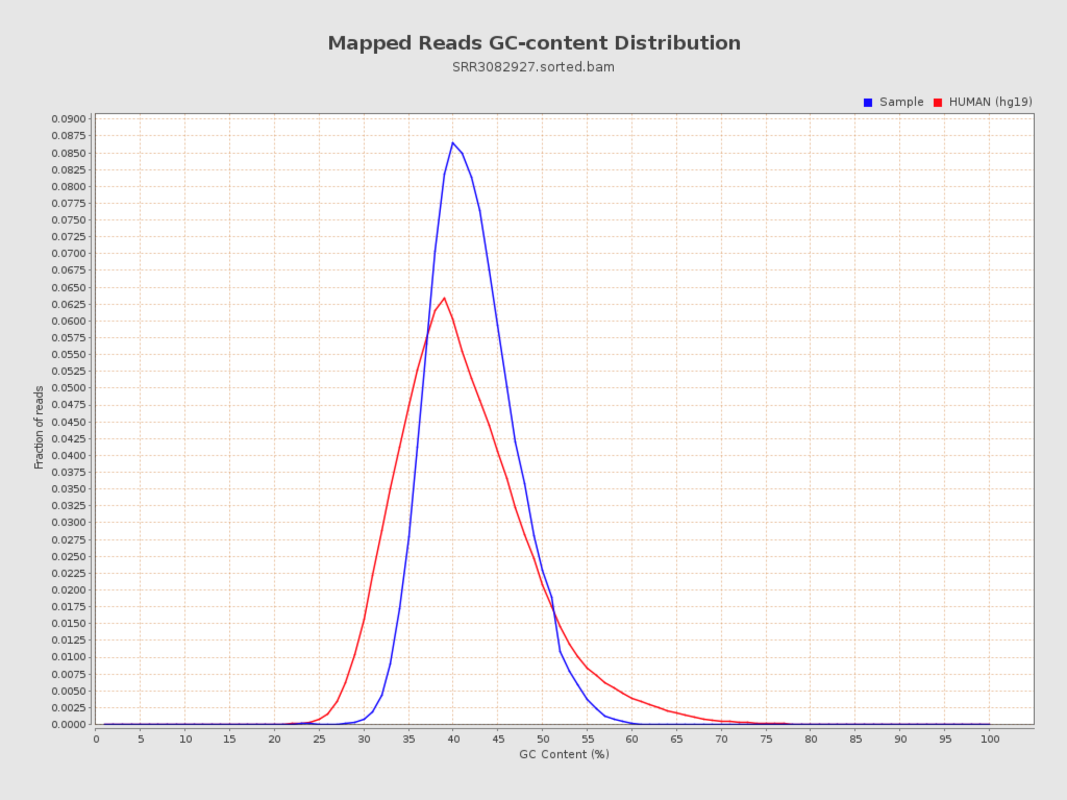
7. Results : Duplication Rate Histogram



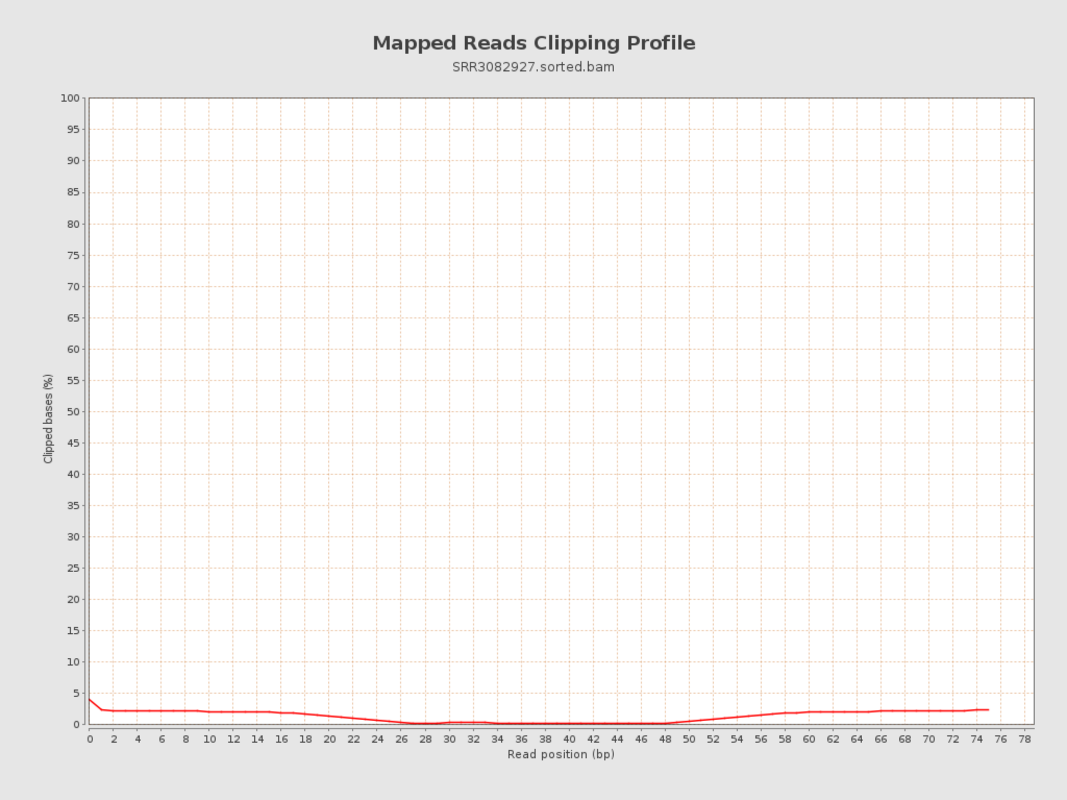
8. Results : Mapped Reads Nucleotide Content



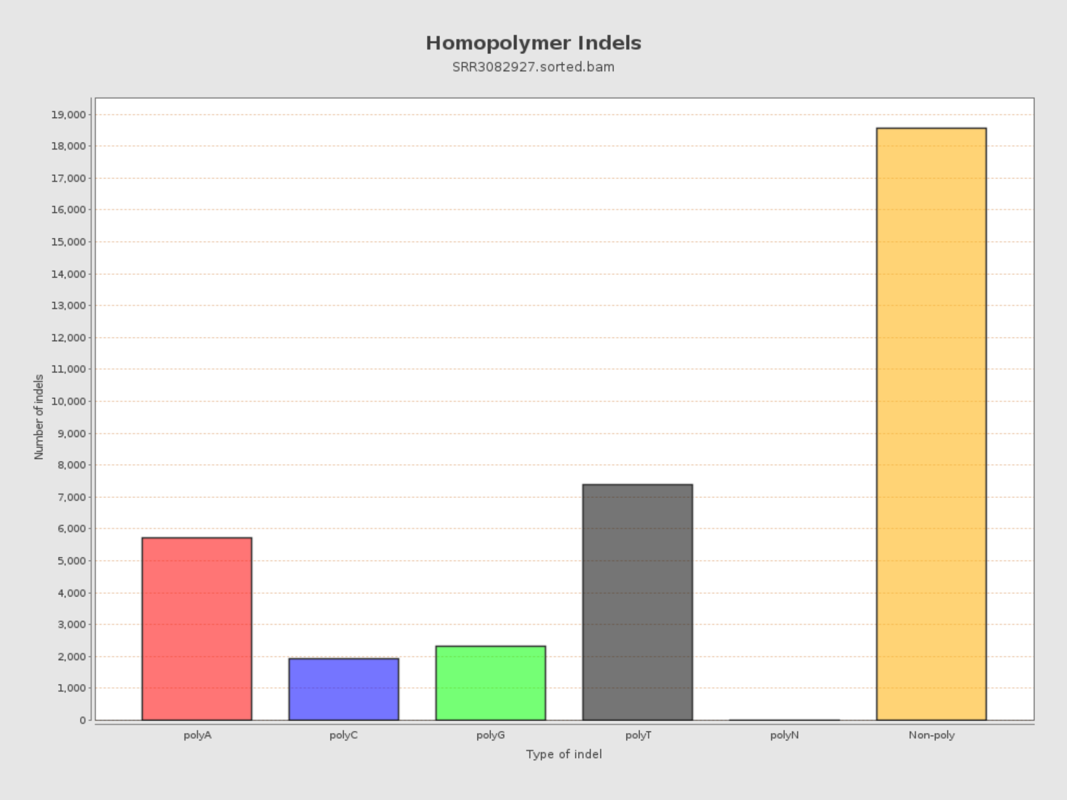
9. Results : Mapped Reads GC-content Distribution



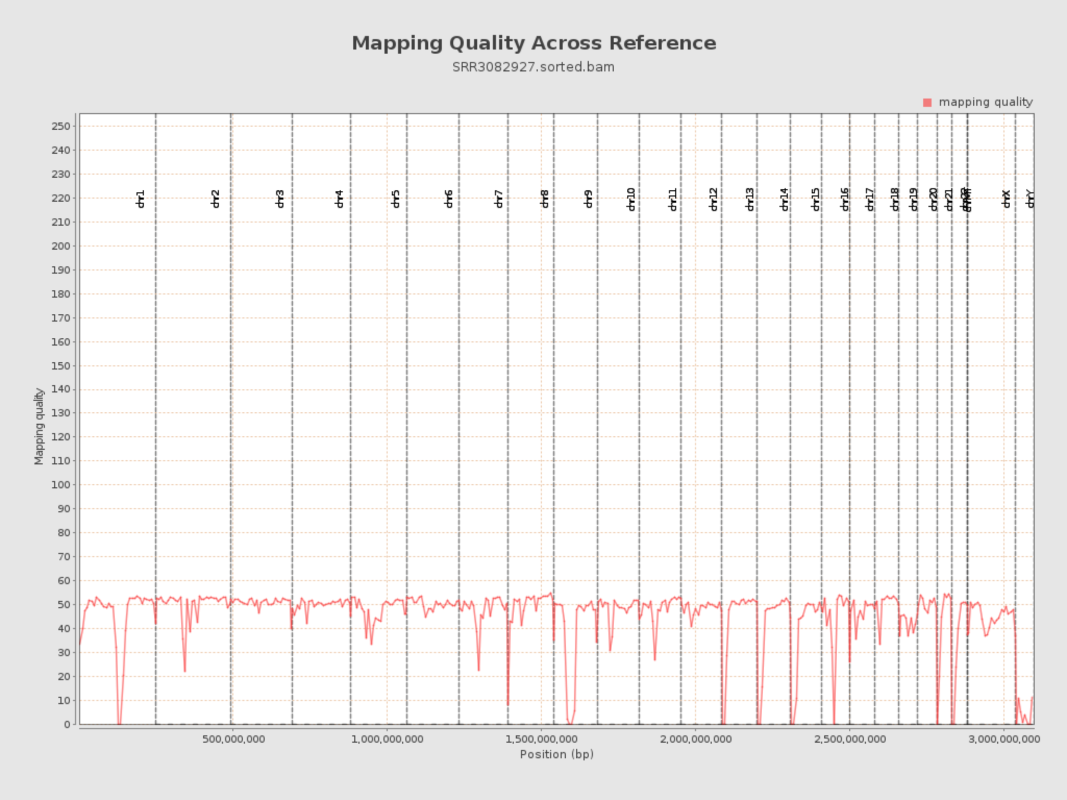
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram