Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:47:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080974.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_SRR3080974 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080974.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:47:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,313,100
Mapped reads	5,534,251 / 87.66%
Unmapped reads	778,849 / 12.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	60,039 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	466,487 / 7.39%
Duplication rate	6.62%
Clipped reads	2,327,243 / 36.86%

2.2. ACGT Content

Number/percentage of A's	105,308,387 / 28.23%
Number/percentage of C's	65,821,223 / 17.64%
Number/percentage of T's	121,421,920 / 32.55%
Number/percentage of G's	79,778,448 / 21.38%
Number/percentage of N's	738,163 / 0.2%
GC Percentage	39.03%

2.3. Coverage

Mean	0.1206

Standard Deviation	0.8829

2.4. Mapping Quality

Mean Mapping Quality	47.13

2.5. Mismatches and indels

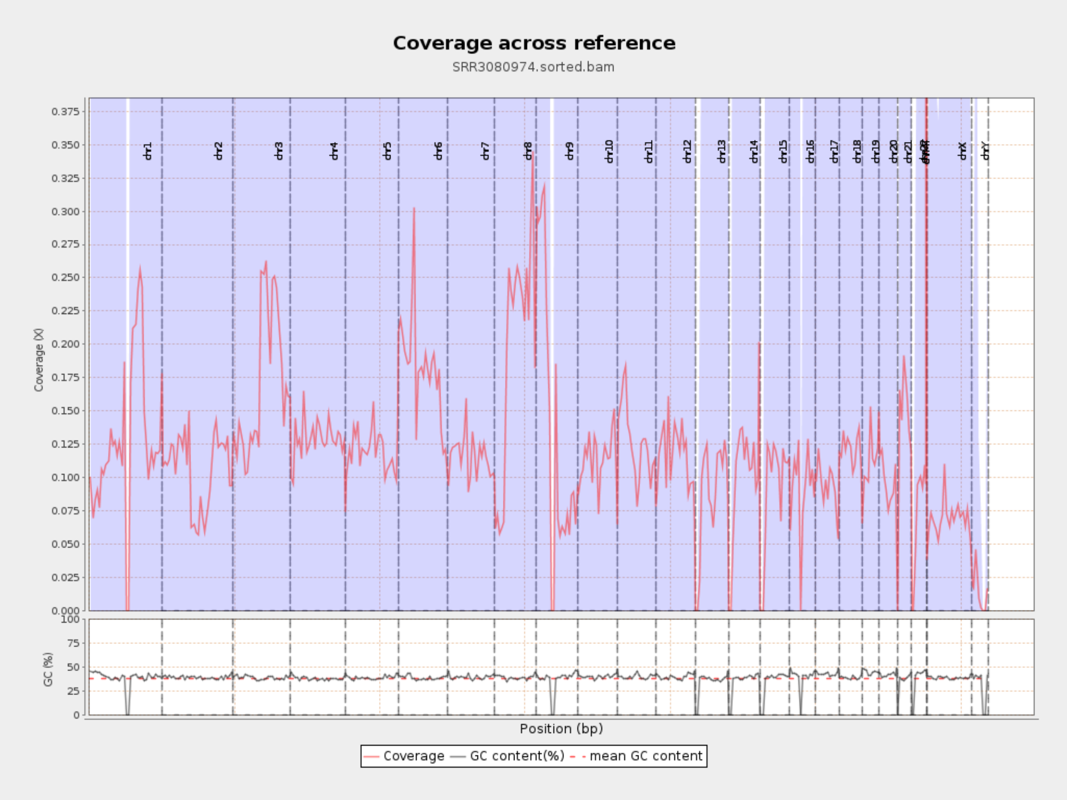
General error rate	1.01%
Mismatches	3,724,577
Insertions	29,563
Mapped reads with at least one insertion	0.53%
Deletions	82,314
Mapped reads with at least one deletion	1.47%
Homopolymer indels	49.4%

2.6. Chromosome stats

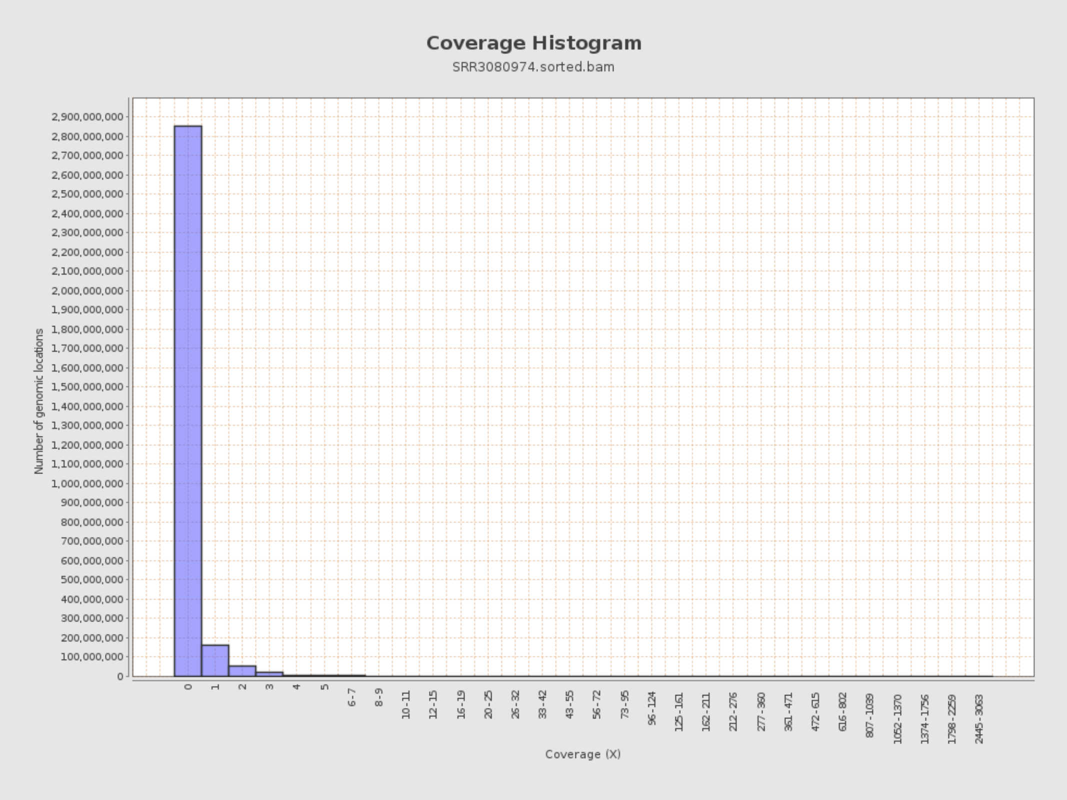
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31830951	0.1277	1.4135
chr2	243199373	25919335	0.1066	0.7449
chr3	198022430	33782755	0.1706	0.5922
chr4	191154276	24636001	0.1289	0.538
chr5	180915260	21709783	0.12	0.4951
chr6	171115067	31219581	0.1824	0.8639
chr7	159138663	18607101	0.1169	0.8713

chr8	146364022	28882971	0.1973	2.0105
chr9	141213431	18933828	0.1341	0.9565
chr10	135534747	15542148	0.1147	0.6491
chr11	135006516	16902039	0.1252	0.7275
chr12	133851895	15685578	0.1172	0.5066
chr13	115169878	9912177	0.0861	0.4132
chr14	107349540	10525734	0.0981	0.5673
chr15	102531392	9350674	0.0912	0.4246
chr16	90354753	8247957	0.0913	0.5259
chr17	81195210	7456062	0.0918	0.4672
chr18	78077248	9484927	0.1215	1.6802
chr19	59128983	6657011	0.1126	1.0476
chr20	63025520	5999410	0.0952	0.4724
chr21	48129895	6757114	0.1404	0.6619
chr22	51304566	3586415	0.0699	0.3636
chrMT	16571	72970	4.4035	3.1354
chrX	155270560	10698078	0.0689	0.4285
chrY	59373566	804024	0.0135	0.247

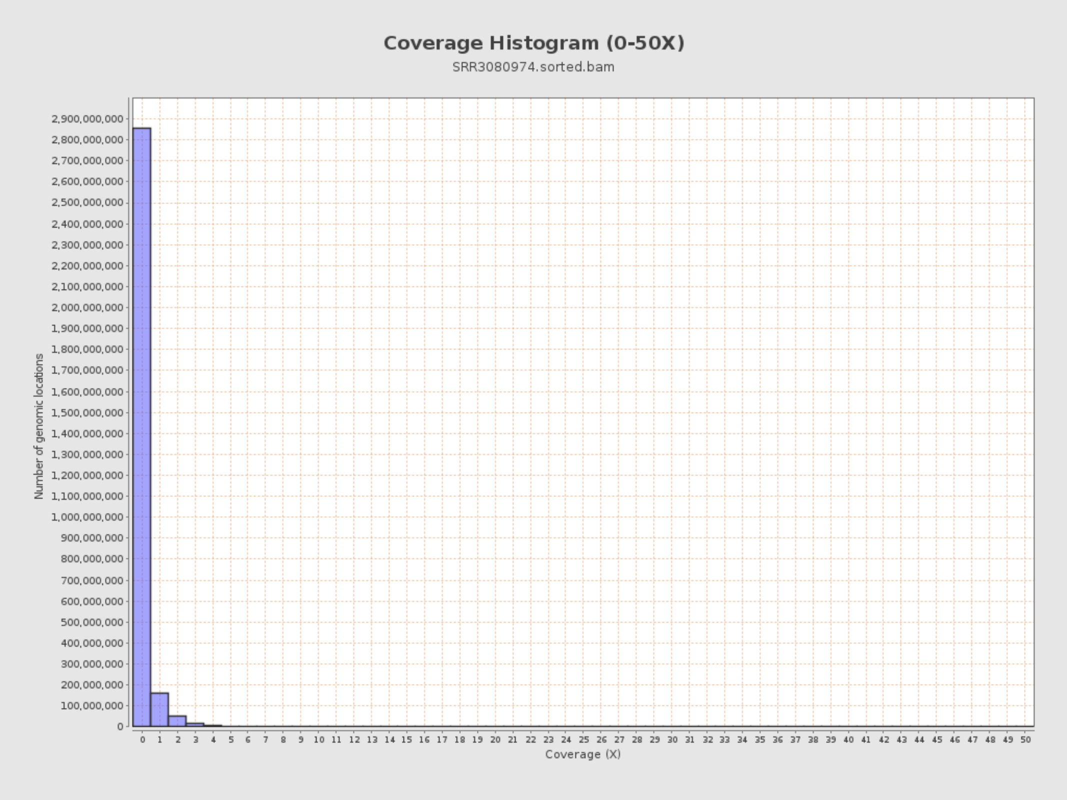
3. Results : Coverage across reference



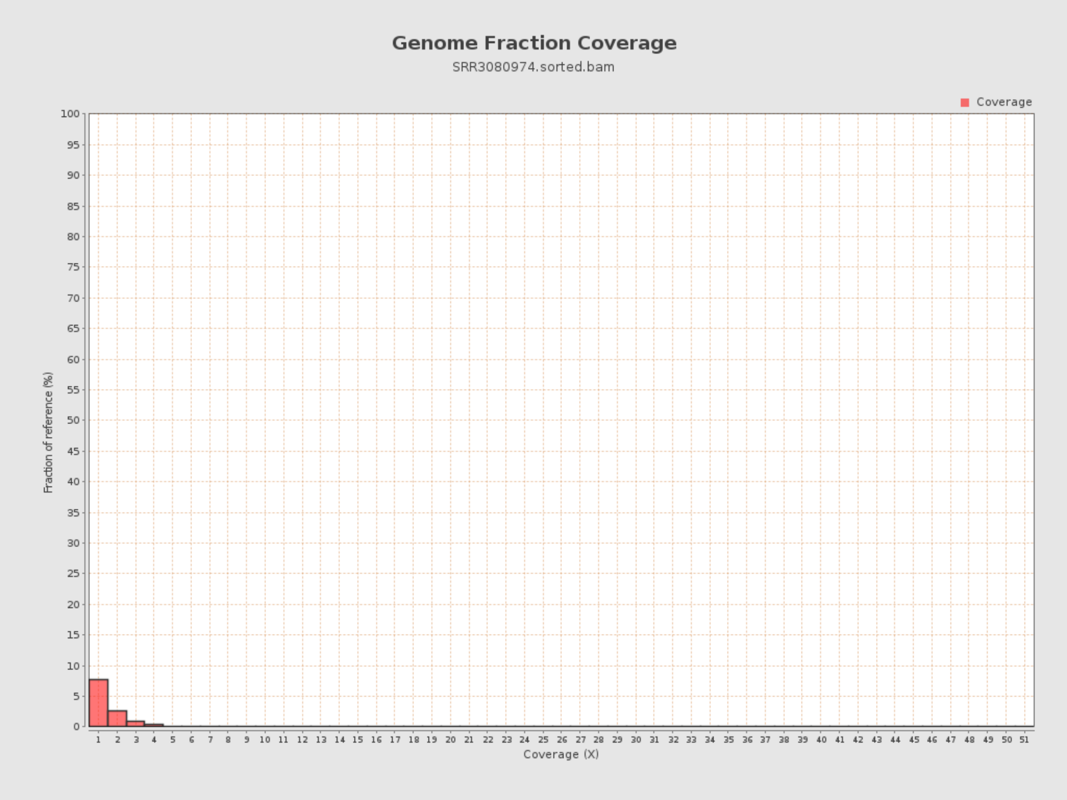
4. Results : Coverage Histogram



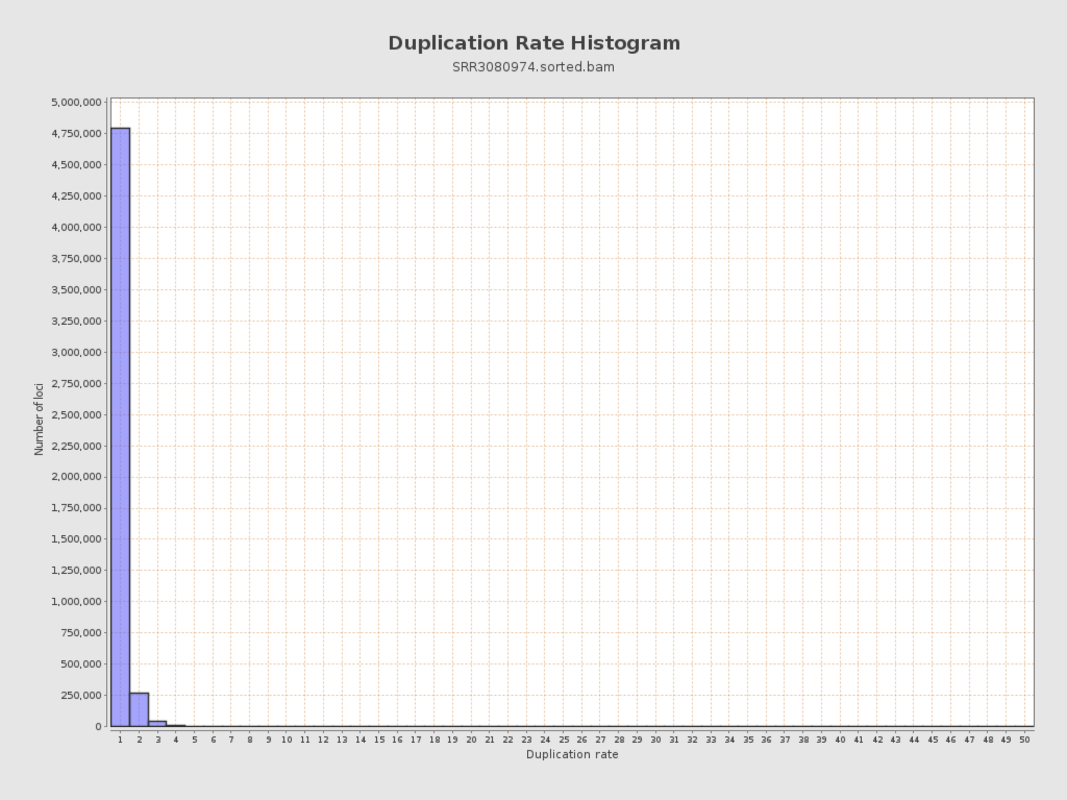
5. Results : Coverage Histogram (0-50X)



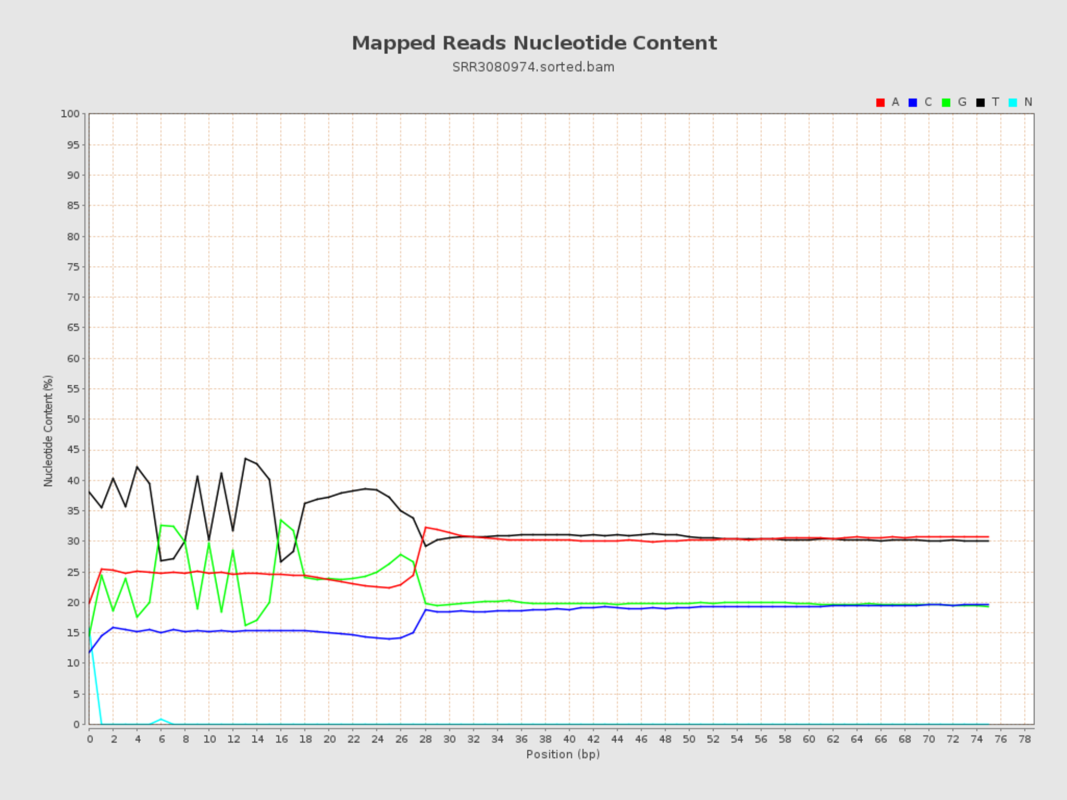
6. Results : Genome Fraction Coverage



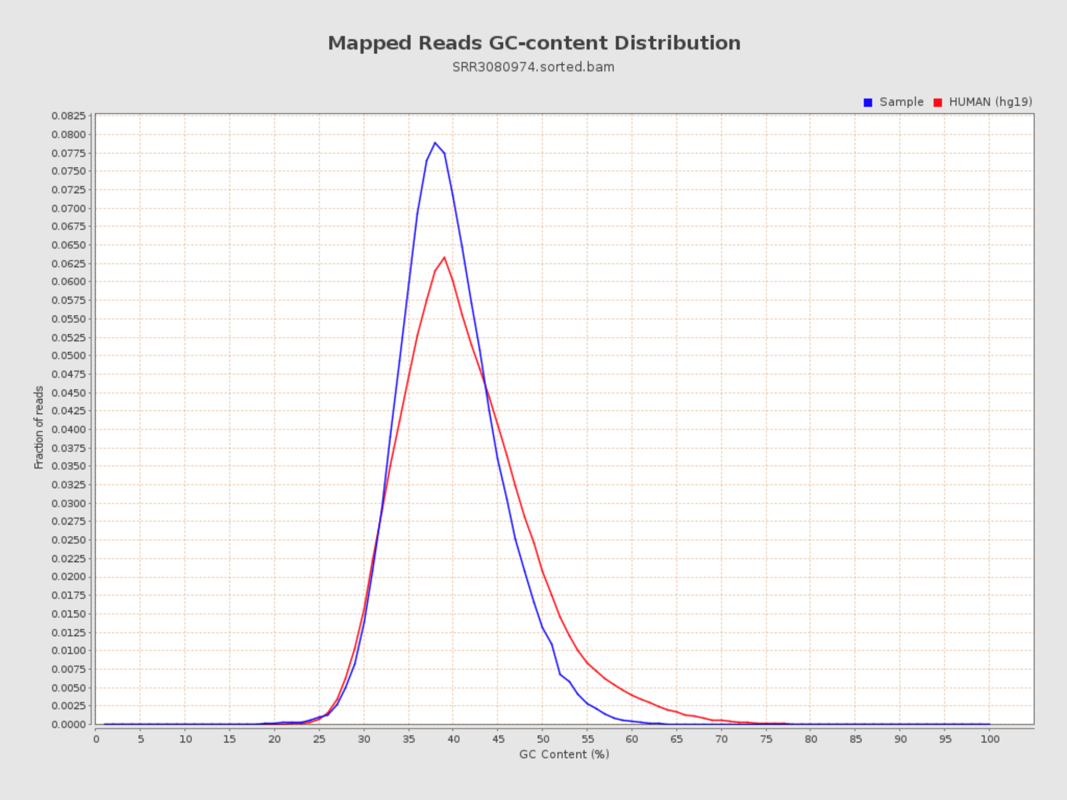
7. Results : Duplication Rate Histogram



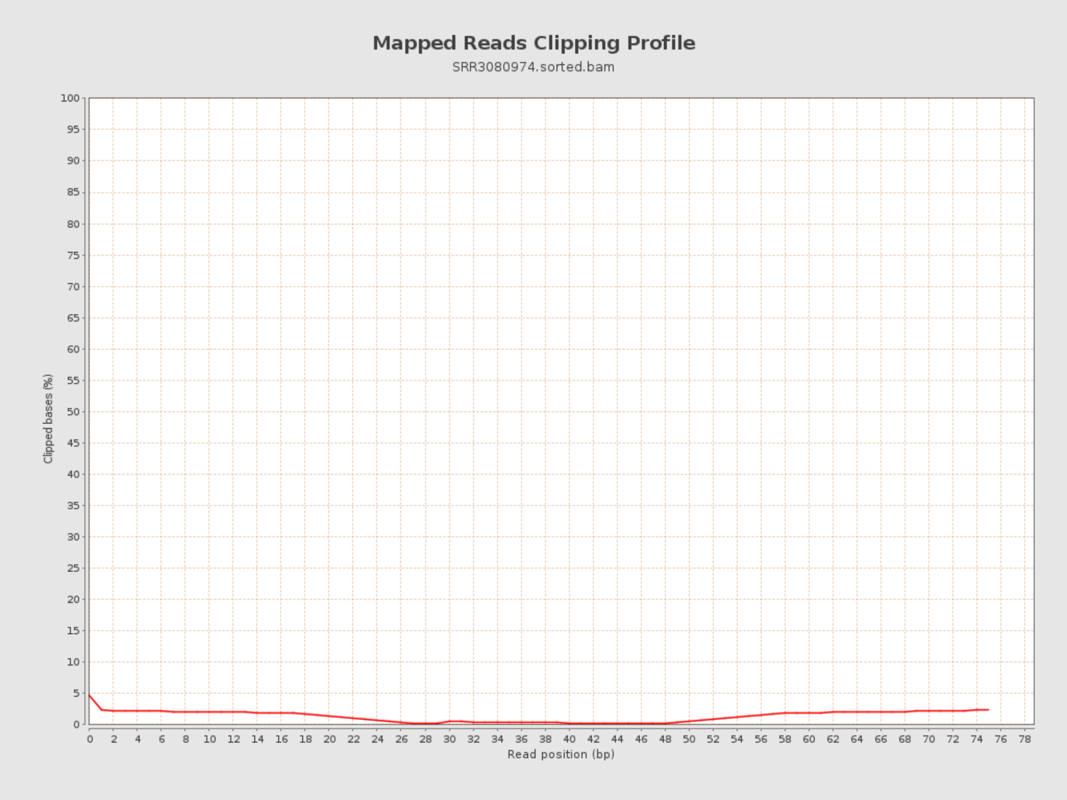
8. Results : Mapped Reads Nucleotide Content



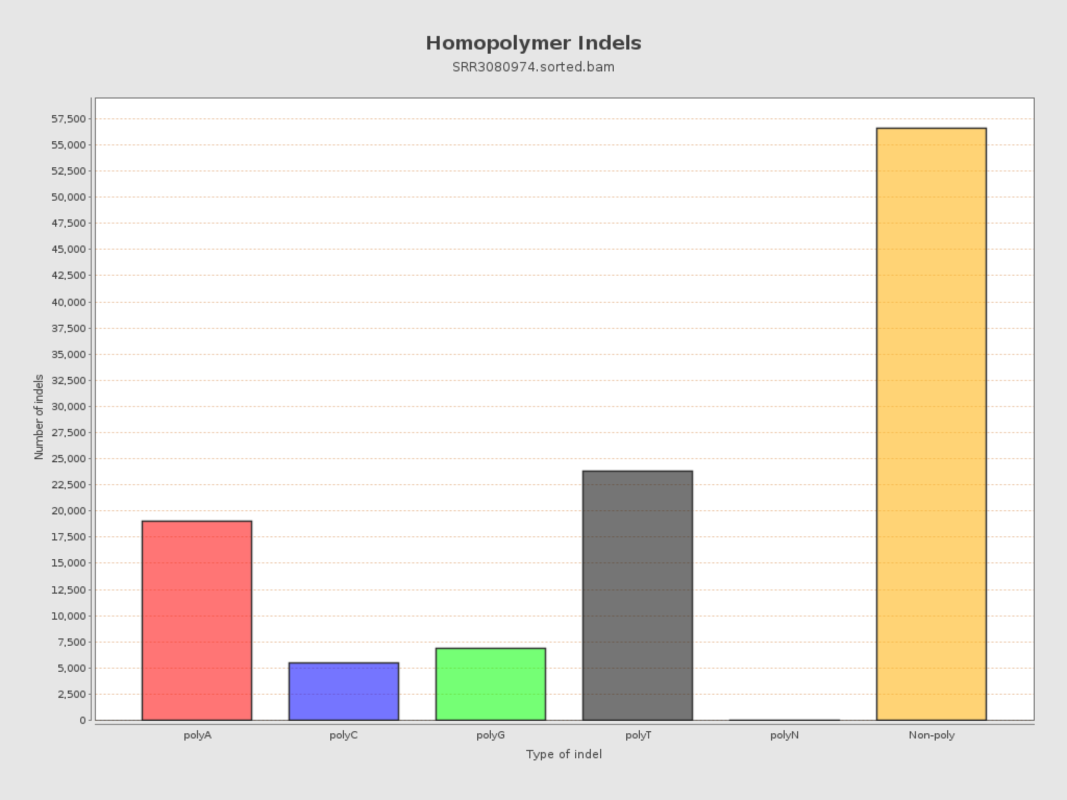
9. Results : Mapped Reads GC-content Distribution



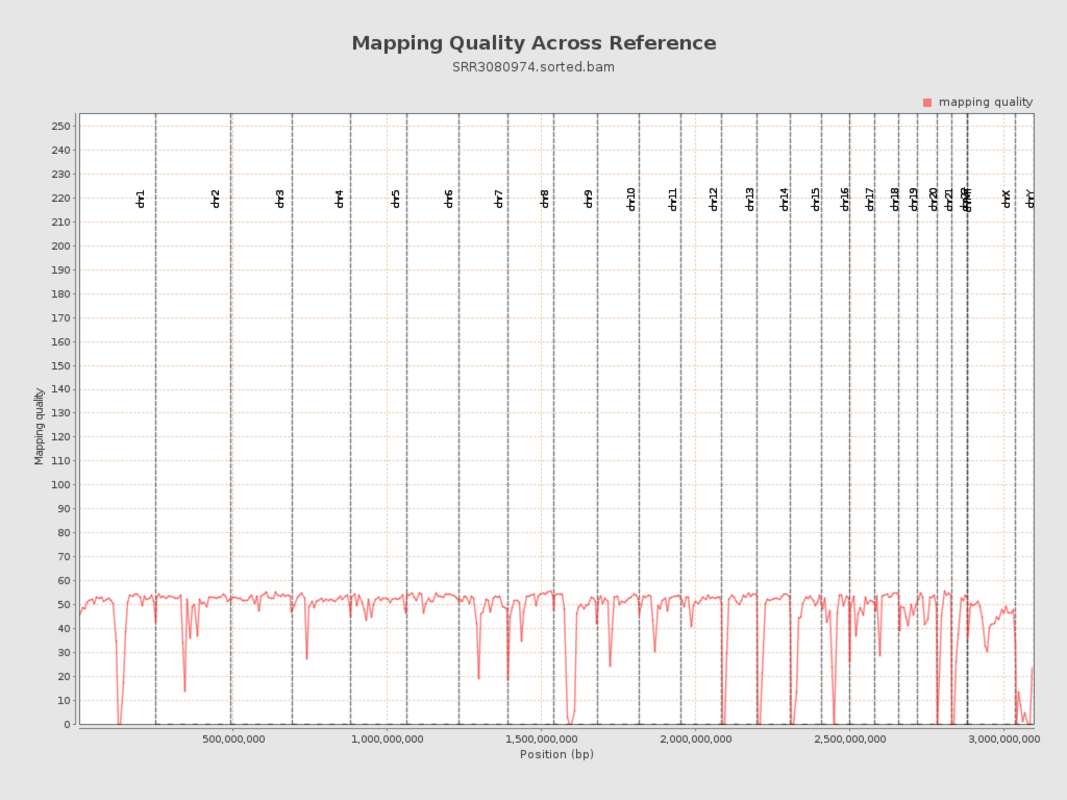
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram