Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:49:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240256.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_SRR6240256 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240256.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:49:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240256.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,722,639
Mapped reads	1,410,366 / 81.87%
Unmapped reads	312,273 / 18.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,437 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	110,346 / 6.41%
Duplication rate	6.5%
Clipped reads	903,069 / 52.42%

2.2. ACGT Content

Number/percentage of A's	24,004,596 / 27.53%
Number/percentage of C's	15,016,738 / 17.22%
Number/percentage of T's	28,641,975 / 32.85%
Number/percentage of G's	19,501,806 / 22.37%
Number/percentage of N's	22,224 / 0.03%
GC Percentage	39.59%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.3039

2.4. Mapping Quality

Mean Mapping Quality	45.8

2.5. Mismatches and indels

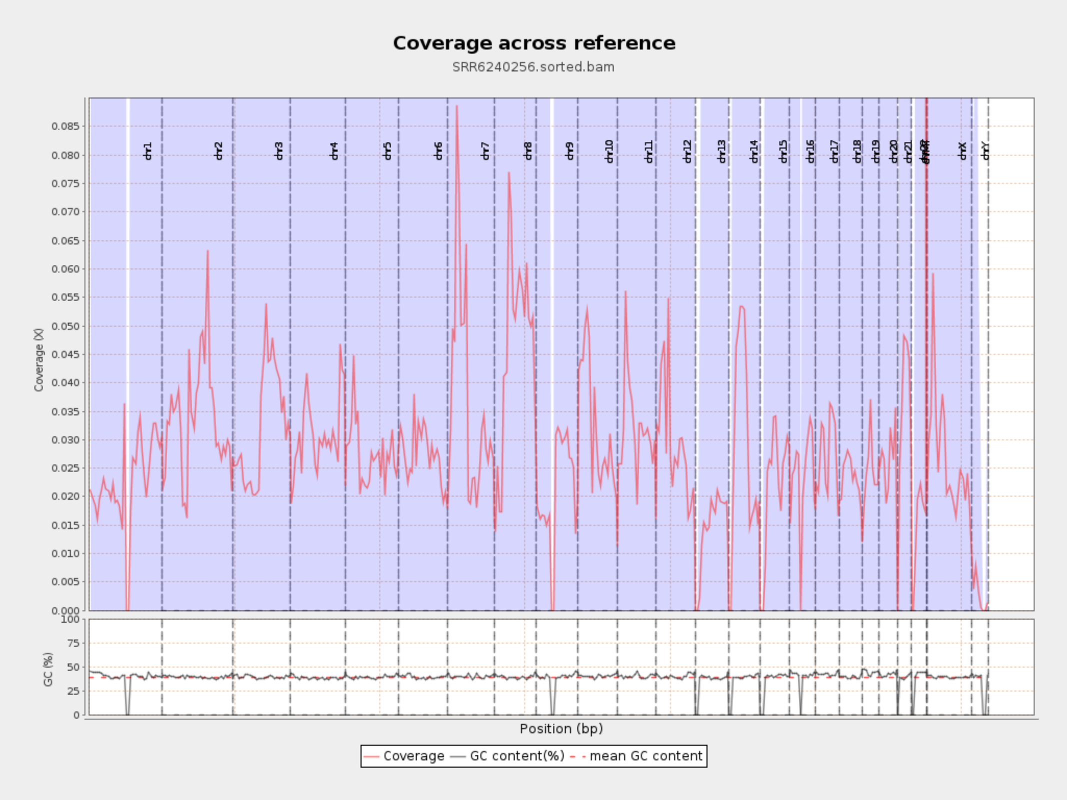
General error rate	0.91%
Mismatches	784,344
Insertions	5,874
Mapped reads with at least one insertion	0.41%
Deletions	28,377
Mapped reads with at least one deletion	1.99%
Homopolymer indels	49.6%

2.6. Chromosome stats

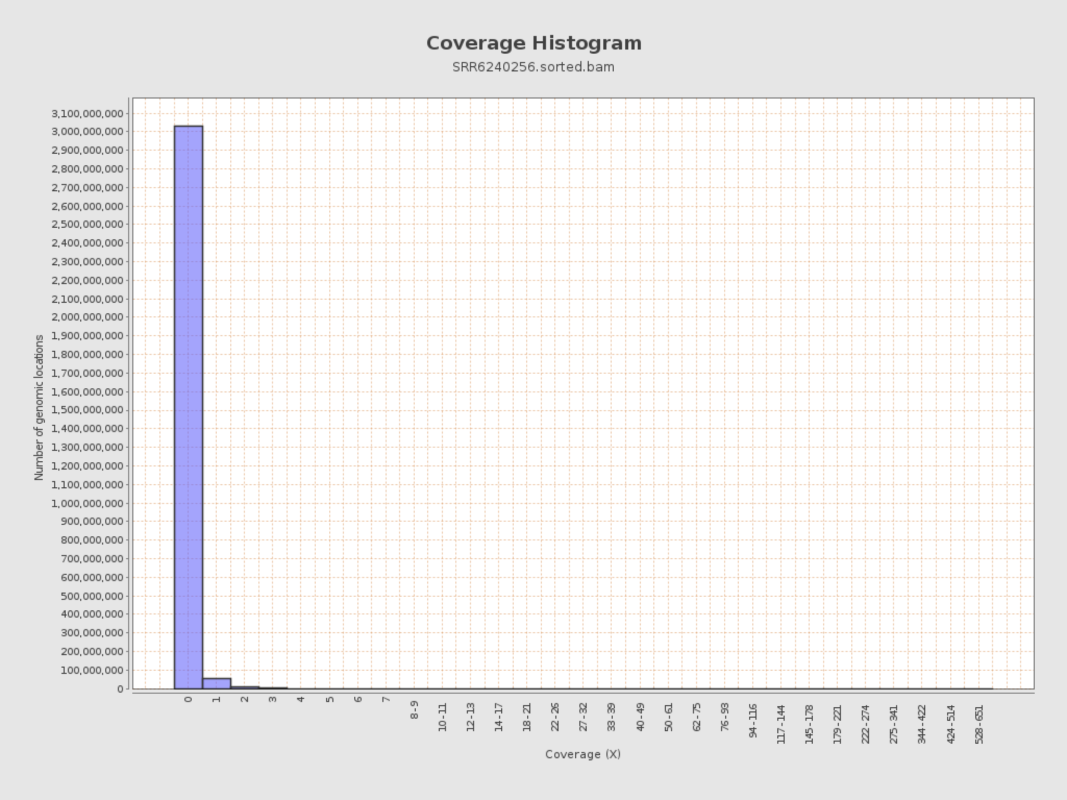
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5589801	0.0224	0.4622
chr2	243199373	8211757	0.0338	0.3054
chr3	198022430	6405607	0.0323	0.2238
chr4	191154276	5915196	0.0309	0.2215
chr5	180915260	4959412	0.0274	0.2071
chr6	171115067	4705345	0.0275	0.2708
chr7	159138663	5989434	0.0376	0.6065

chr8	146364022	6788171	0.0464	0.4123
chr9	141213431	2951931	0.0209	0.243
chr10	135534747	4482012	0.0331	0.2791
chr11	135006516	4315792	0.032	0.2913
chr12	133851895	3944444	0.0295	0.2122
chr13	115169878	1646427	0.0143	0.1455
chr14	107349540	3115820	0.029	0.2203
chr15	102531392	2220891	0.0217	0.1871
chr16	90354753	2147781	0.0238	0.1962
chr17	81195210	2201585	0.0271	0.2402
chr18	78077248	1836543	0.0235	0.3774
chr19	59128983	1453614	0.0246	0.3109
chr20	63025520	1664724	0.0264	0.204
chr21	48129895	1685477	0.035	0.2385
chr22	51304566	717608	0.014	0.1432
chrMT	16571	15109	0.9118	1.3349
chrX	155270560	4110690	0.0265	0.2192
chrY	59373566	160953	0.0027	0.0689

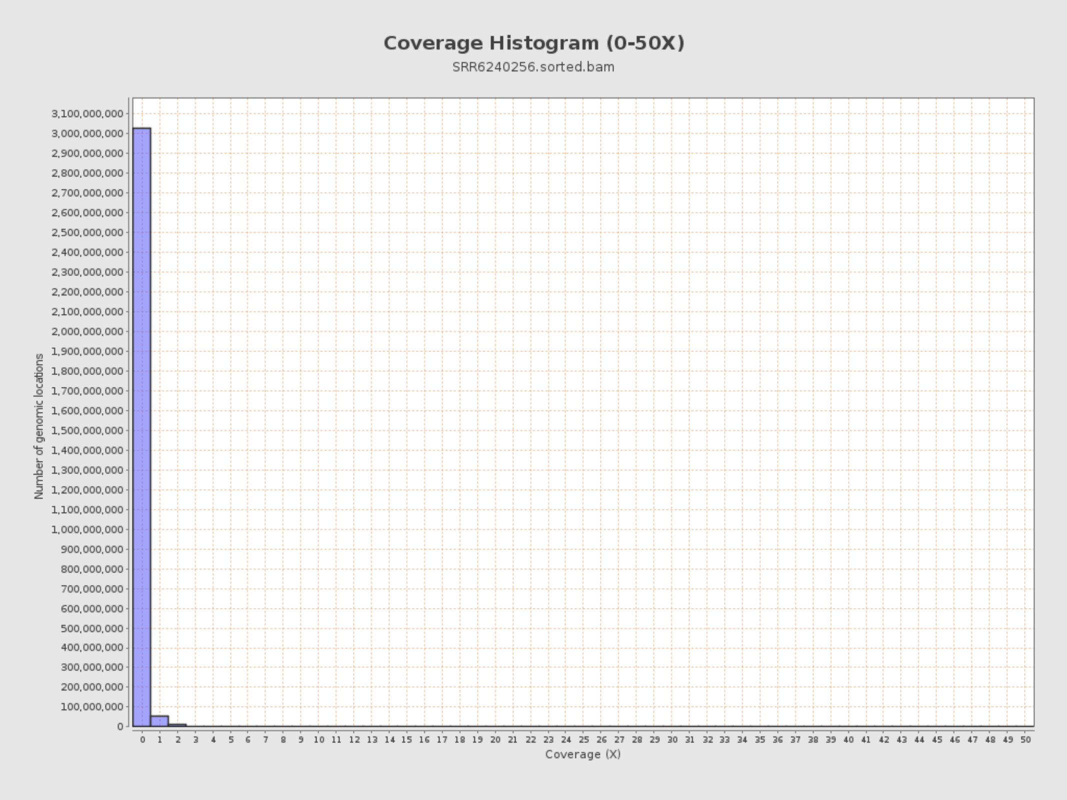
3. Results : Coverage across reference



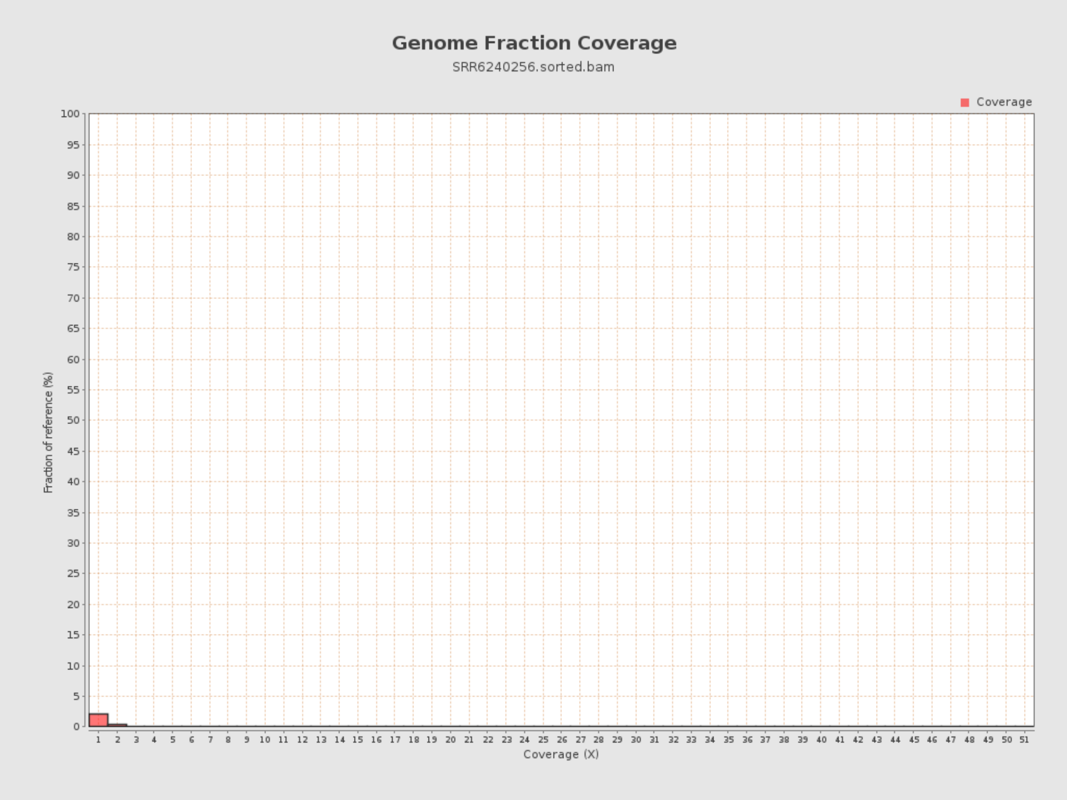
4. Results : Coverage Histogram



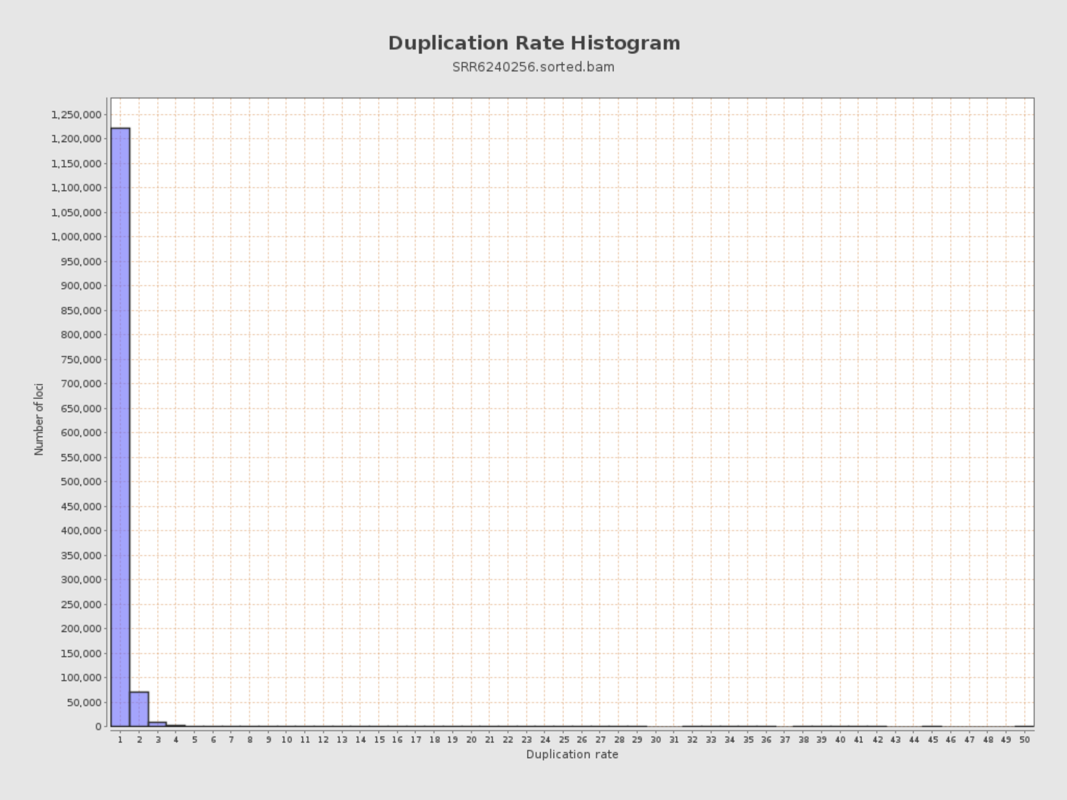
5. Results : Coverage Histogram (0-50X)



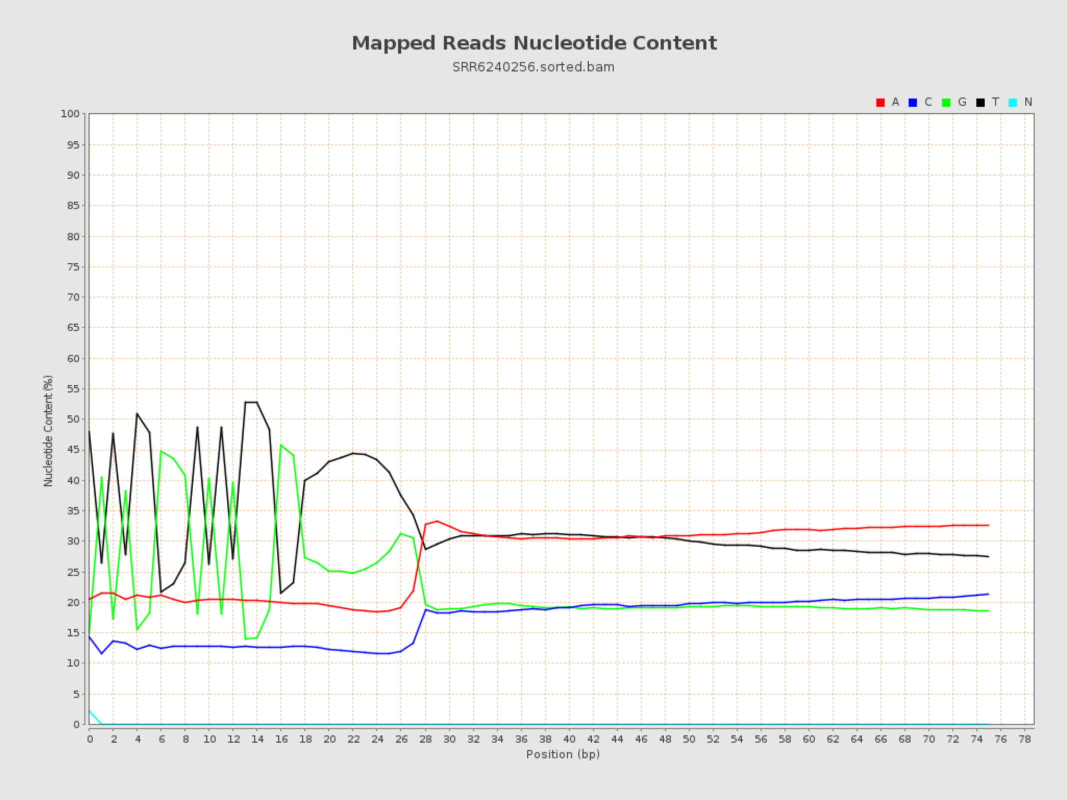
6. Results : Genome Fraction Coverage



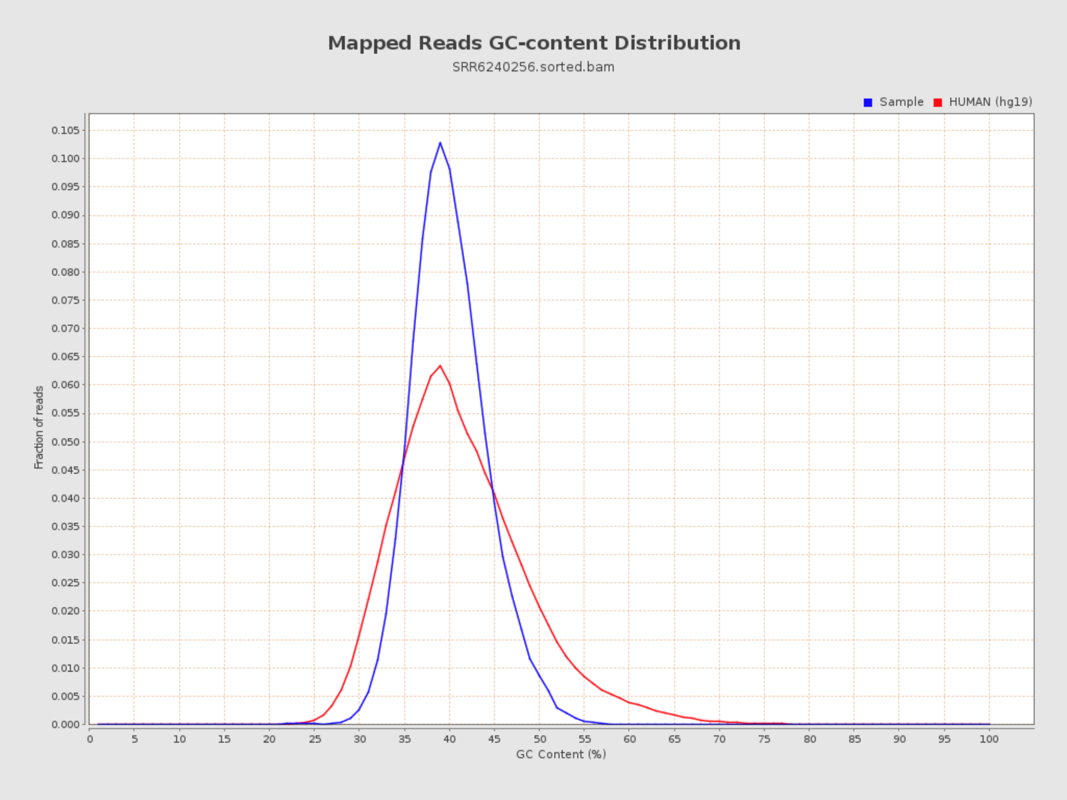
7. Results : Duplication Rate Histogram



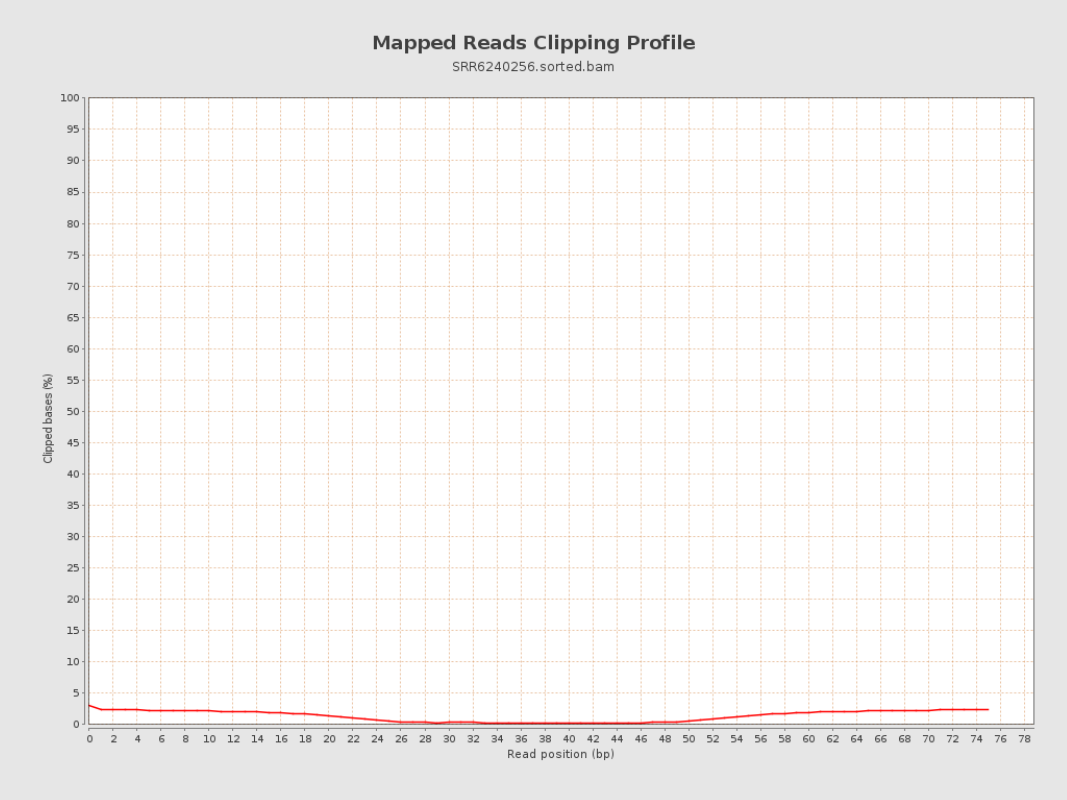
8. Results : Mapped Reads Nucleotide Content



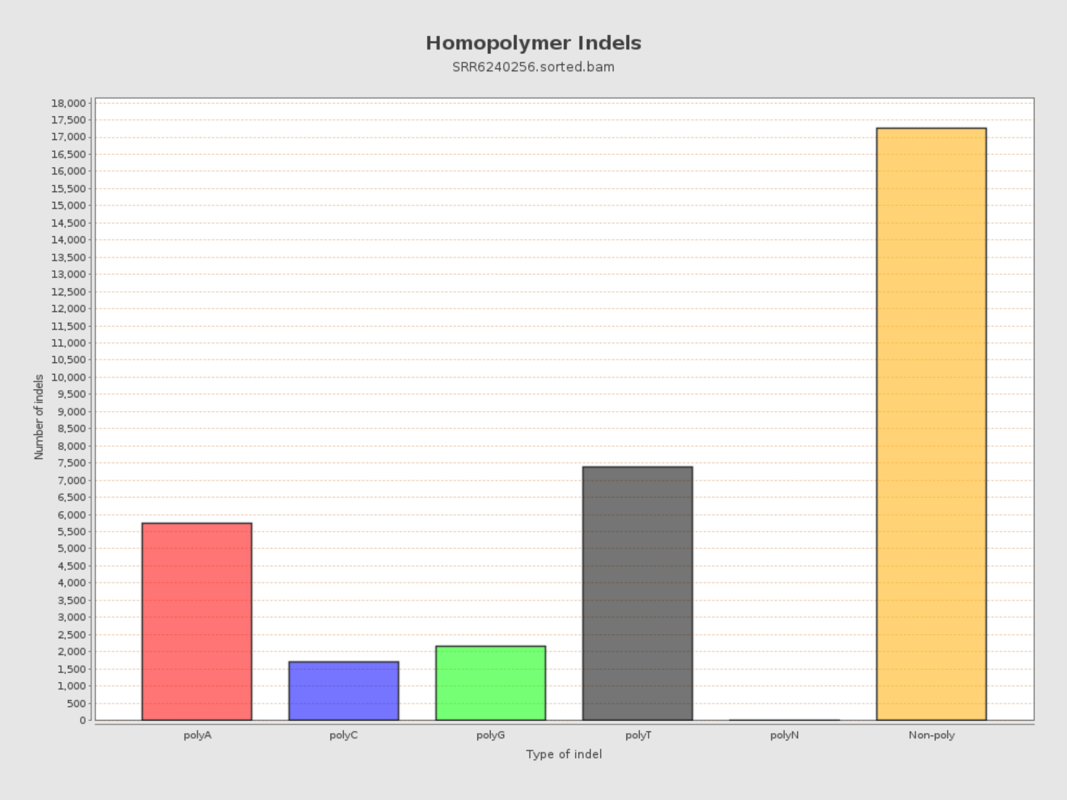
9. Results : Mapped Reads GC-content Distribution



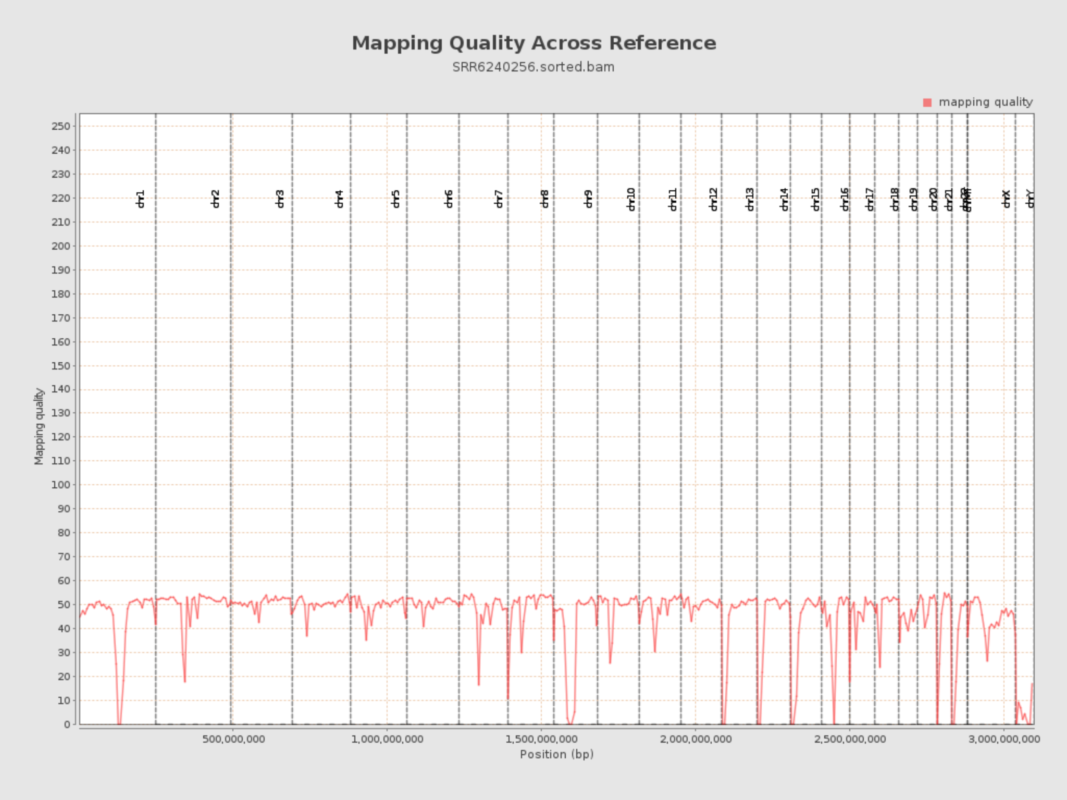
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram