Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:16:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013257.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_SRR6013257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013257.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:16:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,075,344
Mapped reads	1,260,018 / 60.71%
Unmapped reads	815,326 / 39.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,549 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	76,922 / 3.71%
Duplication rate	5.04%
Clipped reads	915,927 / 44.13%

2.2. ACGT Content

Number/percentage of A's	20,175,780 / 27.37%
Number/percentage of C's	12,257,010 / 16.63%
Number/percentage of T's	23,490,435 / 31.87%
Number/percentage of G's	17,767,548 / 24.1%
Number/percentage of N's	23,983 / 0.03%
GC Percentage	40.73%

2.3. Coverage

Mean	0.0238

Standard Deviation	0.2152

2.4. Mapping Quality

Mean Mapping Quality	43.9

2.5. Mismatches and indels

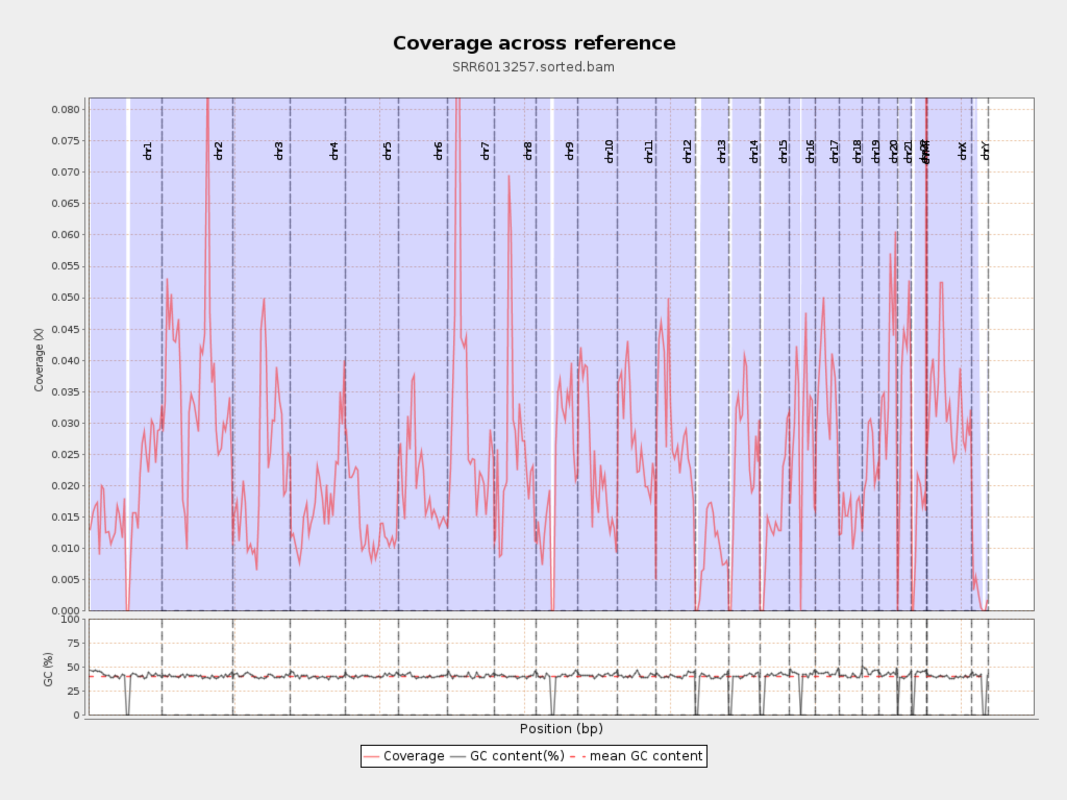
General error rate	1.06%
Mismatches	773,302
Insertions	4,792
Mapped reads with at least one insertion	0.38%
Deletions	20,557
Mapped reads with at least one deletion	1.62%
Homopolymer indels	47.64%

2.6. Chromosome stats

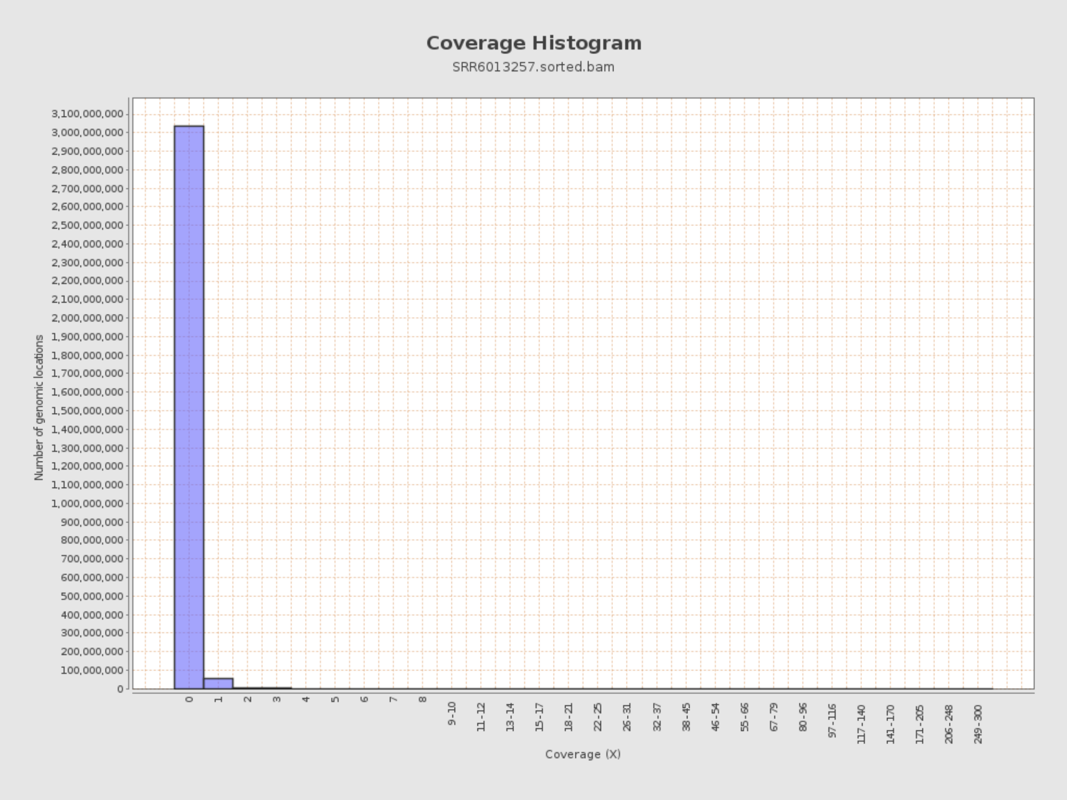
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4317245	0.0173	0.2382
chr2	243199373	8778459	0.0361	0.2772
chr3	198022430	4489335	0.0227	0.1734
chr4	191154276	3417911	0.0179	0.1551
chr5	180915260	2590221	0.0143	0.1392
chr6	171115067	3527209	0.0206	0.2083
chr7	159138663	5415057	0.034	0.3646

chr8	146364022	3789361	0.0259	0.2301
chr9	141213431	3083248	0.0218	0.2
chr10	135534747	3243436	0.0239	0.2064
chr11	135006516	3717156	0.0275	0.2059
chr12	133851895	3999068	0.0299	0.2014
chr13	115169878	1079411	0.0094	0.1112
chr14	107349540	2604879	0.0243	0.1855
chr15	102531392	1473205	0.0144	0.1407
chr16	90354753	2566681	0.0284	0.2011
chr17	81195210	2892700	0.0356	0.2445
chr18	78077248	1178302	0.0151	0.221
chr19	59128983	1415574	0.0239	0.2221
chr20	63025520	2461613	0.0391	0.2353
chr21	48129895	1684956	0.035	0.2251
chr22	51304566	686899	0.0134	0.1324
chrMT	16571	6452	0.3894	0.7473
chrX	155270560	5170683	0.0333	0.2266
chrY	59373566	159111	0.0027	0.0597

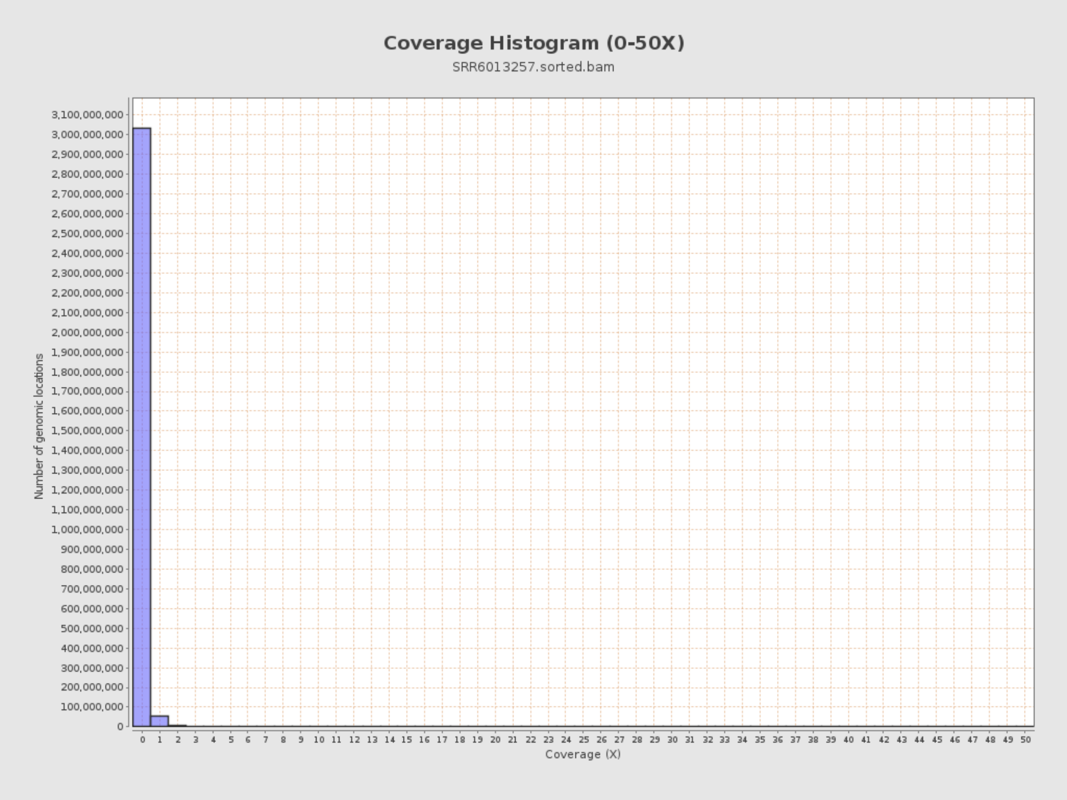
3. Results : Coverage across reference



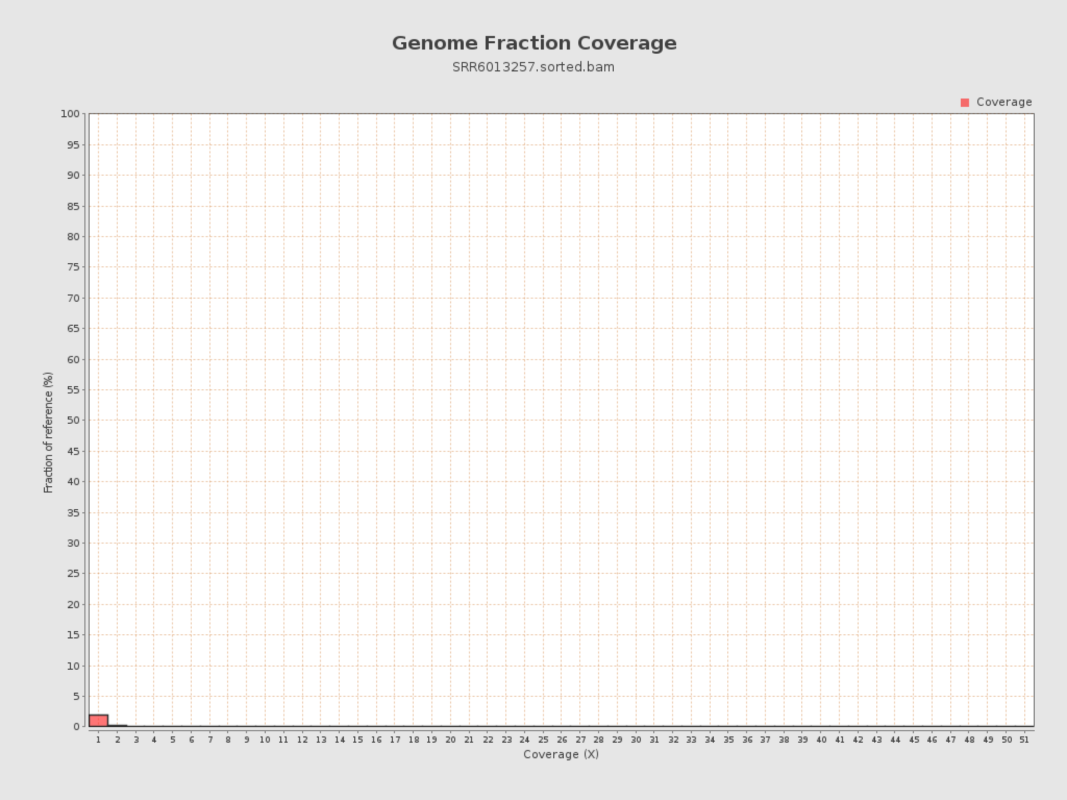
4. Results : Coverage Histogram



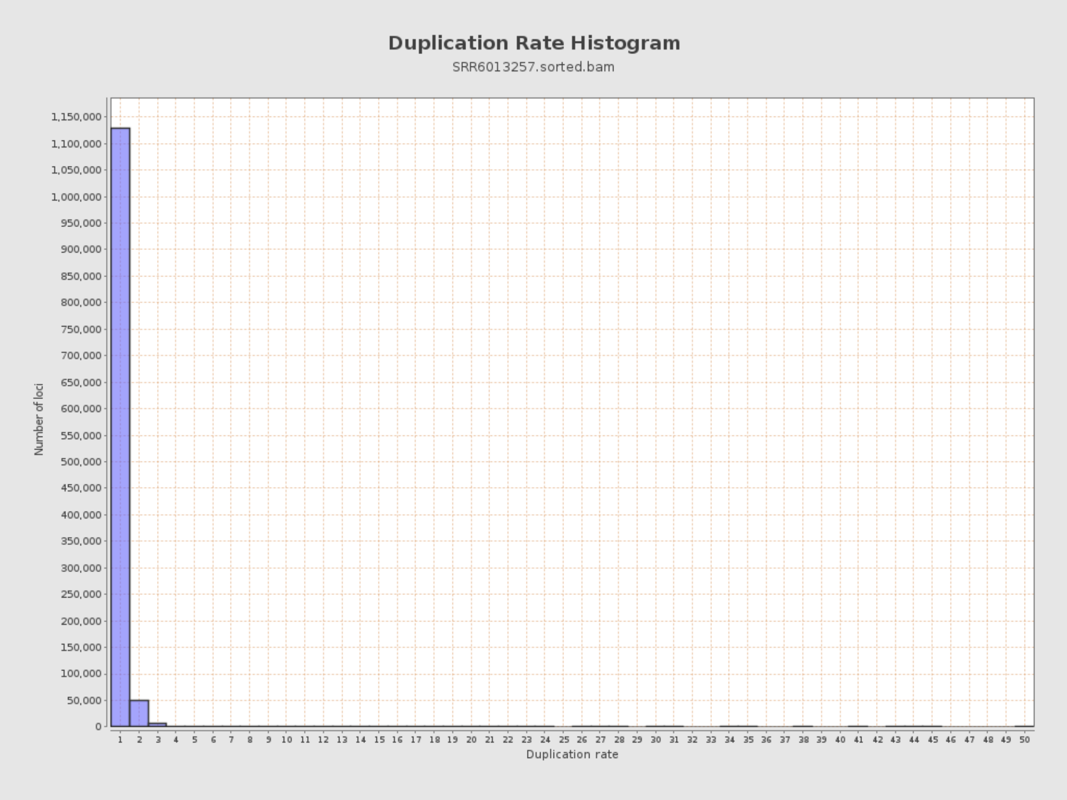
5. Results : Coverage Histogram (0-50X)



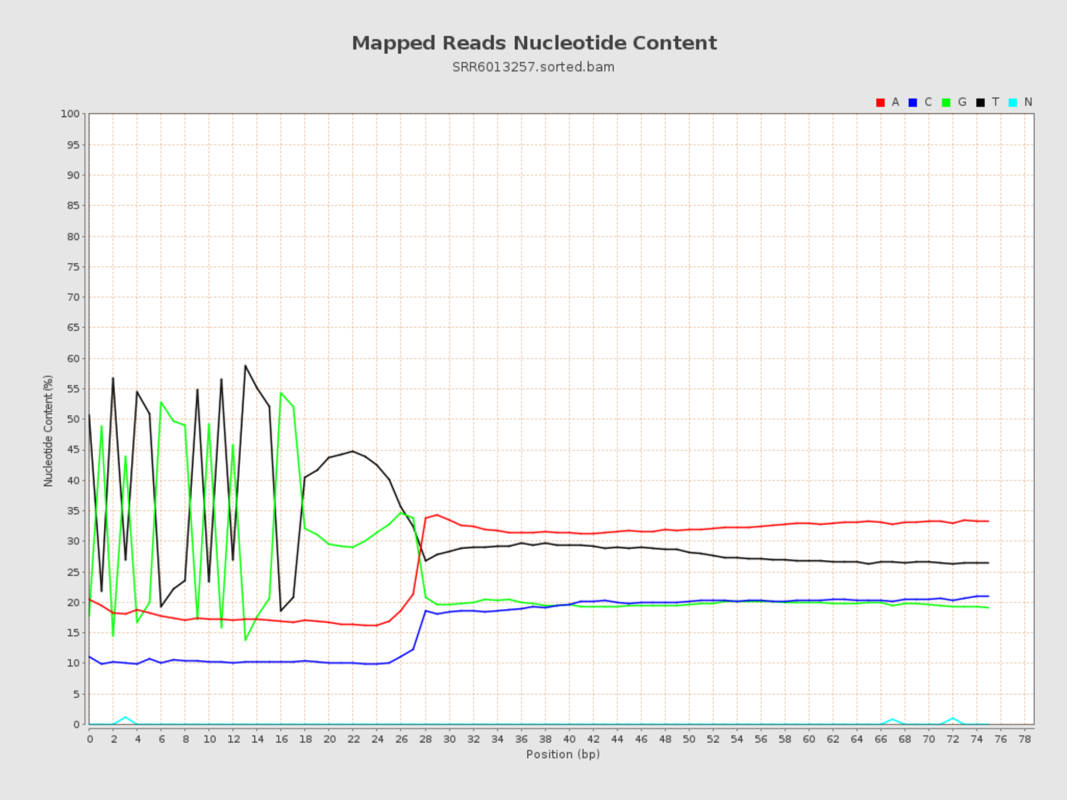
6. Results : Genome Fraction Coverage



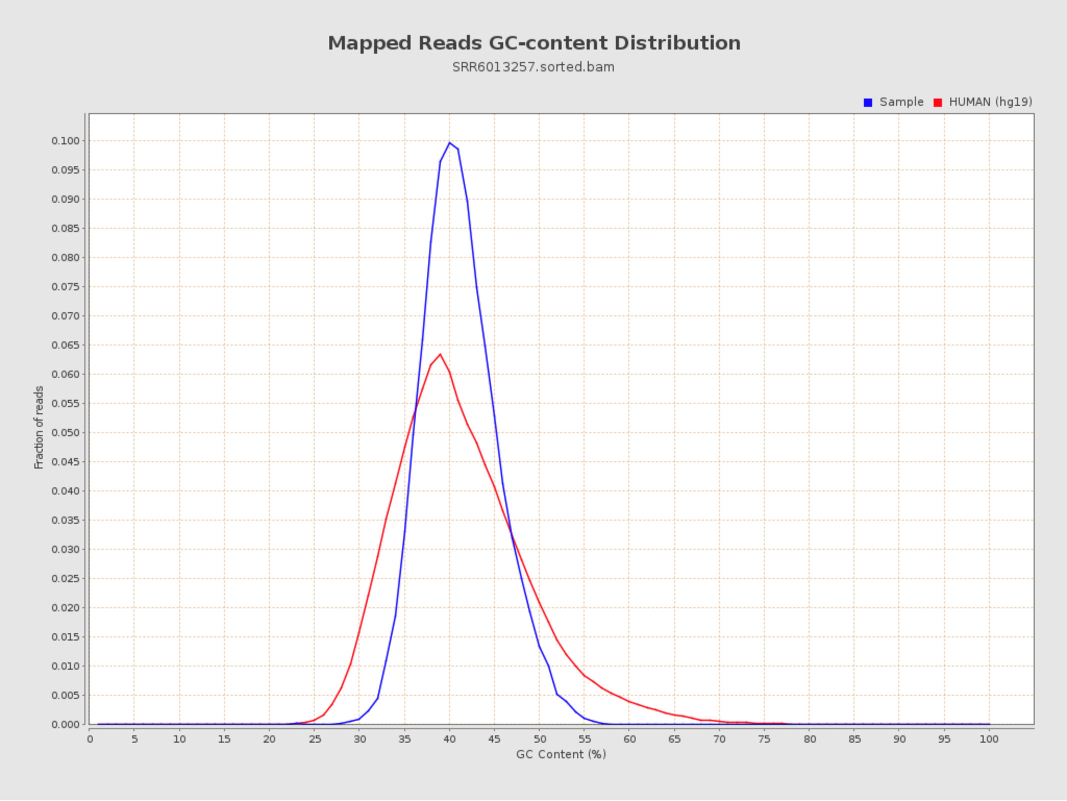
7. Results : Duplication Rate Histogram



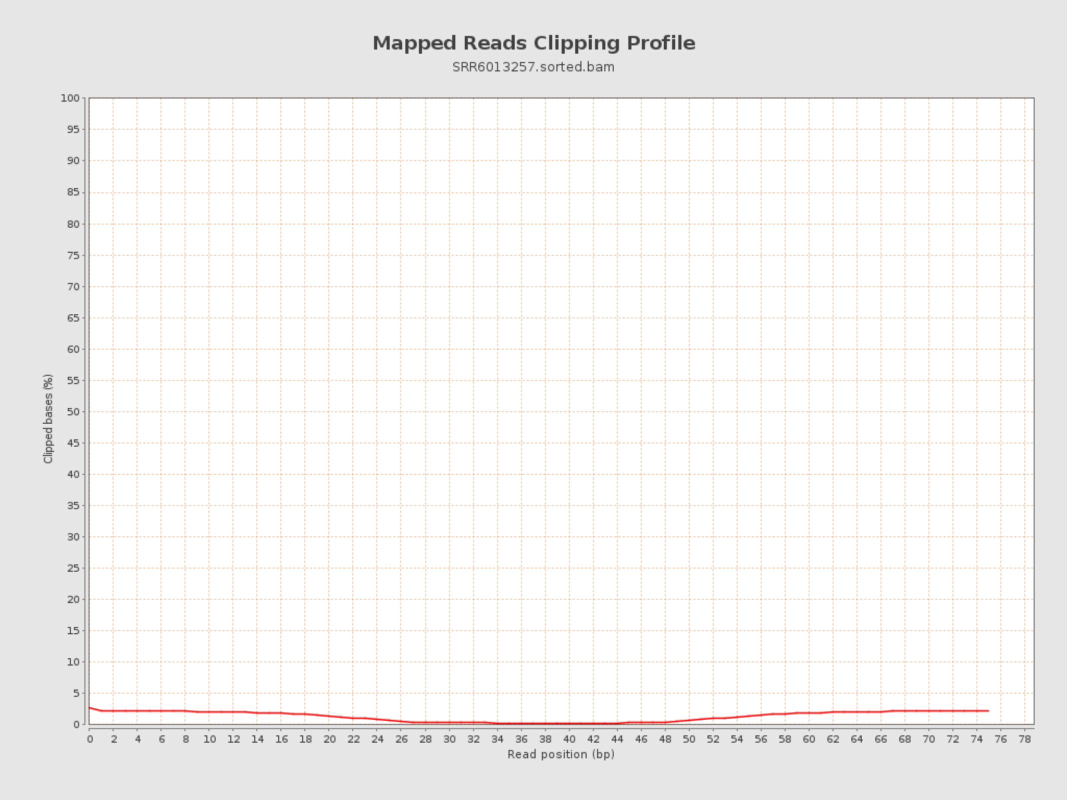
8. Results : Mapped Reads Nucleotide Content



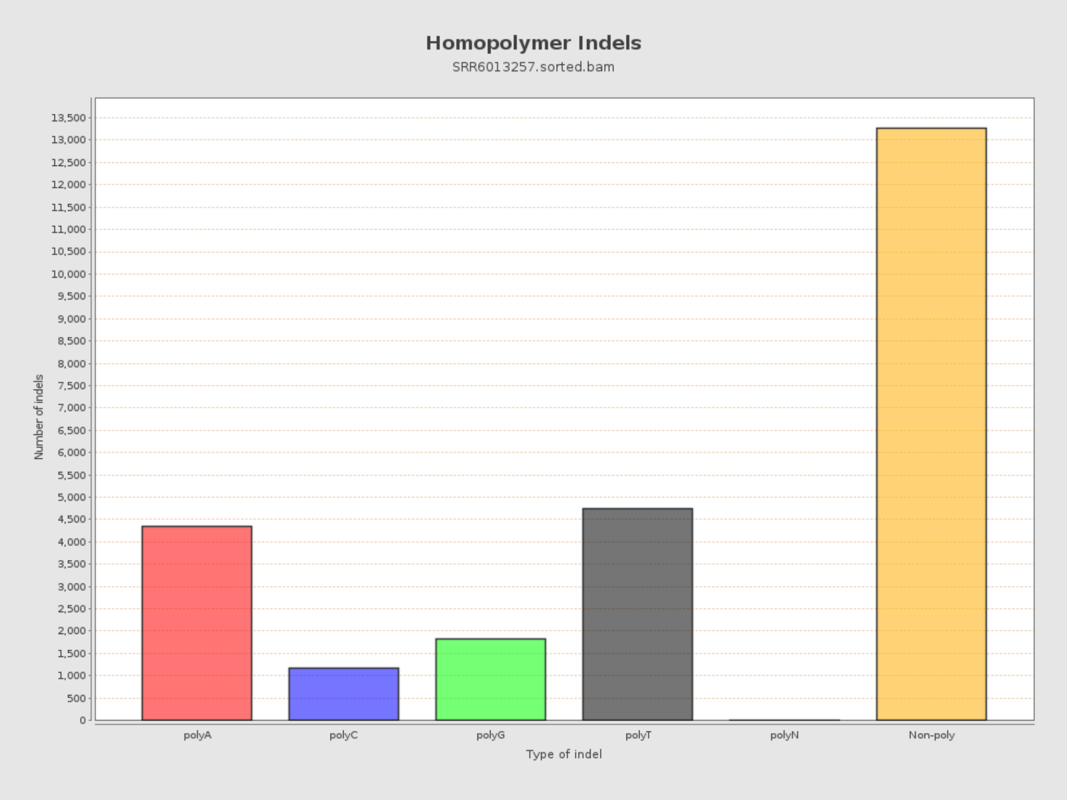
9. Results : Mapped Reads GC-content Distribution



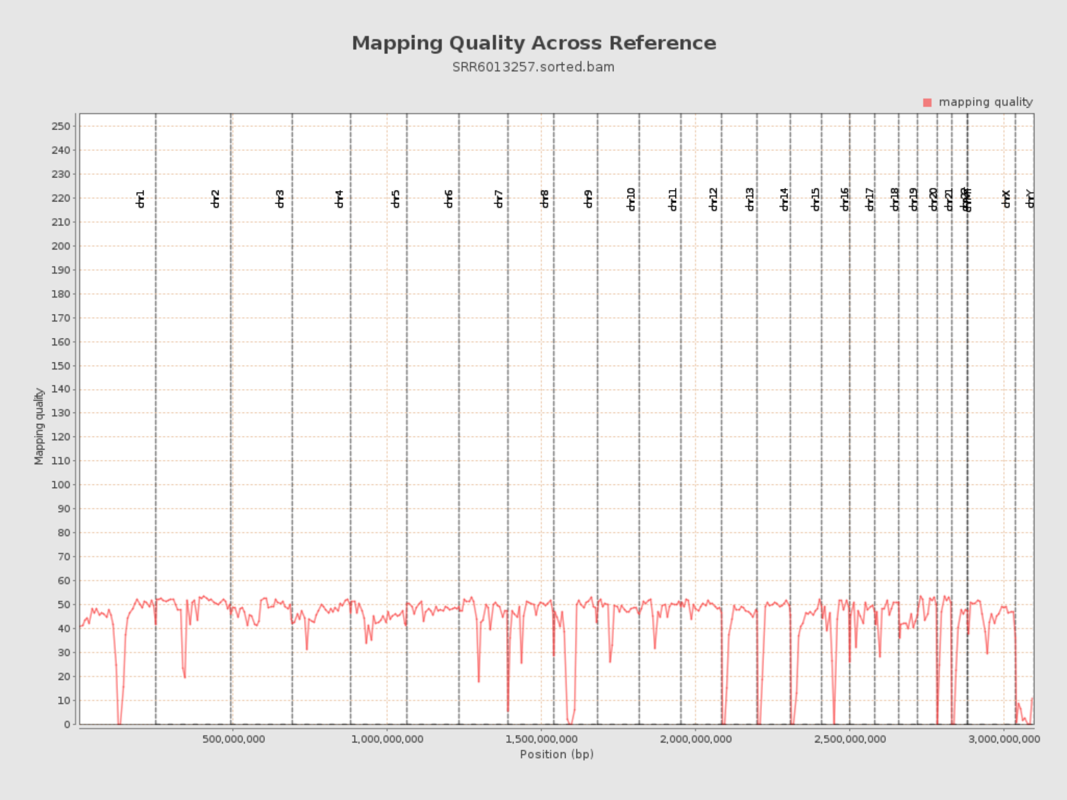
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram