Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:56:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082769.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_SRR3082769 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082769.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:56:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082769.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,635,838
Mapped reads	4,095,995 / 88.36%
Unmapped reads	539,843 / 11.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	39,192 / 0.85%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	226,887 / 4.89%
Duplication rate	4.48%
Clipped reads	1,629,798 / 35.16%

2.2. ACGT Content

Number/percentage of A's	80,788,019 / 28.88%
Number/percentage of C's	51,004,305 / 18.23%
Number/percentage of T's	90,584,311 / 32.38%
Number/percentage of G's	57,390,607 / 20.51%
Number/percentage of N's	15,681 / 0.01%
GC Percentage	38.74%

2.3. Coverage

Mean	0.0904

Standard Deviation	0.6309

2.4. Mapping Quality

Mean Mapping Quality	47.42

2.5. Mismatches and indels

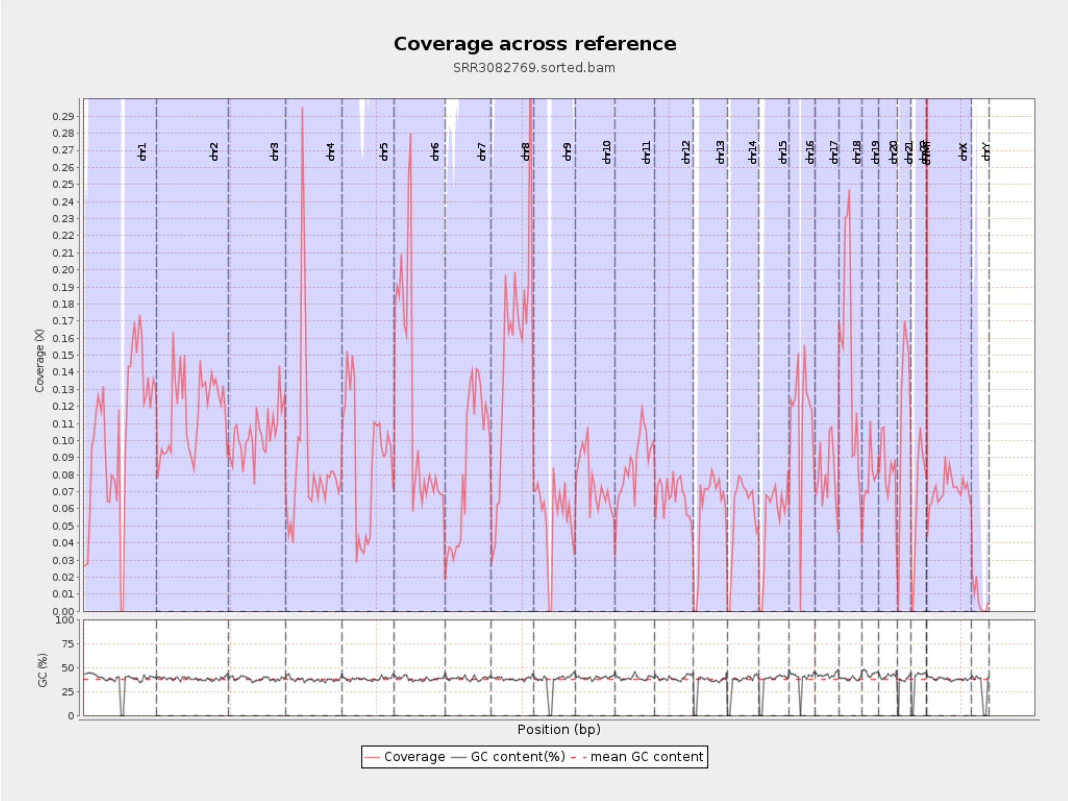
General error rate	0.89%
Mismatches	2,462,783
Insertions	23,160
Mapped reads with at least one insertion	0.56%
Deletions	62,539
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.16%

2.6. Chromosome stats

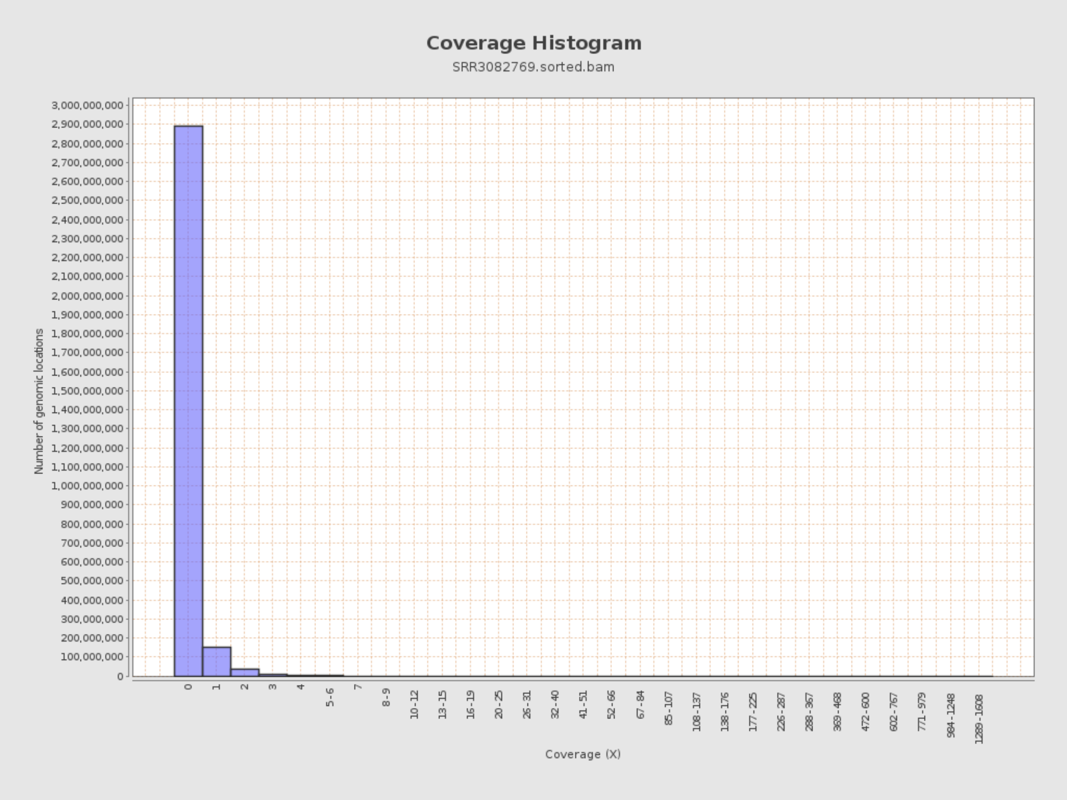
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25902732	0.1039	1.1398
chr2	243199373	28429500	0.1169	0.7451
chr3	198022430	20555215	0.1038	0.4148
chr4	191154276	17111246	0.0895	0.4011
chr5	180915260	16041025	0.0887	0.3884
chr6	171115067	20246016	0.1183	0.6492
chr7	159138663	13647235	0.0858	0.4951

chr8	146364022	22103245	0.151	1.1141
chr9	141213431	7858234	0.0556	0.5295
chr10	135534747	10192140	0.0752	0.4882
chr11	135006516	11690161	0.0866	0.4925
chr12	133851895	8966639	0.067	0.3462
chr13	115169878	6860121	0.0596	0.3139
chr14	107349540	6132508	0.0571	0.3643
chr15	102531392	5438221	0.053	0.2953
chr16	90354753	9970775	0.1104	0.4667
chr17	81195210	6536097	0.0805	0.4496
chr18	78077248	11732287	0.1503	1.1641
chr19	59128983	4634478	0.0784	0.7928
chr20	63025520	5332502	0.0846	0.3957
chr21	48129895	5548247	0.1153	0.4518
chr22	51304566	3361271	0.0655	0.3255
chrMT	16571	155246	9.3685	6.3374
chrX	155270560	11013905	0.0709	0.3881
chrY	59373566	430625	0.0073	0.1383

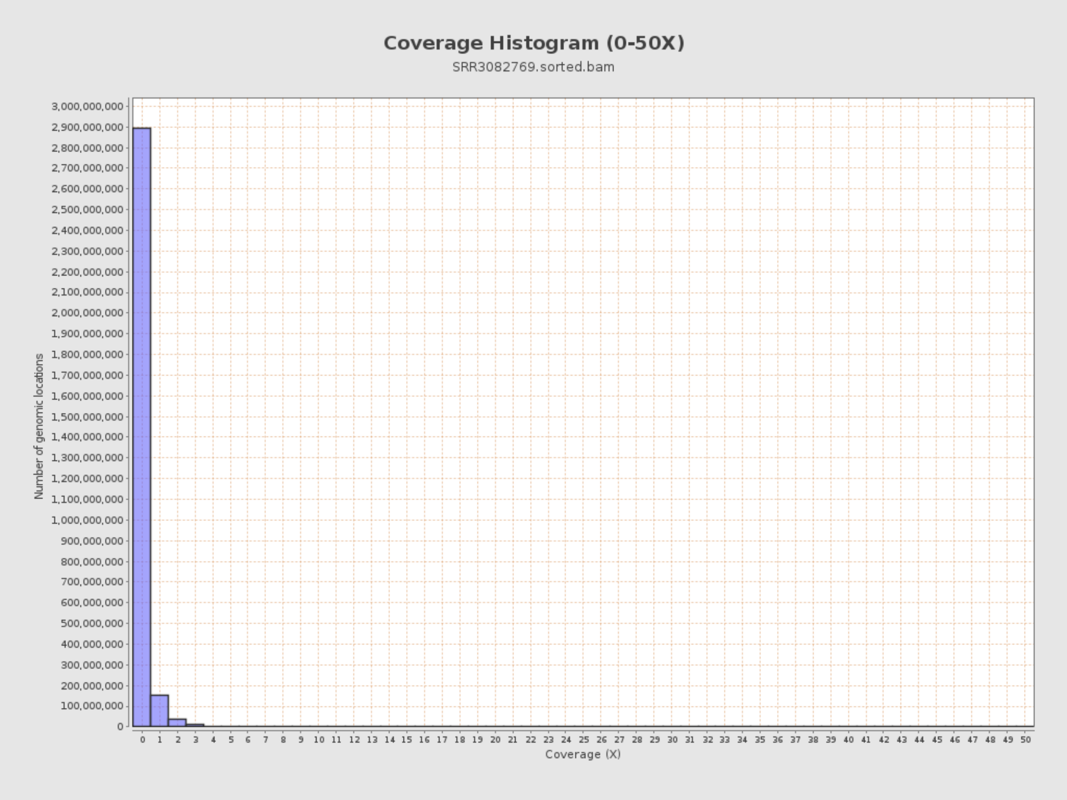
3. Results : Coverage across reference



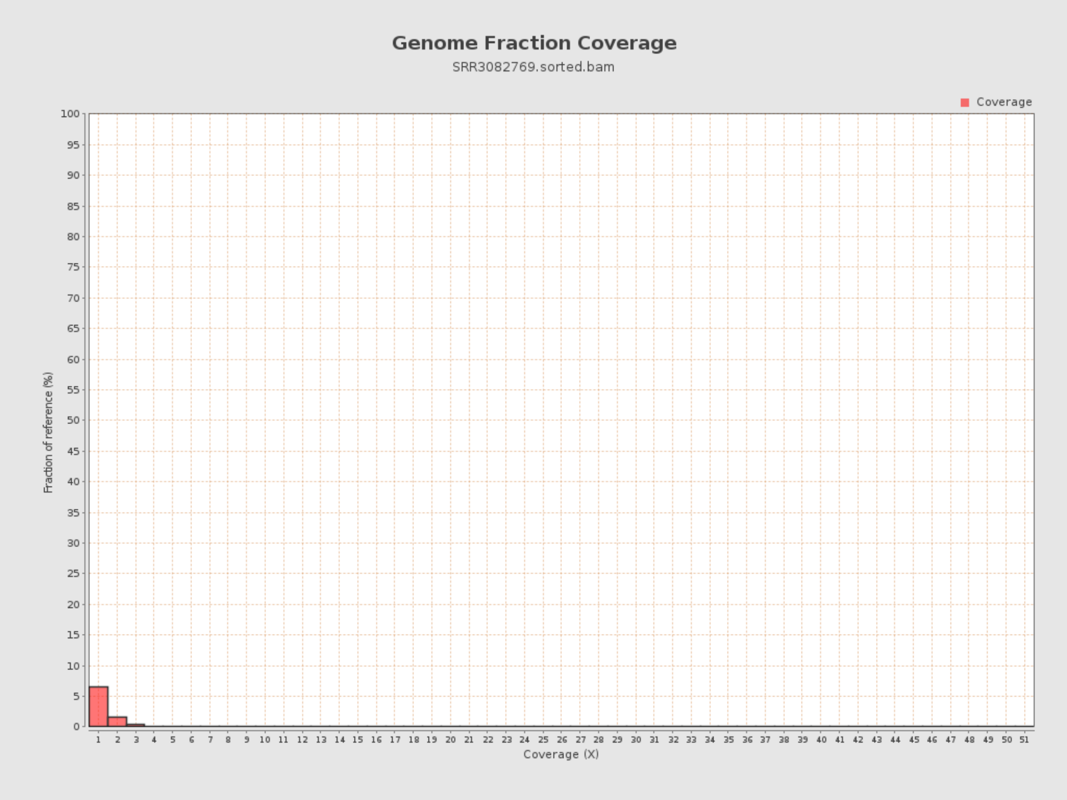
4. Results : Coverage Histogram



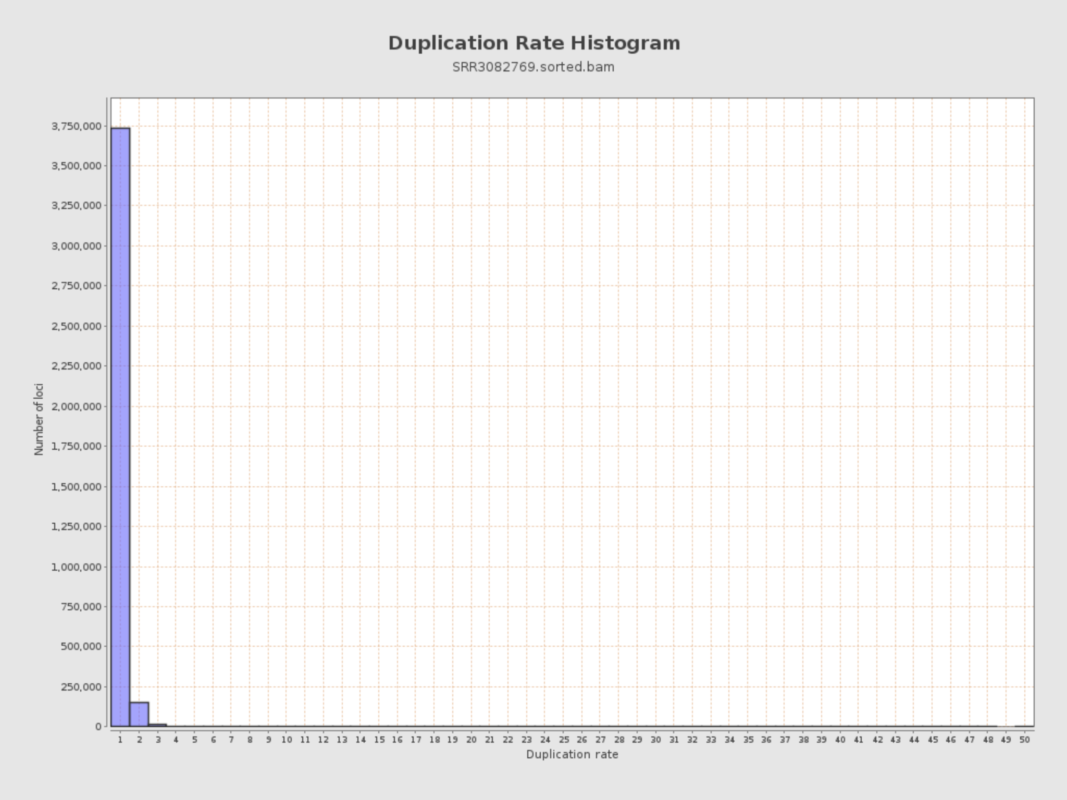
5. Results : Coverage Histogram (0-50X)



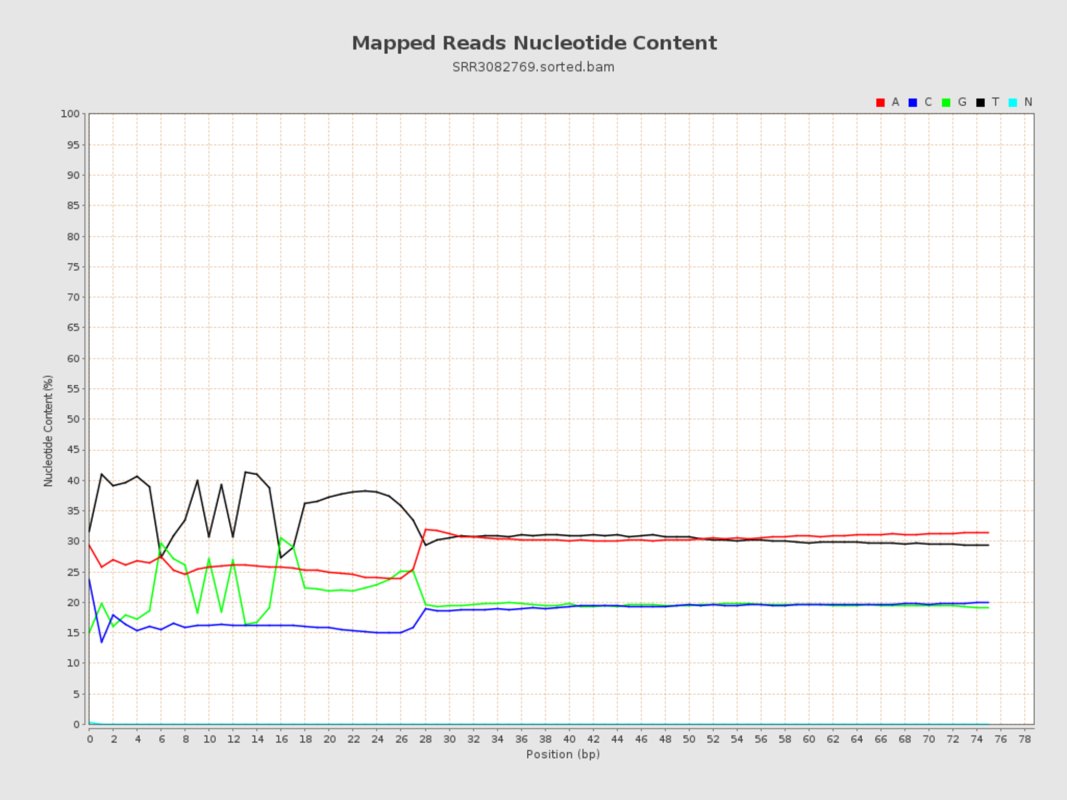
6. Results : Genome Fraction Coverage



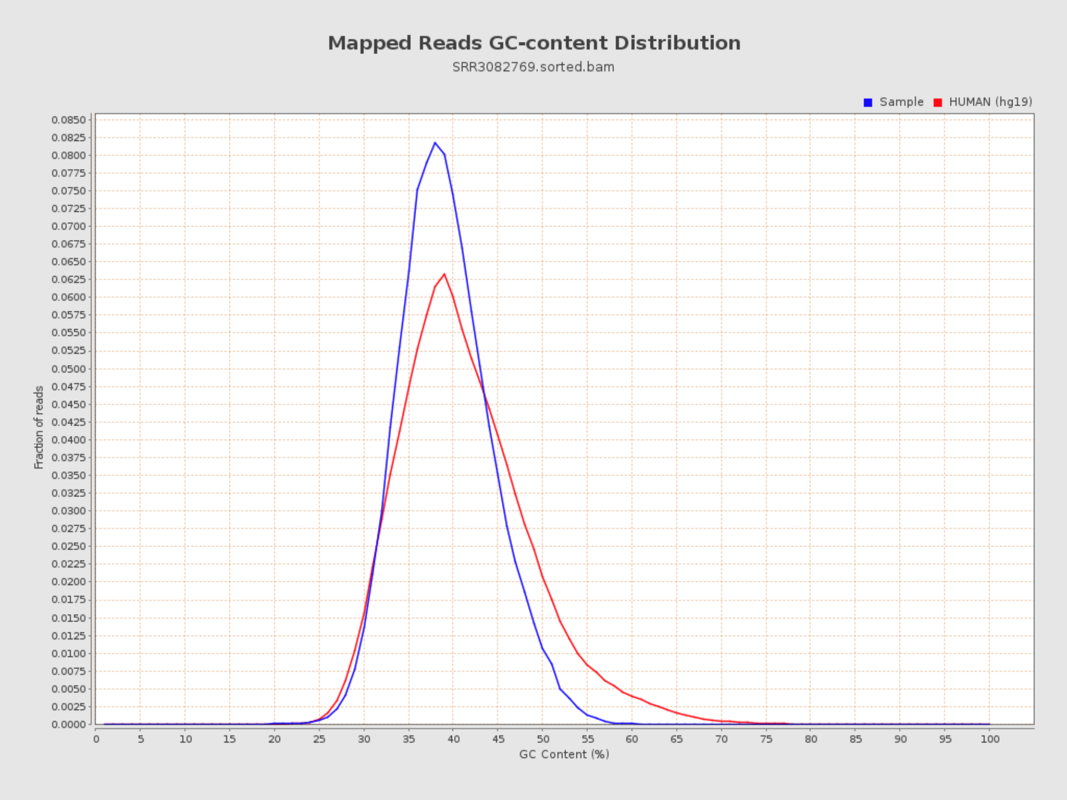
7. Results : Duplication Rate Histogram



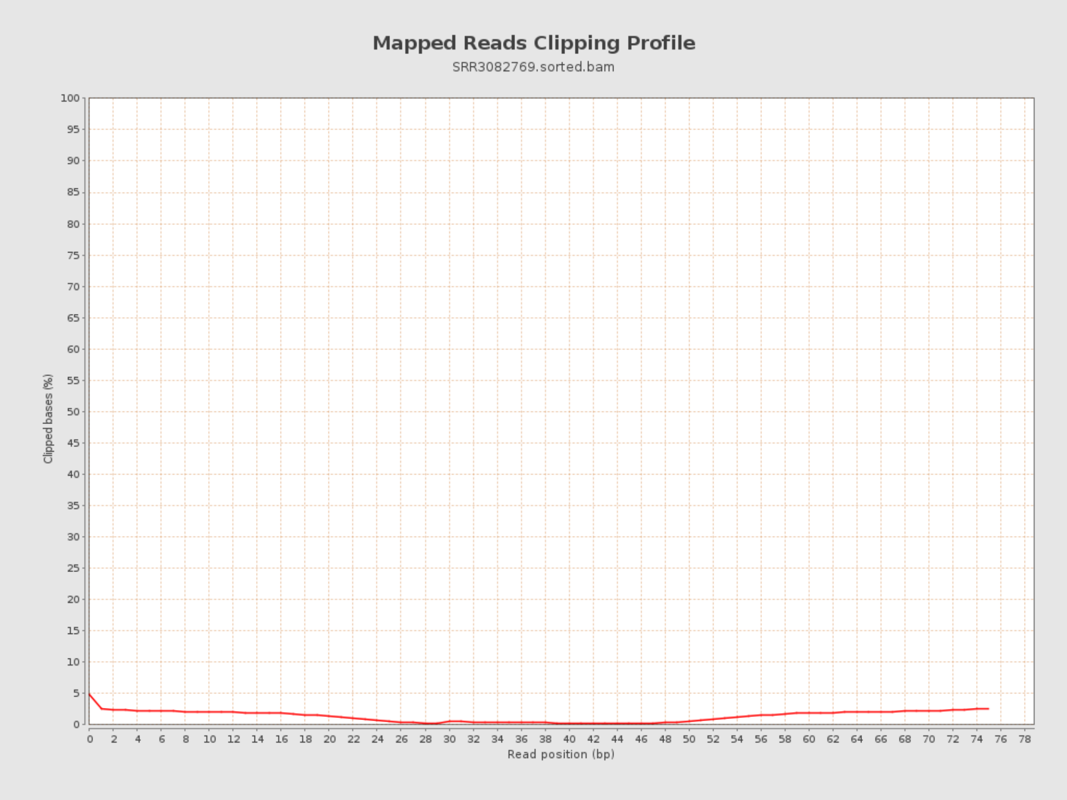
8. Results : Mapped Reads Nucleotide Content



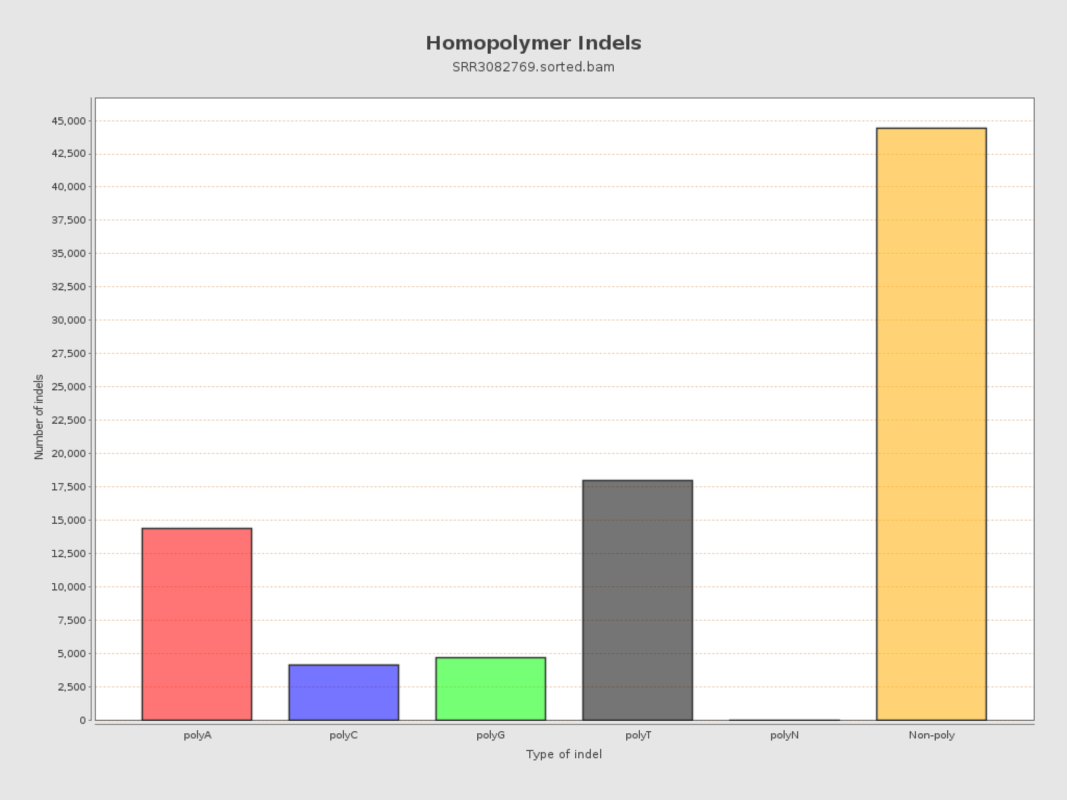
9. Results : Mapped Reads GC-content Distribution



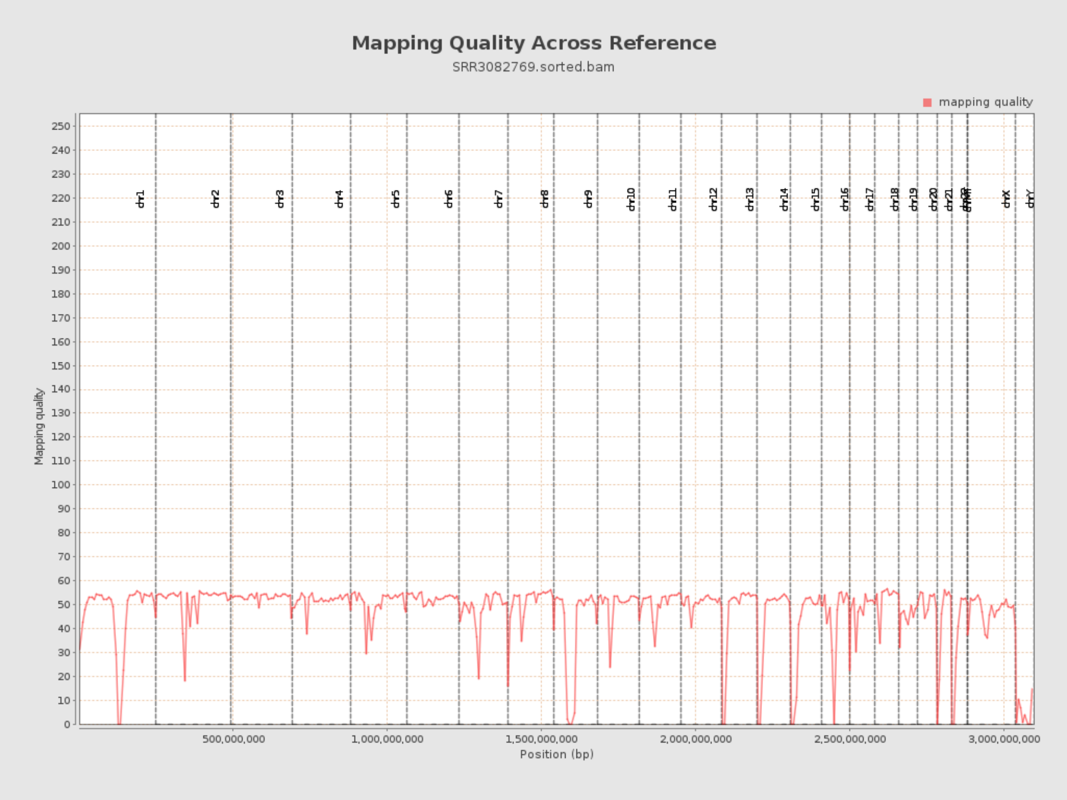
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram