Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:43:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080749.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_SRR3080749 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080749.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:43:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080749.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,214,761
Mapped reads	6,042,276 / 73.55%
Unmapped reads	2,172,485 / 26.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,916 / 0.38%
Read min/max/mean length	30 / 66 / 66.12
Duplicated reads (estimated)	770,112 / 9.37%
Duplication rate	9.72%
Clipped reads	1,139,003 / 13.87%

2.2. ACGT Content

Number/percentage of A's	120,386,155 / 31.61%
Number/percentage of C's	76,853,582 / 20.18%
Number/percentage of T's	94,536,942 / 24.82%
Number/percentage of G's	88,262,252 / 23.17%
Number/percentage of N's	851,050 / 0.22%
GC Percentage	43.35%

2.3. Coverage

Mean	0.1231

Standard Deviation	0.7939

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

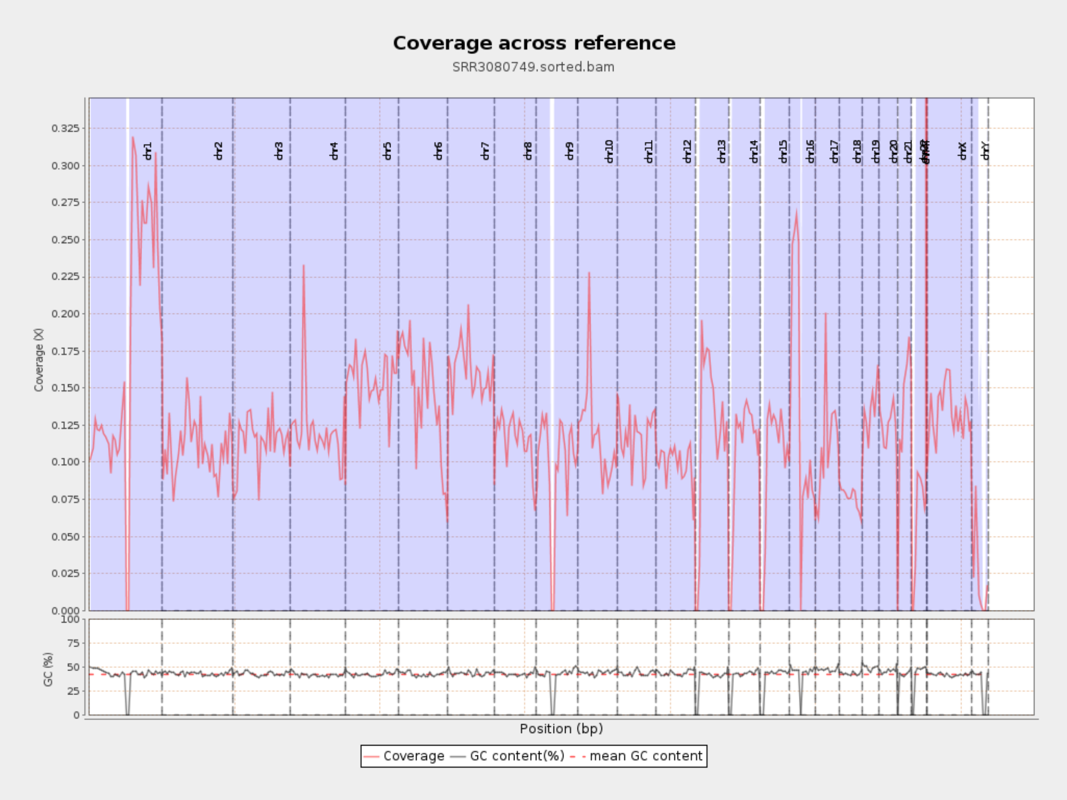
General error rate	1.04%
Mismatches	3,911,868
Insertions	28,446
Mapped reads with at least one insertion	0.47%
Deletions	69,105
Mapped reads with at least one deletion	1.13%
Homopolymer indels	42.34%

2.6. Chromosome stats

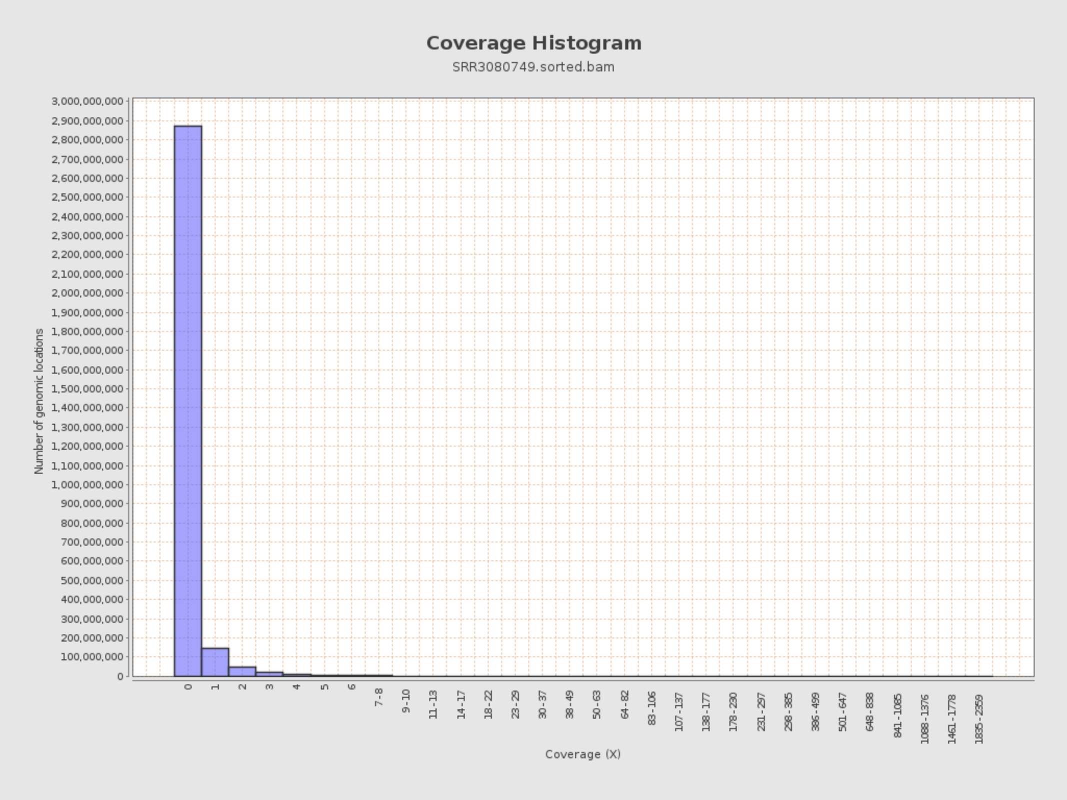
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	43228306	0.1734	1.0451
chr2	243199373	26725617	0.1099	0.7831
chr3	198022430	22646874	0.1144	0.5498
chr4	191154276	23197750	0.1214	0.7353
chr5	180915260	28237370	0.1561	0.6453
chr6	171115067	25057494	0.1464	1.3045
chr7	159138663	25800278	0.1621	0.9484

chr8	146364022	16954959	0.1158	0.8787
chr9	141213431	13849496	0.0981	0.5802
chr10	135534747	16099206	0.1188	0.9996
chr11	135006516	15927343	0.118	0.6875
chr12	133851895	13216206	0.0987	0.5295
chr13	115169878	13974533	0.1213	0.5663
chr14	107349540	11194410	0.1043	0.6011
chr15	102531392	10134194	0.0988	0.5104
chr16	90354753	12426451	0.1375	0.7321
chr17	81195210	9175359	0.113	0.5778
chr18	78077248	5954220	0.0763	0.7762
chr19	59128983	7972318	0.1348	1.1655
chr20	63025520	7837079	0.1243	0.6086
chr21	48129895	6416600	0.1333	0.7638
chr22	51304566	2959841	0.0577	0.3983
chrMT	16571	62821	3.791	4.3055
chrX	155270560	20677482	0.1332	0.6158
chrY	59373566	1296315	0.0218	0.7415

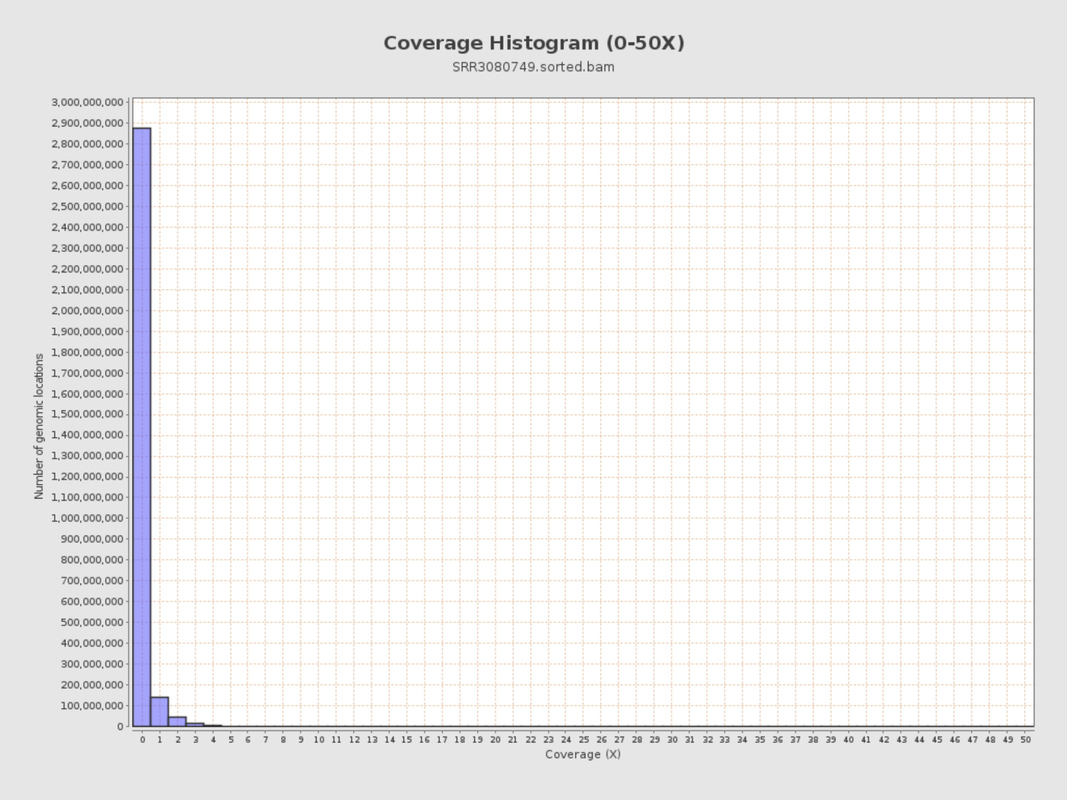
3. Results : Coverage across reference



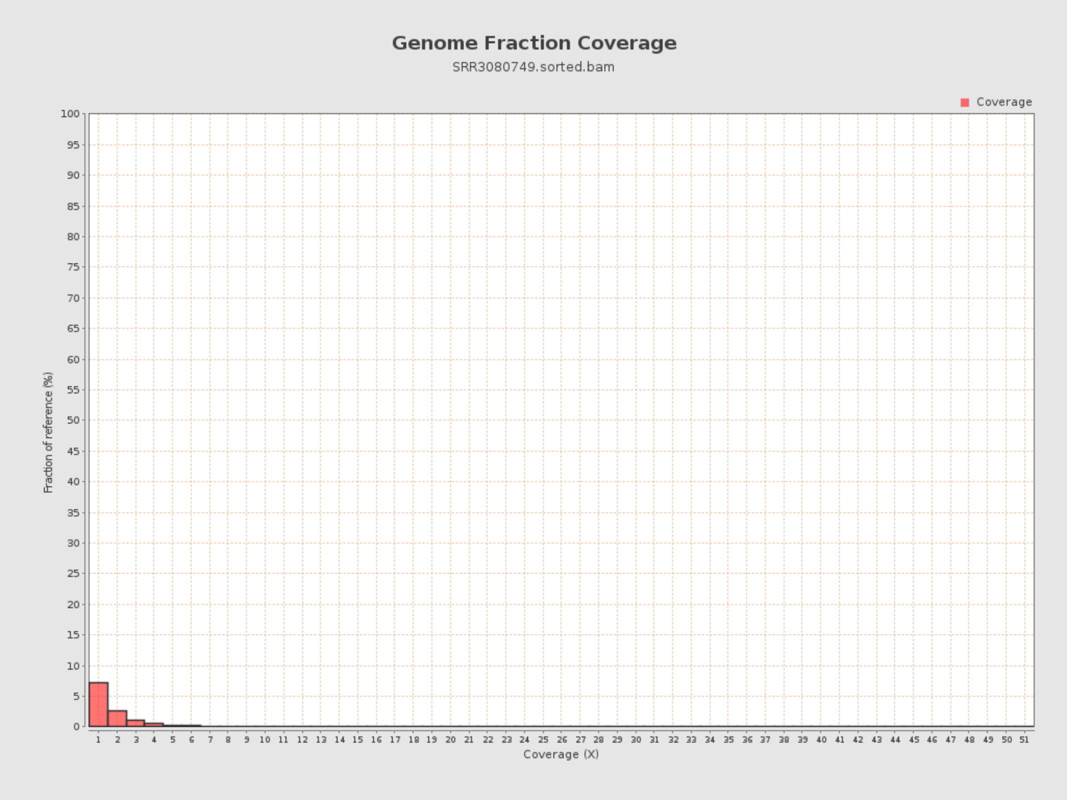
4. Results : Coverage Histogram



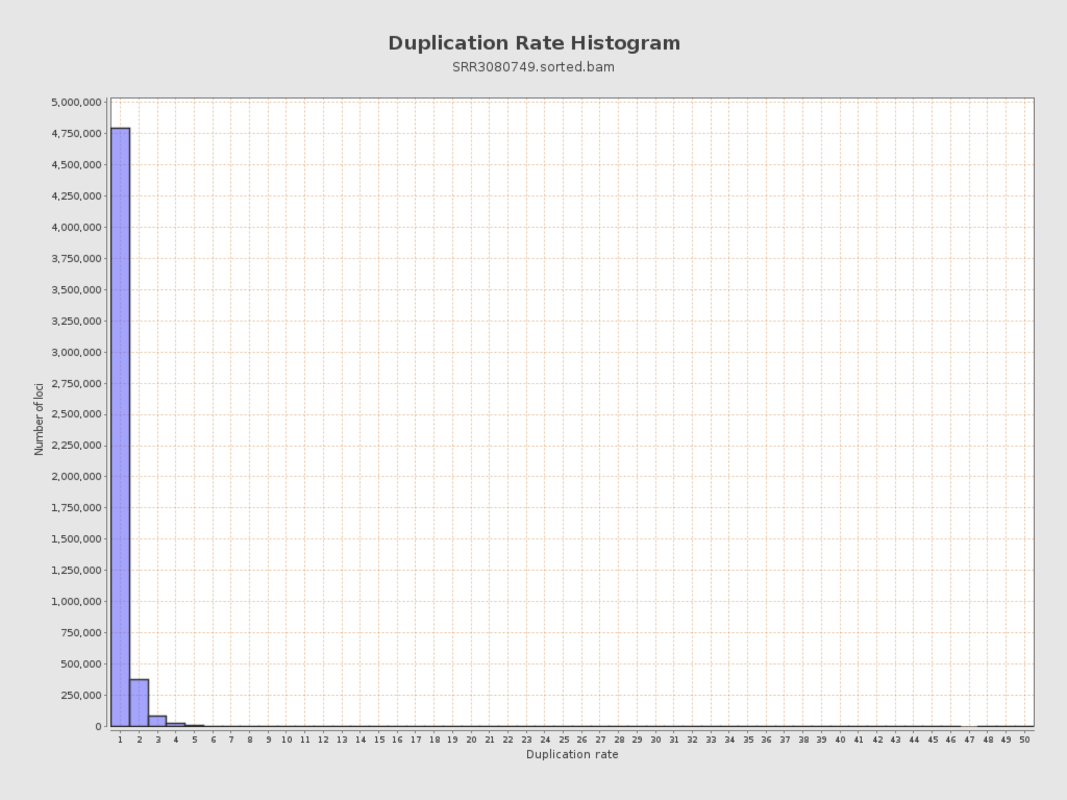
5. Results : Coverage Histogram (0-50X)



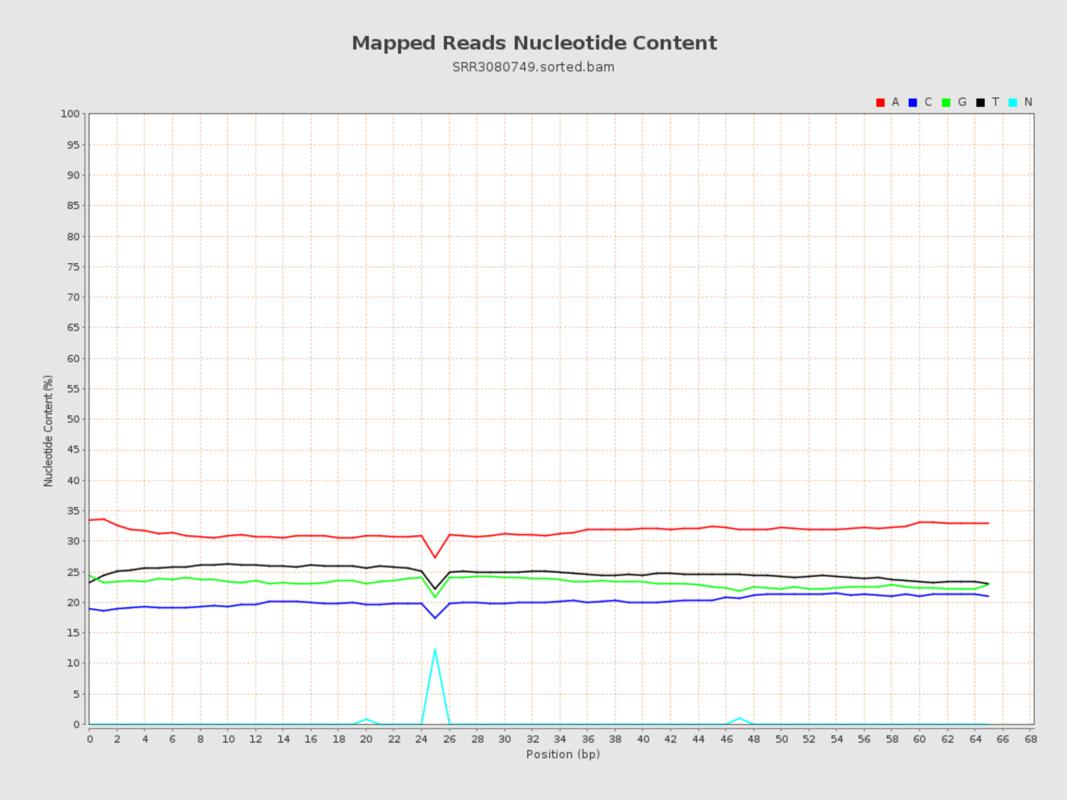
6. Results : Genome Fraction Coverage



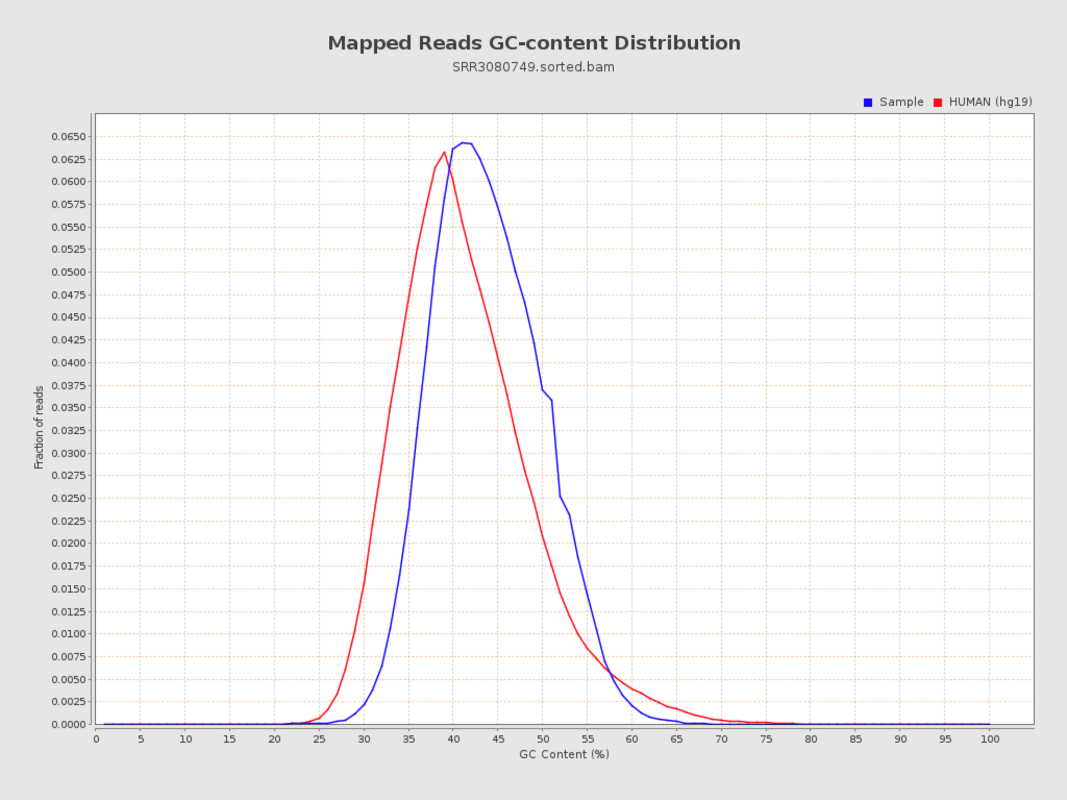
7. Results : Duplication Rate Histogram



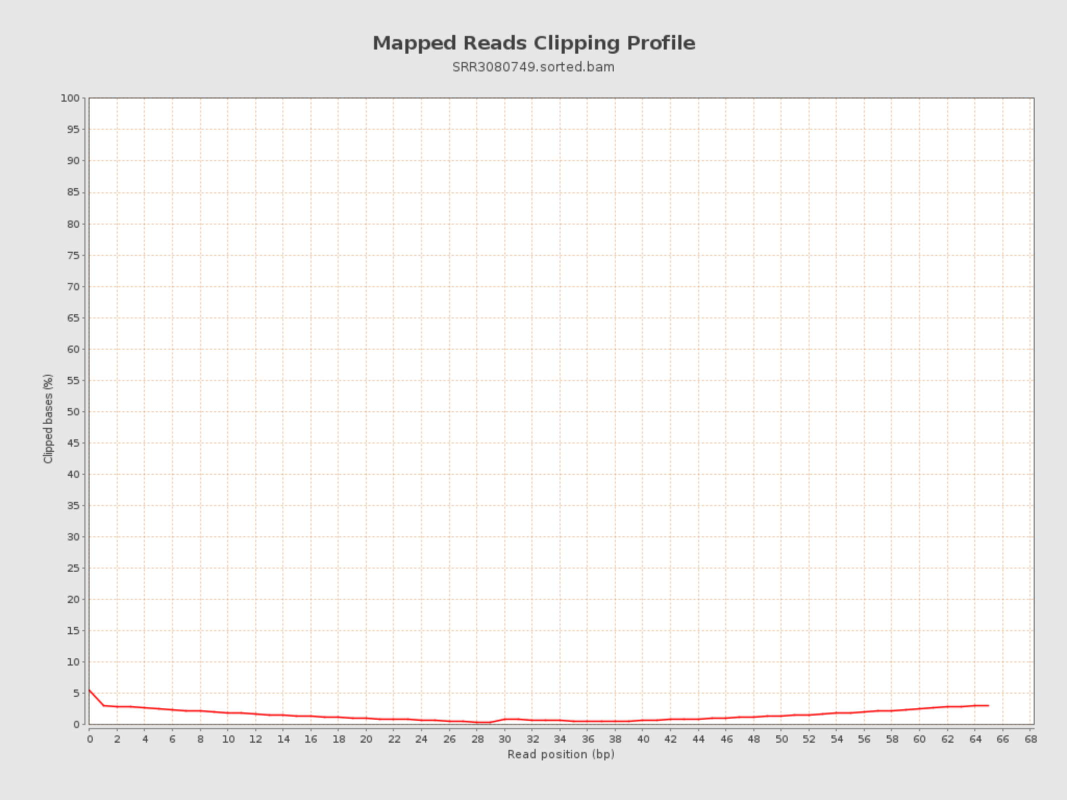
8. Results : Mapped Reads Nucleotide Content



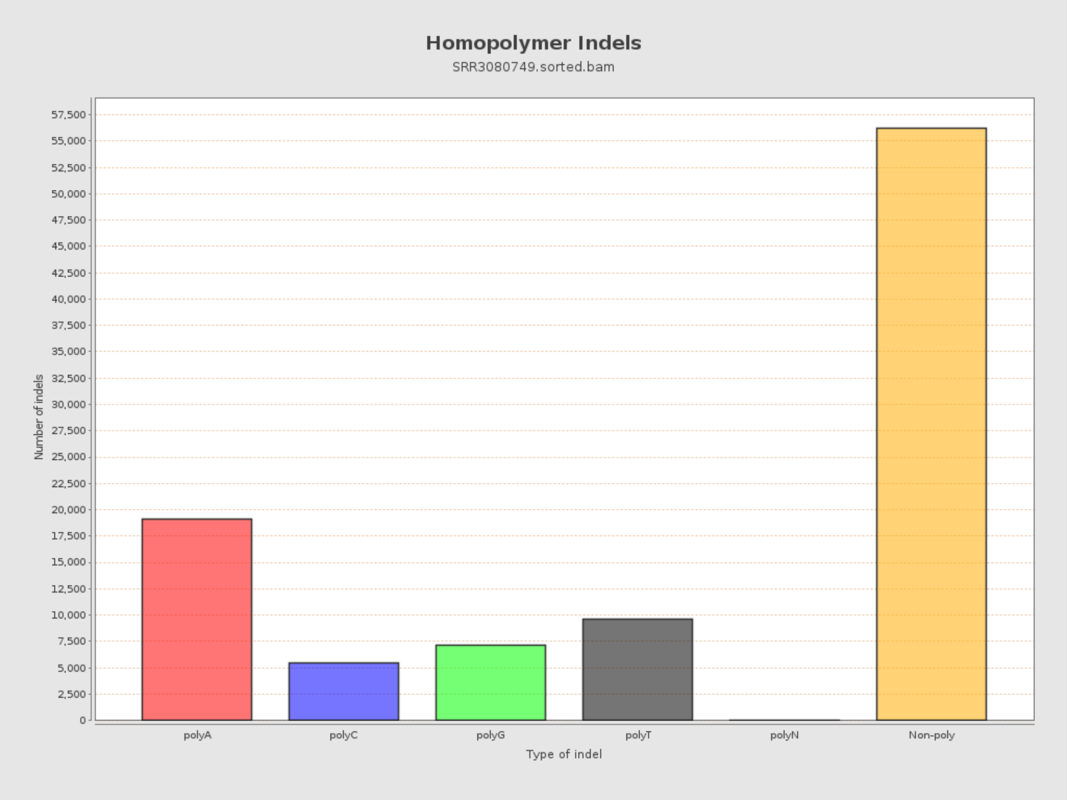
9. Results : Mapped Reads GC-content Distribution



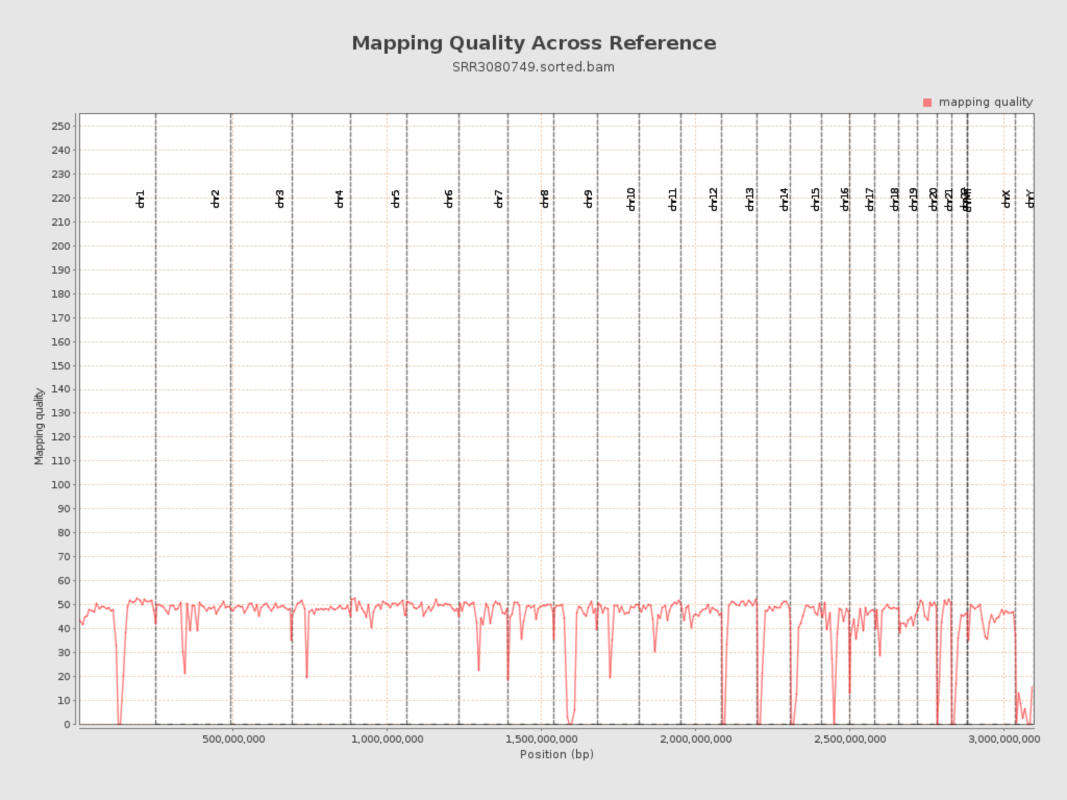
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram