Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:43:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818741.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_SRR1818741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818741.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:43:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818741.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,499,481
Mapped reads	3,391,907 / 96.93%
Unmapped reads	107,574 / 3.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,480 / 0.84%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	1,947,953 / 55.66%
Duplication rate	47.38%
Clipped reads	3,380,119 / 96.59%

2.2. ACGT Content

Number/percentage of A's	63,461,497 / 27.56%
Number/percentage of C's	50,158,072 / 21.78%
Number/percentage of T's	69,020,521 / 29.97%
Number/percentage of G's	47,652,003 / 20.69%
Number/percentage of N's	14,821 / 0.01%
GC Percentage	42.47%

2.3. Coverage

Mean	0.0744

Standard Deviation	0.8555

2.4. Mapping Quality

Mean Mapping Quality	47.83

2.5. Mismatches and indels

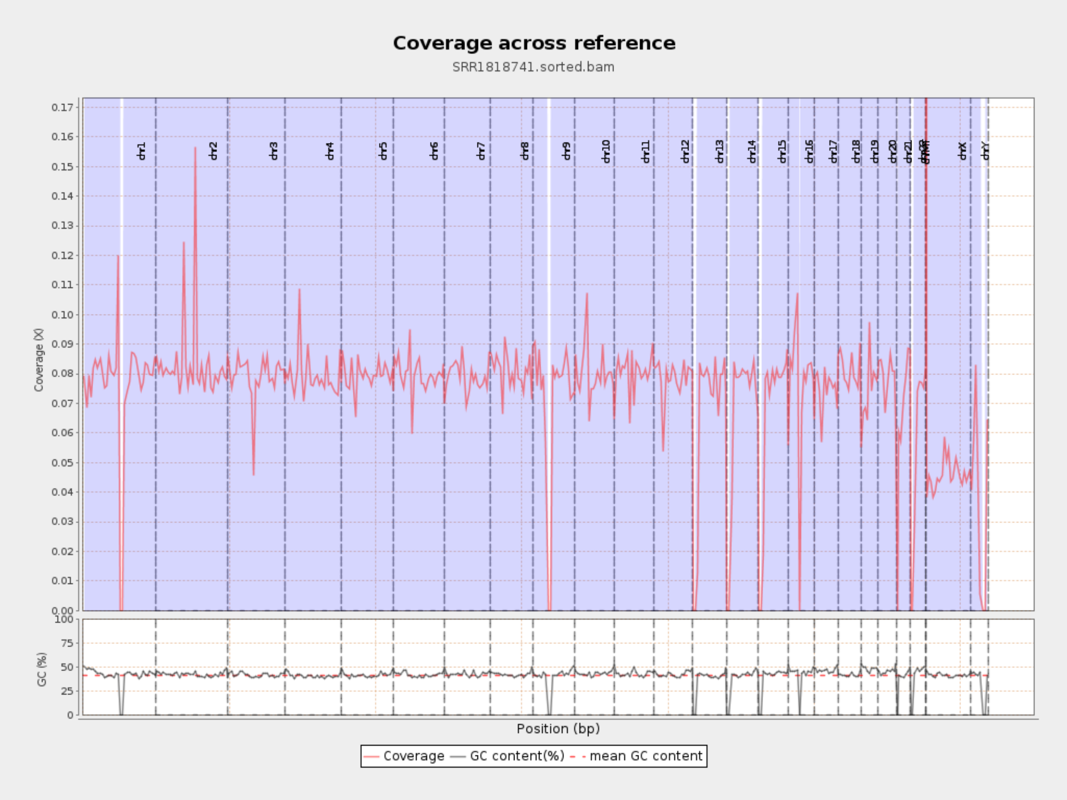
General error rate	0.54%
Mismatches	1,195,017
Insertions	29,466
Mapped reads with at least one insertion	0.86%
Deletions	59,777
Mapped reads with at least one deletion	1.74%
Homopolymer indels	39.11%

2.6. Chromosome stats

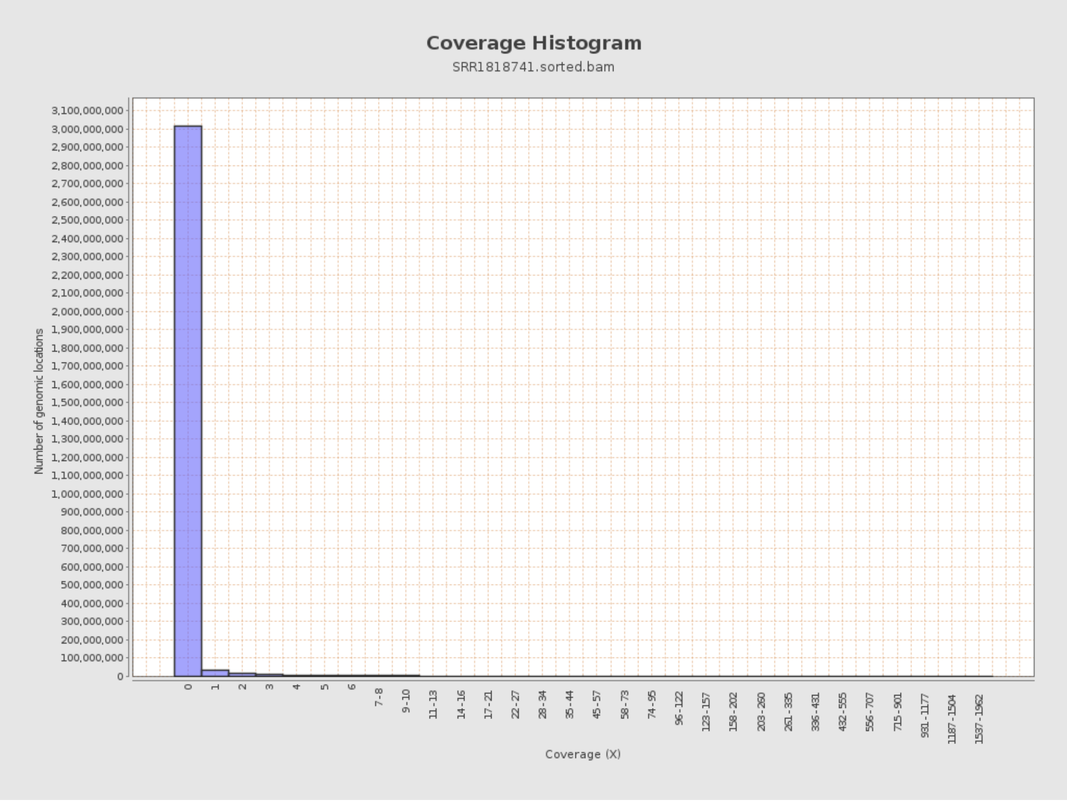
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18990117	0.0762	1.1989
chr2	243199373	20358109	0.0837	1.4134
chr3	198022430	15703556	0.0793	0.6266
chr4	191154276	15222754	0.0796	0.7249
chr5	180915260	14417650	0.0797	0.6683
chr6	171115067	13648483	0.0798	0.6928
chr7	159138663	12599981	0.0792	0.775

chr8	146364022	11820506	0.0808	0.7404
chr9	141213431	9958091	0.0705	0.7141
chr10	135534747	10892201	0.0804	0.8953
chr11	135006516	10852540	0.0804	0.7062
chr12	133851895	10507570	0.0785	0.6562
chr13	115169878	7567878	0.0657	0.5822
chr14	107349540	7152449	0.0666	0.6445
chr15	102531392	6540274	0.0638	0.5668
chr16	90354753	6780903	0.075	0.924
chr17	81195210	6090747	0.075	0.6567
chr18	78077248	6333869	0.0811	1.0571
chr19	59128983	4428594	0.0749	1.0022
chr20	63025520	4987116	0.0791	0.6829
chr21	48129895	3212286	0.0667	0.6228
chr22	51304566	2720361	0.053	0.5794
chrMT	16571	295192	17.8138	15.083
chrX	155270560	7123389	0.0459	0.5548
chrY	59373566	2197656	0.037	1.3049

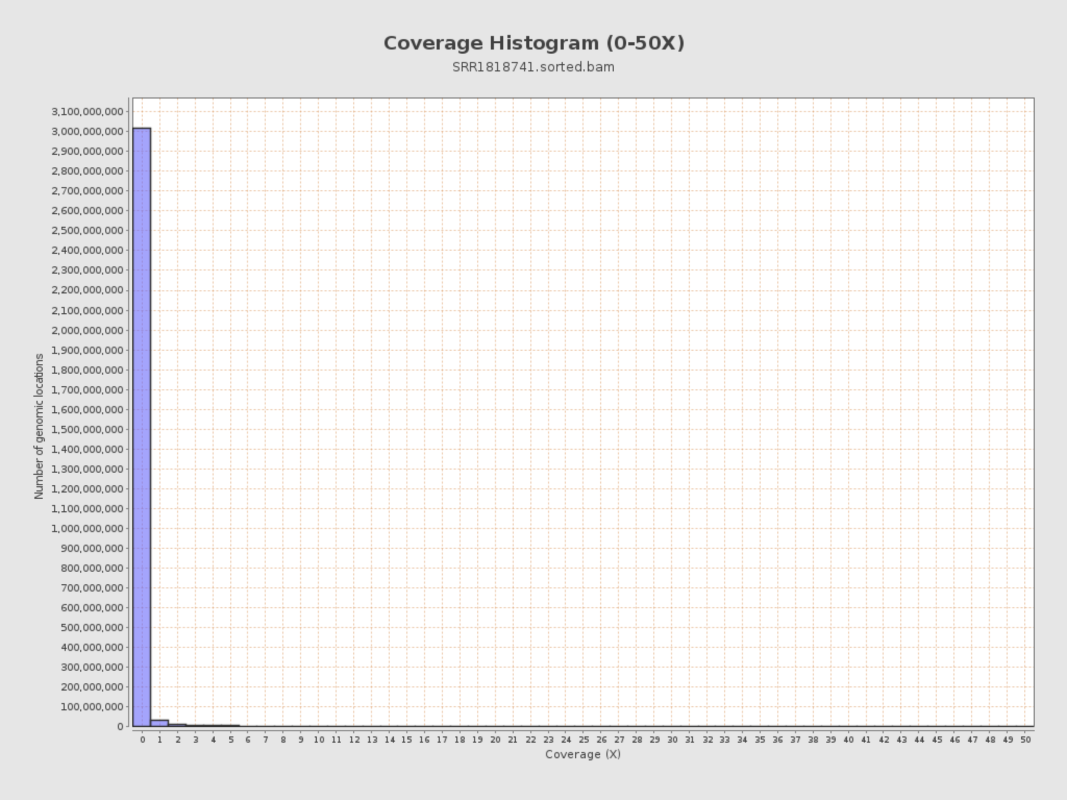
3. Results : Coverage across reference



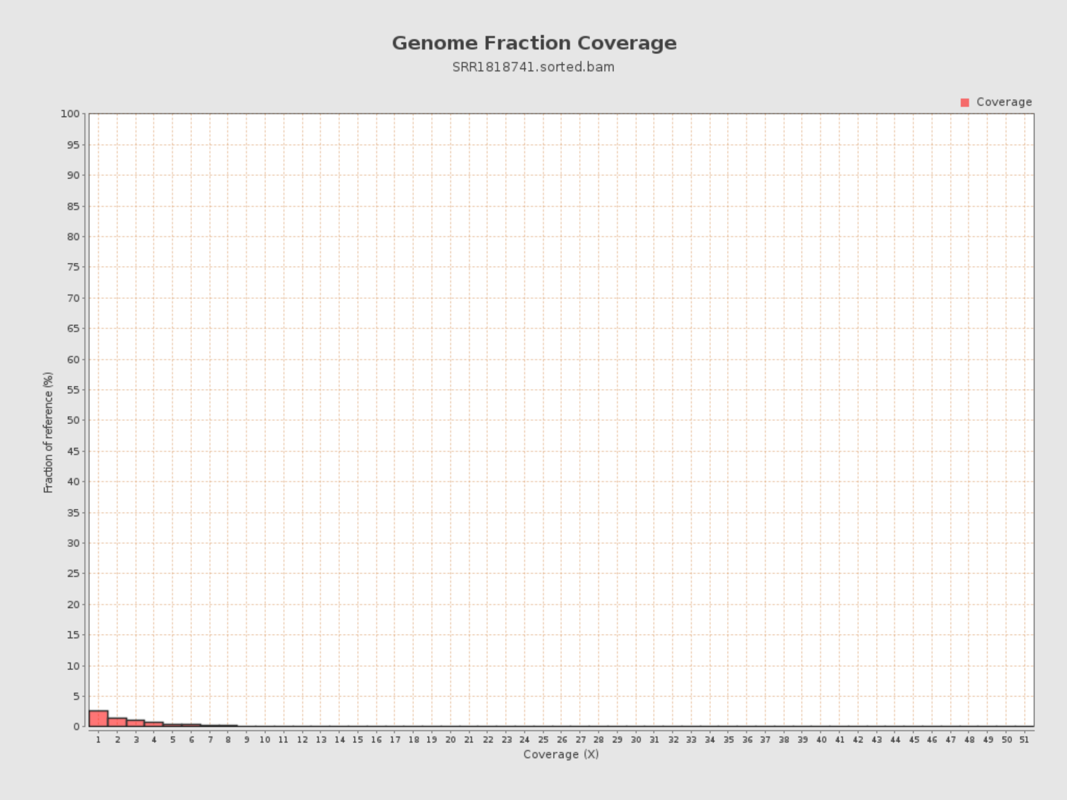
4. Results : Coverage Histogram



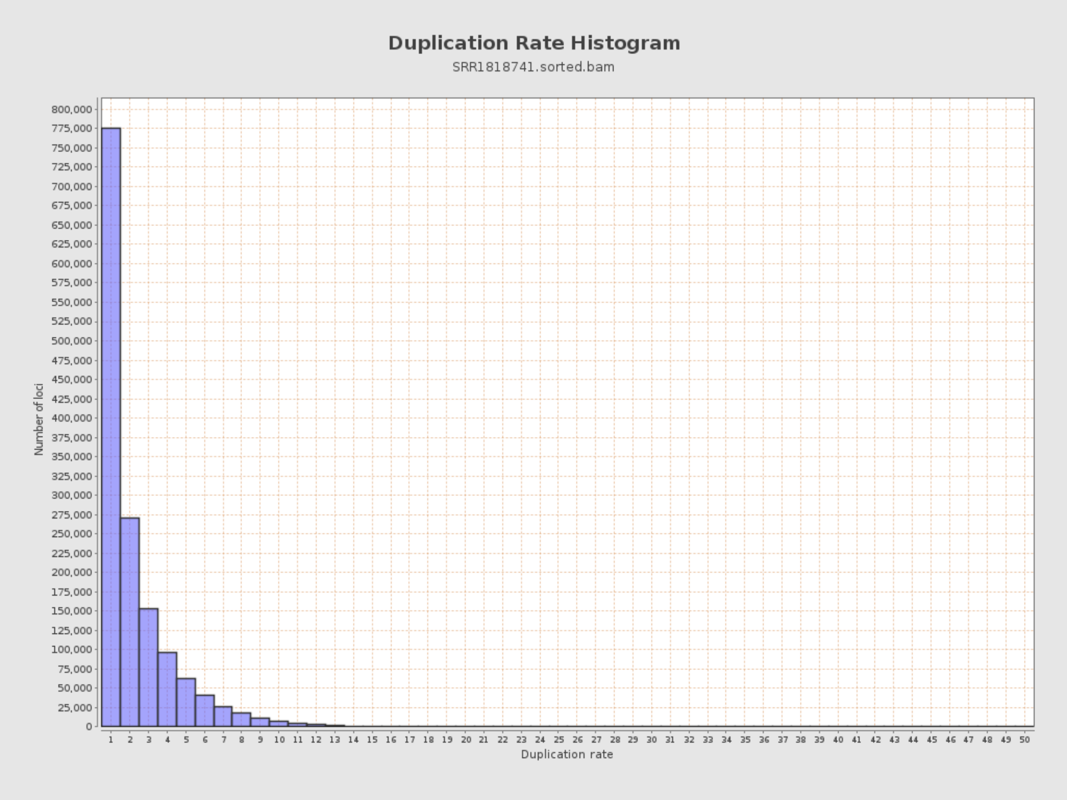
5. Results : Coverage Histogram (0-50X)



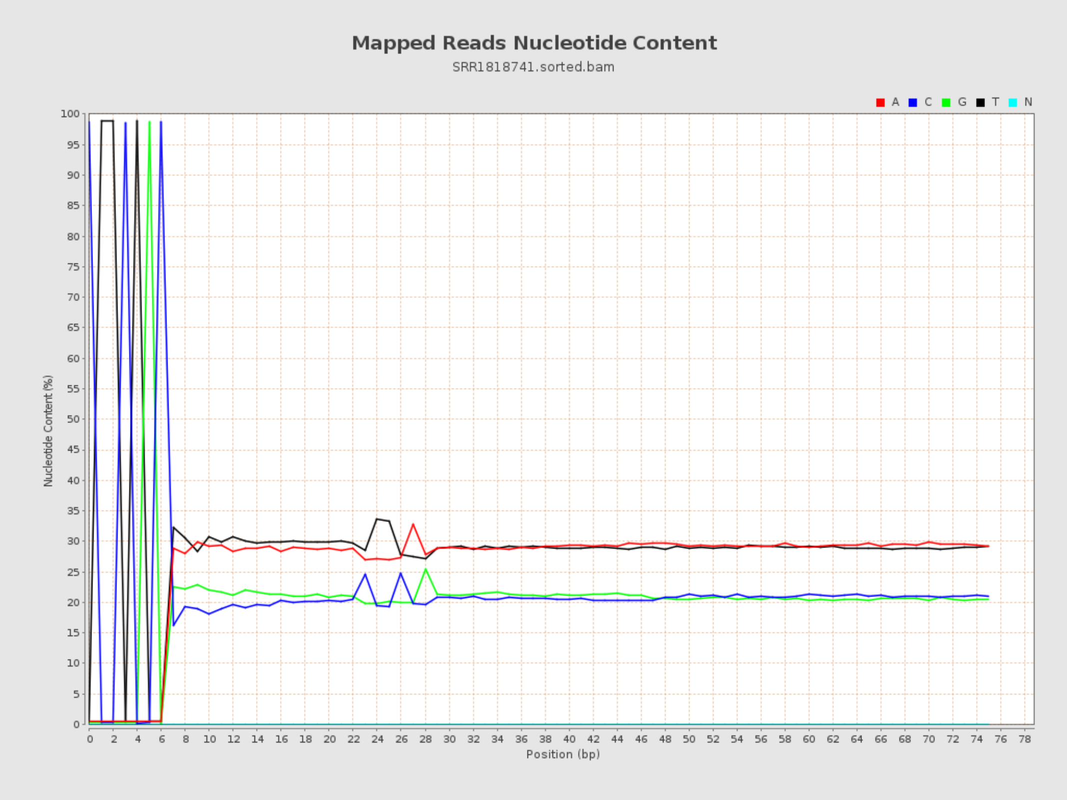
6. Results : Genome Fraction Coverage



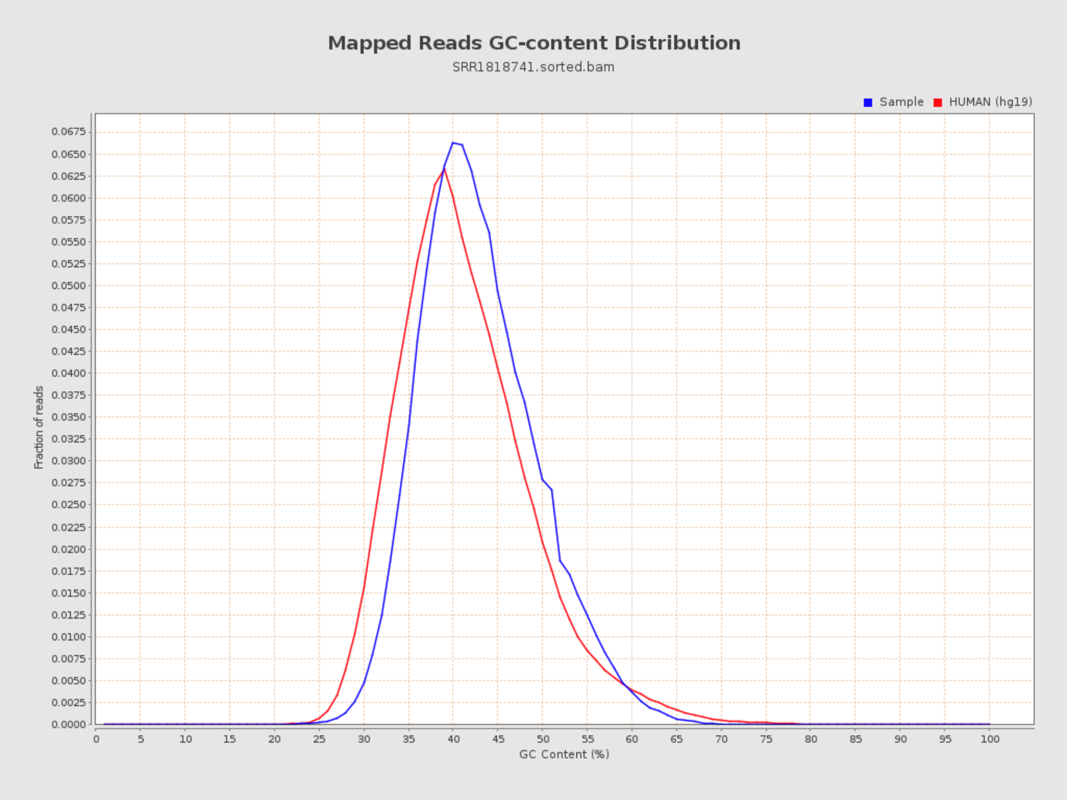
7. Results : Duplication Rate Histogram



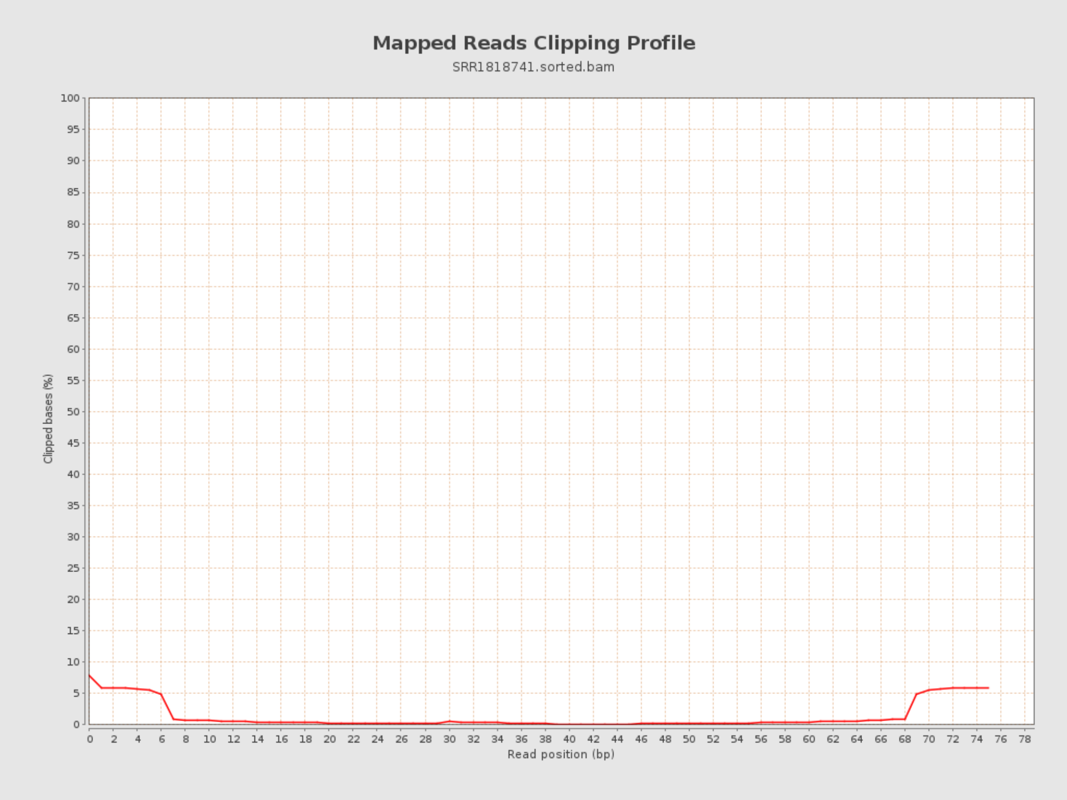
8. Results : Mapped Reads Nucleotide Content



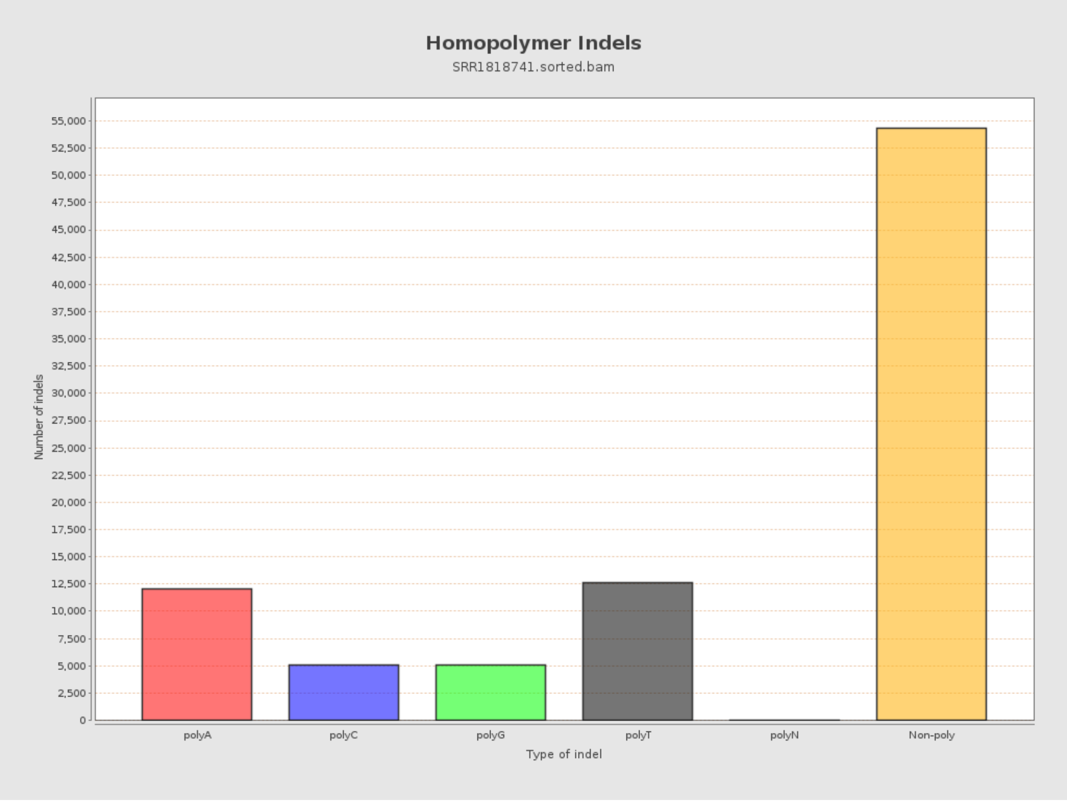
9. Results : Mapped Reads GC-content Distribution



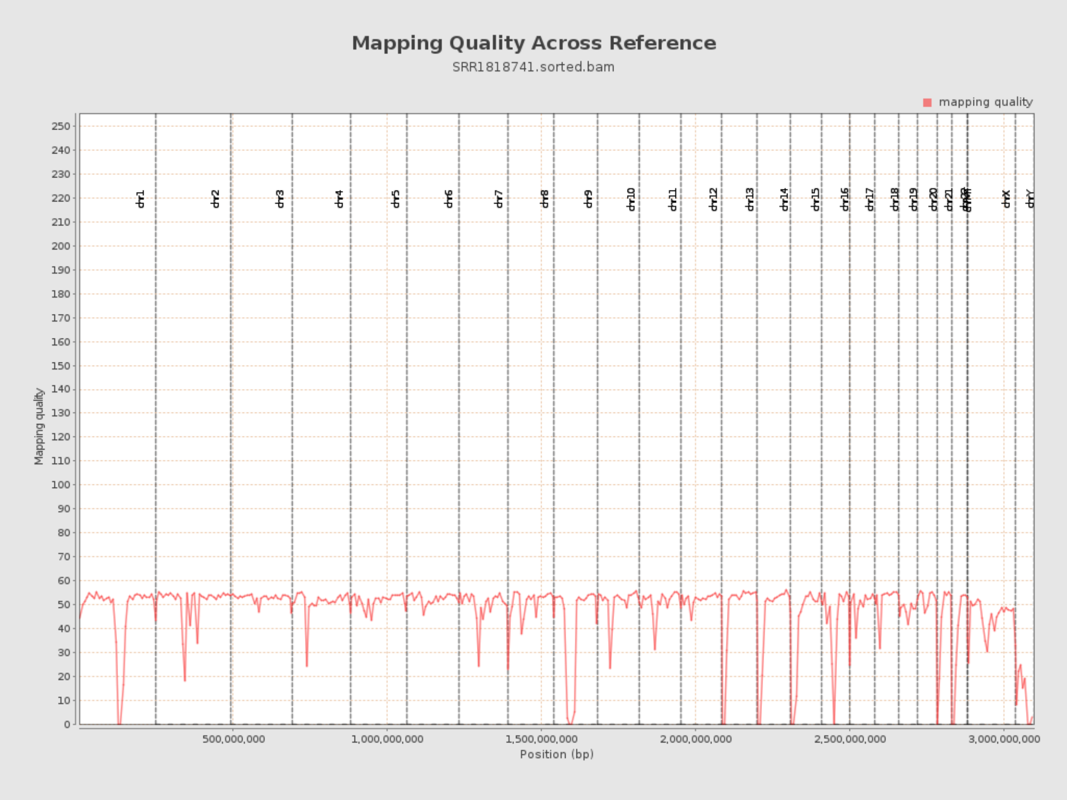
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram