Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:24:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080757.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_SRR3080757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080757.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:24:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,342,984
Mapped reads	4,564,757 / 71.97%
Unmapped reads	1,778,227 / 28.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,258 / 0.67%
Read min/max/mean length	30 / 66 / 66.22
Duplicated reads (estimated)	298,402 / 4.7%
Duplication rate	5.4%
Clipped reads	915,549 / 14.43%

2.2. ACGT Content

Number/percentage of A's	88,952,614 / 30.92%
Number/percentage of C's	57,739,100 / 20.07%
Number/percentage of T's	73,933,213 / 25.7%
Number/percentage of G's	66,922,556 / 23.27%
Number/percentage of N's	98,530 / 0.03%
GC Percentage	43.34%

2.3. Coverage

Mean	0.093

Standard Deviation	0.6113

2.4. Mapping Quality

Mean Mapping Quality	43.13

2.5. Mismatches and indels

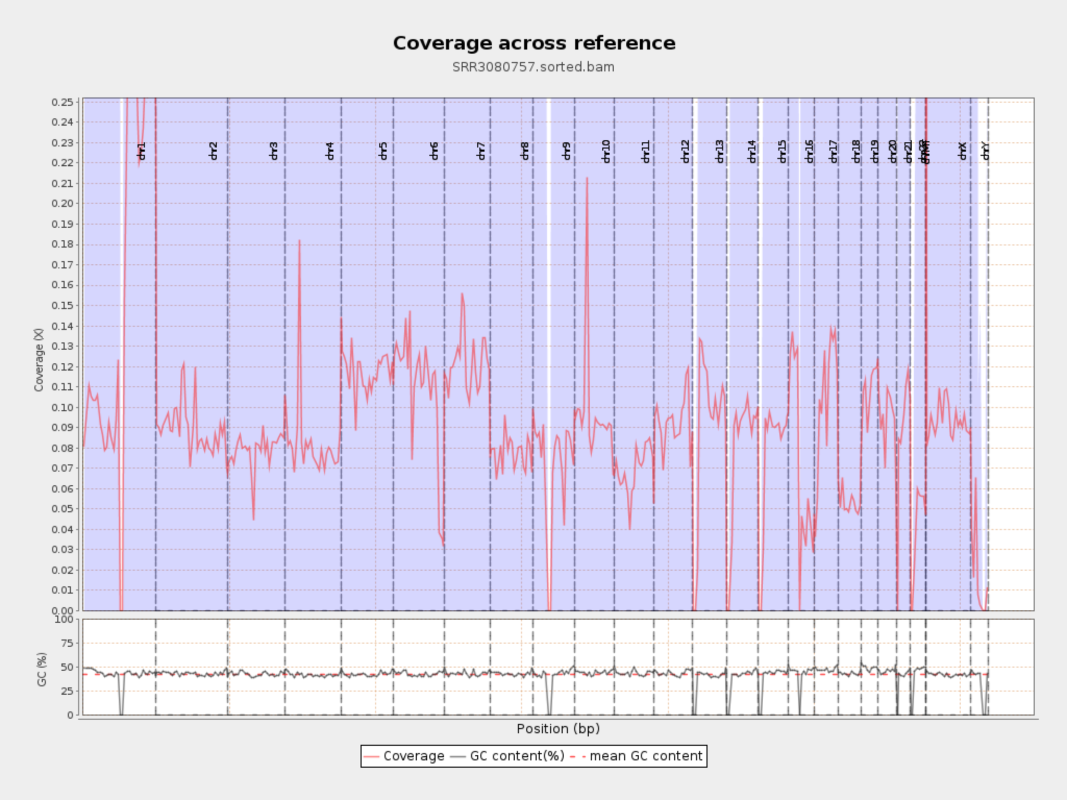
General error rate	0.85%
Mismatches	2,410,657
Insertions	23,617
Mapped reads with at least one insertion	0.51%
Deletions	54,050
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.08%

2.6. Chromosome stats

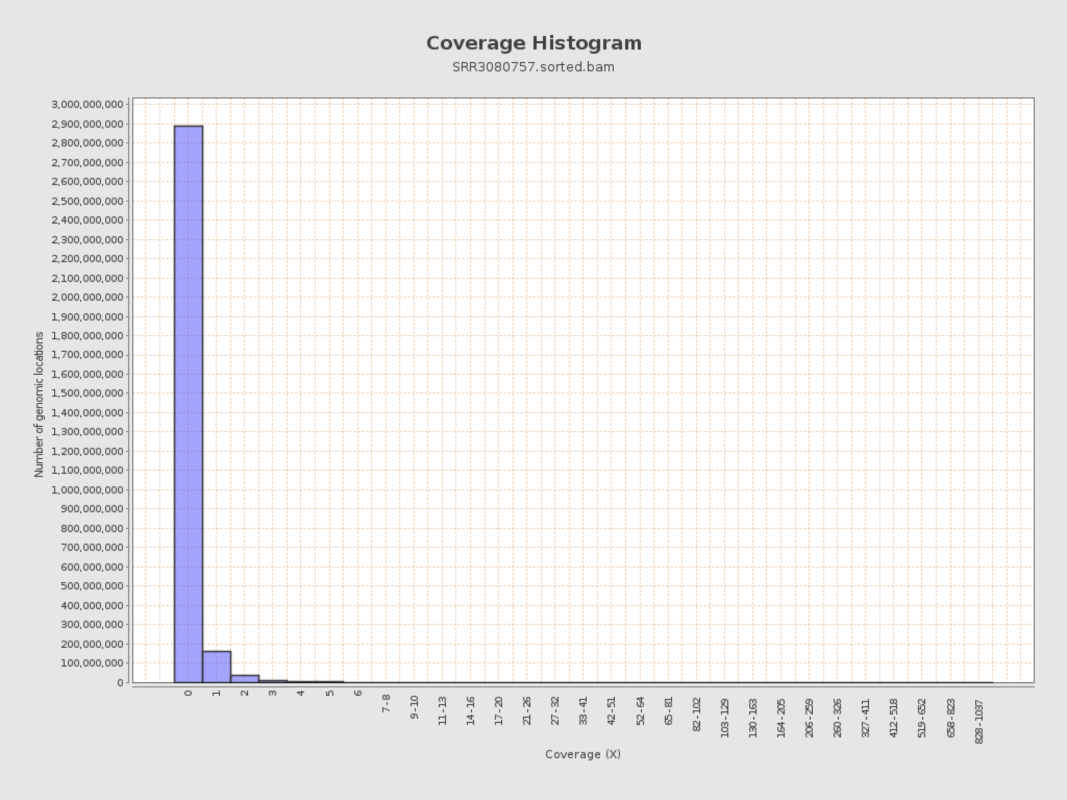
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39235902	0.1574	0.8633
chr2	243199373	21890025	0.09	0.6433
chr3	198022430	15614186	0.0789	0.3662
chr4	191154276	15803718	0.0827	0.5538
chr5	180915260	21203524	0.1172	0.4558
chr6	171115067	18760456	0.1096	0.7417
chr7	159138663	19460954	0.1223	0.9054

chr8	146364022	11302596	0.0772	0.5485
chr9	141213431	9831114	0.0696	0.4329
chr10	135534747	13204680	0.0974	1.0915
chr11	135006516	9311270	0.069	0.4367
chr12	133851895	12491879	0.0933	0.4117
chr13	115169878	10447718	0.0907	0.4
chr14	107349540	8407625	0.0783	0.4289
chr15	102531392	7555072	0.0737	0.3542
chr16	90354753	6350285	0.0703	0.4595
chr17	81195210	8461412	0.1042	0.4889
chr18	78077248	4130608	0.0529	0.7075
chr19	59128983	6393222	0.1081	0.7344
chr20	63025520	5972131	0.0948	0.4339
chr21	48129895	4326403	0.0899	0.5519
chr22	51304566	2030328	0.0396	0.2562
chrMT	16571	30274	1.8269	2.0312
chrX	155270560	14522329	0.0935	0.4369
chrY	59373566	1009838	0.017	0.5847

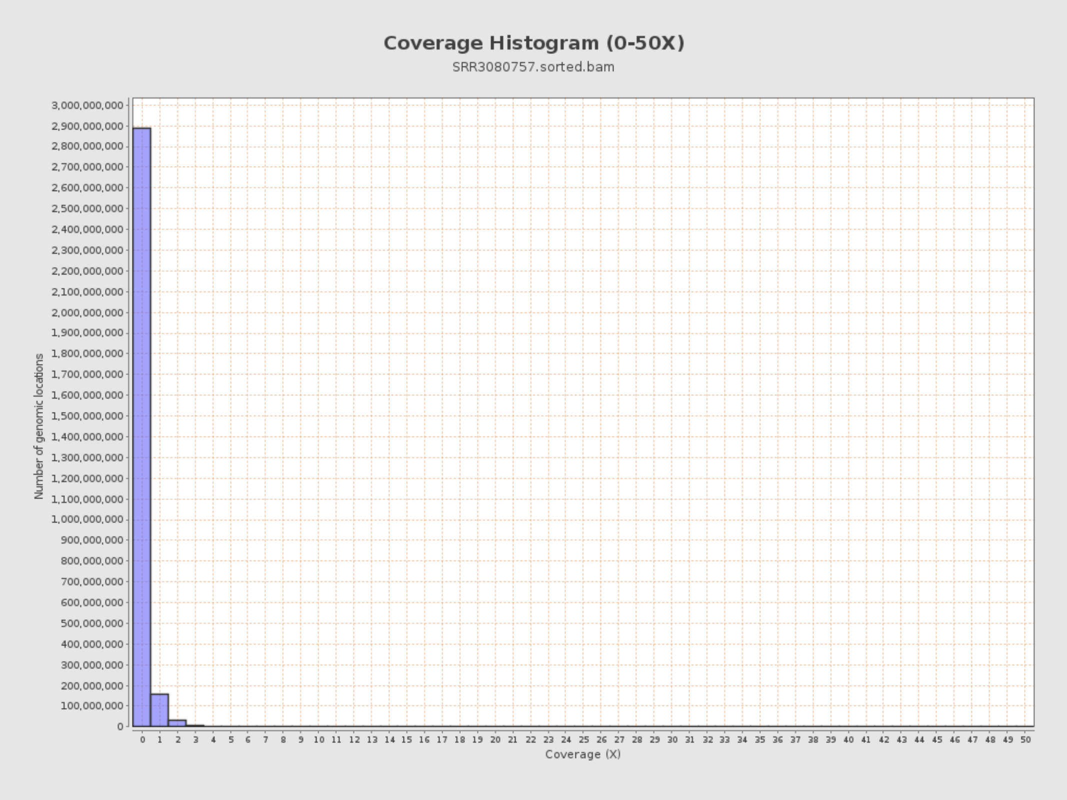
3. Results : Coverage across reference



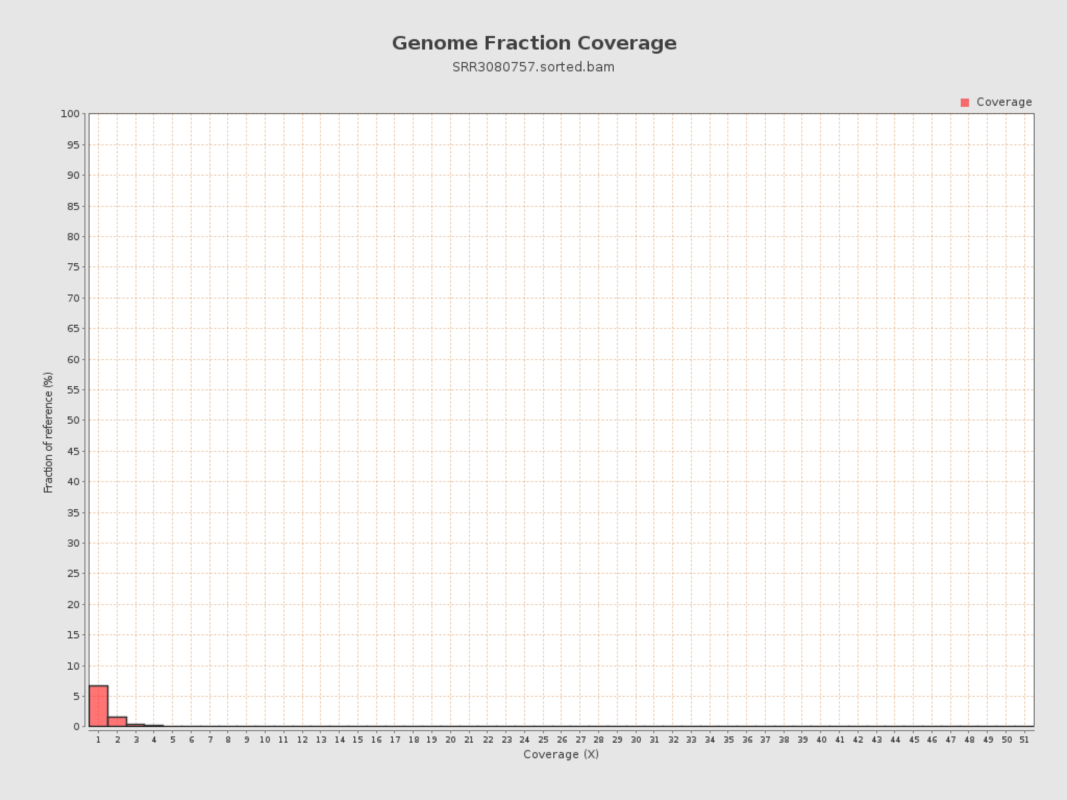
4. Results : Coverage Histogram



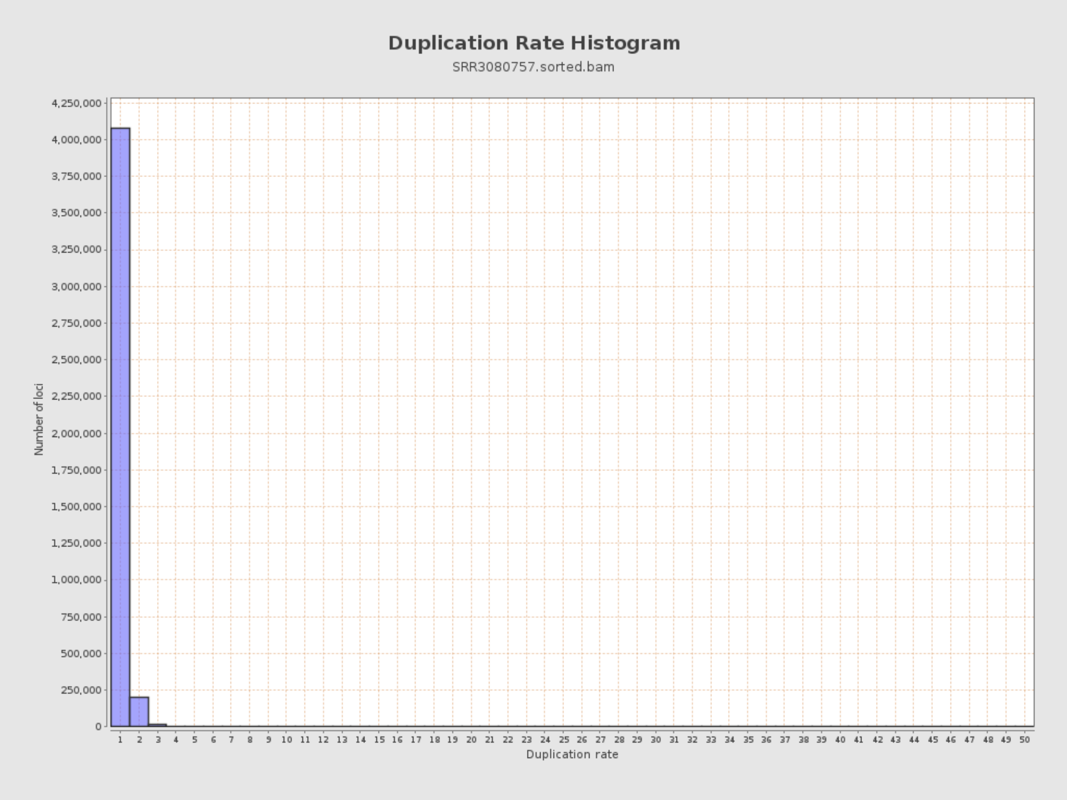
5. Results : Coverage Histogram (0-50X)



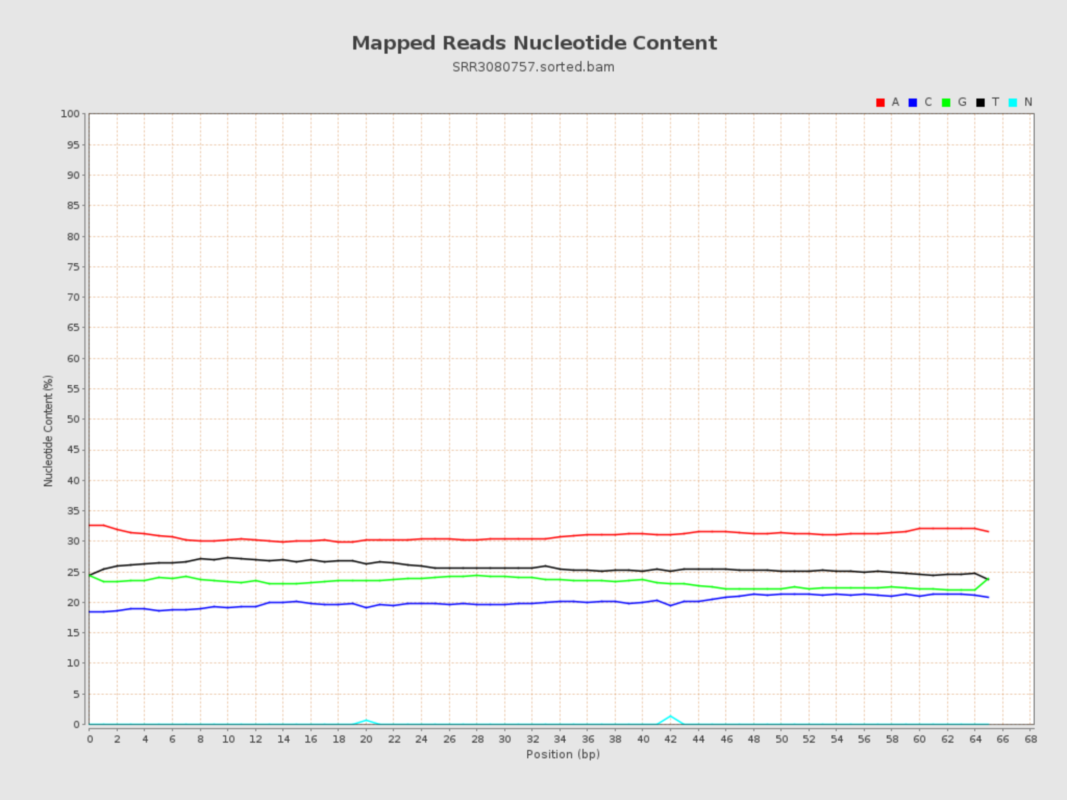
6. Results : Genome Fraction Coverage



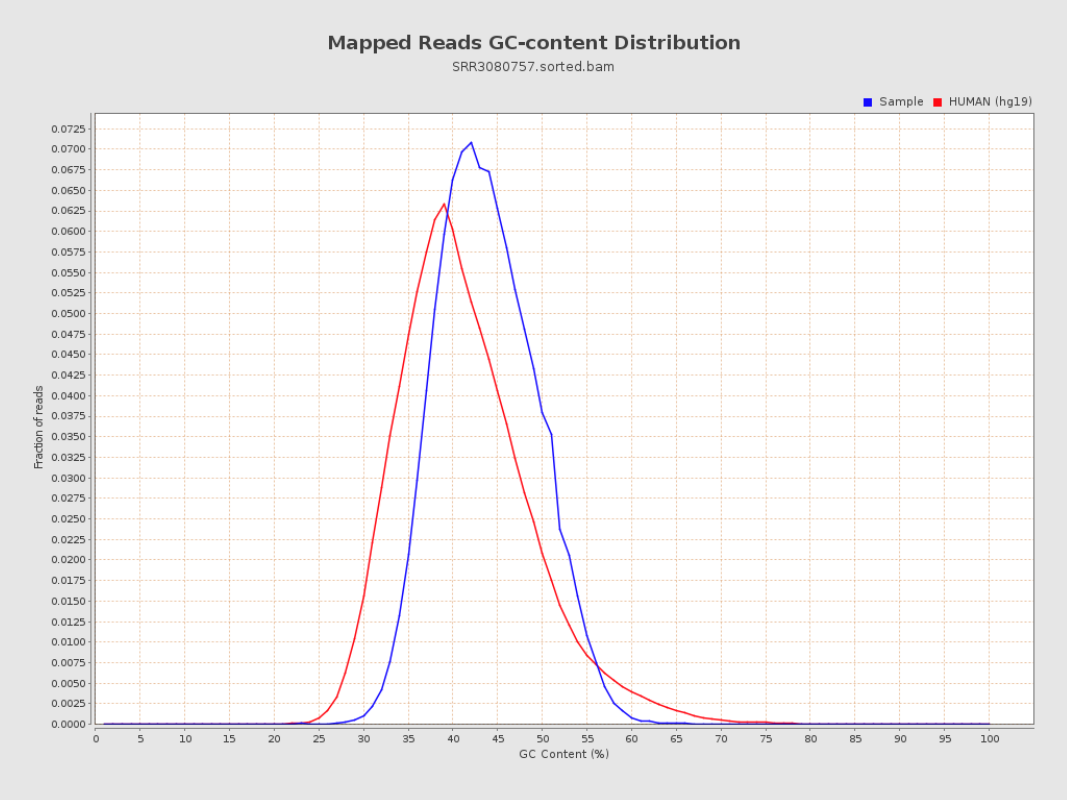
7. Results : Duplication Rate Histogram



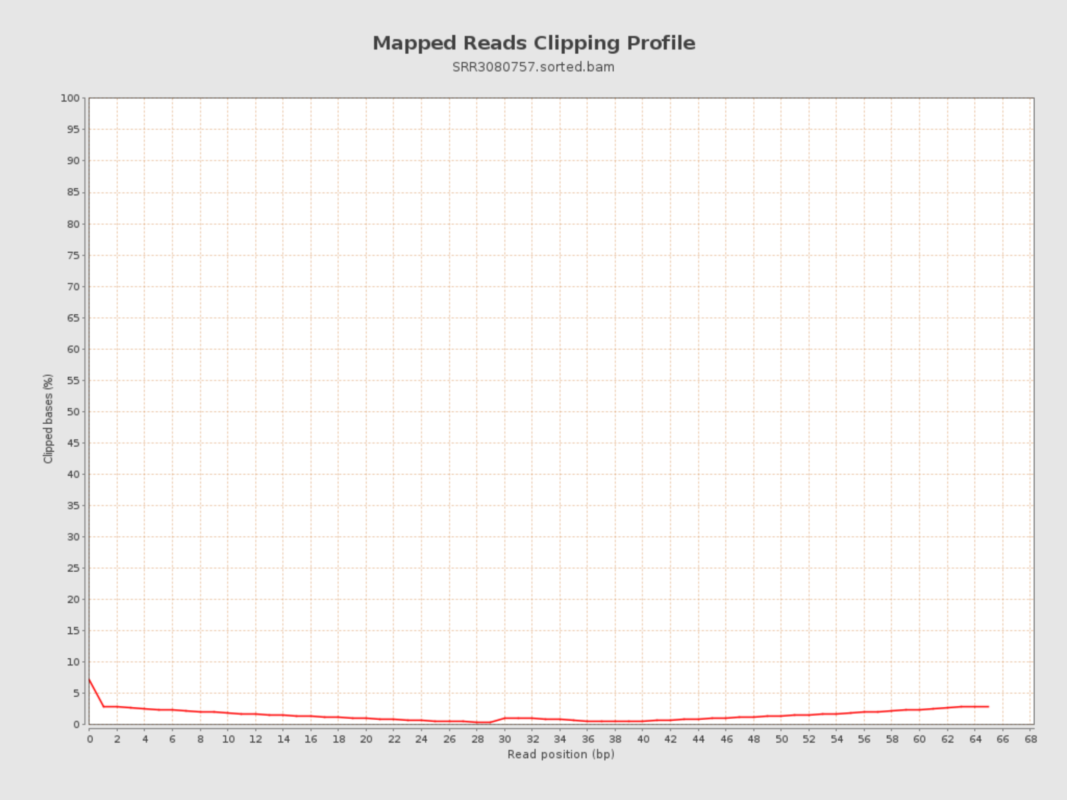
8. Results : Mapped Reads Nucleotide Content



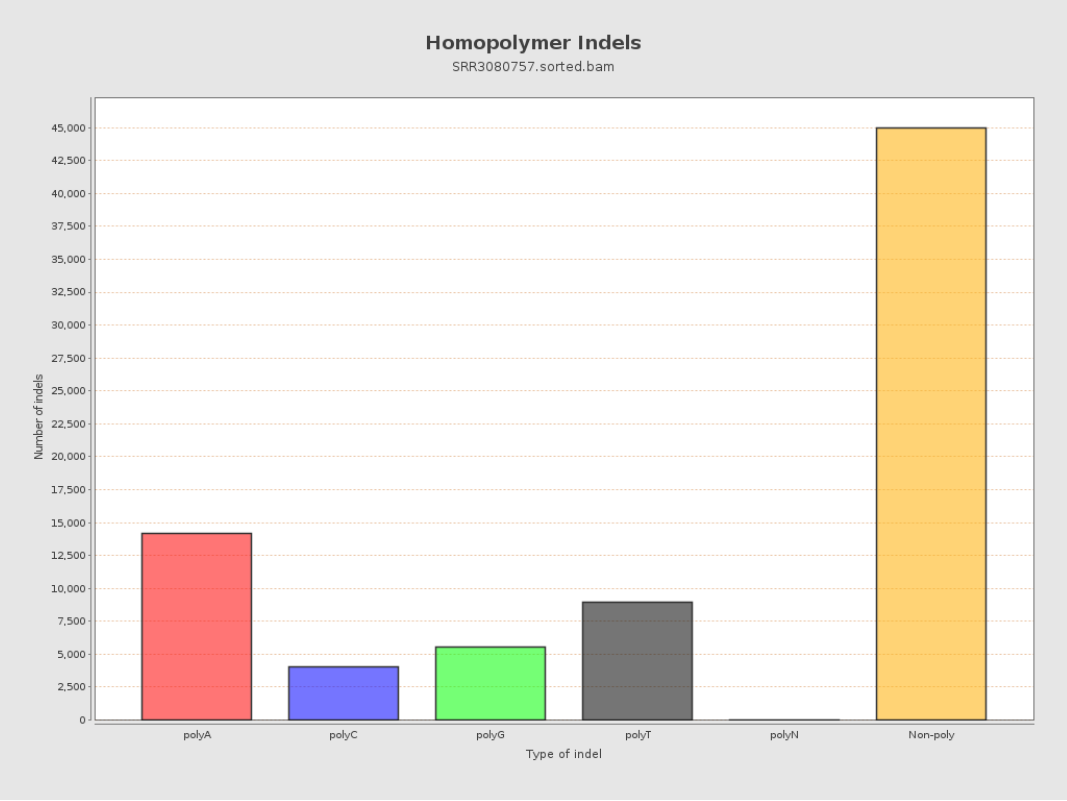
9. Results : Mapped Reads GC-content Distribution



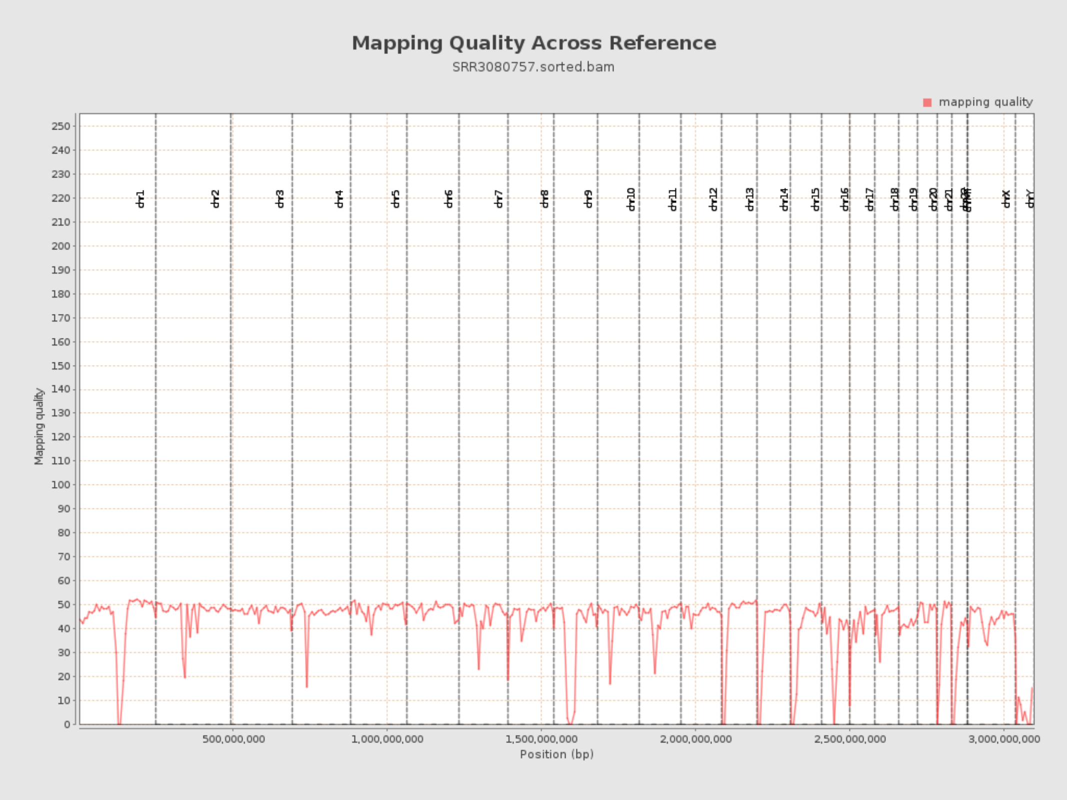
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram