Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:52:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240066.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_SRR6240066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240066.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:52:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240066.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,577,943
Mapped reads	2,105,278 / 81.67%
Unmapped reads	472,665 / 18.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,814 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	418,037 / 16.22%
Duplication rate	12.98%
Clipped reads	1,033,263 / 40.08%

2.2. ACGT Content

Number/percentage of A's	37,947,489 / 27.5%
Number/percentage of C's	24,658,222 / 17.87%
Number/percentage of T's	45,028,948 / 32.63%
Number/percentage of G's	30,330,223 / 21.98%
Number/percentage of N's	12,633 / 0.01%
GC Percentage	39.85%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.6306

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

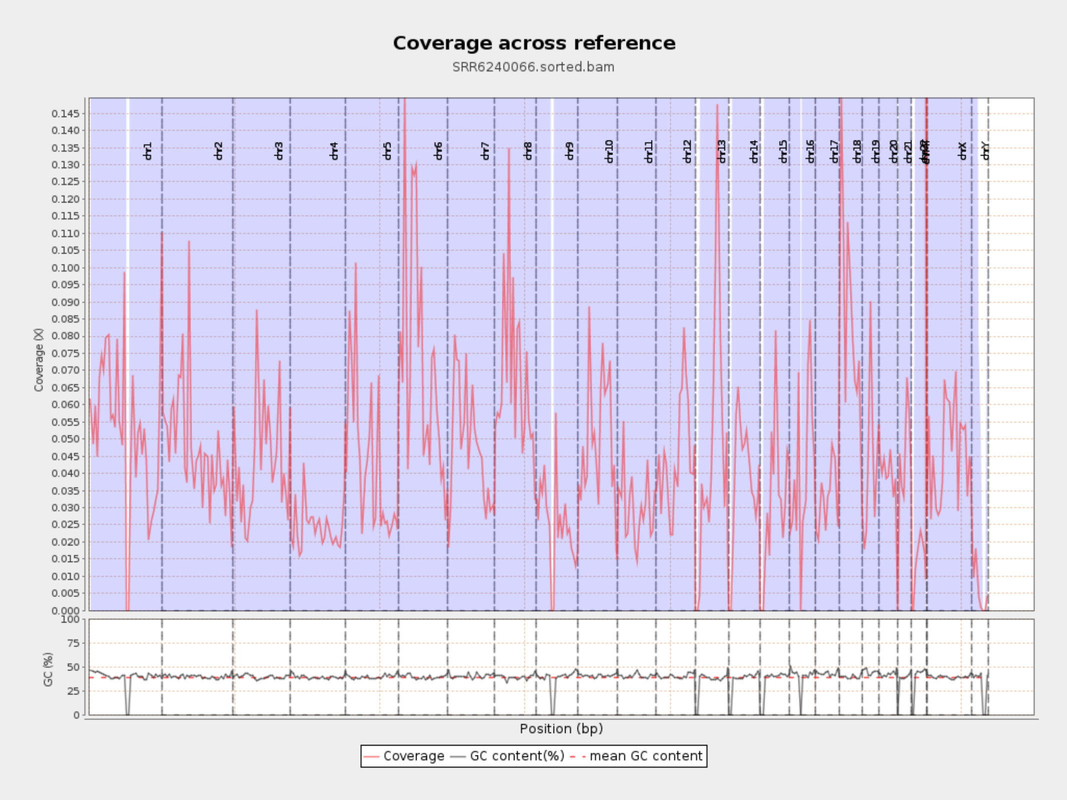
General error rate	0.83%
Mismatches	1,124,318
Insertions	10,041
Mapped reads with at least one insertion	0.47%
Deletions	31,037
Mapped reads with at least one deletion	1.46%
Homopolymer indels	49.08%

2.6. Chromosome stats

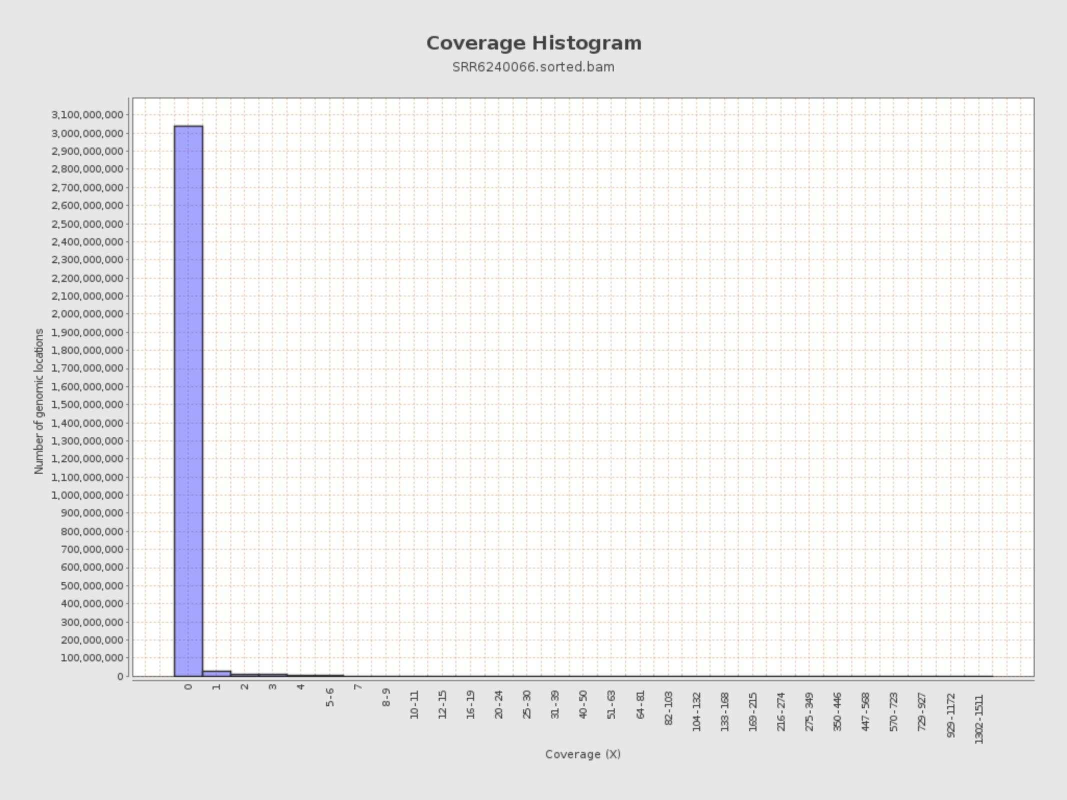
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12901926	0.0518	1.0474
chr2	243199373	11579681	0.0476	0.7822
chr3	198022430	8702968	0.0439	0.4197
chr4	191154276	4616546	0.0242	0.3091
chr5	180915260	7858883	0.0434	0.4214
chr6	171115067	12259540	0.0716	0.6284
chr7	159138663	7777613	0.0489	0.5776

chr8	146364022	9828912	0.0672	1.0735
chr9	141213431	3518072	0.0249	0.5159
chr10	135534747	6842442	0.0505	0.5133
chr11	135006516	4009388	0.0297	0.4204
chr12	133851895	6100465	0.0456	0.4349
chr13	115169878	5367239	0.0466	0.4393
chr14	107349540	4029264	0.0375	0.4001
chr15	102531392	3210582	0.0313	0.3526
chr16	90354753	3777211	0.0418	0.4208
chr17	81195210	2622546	0.0323	0.404
chr18	78077248	6766171	0.0867	0.9643
chr19	59128983	2579632	0.0436	0.7003
chr20	63025520	2490269	0.0395	0.3994
chr21	48129895	2060387	0.0428	0.4223
chr22	51304566	708302	0.0138	0.2139
chrMT	16571	907247	54.7491	36.9155
chrX	155270560	7141900	0.046	0.4618
chrY	59373566	372905	0.0063	0.1633

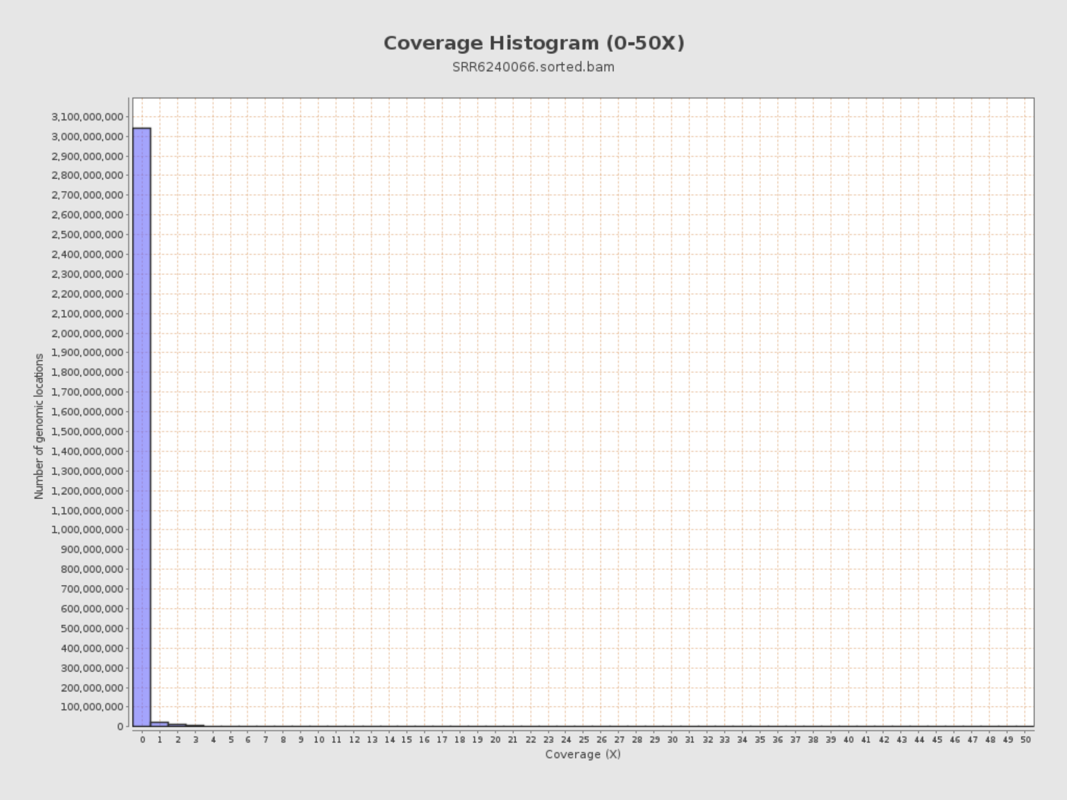
3. Results : Coverage across reference



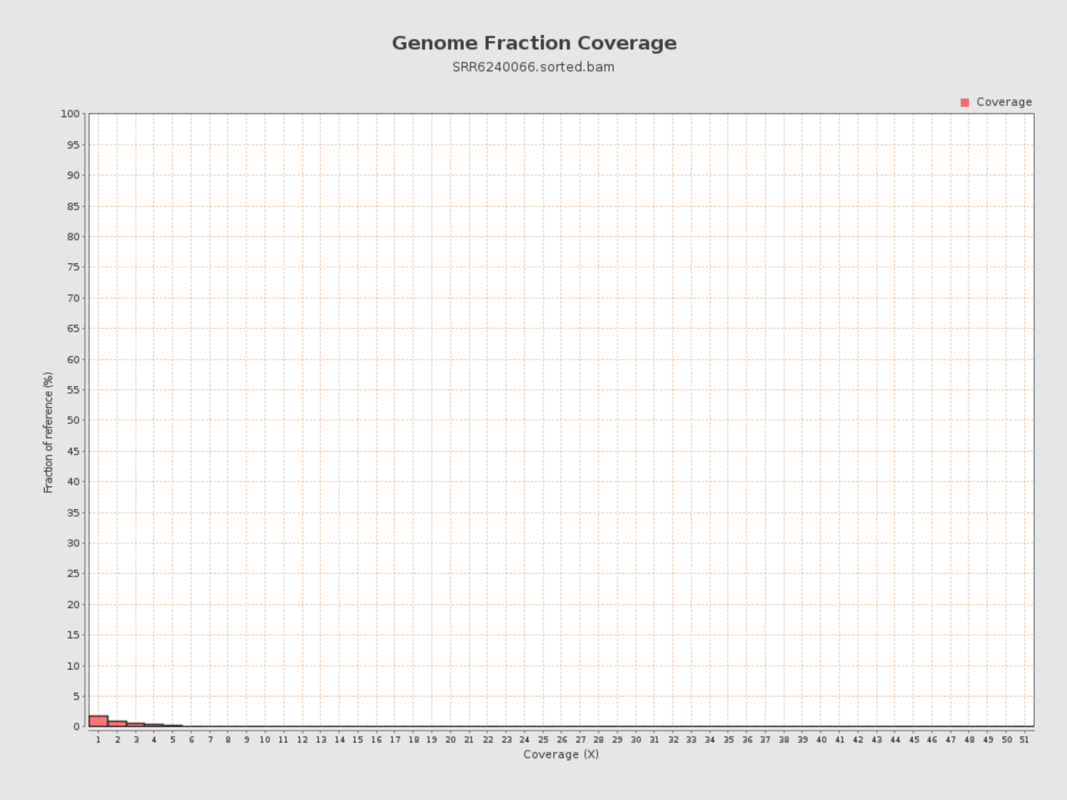
4. Results : Coverage Histogram



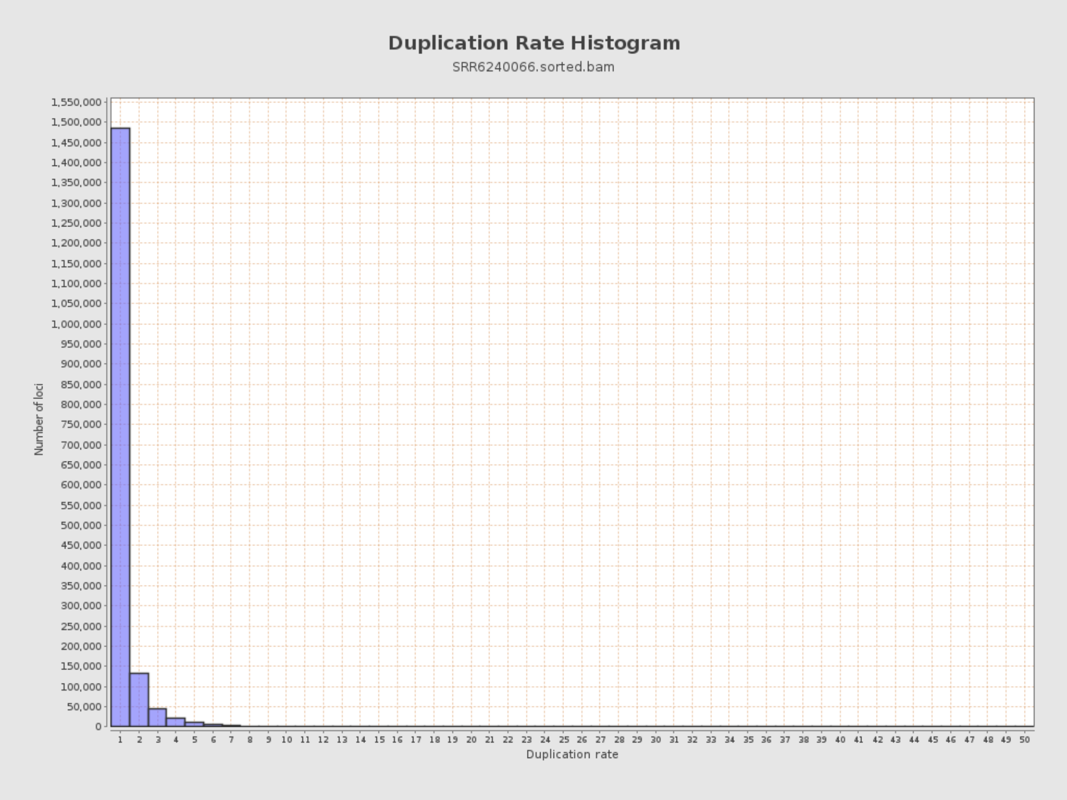
5. Results : Coverage Histogram (0-50X)



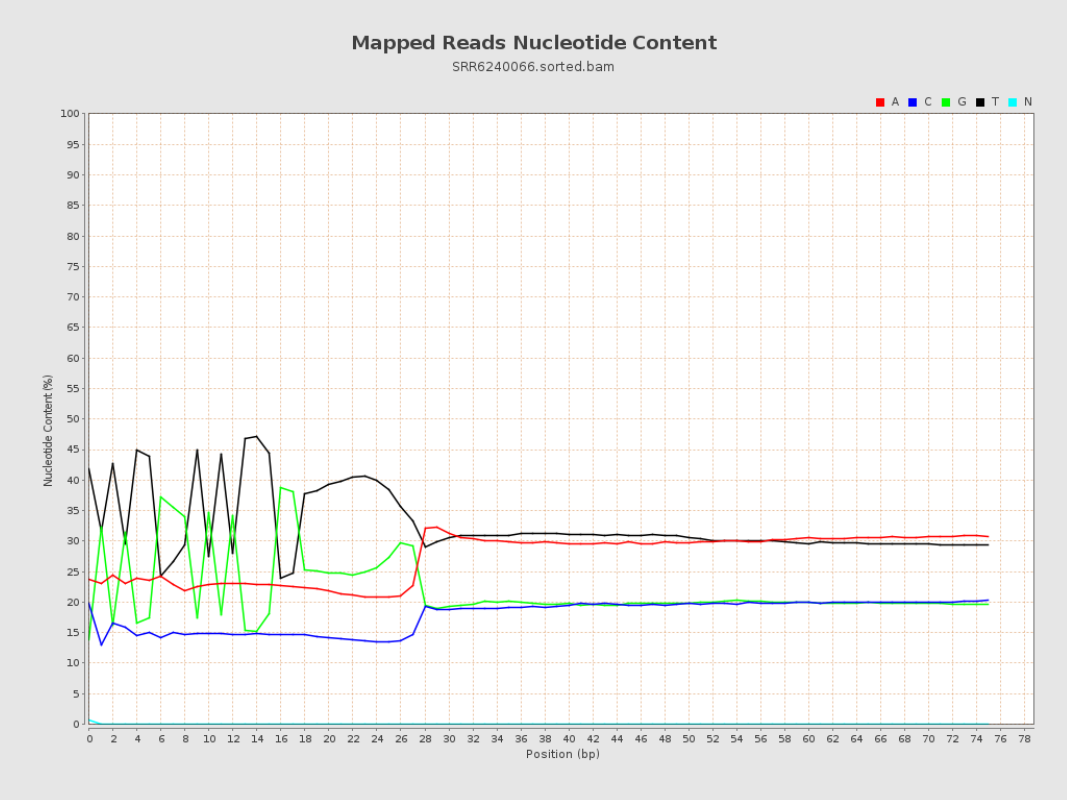
6. Results : Genome Fraction Coverage



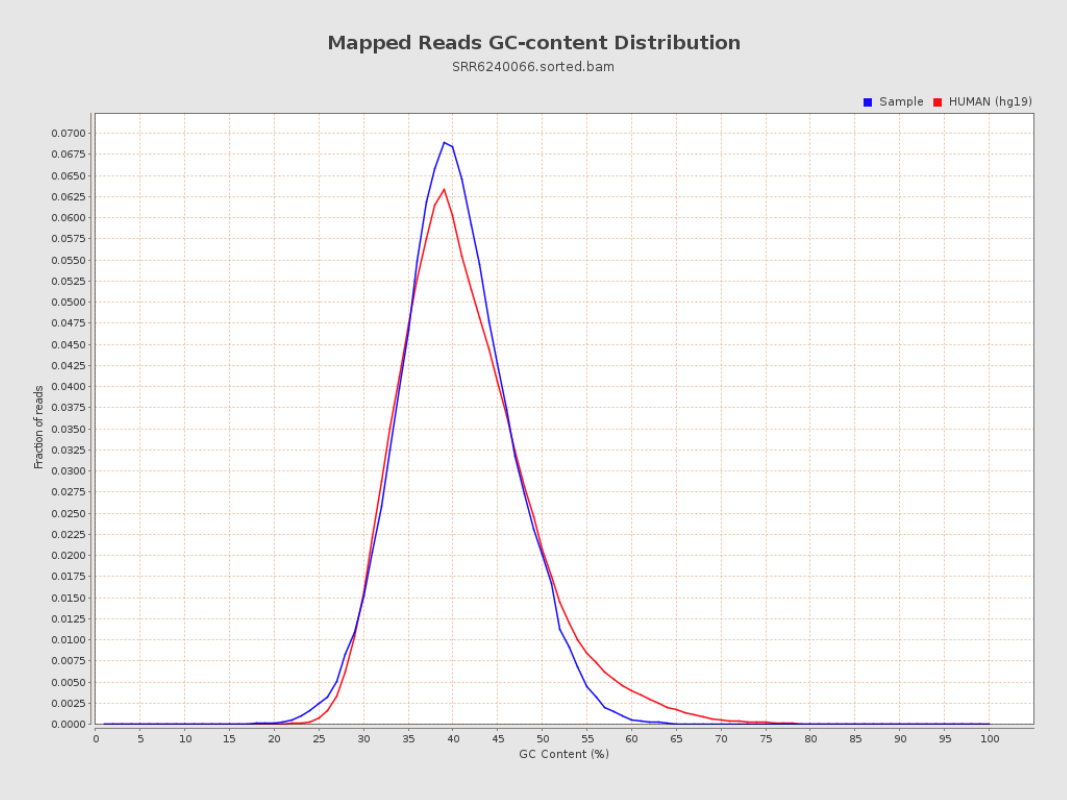
7. Results : Duplication Rate Histogram



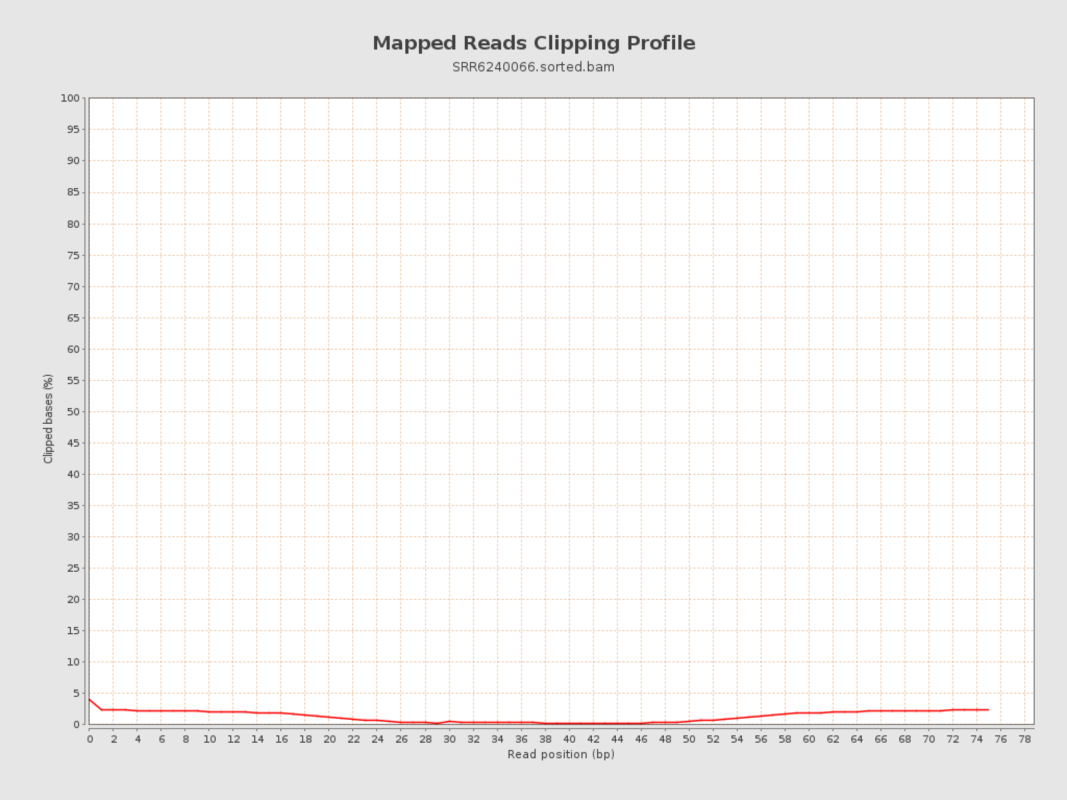
8. Results : Mapped Reads Nucleotide Content



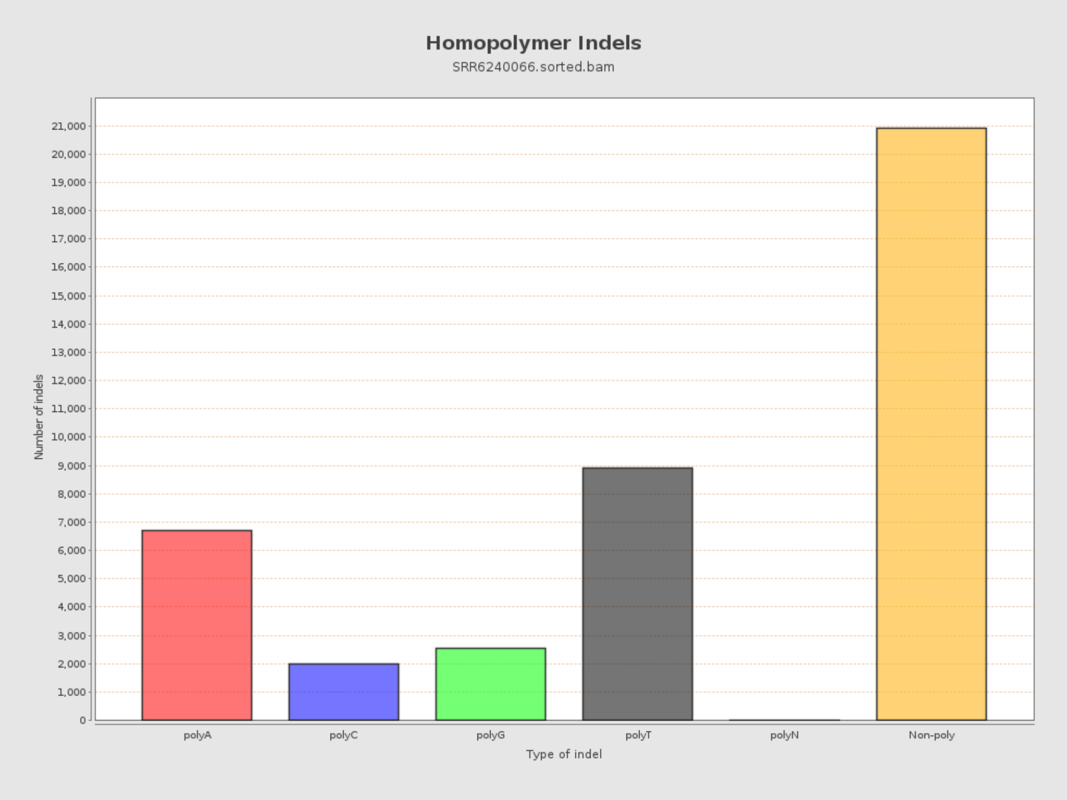
9. Results : Mapped Reads GC-content Distribution



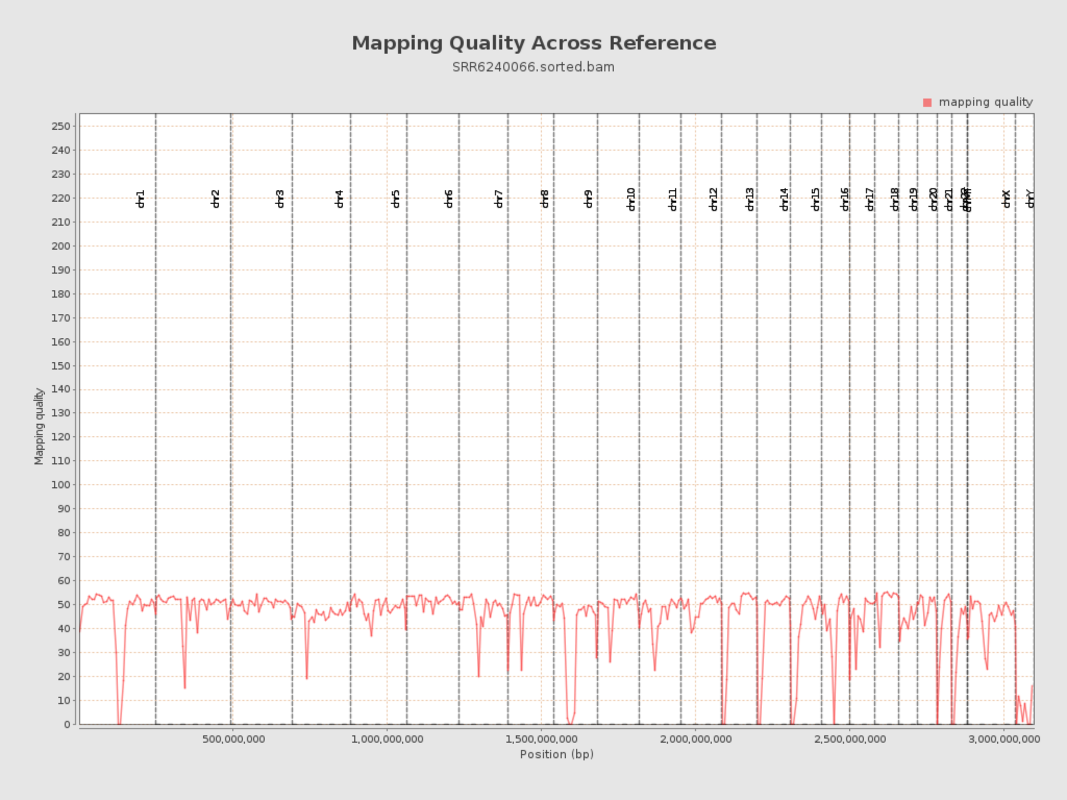
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram