Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:57:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240196.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_SRR6240196 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240196.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:57:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240196.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,708,504
Mapped reads	1,306,076 / 76.45%
Unmapped reads	402,428 / 23.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,736 / 0.39%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	146,455 / 8.57%
Duplication rate	9.35%
Clipped reads	871,415 / 51%

2.2. ACGT Content

Number/percentage of A's	21,337,063 / 26.65%
Number/percentage of C's	13,574,389 / 16.96%
Number/percentage of T's	26,644,610 / 33.28%
Number/percentage of G's	18,477,042 / 23.08%
Number/percentage of N's	18,931 / 0.02%
GC Percentage	40.04%

2.3. Coverage

Mean	0.0259

Standard Deviation	0.2721

2.4. Mapping Quality

Mean Mapping Quality	45.66

2.5. Mismatches and indels

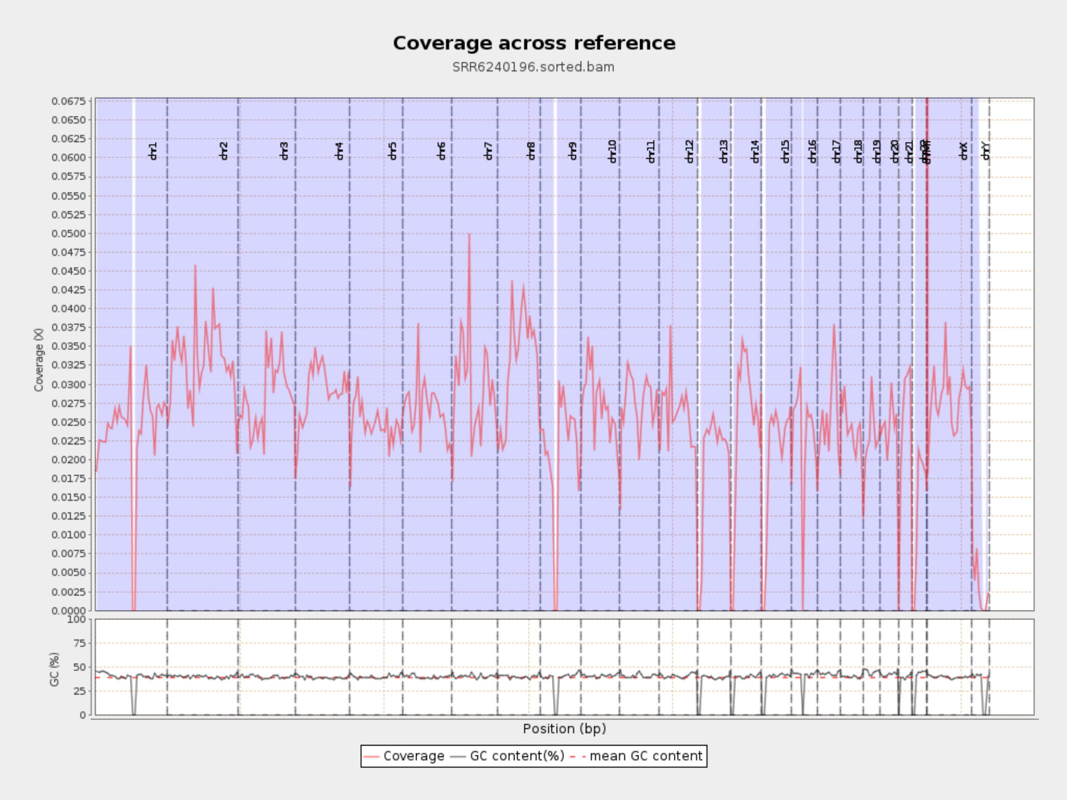
General error rate	0.94%
Mismatches	744,448
Insertions	5,601
Mapped reads with at least one insertion	0.43%
Deletions	25,547
Mapped reads with at least one deletion	1.93%
Homopolymer indels	49.52%

2.6. Chromosome stats

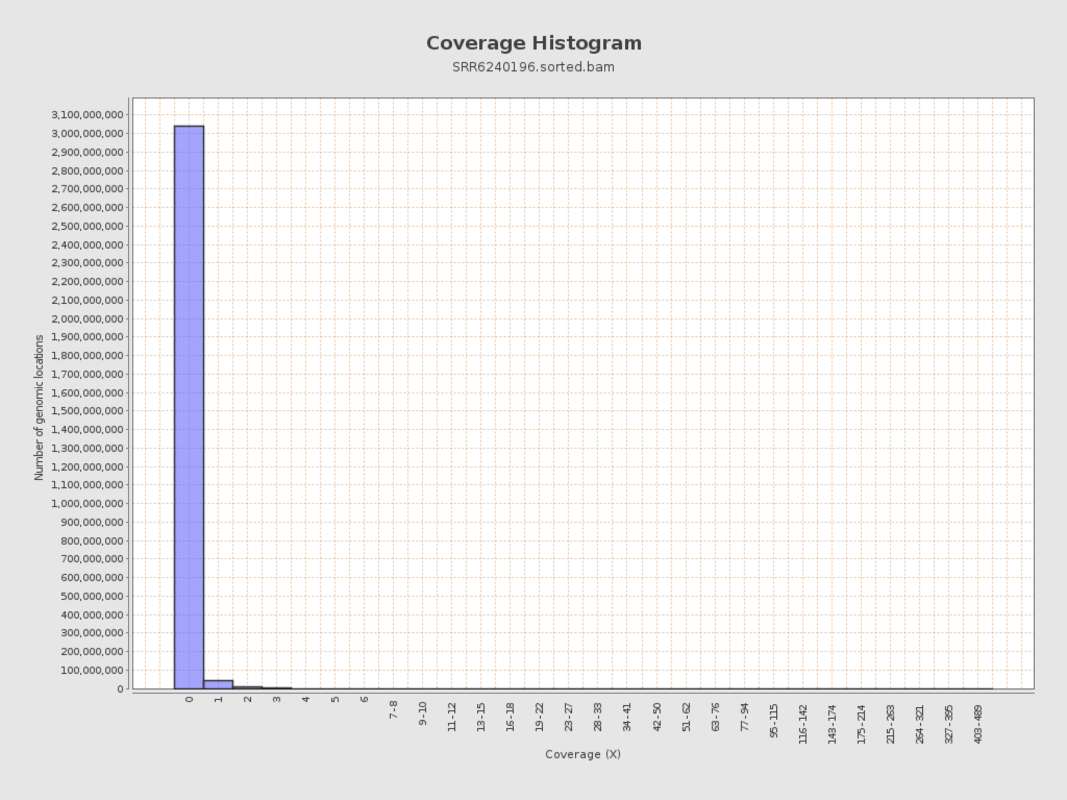
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5937752	0.0238	0.3556
chr2	243199373	8062827	0.0332	0.3324
chr3	198022430	5637989	0.0285	0.2268
chr4	191154276	5544721	0.029	0.2331
chr5	180915260	4509109	0.0249	0.2117
chr6	171115067	4587182	0.0268	0.2472
chr7	159138663	4744618	0.0298	0.4246

chr8	146364022	4876436	0.0333	0.3814
chr9	141213431	2964123	0.021	0.2405
chr10	135534747	3707058	0.0274	0.2488
chr11	135006516	3708732	0.0275	0.2603
chr12	133851895	3485618	0.026	0.2177
chr13	115169878	2221212	0.0193	0.1869
chr14	107349540	2651740	0.0247	0.2203
chr15	102531392	2027608	0.0198	0.1938
chr16	90354753	2066314	0.0229	0.202
chr17	81195210	2088916	0.0257	0.2233
chr18	78077248	1883607	0.0241	0.337
chr19	59128983	1368403	0.0231	0.2733
chr20	63025520	1522356	0.0242	0.2095
chr21	48129895	1185672	0.0246	0.2126
chr22	51304566	702645	0.0137	0.1505
chrMT	16571	51235	3.0918	3.451
chrX	155270560	4384693	0.0282	0.2374
chrY	59373566	174715	0.0029	0.0746

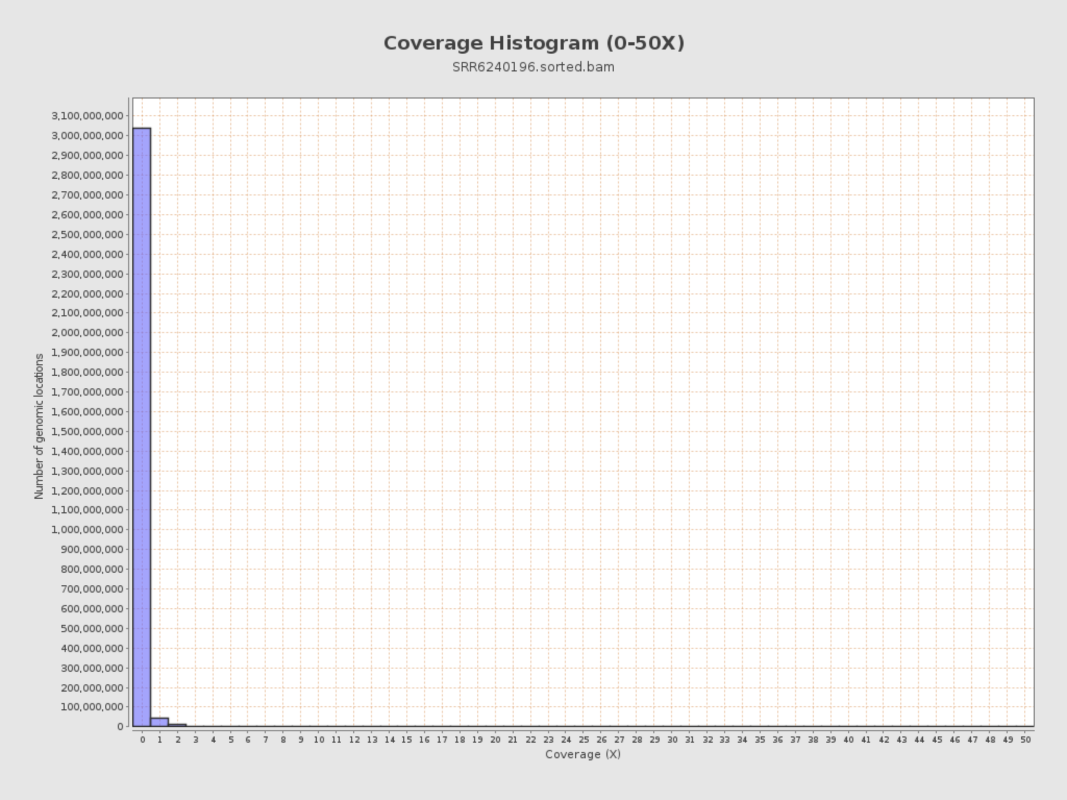
3. Results : Coverage across reference



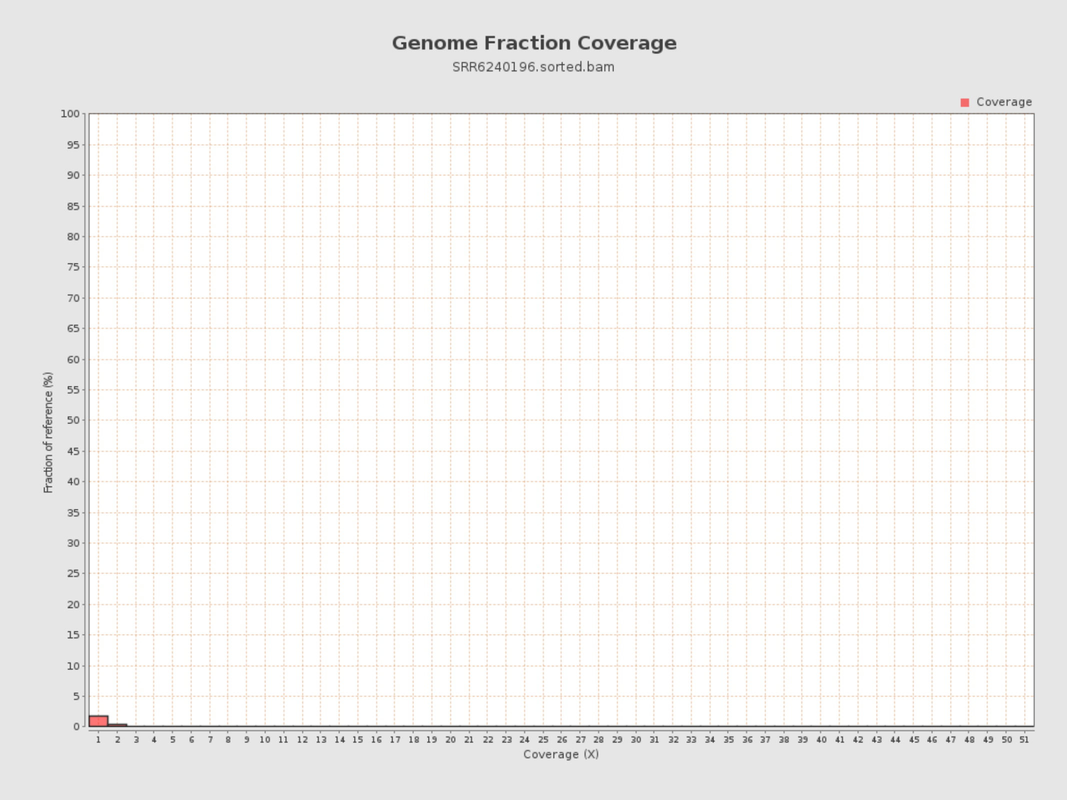
4. Results : Coverage Histogram



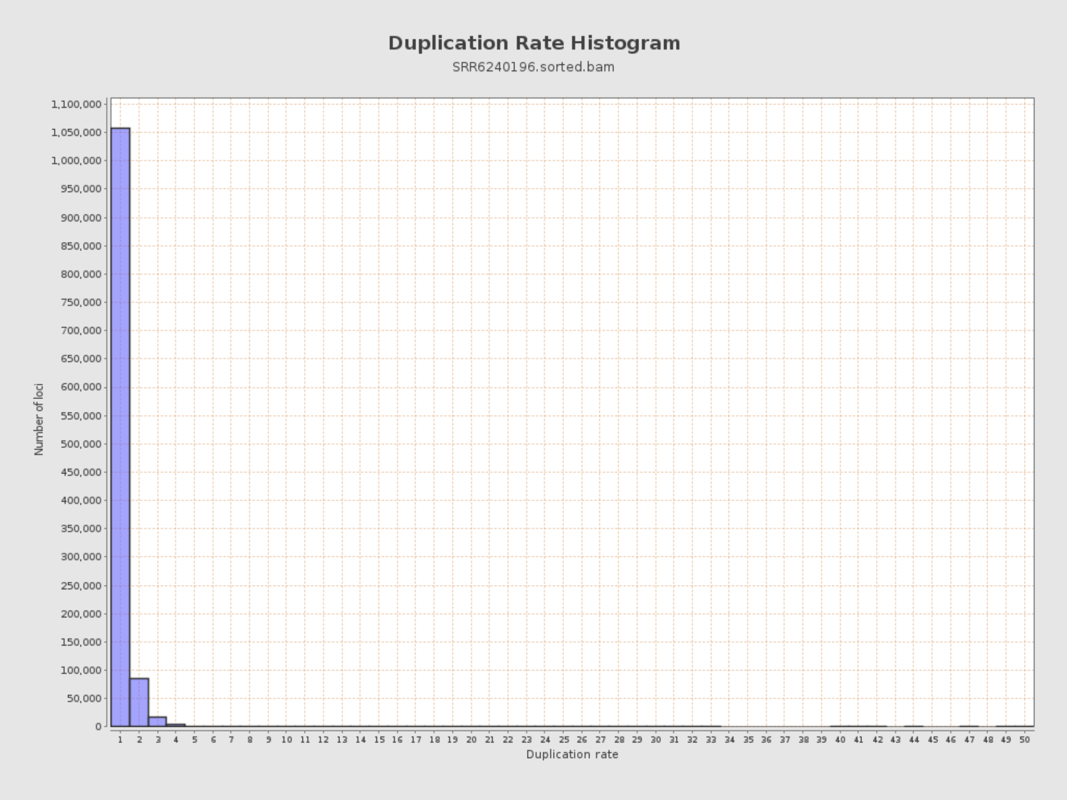
5. Results : Coverage Histogram (0-50X)



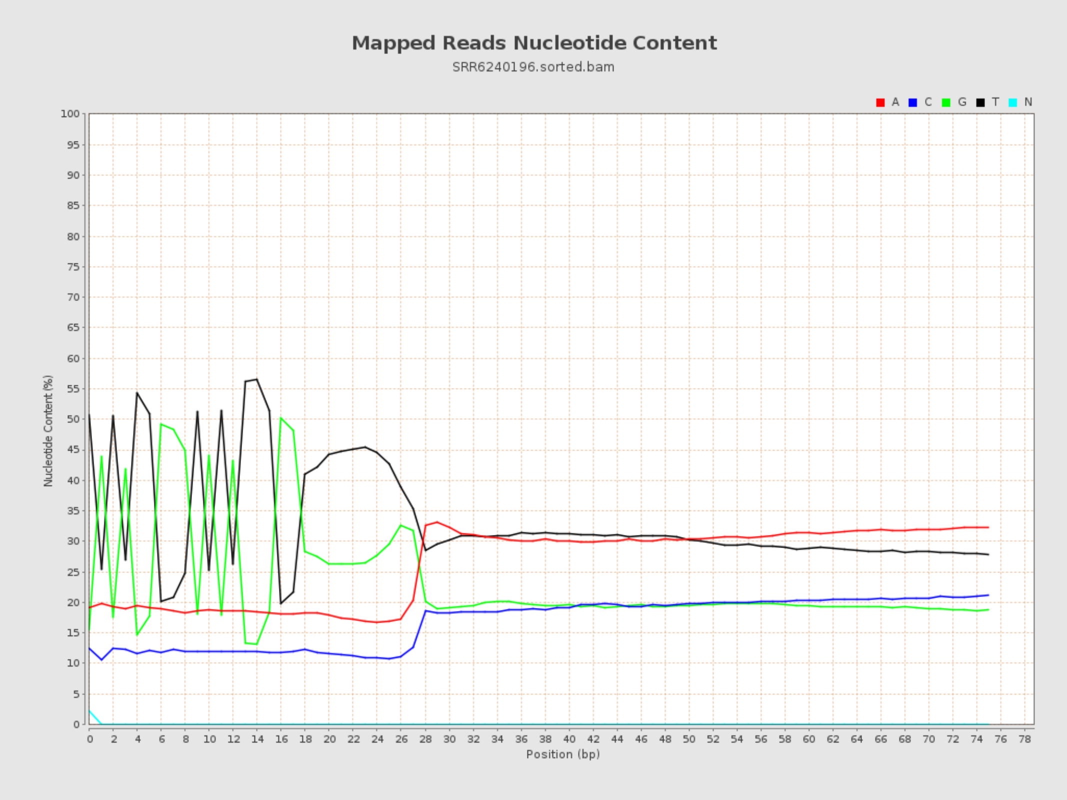
6. Results : Genome Fraction Coverage



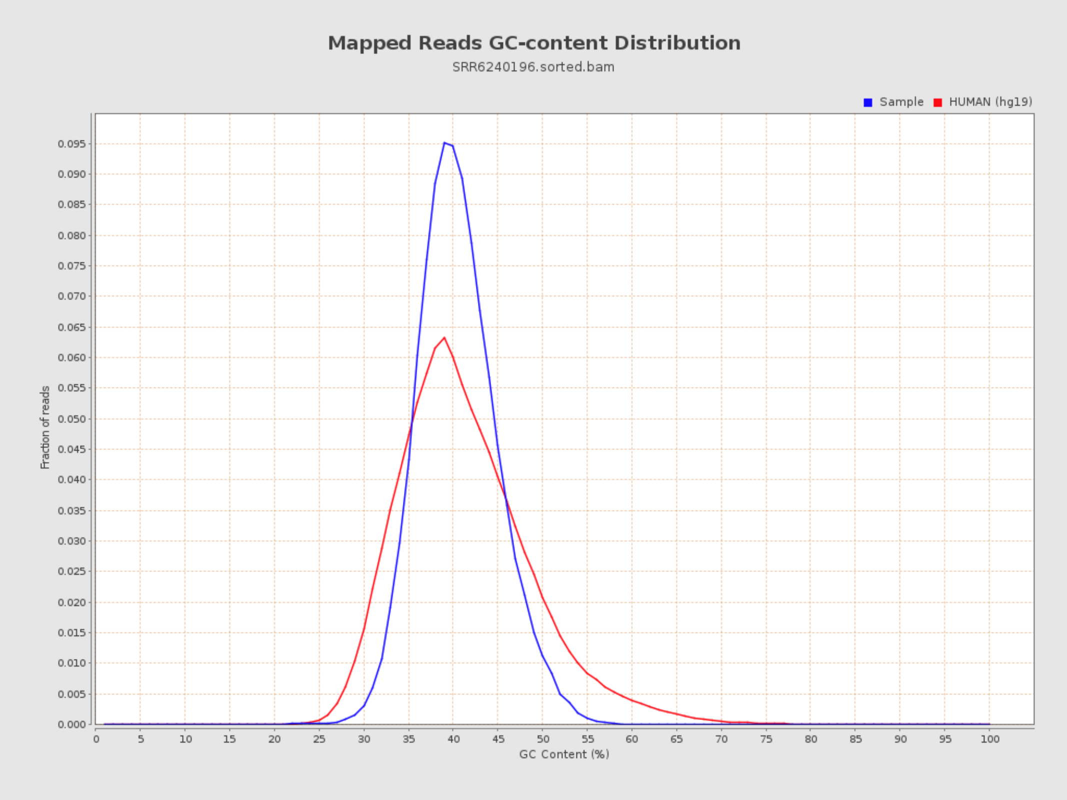
7. Results : Duplication Rate Histogram



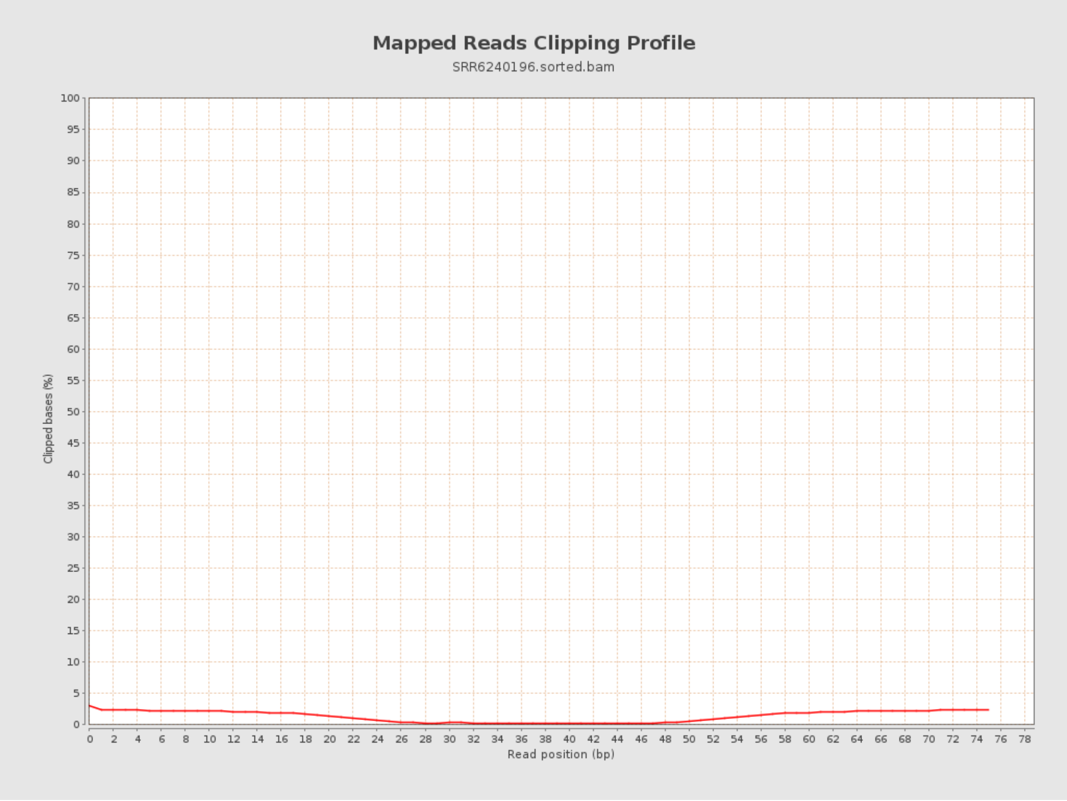
8. Results : Mapped Reads Nucleotide Content



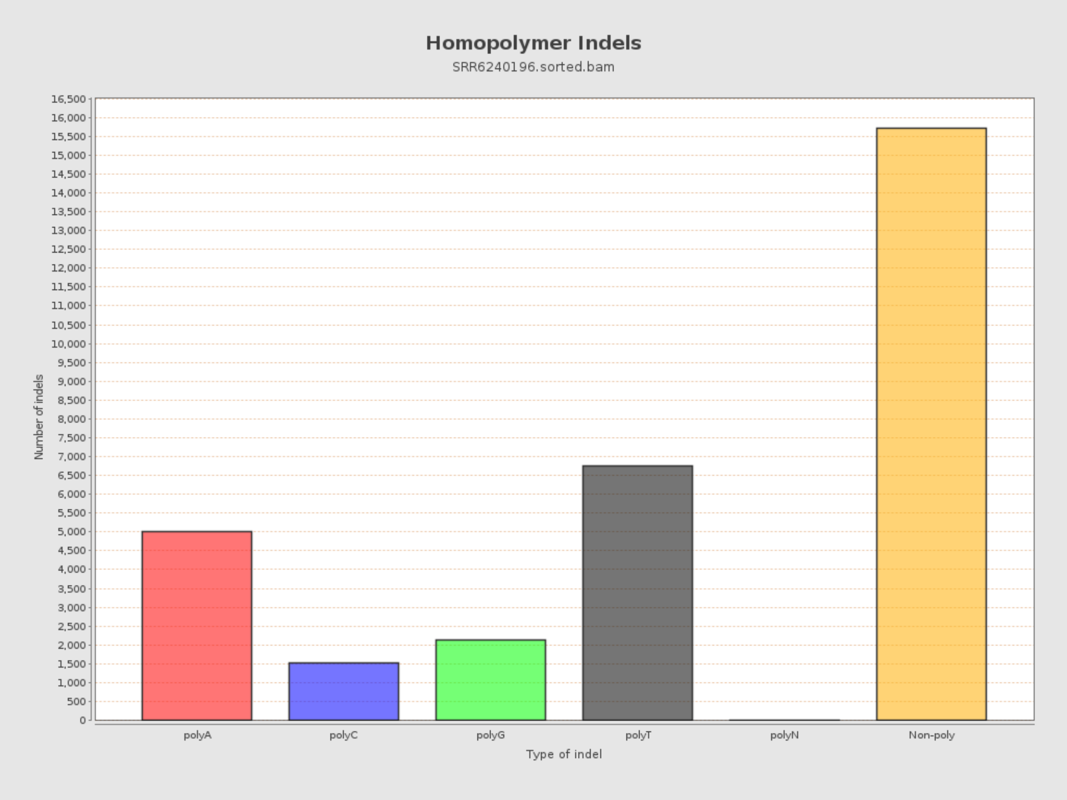
9. Results : Mapped Reads GC-content Distribution



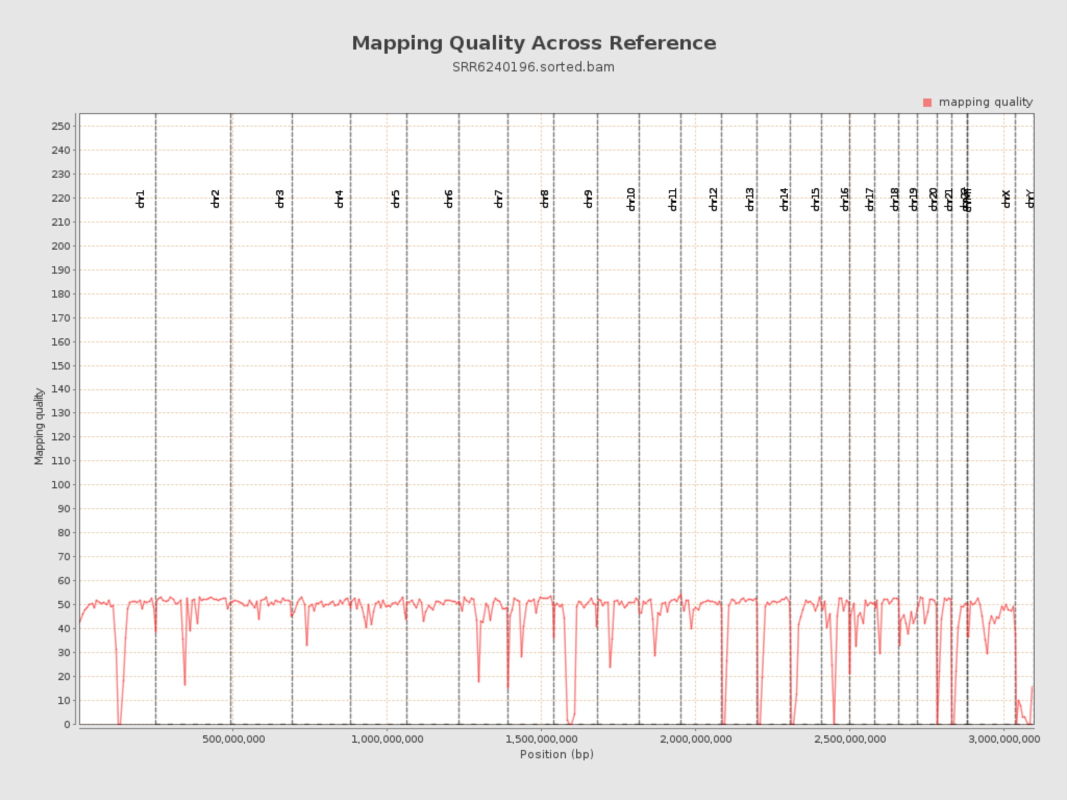
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram