Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:38:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083627.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_SRR3083627 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083627.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:38:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083627.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,371,359
Mapped reads	1,267,562 / 92.43%
Unmapped reads	103,797 / 7.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,540 / 0.84%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	53,686 / 3.91%
Duplication rate	3.44%
Clipped reads	548,072 / 39.97%

2.2. ACGT Content

Number/percentage of A's	23,111,162 / 27.25%
Number/percentage of C's	15,676,591 / 18.49%
Number/percentage of T's	26,845,717 / 31.66%
Number/percentage of G's	19,166,661 / 22.6%
Number/percentage of N's	4,667 / 0.01%
GC Percentage	41.09%

2.3. Coverage

Mean	0.0274

Standard Deviation	0.287

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

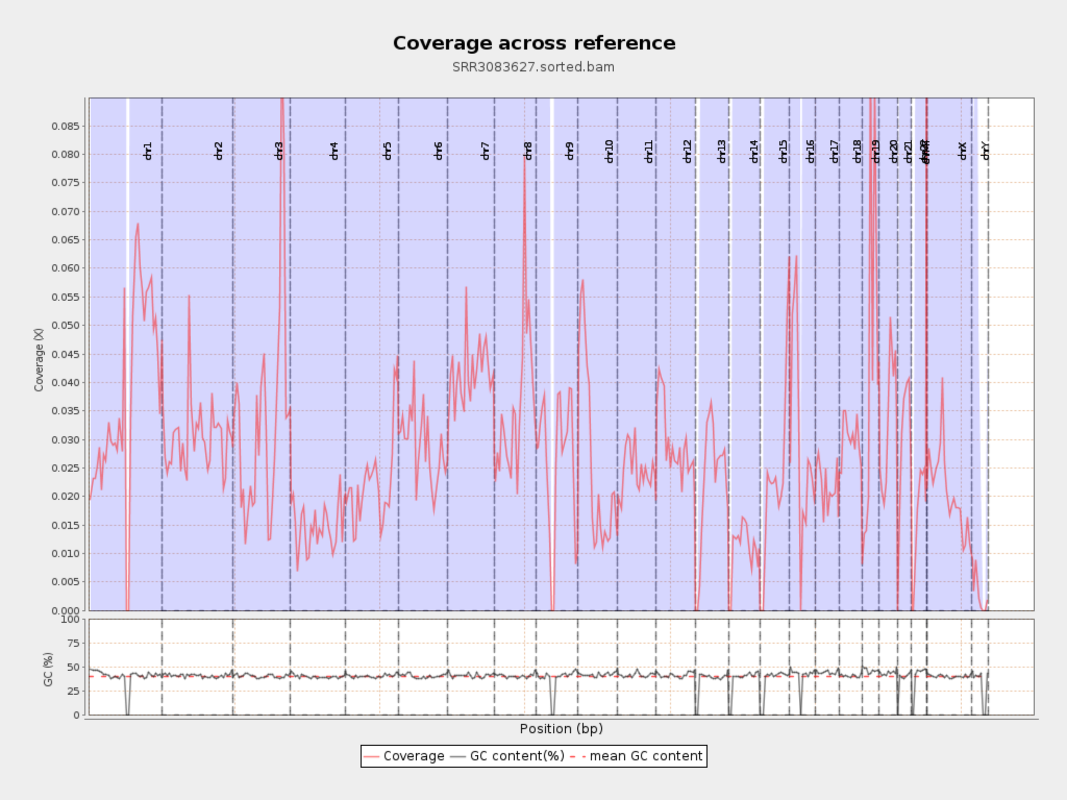
General error rate	0.71%
Mismatches	593,371
Insertions	6,650
Mapped reads with at least one insertion	0.52%
Deletions	19,595
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.28%

2.6. Chromosome stats

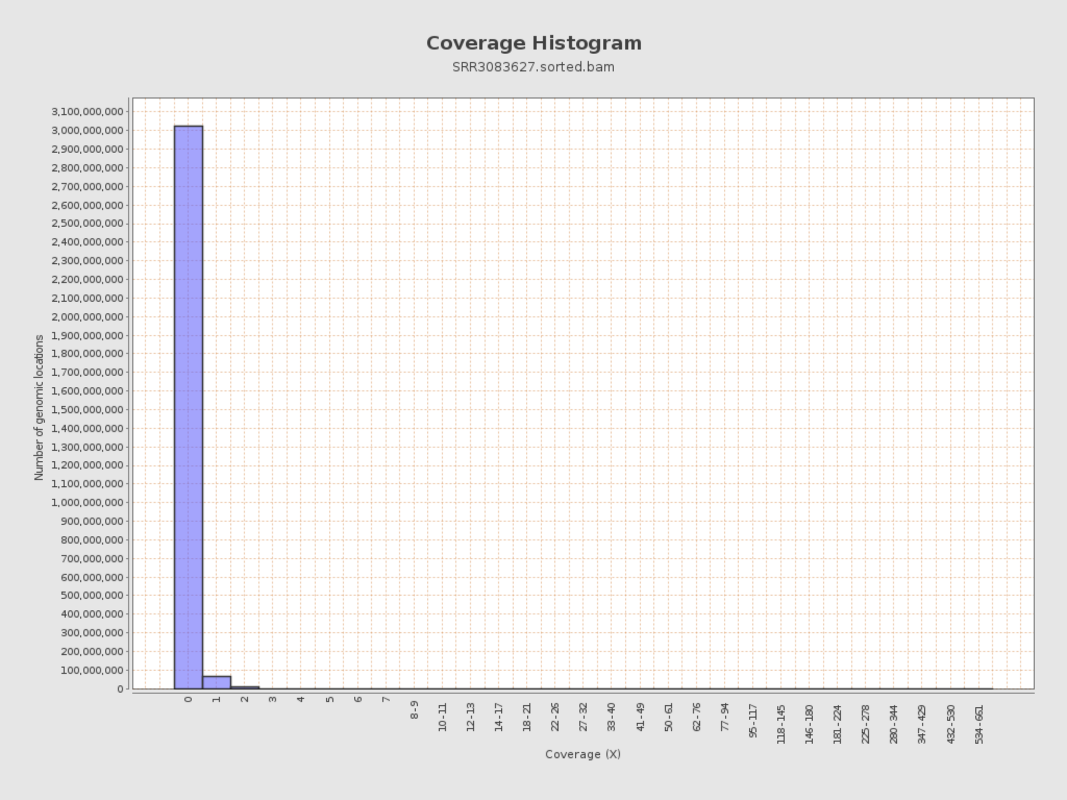
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9361410	0.0376	0.6064
chr2	243199373	7392164	0.0304	0.3423
chr3	198022430	6545882	0.0331	0.2048
chr4	191154276	2823180	0.0148	0.1426
chr5	180915260	4032675	0.0223	0.1673
chr6	171115067	4959089	0.029	0.2206
chr7	159138663	6673472	0.0419	0.4109

chr8	146364022	5287819	0.0361	0.2698
chr9	141213431	3711452	0.0263	0.2217
chr10	135534747	3569875	0.0263	0.2349
chr11	135006516	3299325	0.0244	0.2085
chr12	133851895	3949786	0.0295	0.192
chr13	115169878	2592178	0.0225	0.1683
chr14	107349540	1142152	0.0106	0.1193
chr15	102531392	2314872	0.0226	0.1739
chr16	90354753	2717334	0.0301	0.2028
chr17	81195210	1768732	0.0218	0.1699
chr18	78077248	2353900	0.0301	0.3881
chr19	59128983	2593688	0.0439	0.4181
chr20	63025520	2074160	0.0329	0.2059
chr21	48129895	1408763	0.0293	0.1938
chr22	51304566	814356	0.0159	0.1387
chrMT	16571	2527	0.1525	0.4616
chrX	155270560	3272075	0.0211	0.1693
chrY	59373566	175515	0.003	0.072

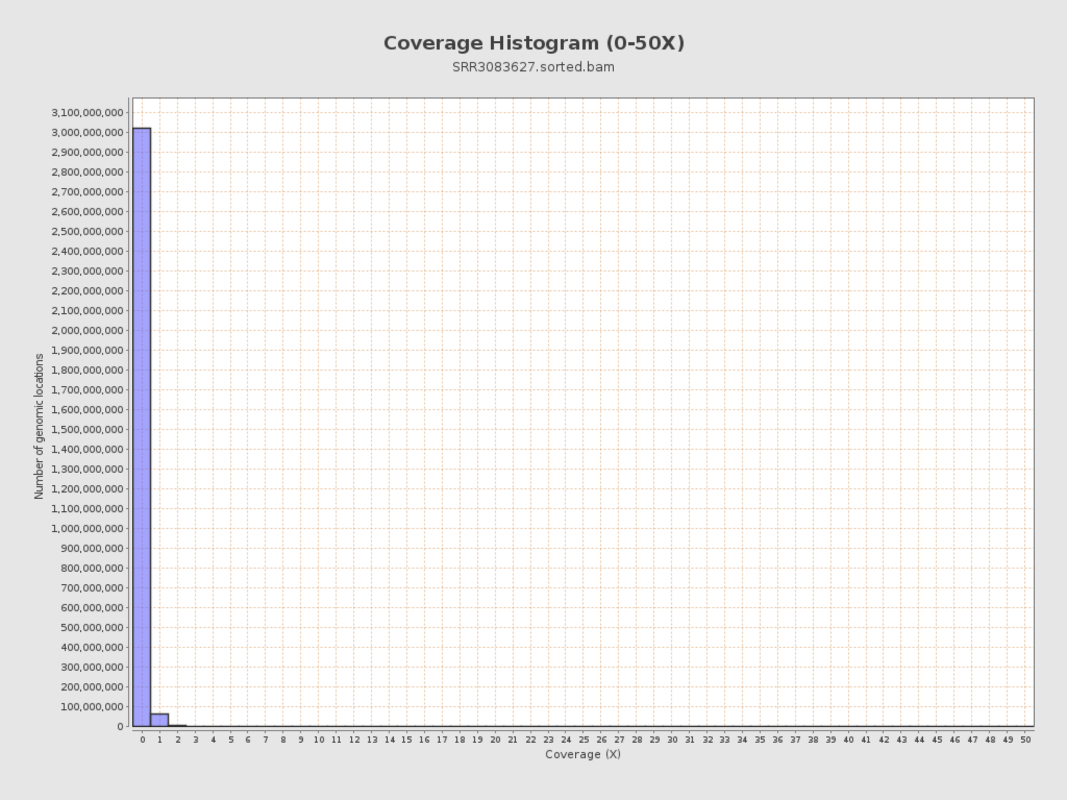
3. Results : Coverage across reference



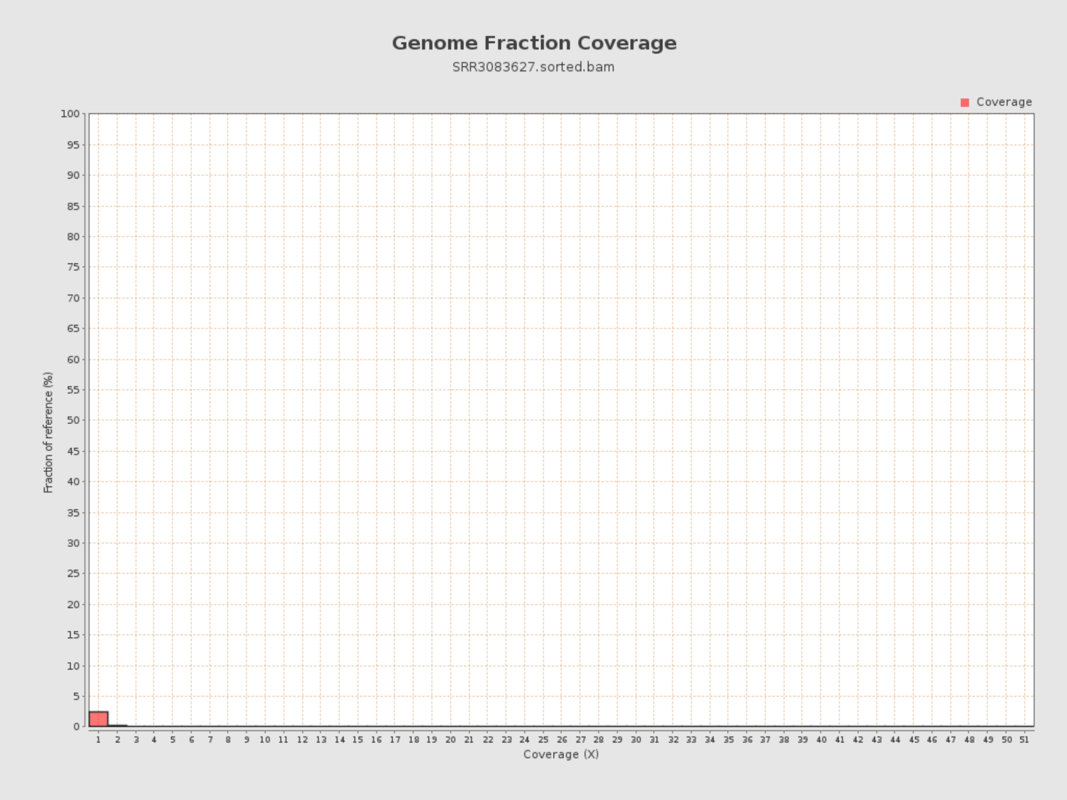
4. Results : Coverage Histogram



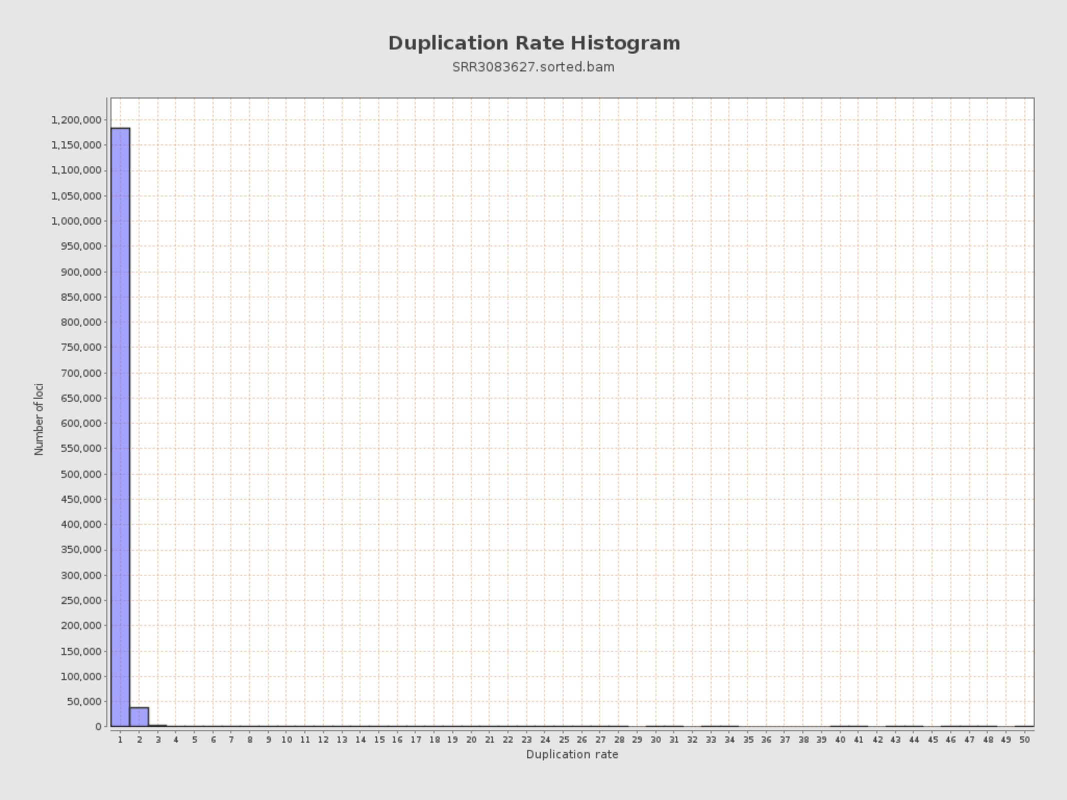
5. Results : Coverage Histogram (0-50X)



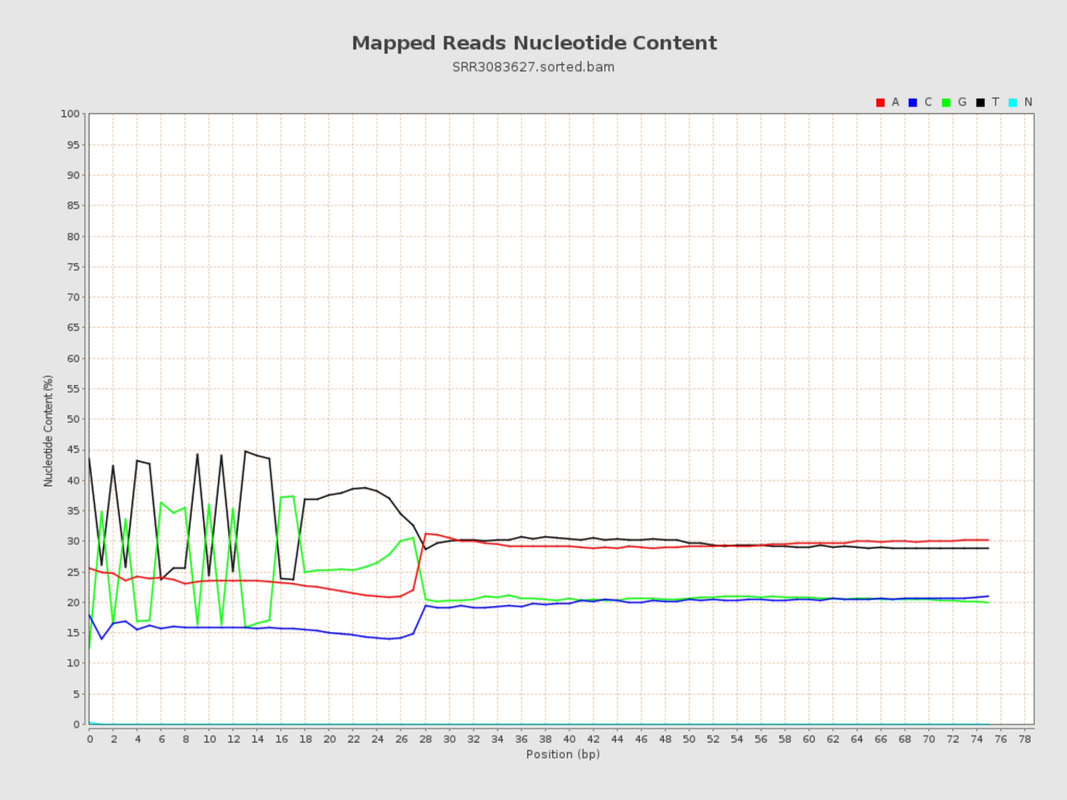
6. Results : Genome Fraction Coverage



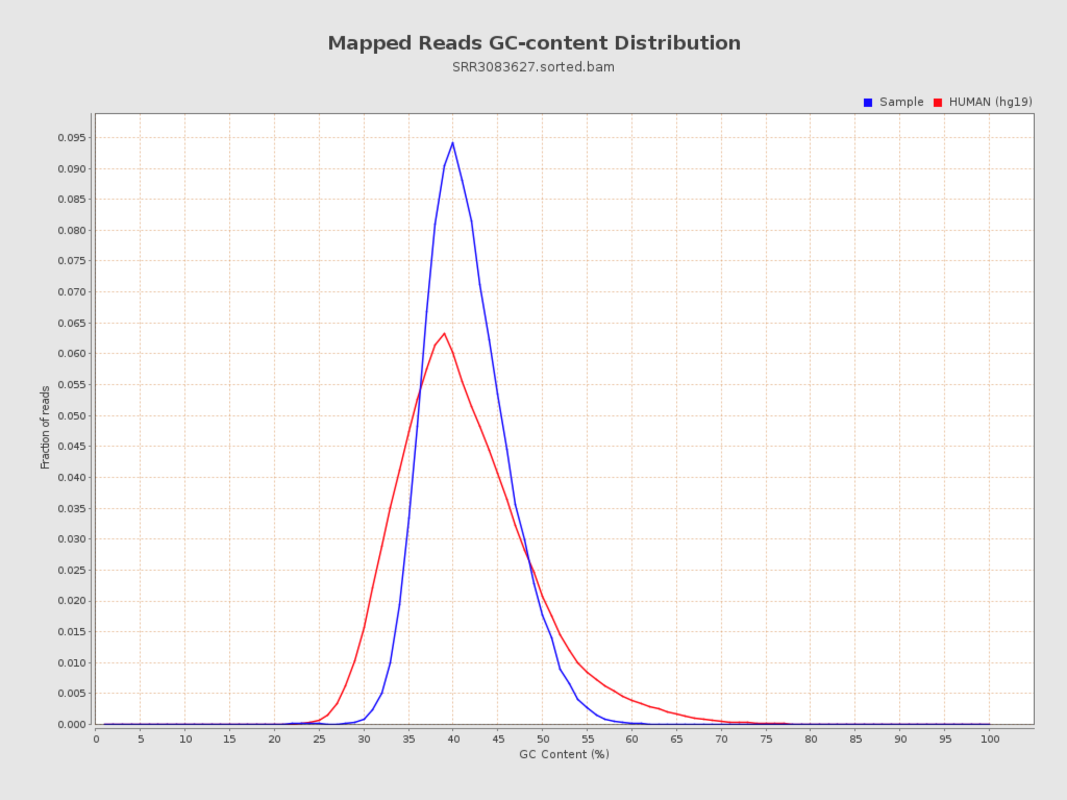
7. Results : Duplication Rate Histogram



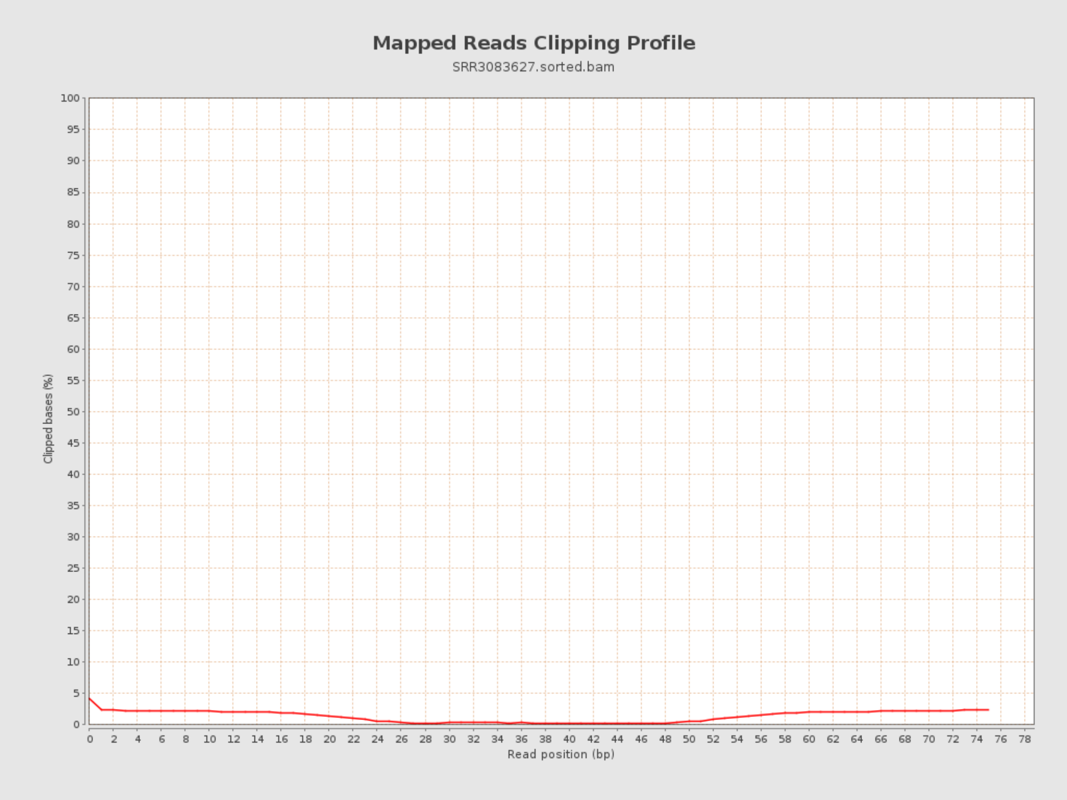
8. Results : Mapped Reads Nucleotide Content



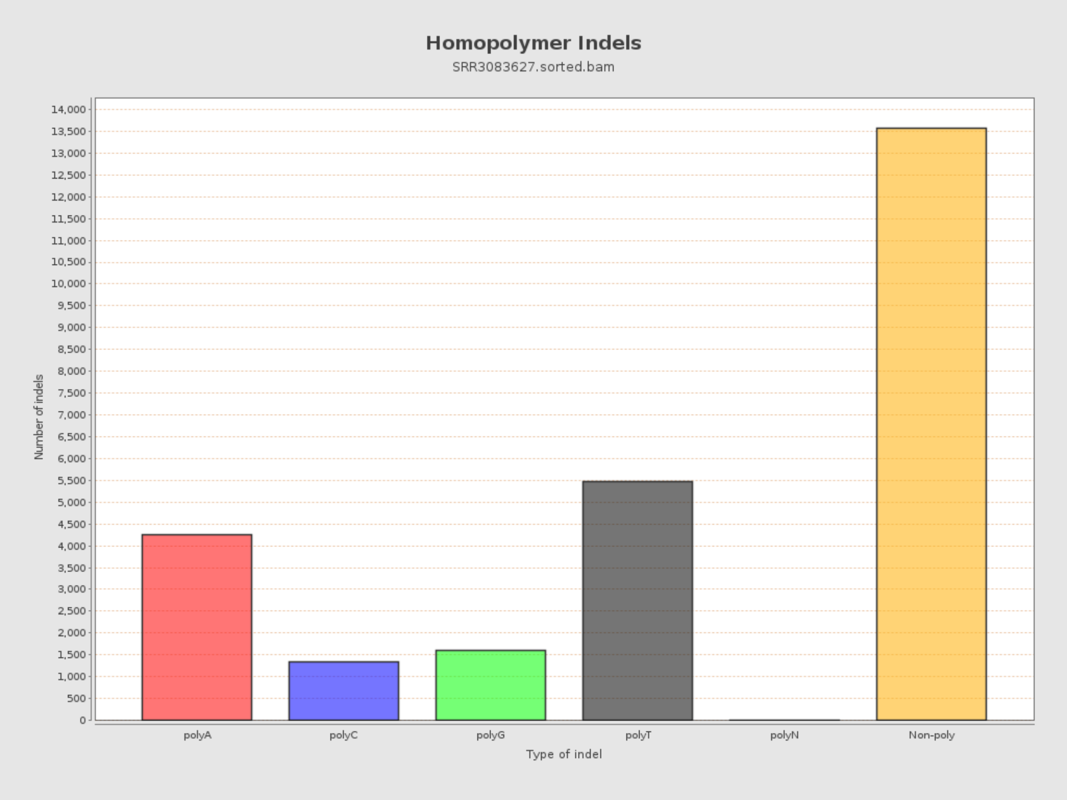
9. Results : Mapped Reads GC-content Distribution



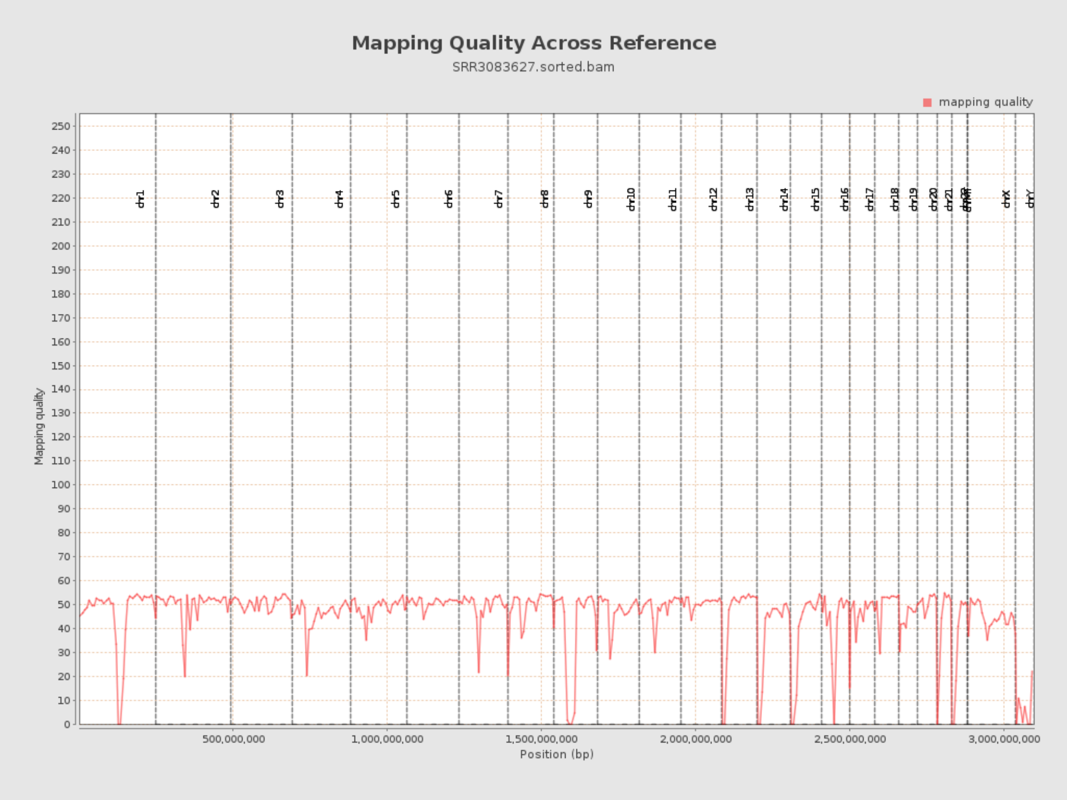
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram