Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:05:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080724.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_SRR3080724 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080724.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:05:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080724.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,071,492
Mapped reads	1,945,927 / 93.94%
Unmapped reads	125,565 / 6.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,679 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	88,922 / 4.29%
Duplication rate	3.83%
Clipped reads	652,156 / 31.48%

2.2. ACGT Content

Number/percentage of A's	39,199,270 / 29.06%
Number/percentage of C's	24,886,220 / 18.45%
Number/percentage of T's	43,026,263 / 31.9%
Number/percentage of G's	27,774,834 / 20.59%
Number/percentage of N's	1,972 / 0%
GC Percentage	39.04%

2.3. Coverage

Mean	0.0436

Standard Deviation	0.387

2.4. Mapping Quality

Mean Mapping Quality	47.07

2.5. Mismatches and indels

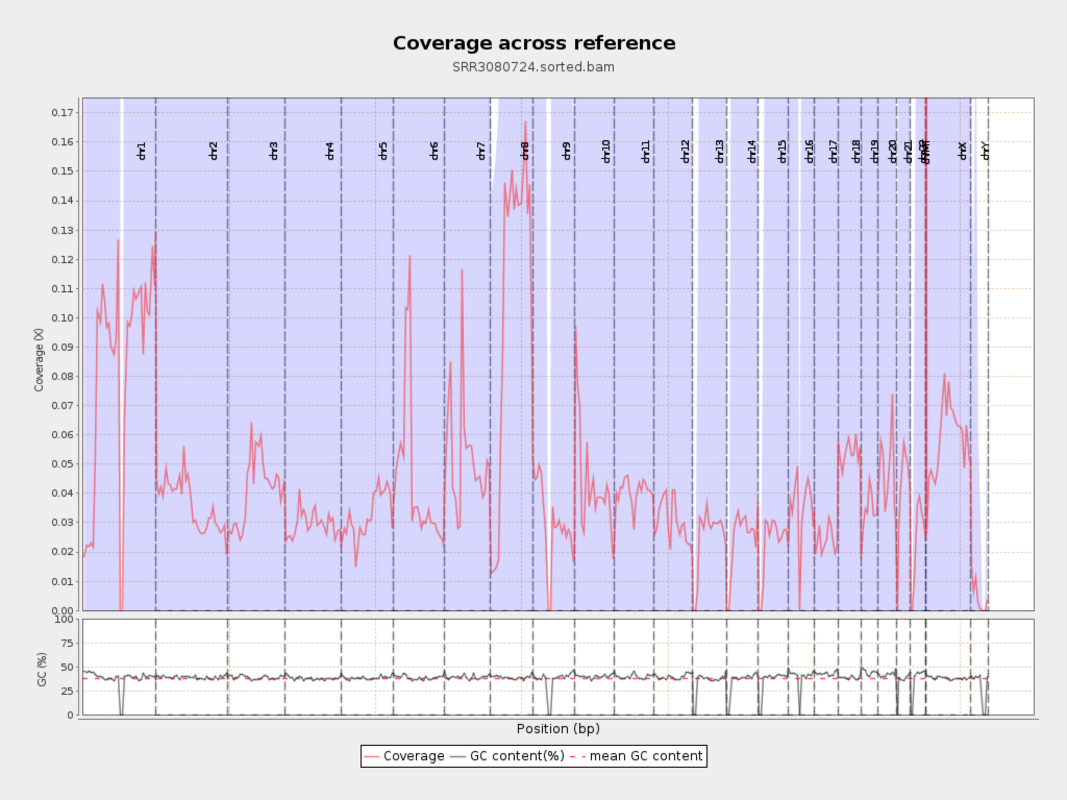
General error rate	0.82%
Mismatches	1,087,245
Insertions	9,740
Mapped reads with at least one insertion	0.5%
Deletions	28,840
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.15%

2.6. Chromosome stats

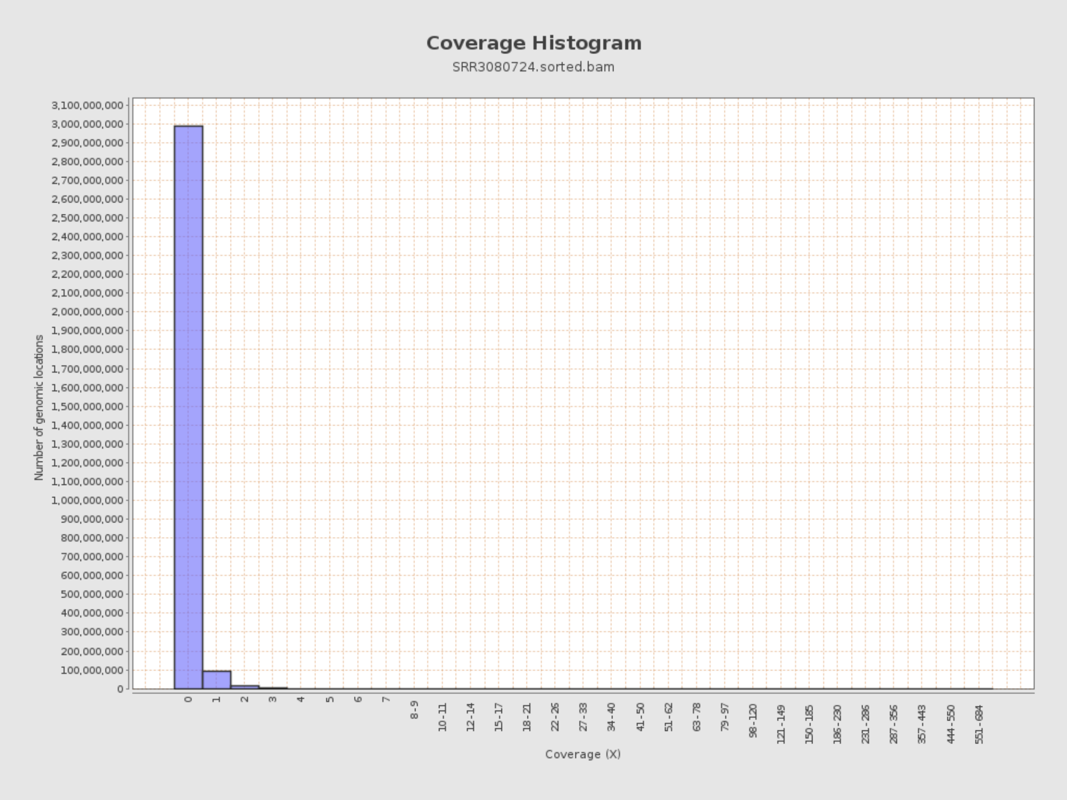
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20379190	0.0818	0.6515
chr2	243199373	8825300	0.0363	0.3047
chr3	198022430	8178725	0.0413	0.2374
chr4	191154276	5667215	0.0296	0.2067
chr5	180915260	5825648	0.0322	0.2082
chr6	171115067	7749341	0.0453	0.3142
chr7	159138663	8395059	0.0528	0.9406

chr8	146364022	15580367	0.1064	0.5623
chr9	141213431	4144806	0.0294	0.2452
chr10	135534747	6012687	0.0444	0.331
chr11	135006516	5438856	0.0403	0.2654
chr12	133851895	4072466	0.0304	0.2026
chr13	115169878	2879246	0.025	0.1827
chr14	107349540	2599587	0.0242	0.1861
chr15	102531392	2292460	0.0224	0.1734
chr16	90354753	3080092	0.0341	0.2255
chr17	81195210	1956957	0.0241	0.1908
chr18	78077248	4218195	0.054	0.4285
chr19	59128983	2045542	0.0346	0.3697
chr20	63025520	3049062	0.0484	0.2572
chr21	48129895	1977785	0.0411	0.2435
chr22	51304566	1211969	0.0236	0.1764
chrMT	16571	23858	1.4397	1.5931
chrX	155270560	9063077	0.0584	0.3043
chrY	59373566	272477	0.0046	0.0973

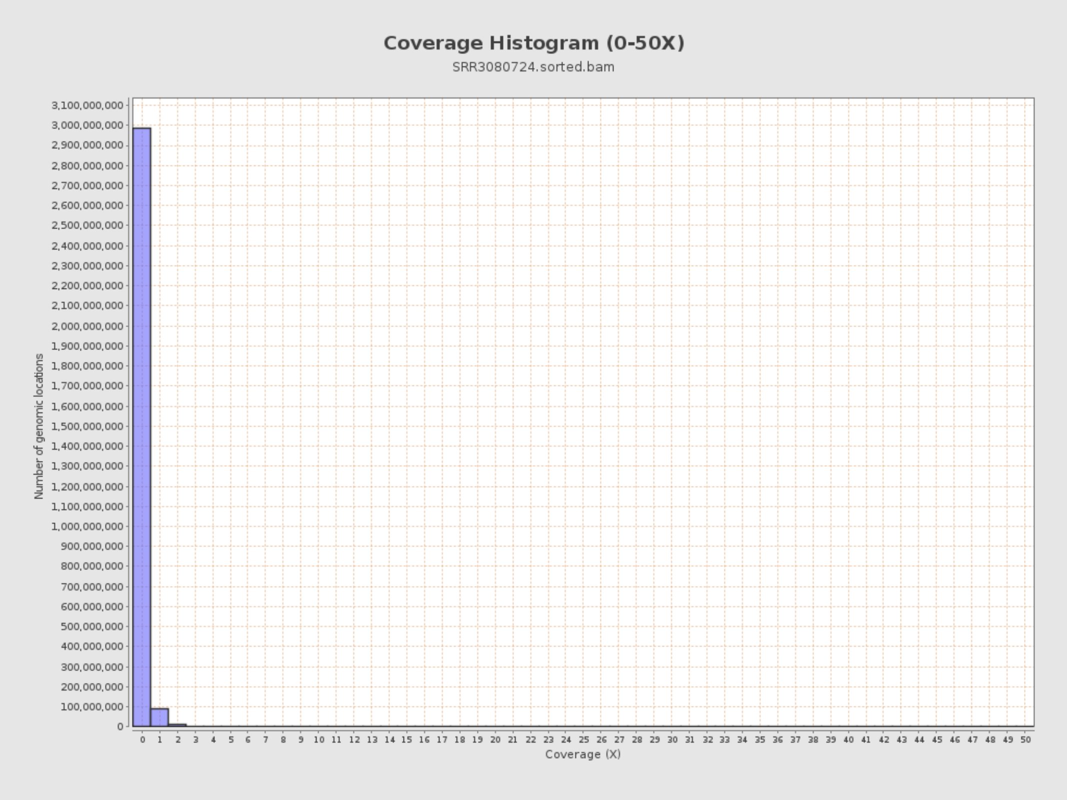
3. Results : Coverage across reference



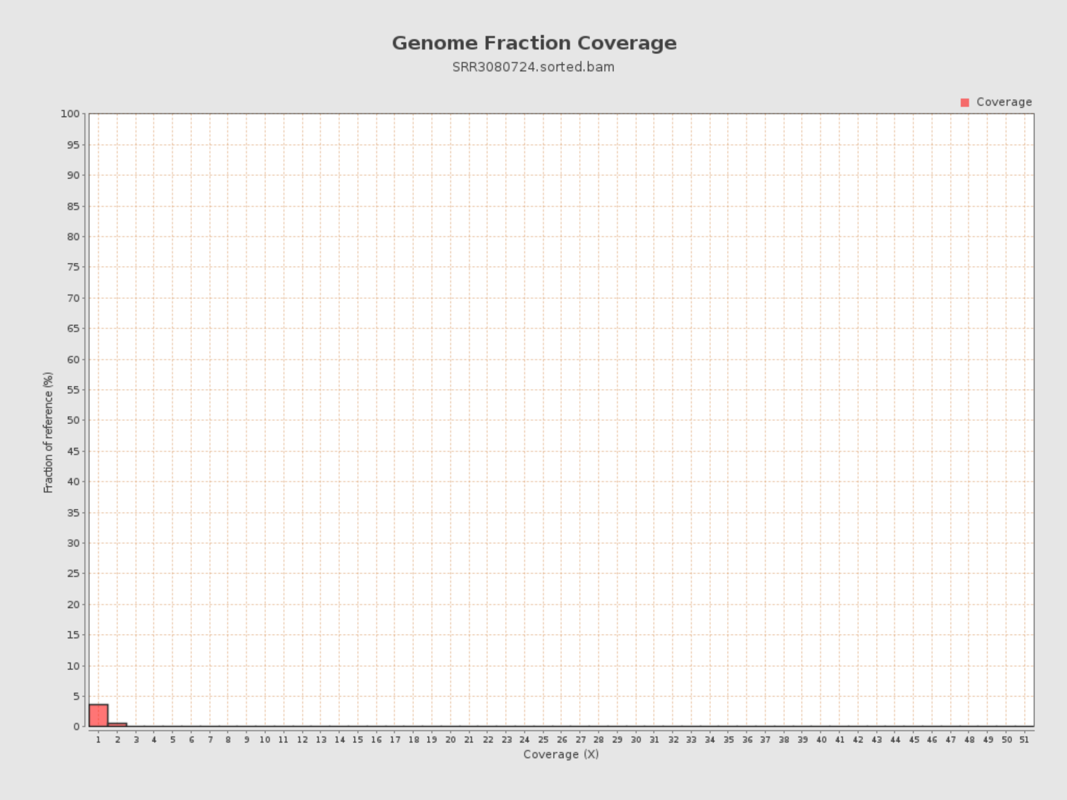
4. Results : Coverage Histogram



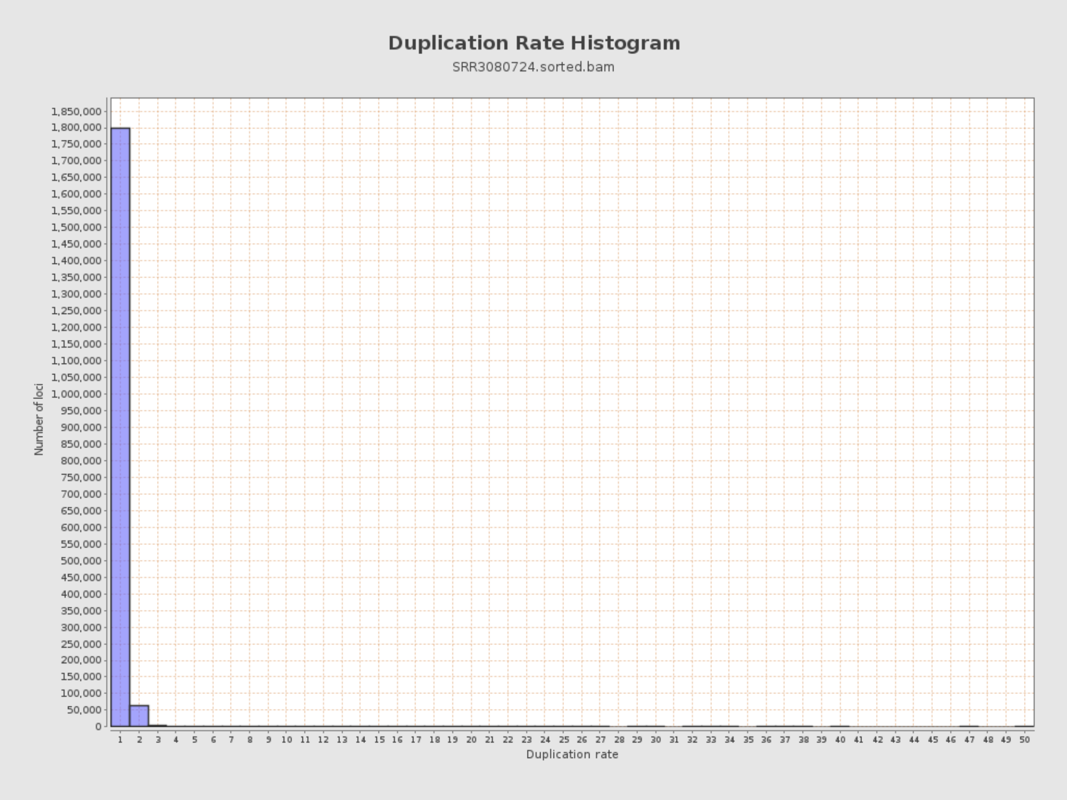
5. Results : Coverage Histogram (0-50X)



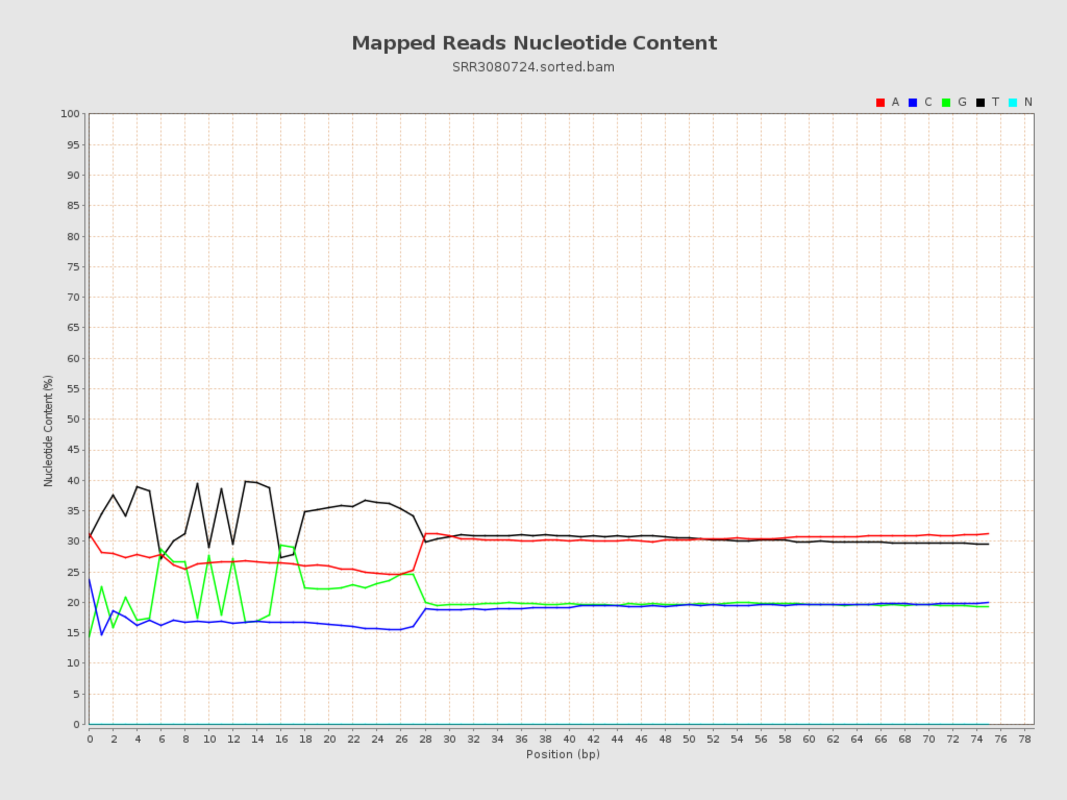
6. Results : Genome Fraction Coverage



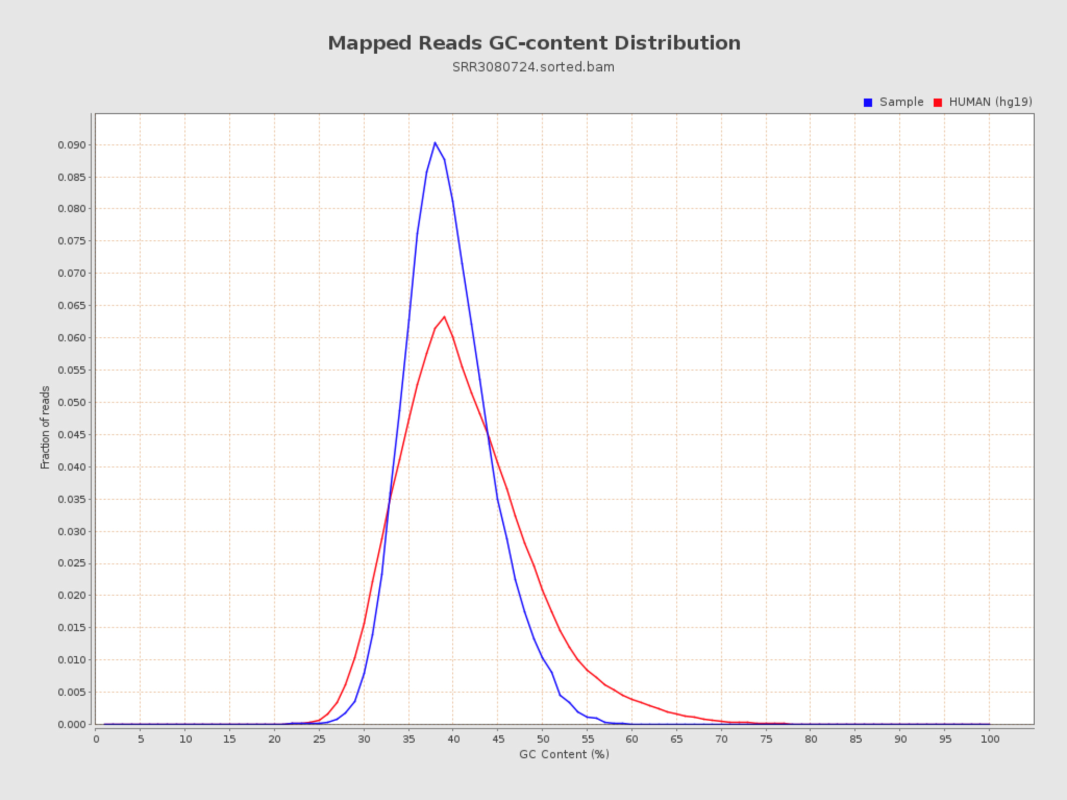
7. Results : Duplication Rate Histogram



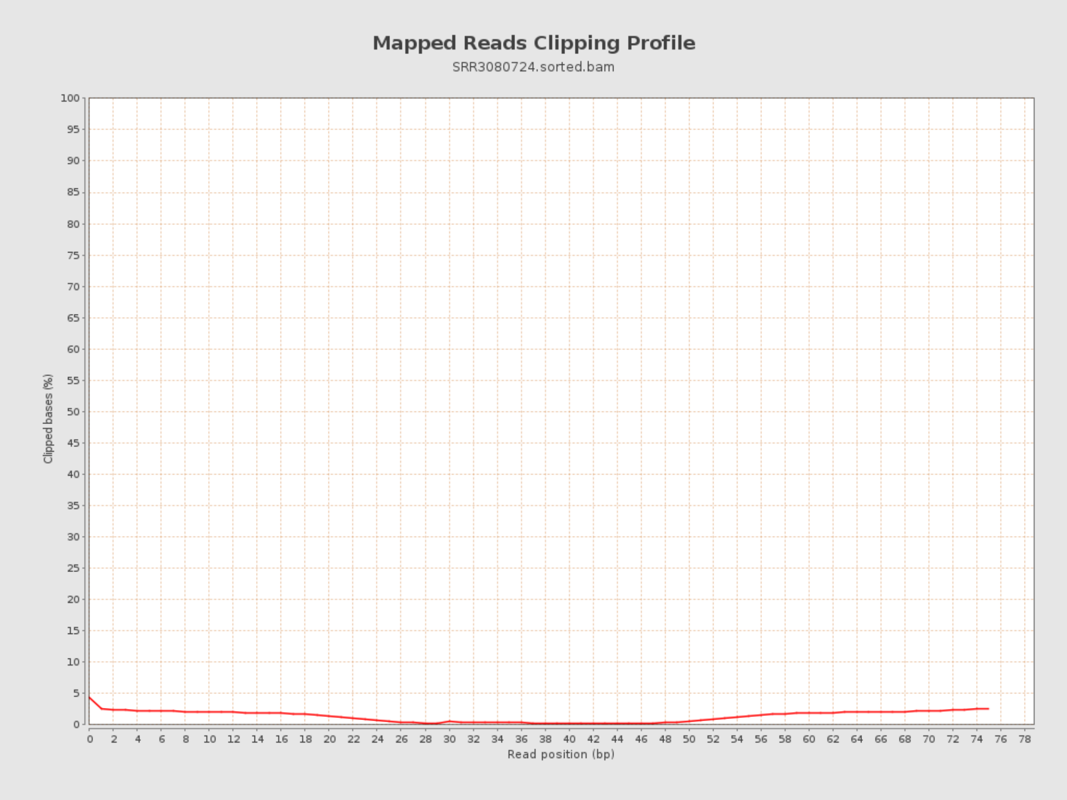
8. Results : Mapped Reads Nucleotide Content



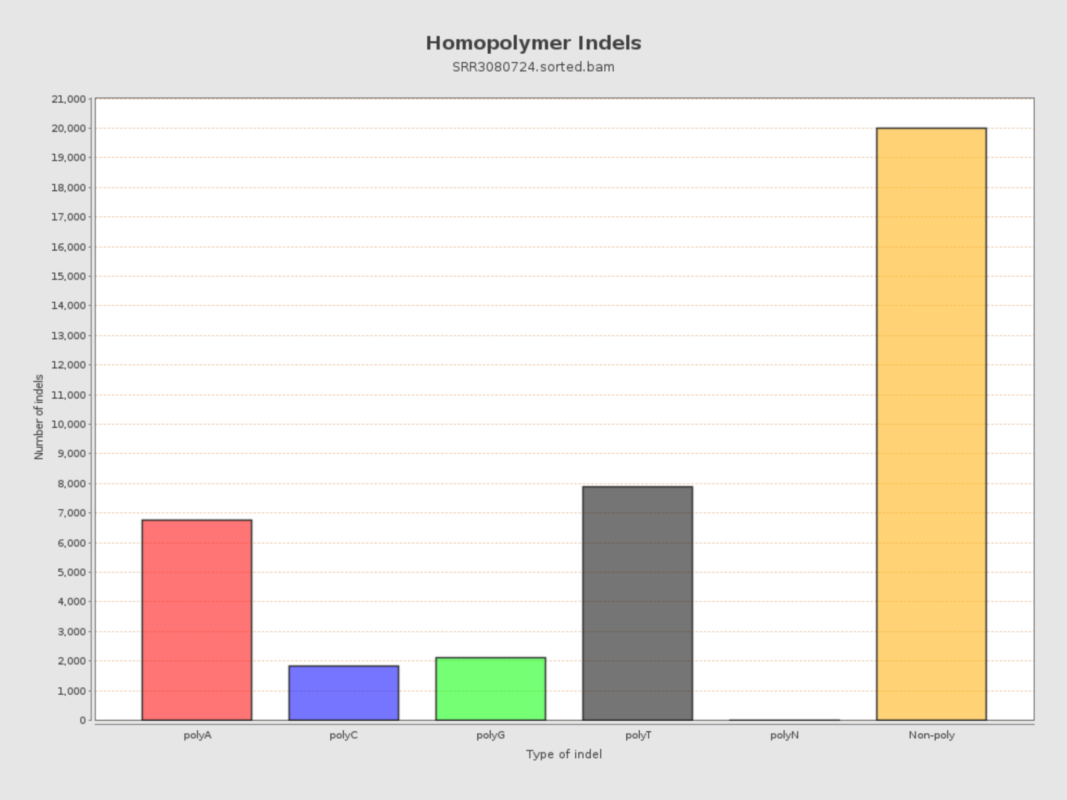
9. Results : Mapped Reads GC-content Distribution



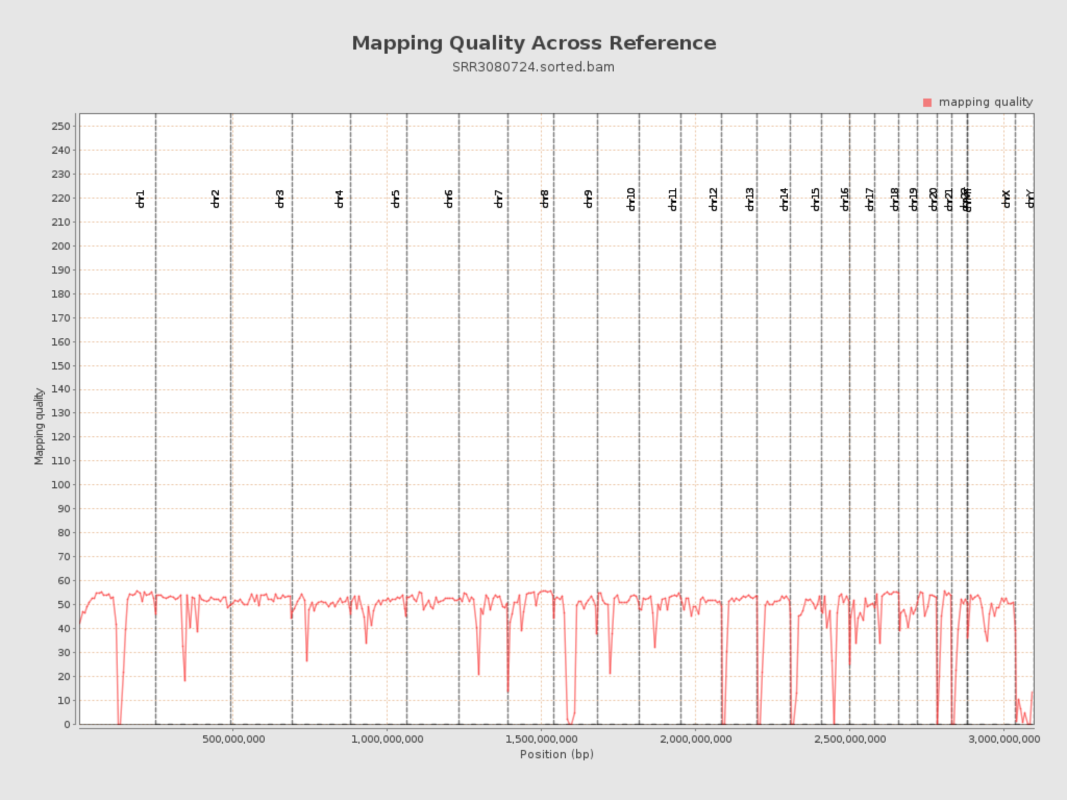
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram