Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/19 00:07:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536760.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_SRR536760 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536760.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 19 00:07:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536760.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,281,356
Mapped reads	23,711,124 / 97.65%
Unmapped reads	570,232 / 2.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	694 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	327,099 / 1.35%
Duplication rate	1.36%
Clipped reads	294,458 / 1.21%

2.2. ACGT Content

Number/percentage of A's	367,045,834 / 31.04%
Number/percentage of C's	222,180,036 / 18.79%
Number/percentage of T's	367,253,198 / 31.05%
Number/percentage of G's	226,154,507 / 19.12%
Number/percentage of N's	41,008 / 0%
GC Percentage	37.91%

2.3. Coverage

Mean	0.3821

Standard Deviation	0.7838

2.4. Mapping Quality

Mean Mapping Quality	46.61

2.5. Mismatches and indels

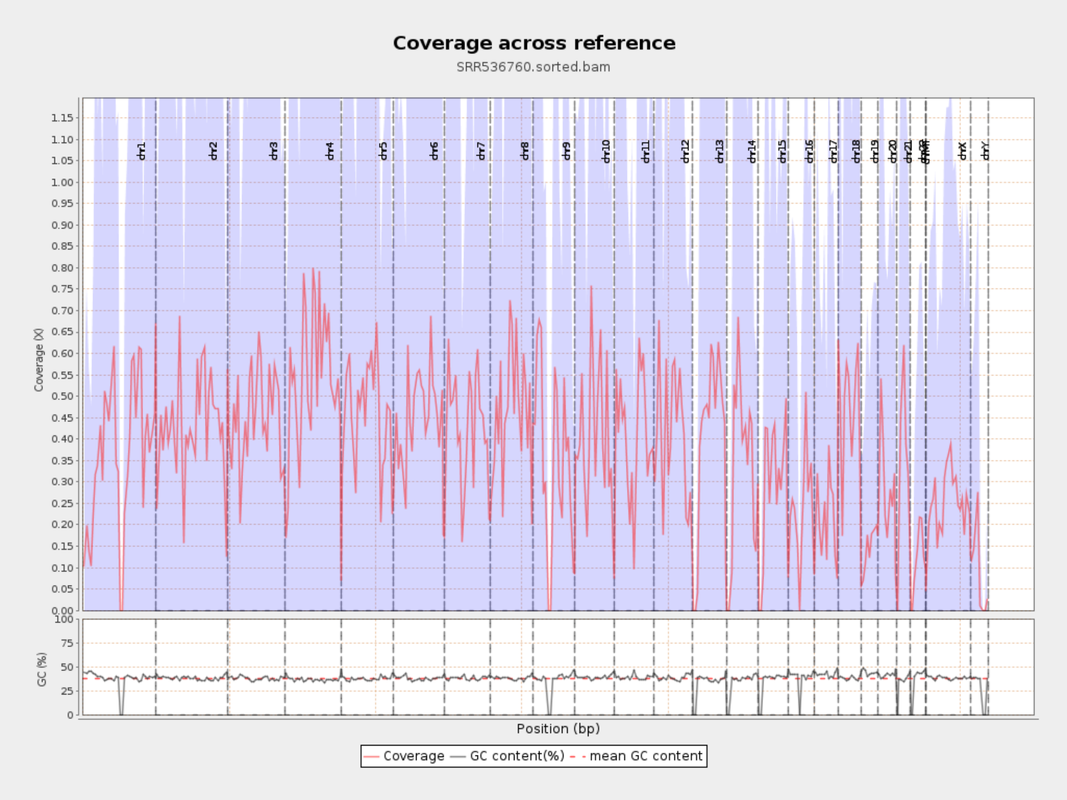
General error rate	0.2%
Mismatches	2,228,946
Insertions	70,256
Mapped reads with at least one insertion	0.3%
Deletions	62,952
Mapped reads with at least one deletion	0.26%
Homopolymer indels	49.21%

2.6. Chromosome stats

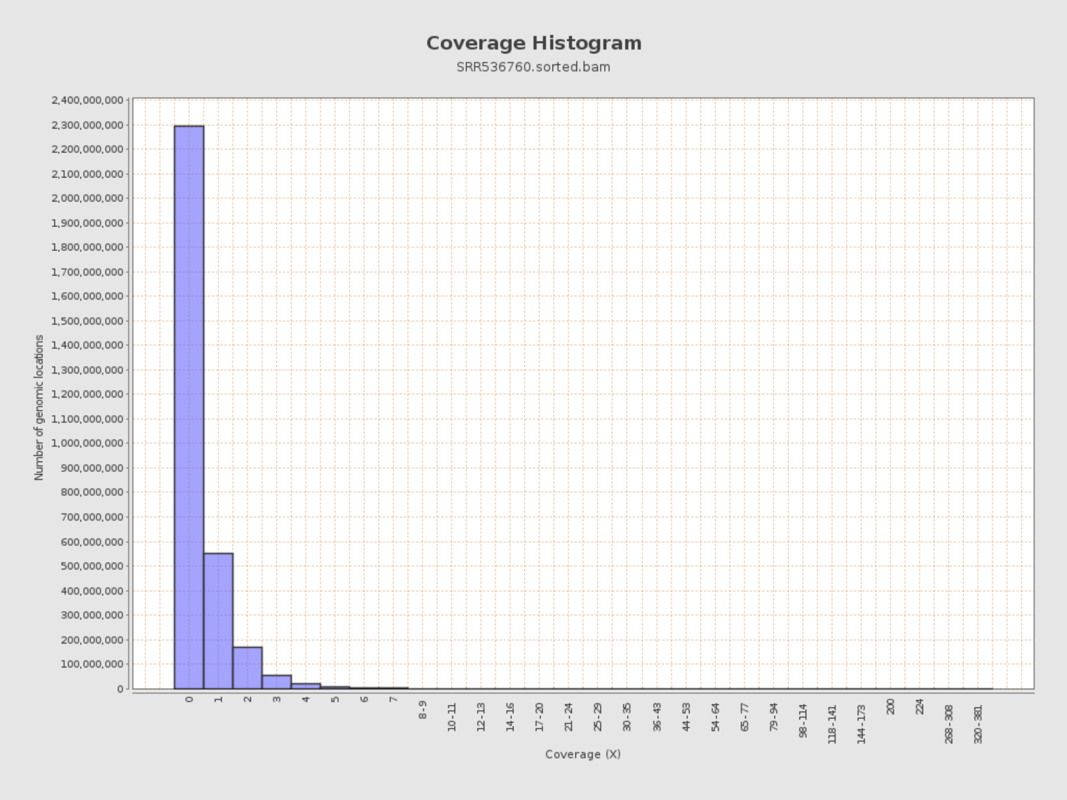
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	90388856	0.3626	0.7784
chr2	243199373	103766078	0.4267	0.8197
chr3	198022430	89542855	0.4522	0.8369
chr4	191154276	104508444	0.5467	0.9371
chr5	180915260	81864399	0.4525	0.8354
chr6	171115067	77767754	0.4545	0.8434
chr7	159138663	67201114	0.4223	0.8169

chr8	146364022	68446508	0.4676	0.8623
chr9	141213431	50719801	0.3592	0.7589
chr10	135534747	56056224	0.4136	0.8032
chr11	135006516	54489933	0.4036	0.7998
chr12	133851895	54524411	0.4073	0.8029
chr13	115169878	47023237	0.4083	0.8107
chr14	107349540	36570207	0.3407	0.7479
chr15	102531392	29872760	0.2914	0.6906
chr16	90354753	20864672	0.2309	0.5911
chr17	81195210	17777420	0.2189	0.5833
chr18	78077248	36958864	0.4734	0.8528
chr19	59128983	8604015	0.1455	0.4536
chr20	63025520	18587797	0.2949	0.6792
chr21	48129895	15777296	0.3278	0.7547
chr22	51304566	6177284	0.1204	0.4196
chrMT	16571	750	0.0453	0.2341
chrX	155270560	39531719	0.2546	0.6125
chrY	59373566	5756765	0.097	0.3863

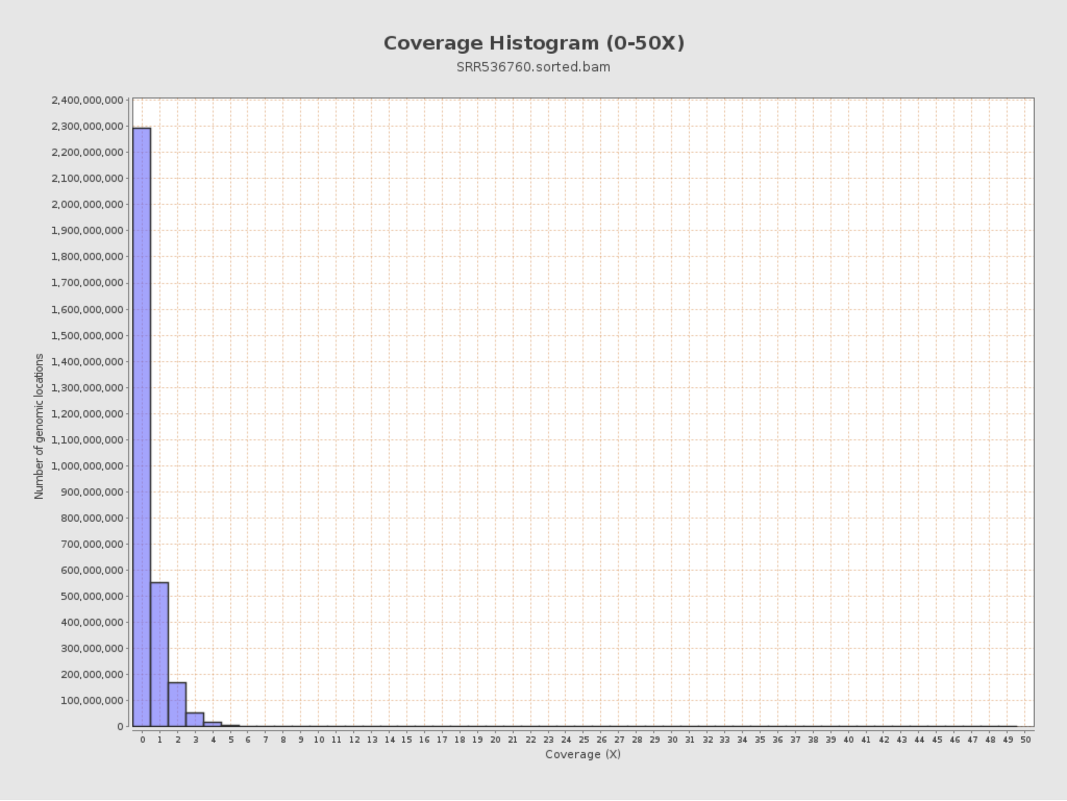
3. Results : Coverage across reference



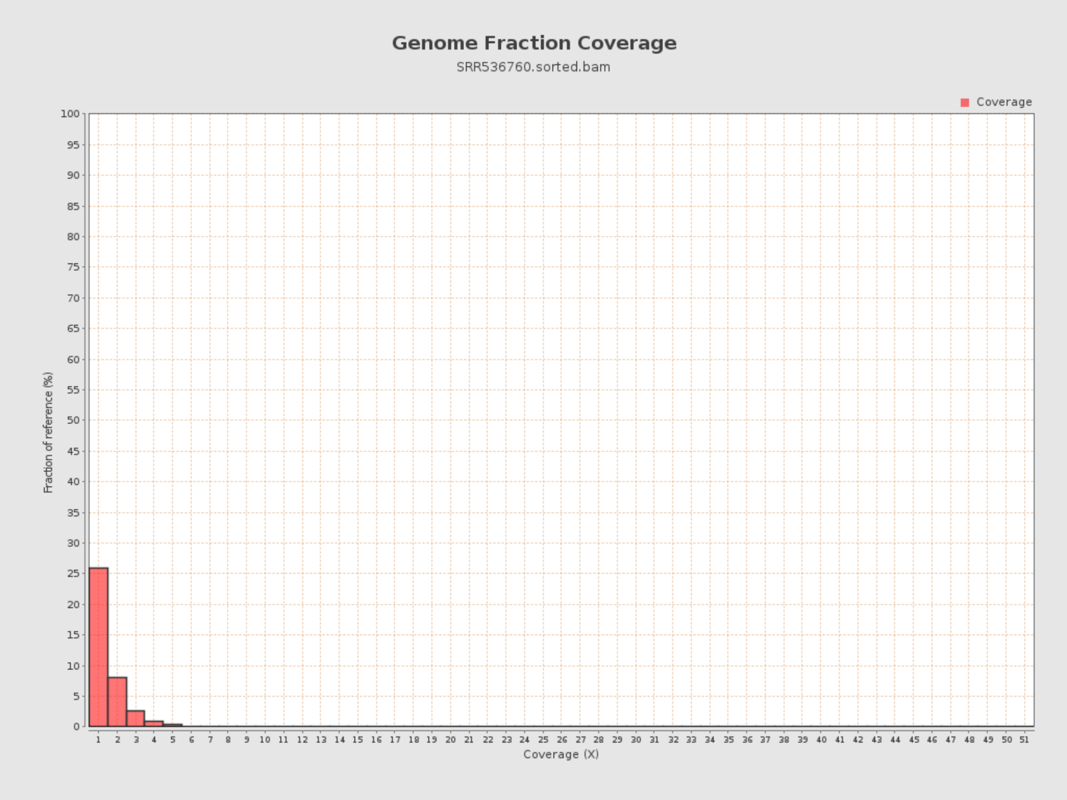
4. Results : Coverage Histogram



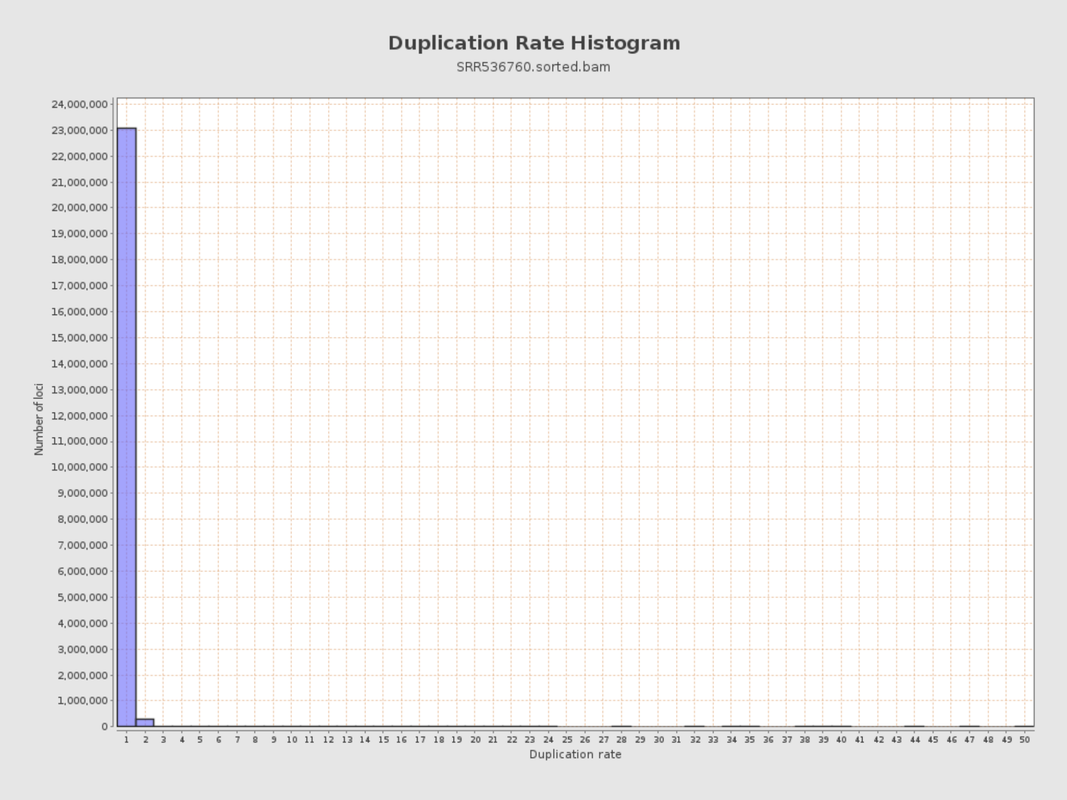
5. Results : Coverage Histogram (0-50X)



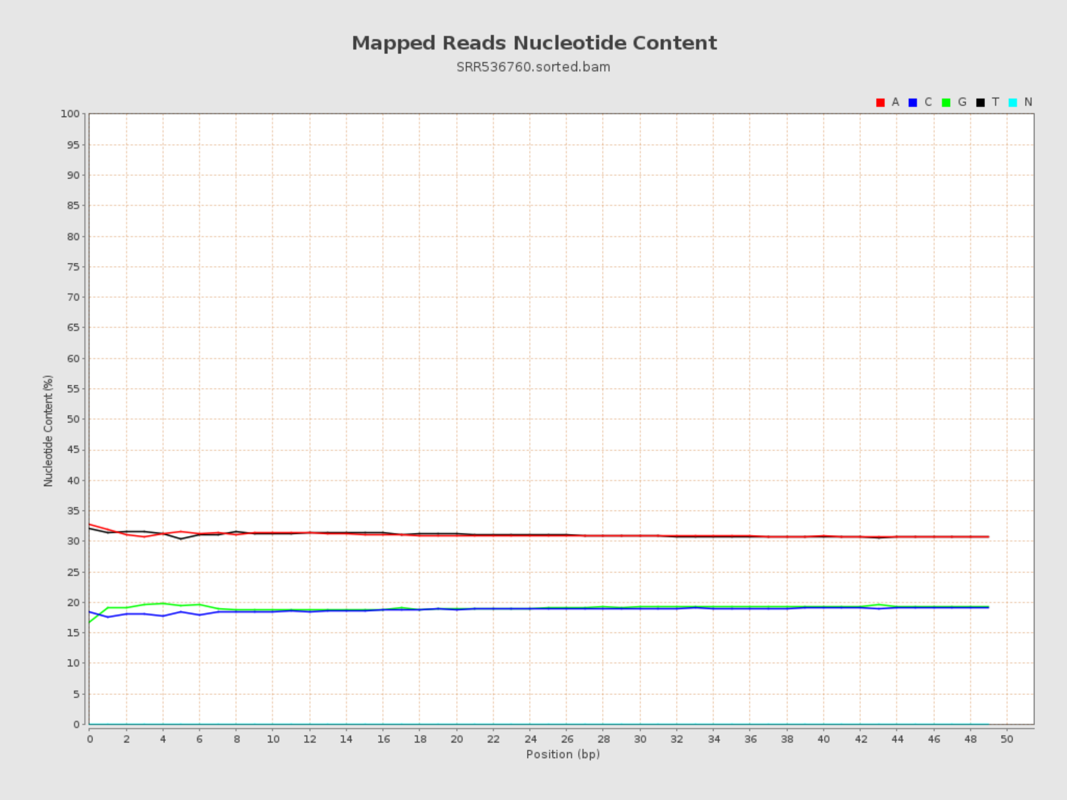
6. Results : Genome Fraction Coverage



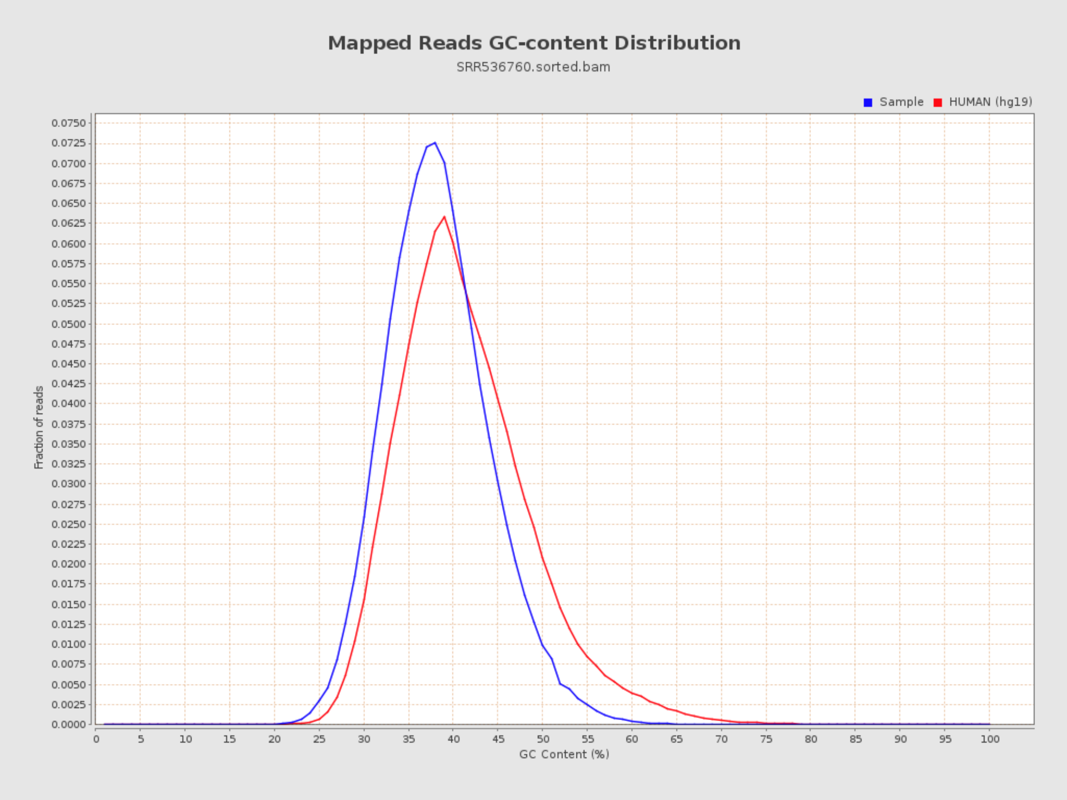
7. Results : Duplication Rate Histogram



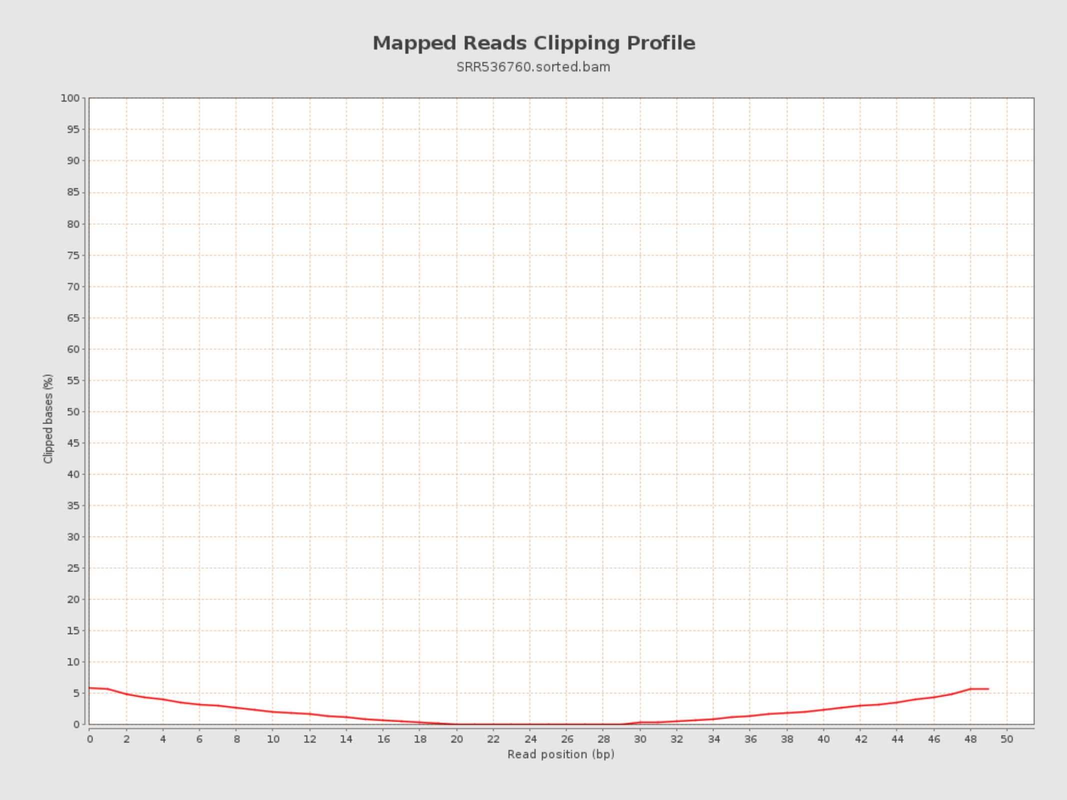
8. Results : Mapped Reads Nucleotide Content



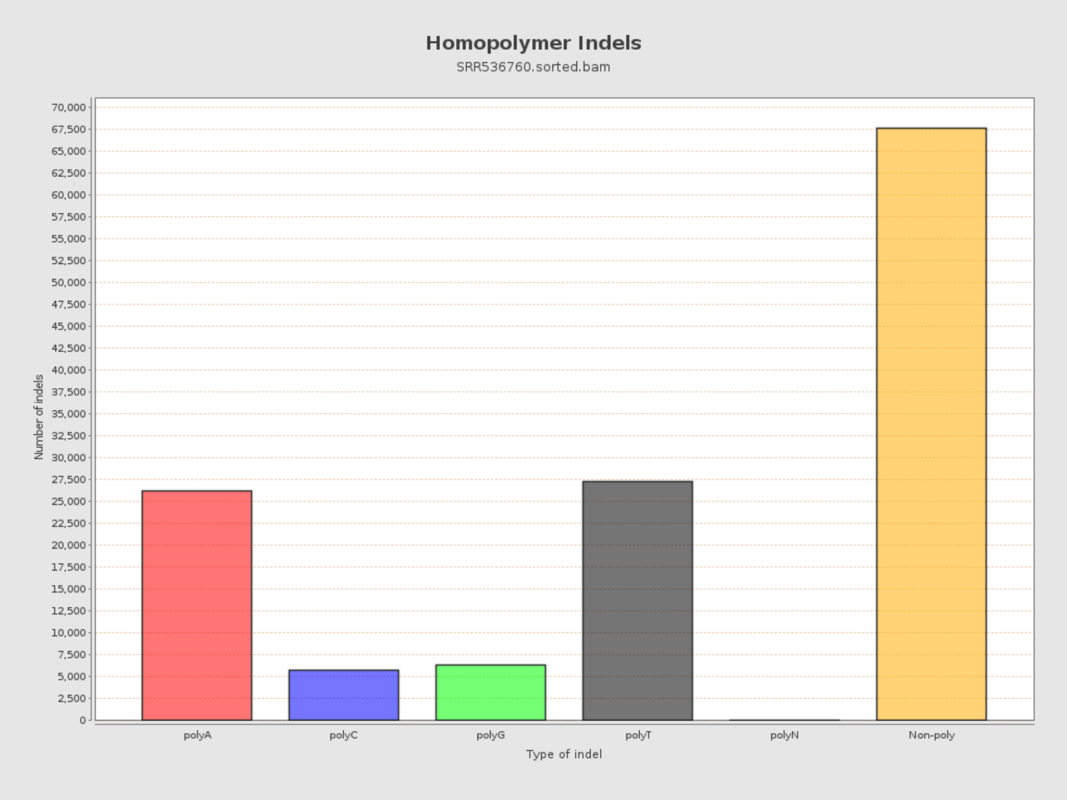
9. Results : Mapped Reads GC-content Distribution



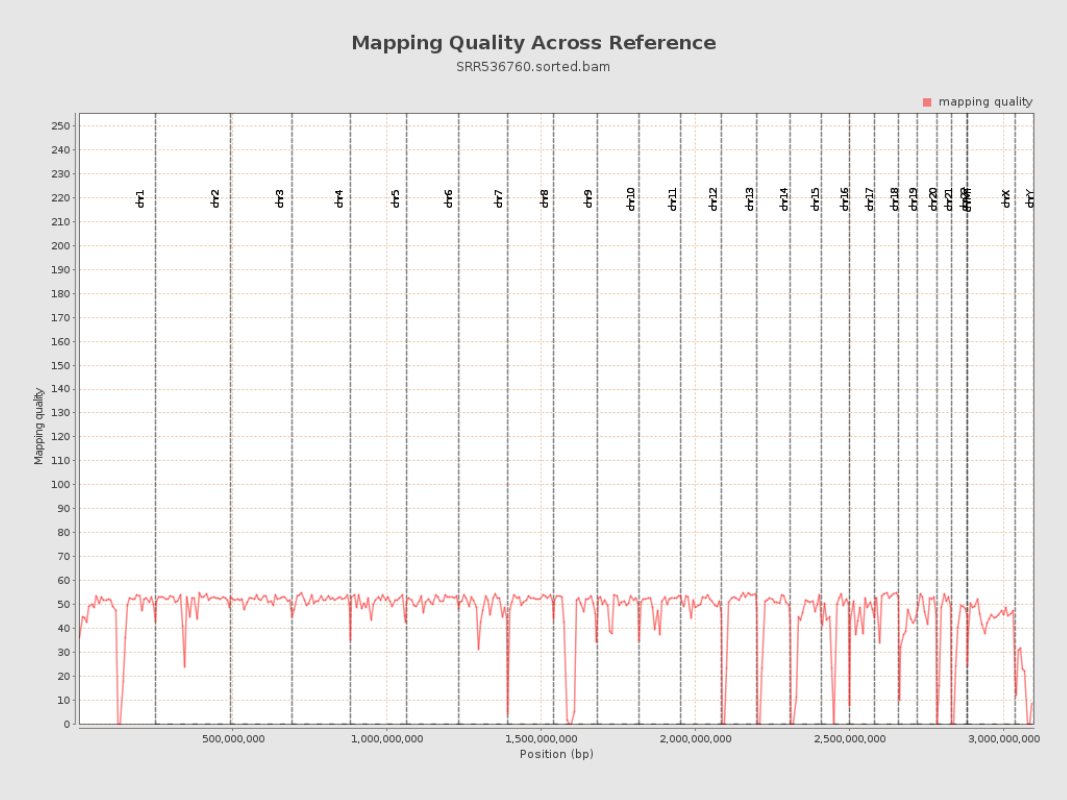
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram