Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:50:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080723.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_SRR3080723 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080723.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:50:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080723.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,592,100
Mapped reads	2,420,075 / 93.36%
Unmapped reads	172,025 / 6.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,567 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	103,463 / 3.99%
Duplication rate	3.52%
Clipped reads	747,960 / 28.86%

2.2. ACGT Content

Number/percentage of A's	49,257,460 / 29.14%
Number/percentage of C's	31,487,910 / 18.62%
Number/percentage of T's	53,557,016 / 31.68%
Number/percentage of G's	34,759,634 / 20.56%
Number/percentage of N's	2,449 / 0%
GC Percentage	39.18%

2.3. Coverage

Mean	0.0546

Standard Deviation	0.426

2.4. Mapping Quality

Mean Mapping Quality	47

2.5. Mismatches and indels

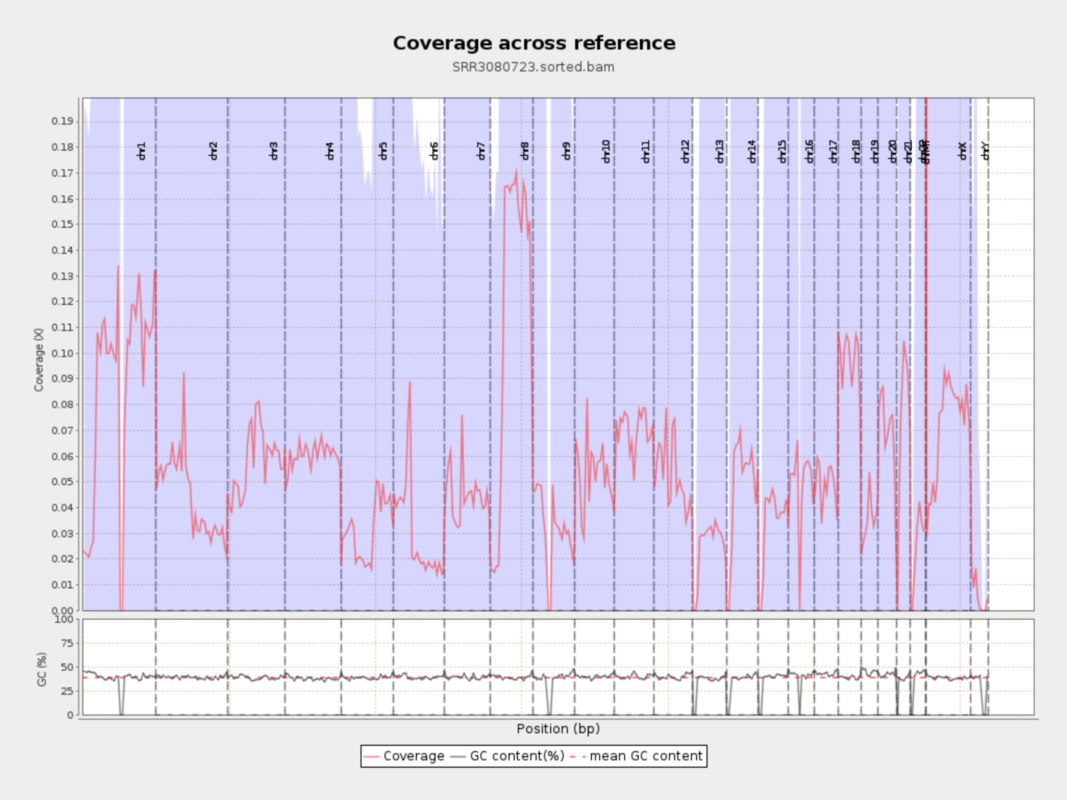
General error rate	0.8%
Mismatches	1,325,484
Insertions	12,371
Mapped reads with at least one insertion	0.51%
Deletions	36,491
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.41%

2.6. Chromosome stats

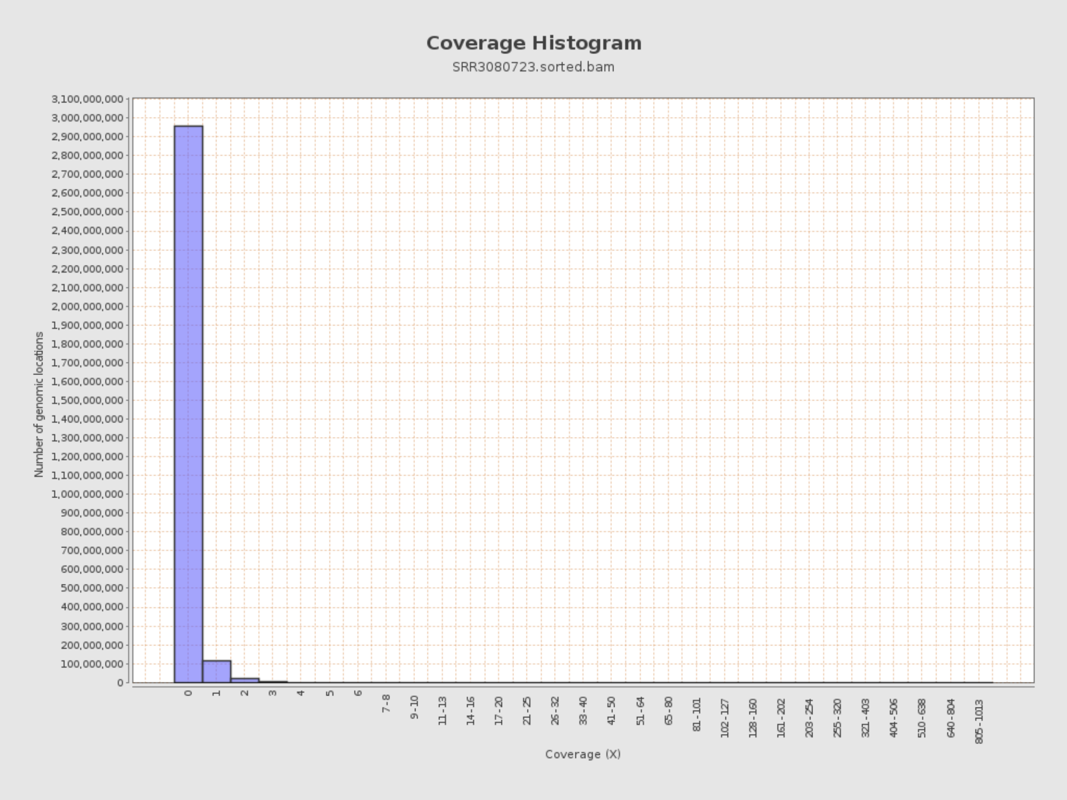
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21718744	0.0871	0.7996
chr2	243199373	10761529	0.0442	0.4202
chr3	198022430	11546003	0.0583	0.2812
chr4	191154276	11561035	0.0605	0.2948
chr5	180915260	5670925	0.0313	0.2046
chr6	171115067	5186011	0.0303	0.26
chr7	159138663	7163303	0.045	0.5466

chr8	146364022	17055048	0.1165	0.7646
chr9	141213431	4515781	0.032	0.3184
chr10	135534747	7230074	0.0533	0.4413
chr11	135006516	9392243	0.0696	0.3764
chr12	133851895	7028464	0.0525	0.2681
chr13	115169878	2867758	0.0249	0.1801
chr14	107349540	5224934	0.0487	0.2677
chr15	102531392	3397346	0.0331	0.2083
chr16	90354753	4320942	0.0478	0.2685
chr17	81195210	4031422	0.0497	0.2837
chr18	78077248	7694646	0.0986	0.5969
chr19	59128983	2120150	0.0359	0.5073
chr20	63025520	4499410	0.0714	0.318
chr21	48129895	3477186	0.0722	0.3247
chr22	51304566	1261744	0.0246	0.1779
chrMT	16571	52635	3.1763	2.3625
chrX	155270560	10987377	0.0708	0.3348
chrY	59373566	364531	0.0061	0.1254

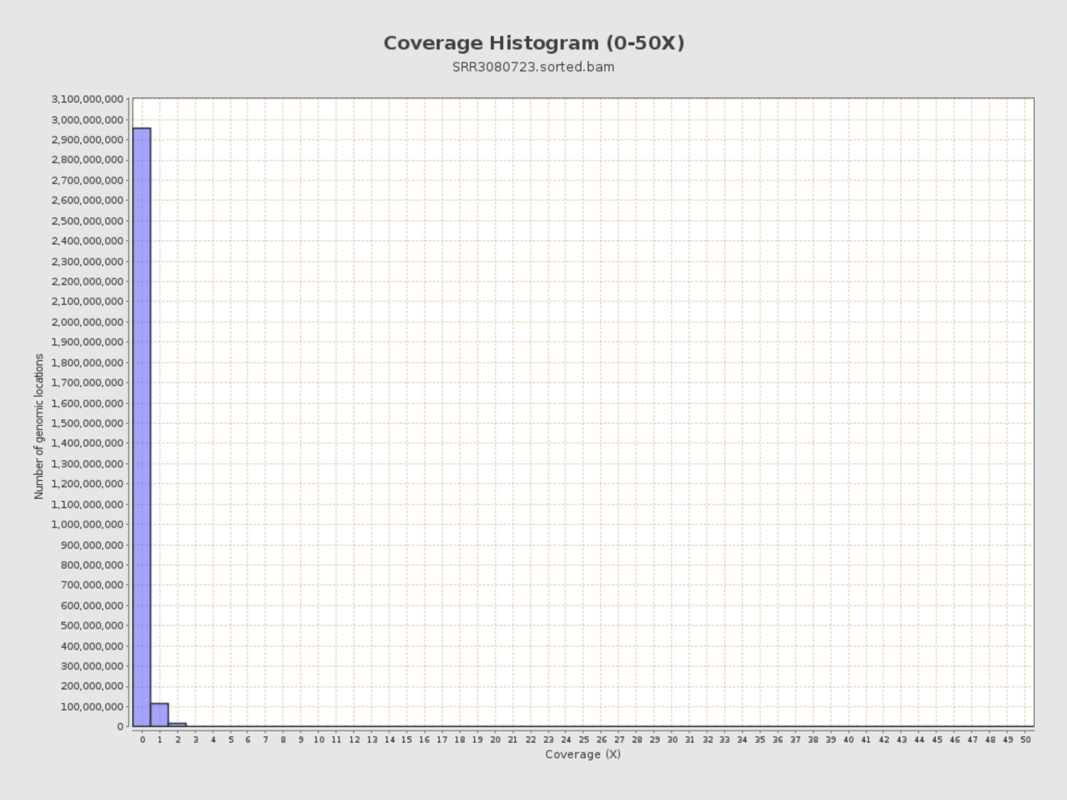
3. Results : Coverage across reference



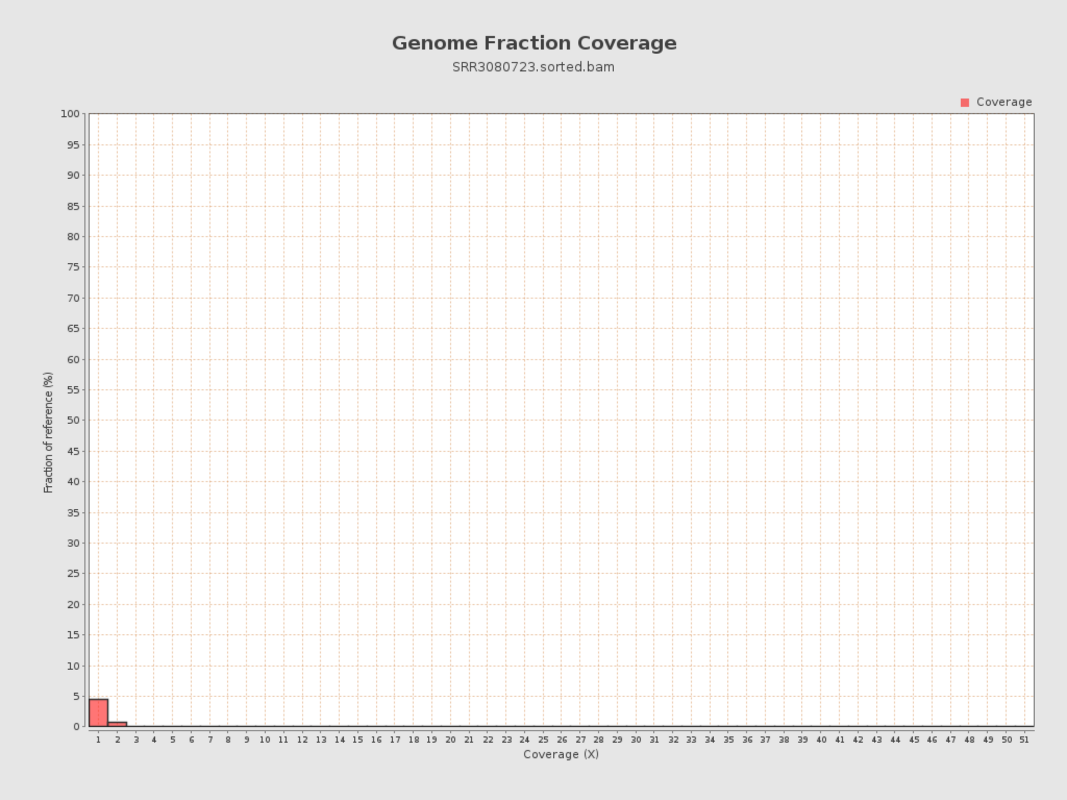
4. Results : Coverage Histogram



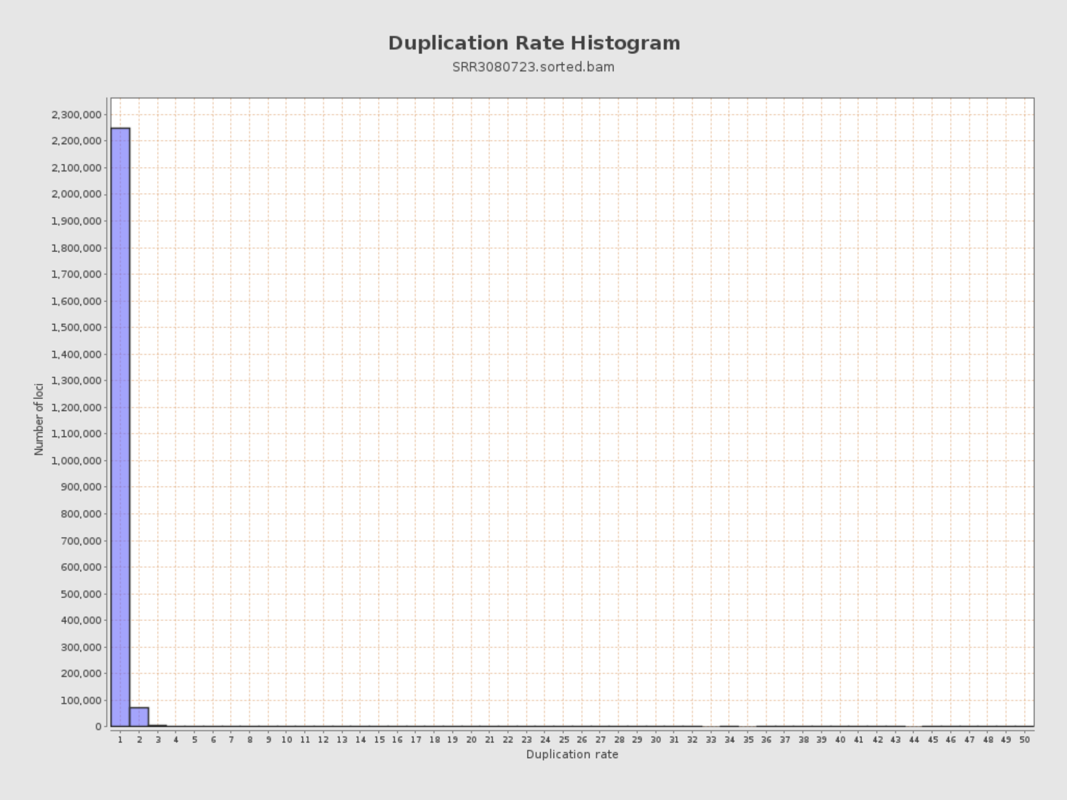
5. Results : Coverage Histogram (0-50X)



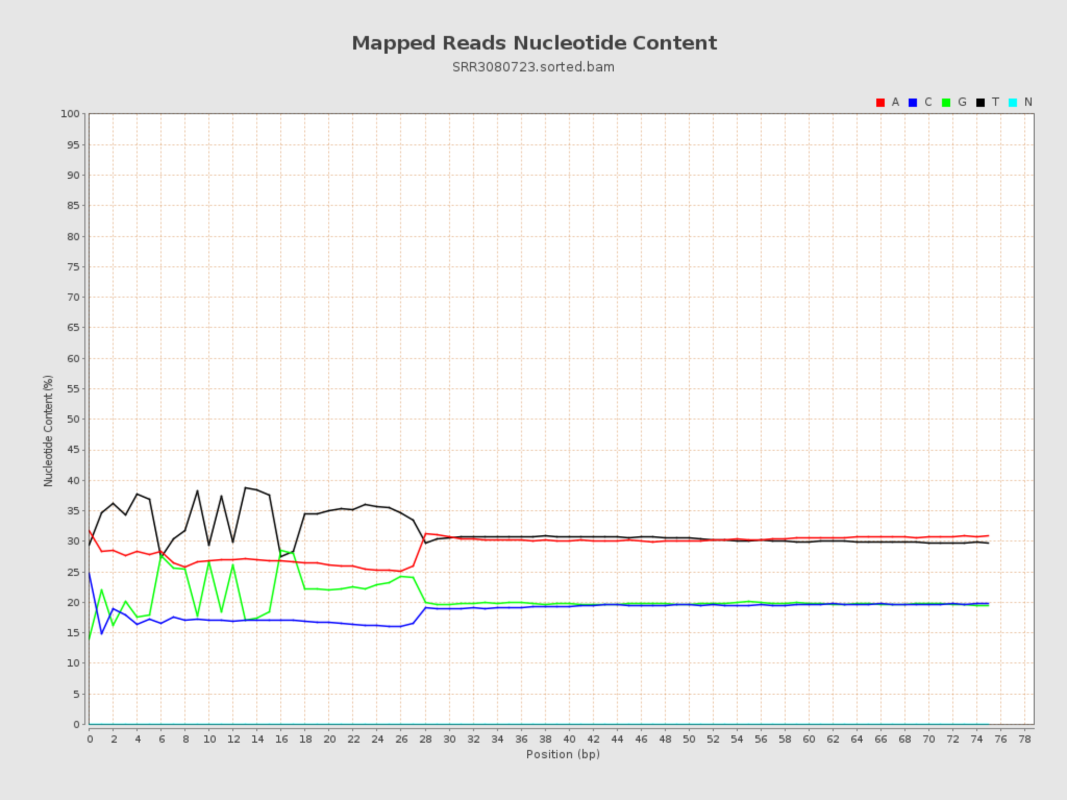
6. Results : Genome Fraction Coverage



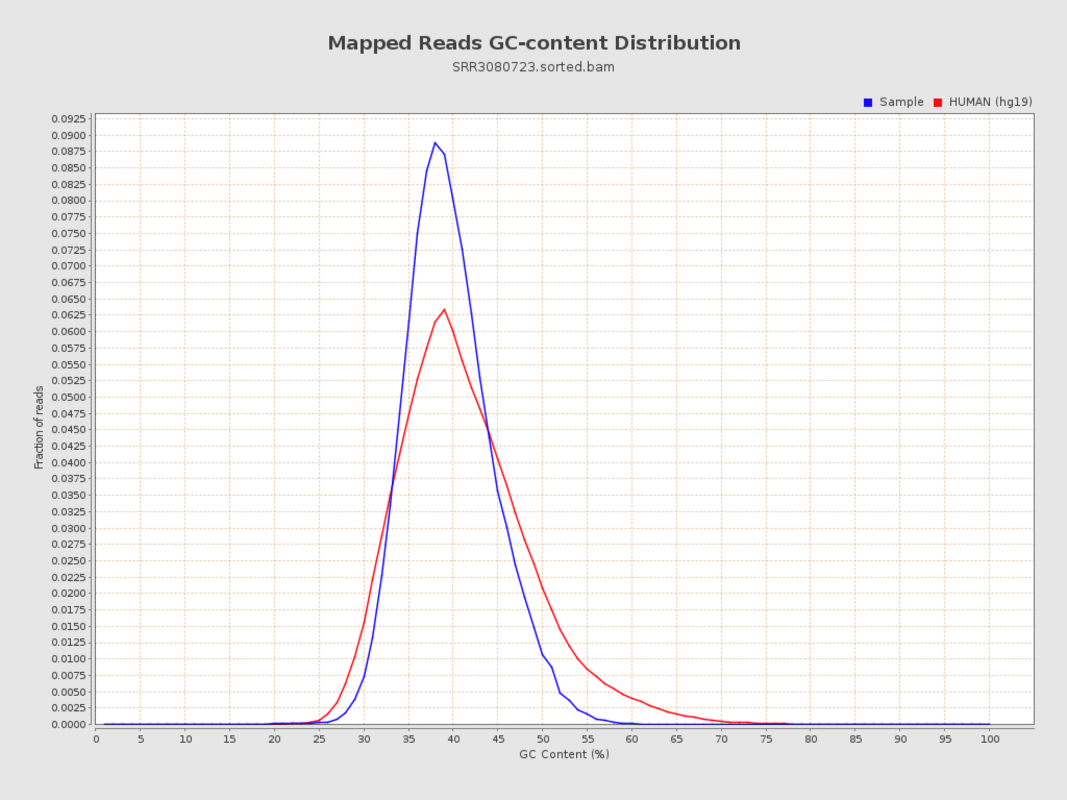
7. Results : Duplication Rate Histogram



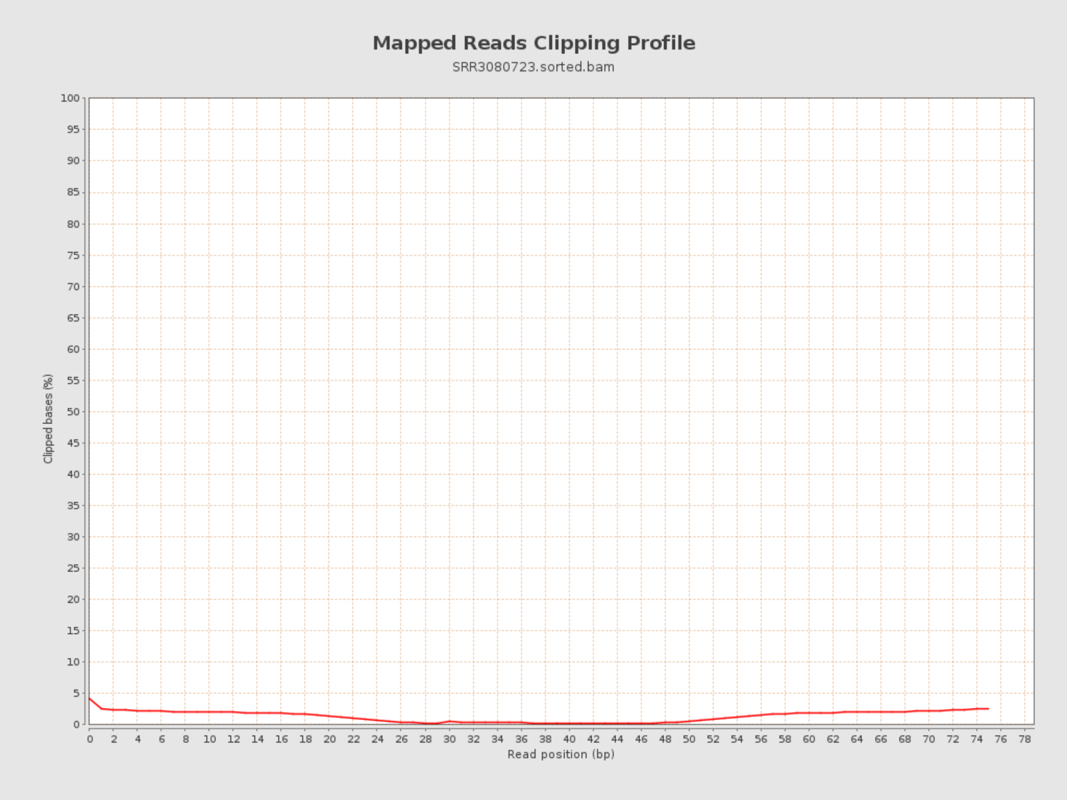
8. Results : Mapped Reads Nucleotide Content



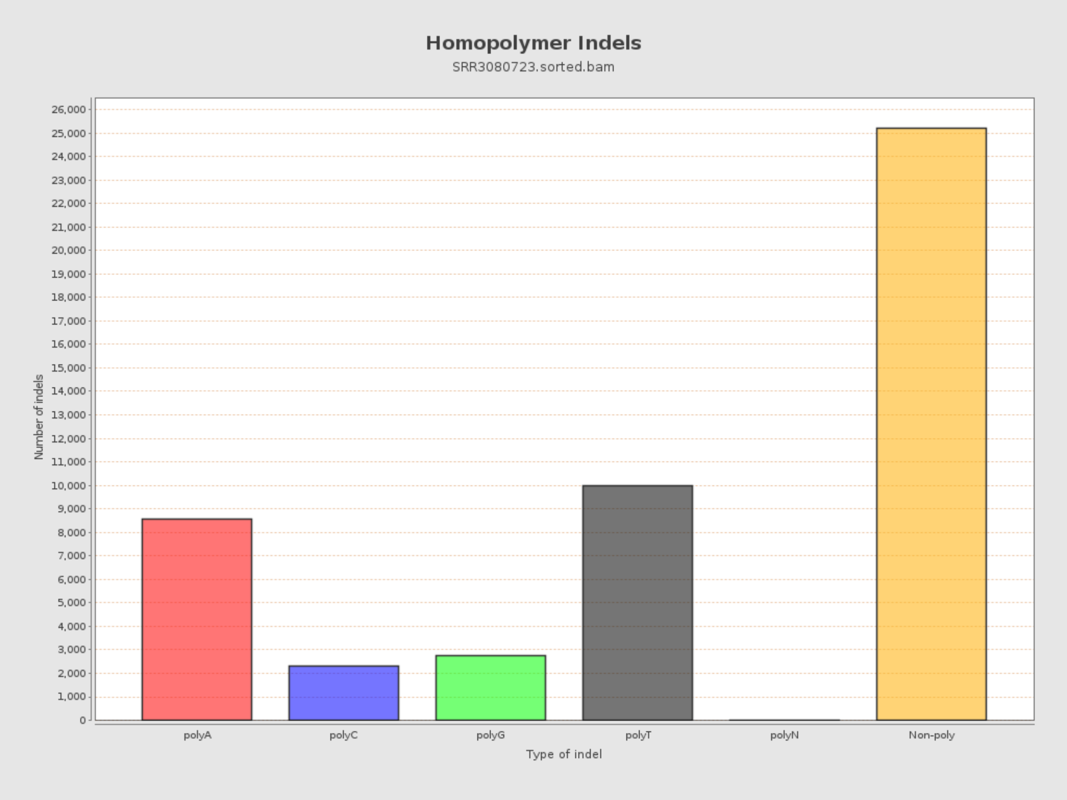
9. Results : Mapped Reads GC-content Distribution



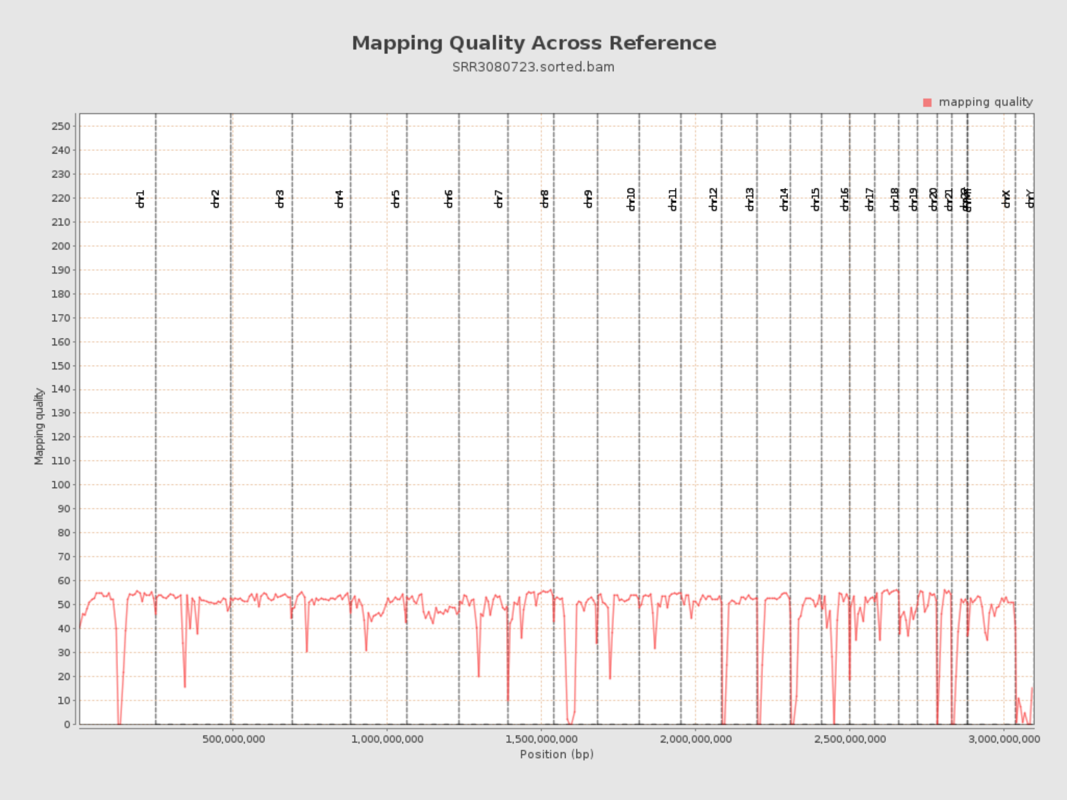
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram