Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:09:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013254.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_SRR6013254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013254.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:09:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,169,729
Mapped reads	1,939,351 / 89.38%
Unmapped reads	230,378 / 10.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,849 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	91,726 / 4.23%
Duplication rate	3.66%
Clipped reads	814,598 / 37.54%

2.2. ACGT Content

Number/percentage of A's	36,441,214 / 27.96%
Number/percentage of C's	23,858,439 / 18.31%
Number/percentage of T's	41,588,622 / 31.91%
Number/percentage of G's	28,442,748 / 21.82%
Number/percentage of N's	1,790 / 0%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0421

Standard Deviation	0.3686

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

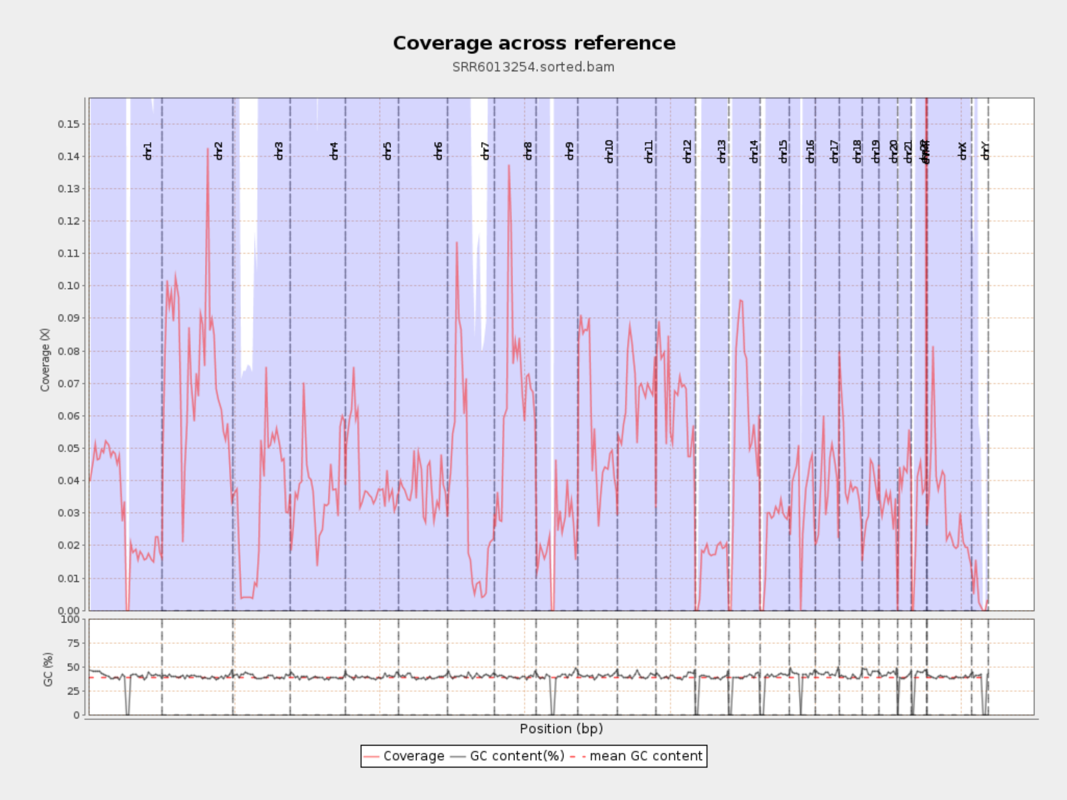
General error rate	0.74%
Mismatches	941,854
Insertions	9,842
Mapped reads with at least one insertion	0.5%
Deletions	35,273
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.6%

2.6. Chromosome stats

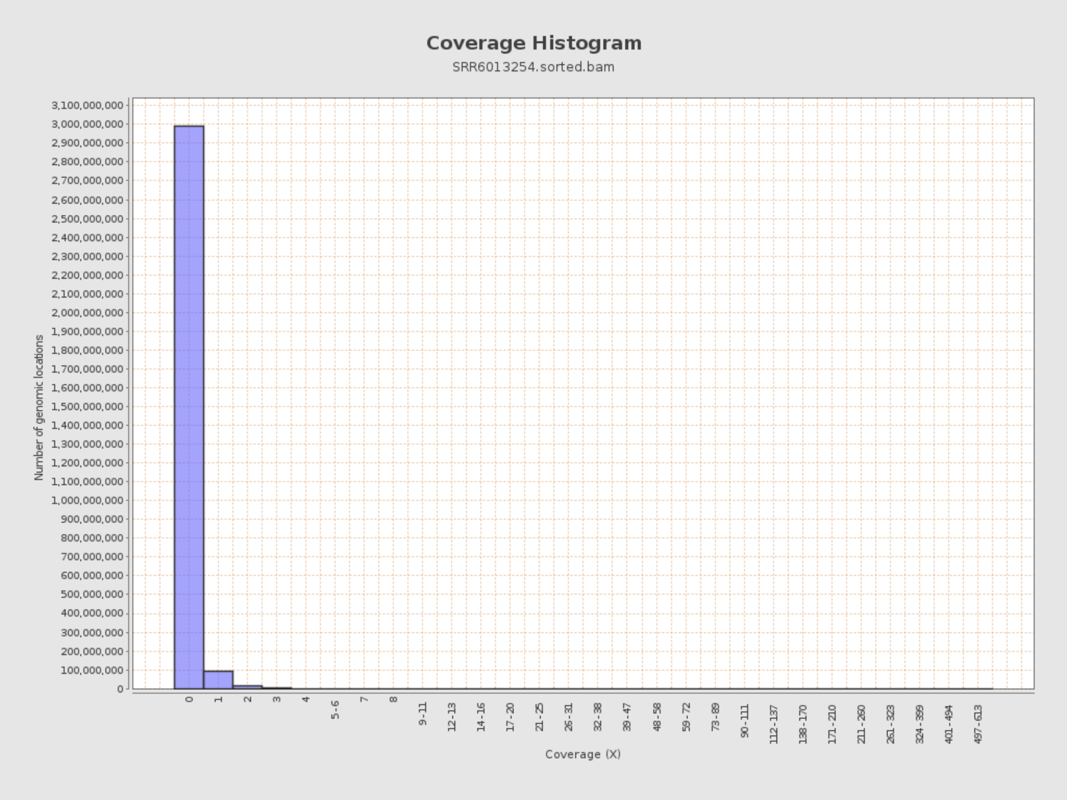
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7633227	0.0306	0.3963
chr2	243199373	18055209	0.0742	0.5076
chr3	198022430	6254484	0.0316	0.2075
chr4	191154276	7187614	0.0376	0.2599
chr5	180915260	7580914	0.0419	0.2408
chr6	171115067	6449514	0.0377	0.2879
chr7	159138663	5706447	0.0359	0.5584

chr8	146364022	9860441	0.0674	0.5117
chr9	141213431	3209403	0.0227	0.3288
chr10	135534747	7786979	0.0575	0.4376
chr11	135006516	9030700	0.0669	0.541
chr12	133851895	8836814	0.066	0.3032
chr13	115169878	1799568	0.0156	0.1453
chr14	107349540	6192833	0.0577	0.2905
chr15	102531392	2498939	0.0244	0.1899
chr16	90354753	3221289	0.0357	0.2492
chr17	81195210	3157633	0.0389	0.2975
chr18	78077248	3376702	0.0432	0.6885
chr19	59128983	2036908	0.0344	0.3361
chr20	63025520	2007537	0.0319	0.2145
chr21	48129895	1938387	0.0403	0.2564
chr22	51304566	1456588	0.0284	0.1929
chrMT	16571	14143	0.8535	1.2943
chrX	155270560	4839885	0.0312	0.2558
chrY	59373566	261419	0.0044	0.1271

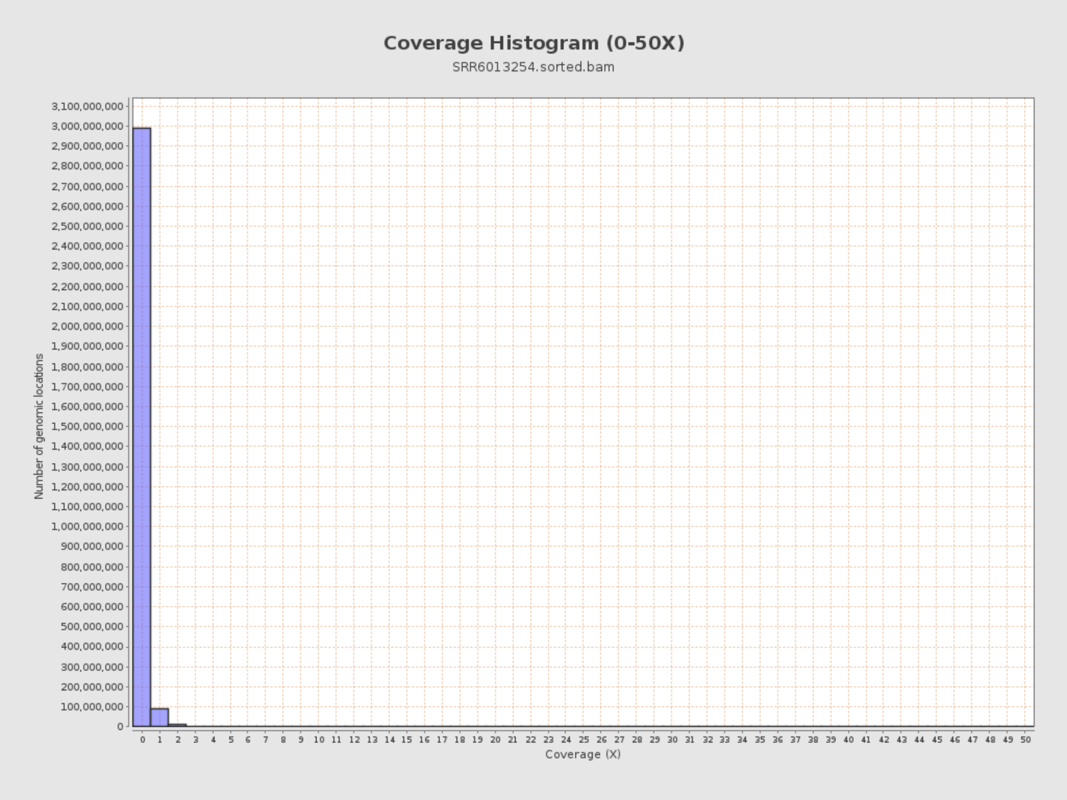
3. Results : Coverage across reference



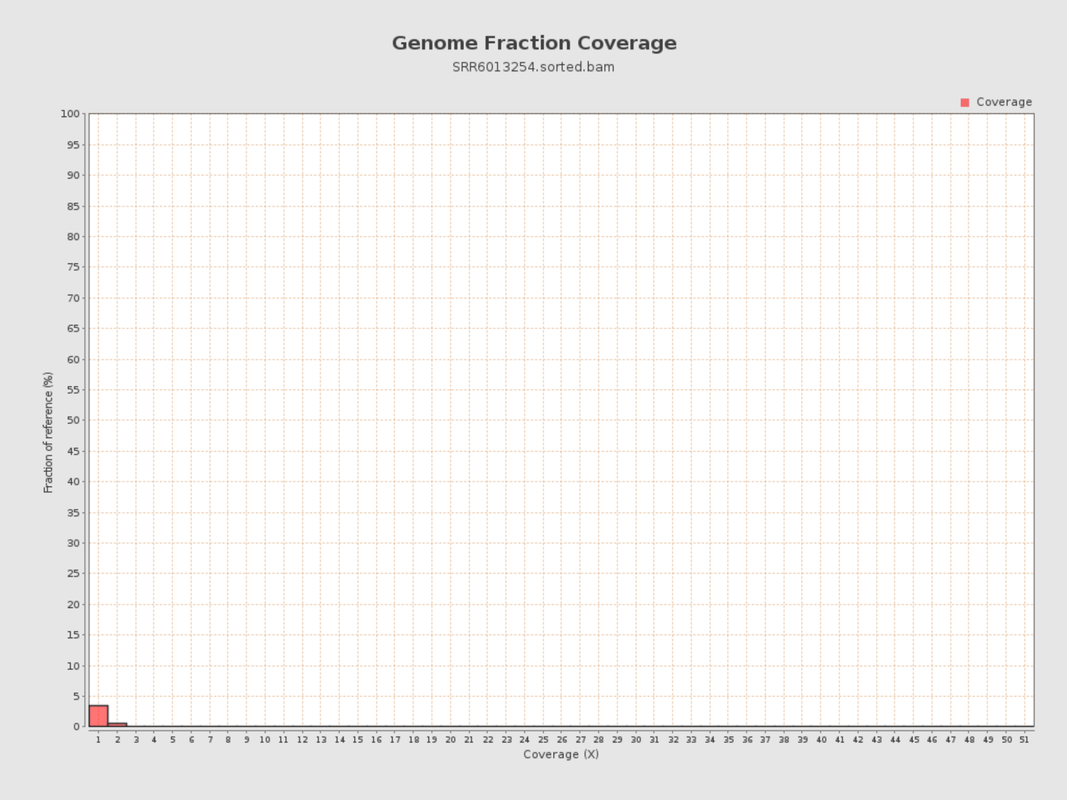
4. Results : Coverage Histogram



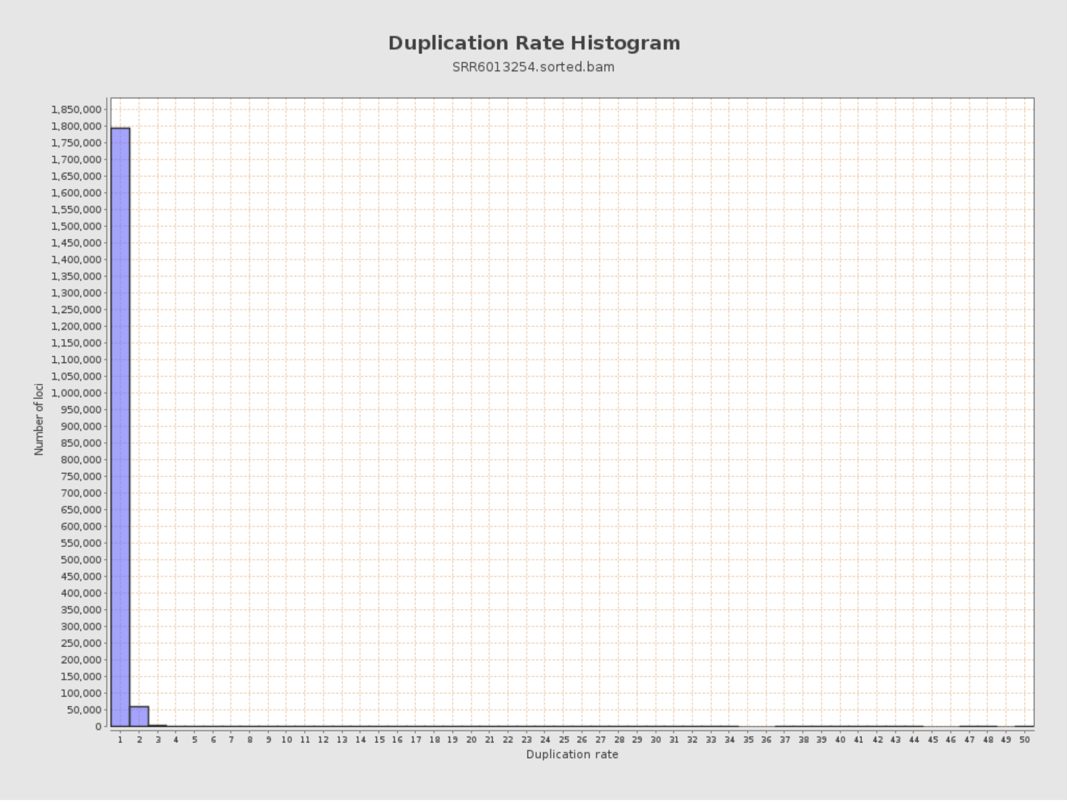
5. Results : Coverage Histogram (0-50X)



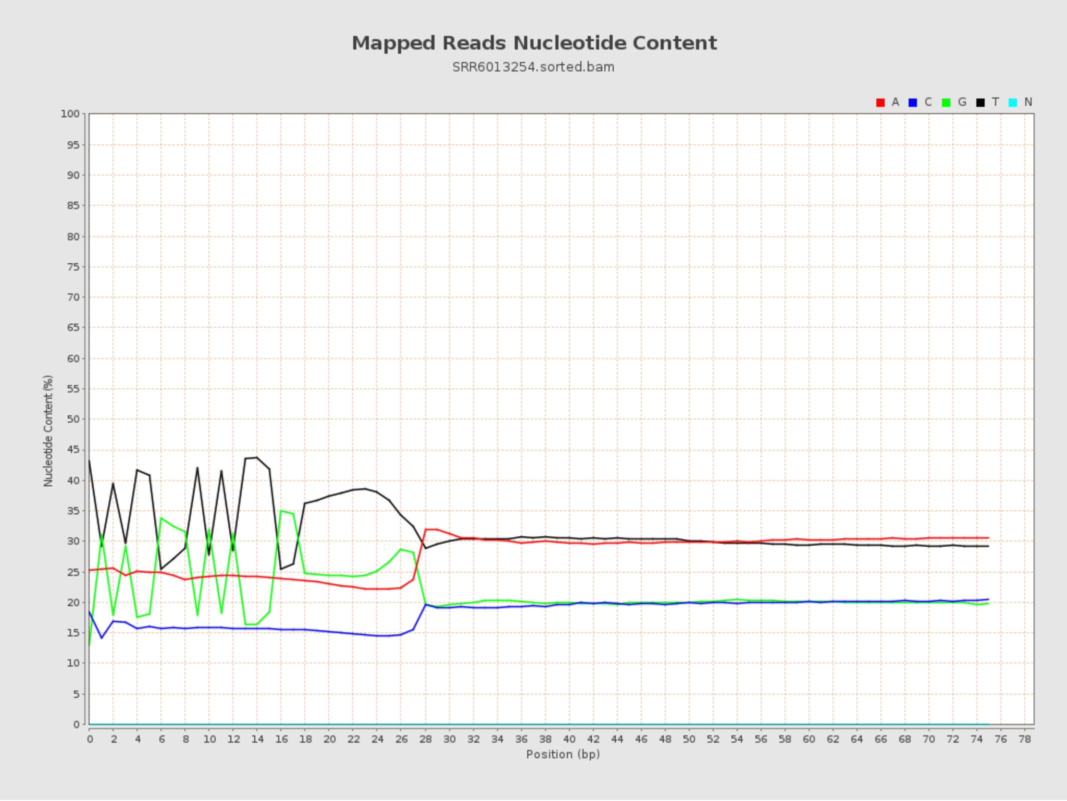
6. Results : Genome Fraction Coverage



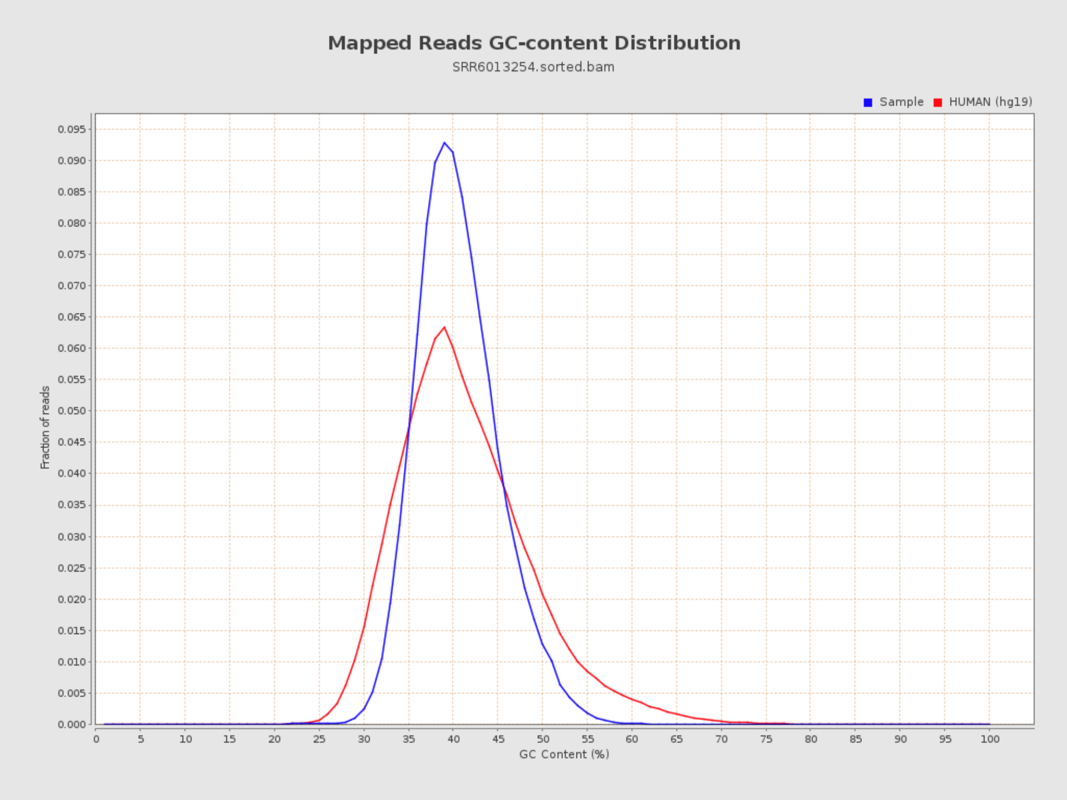
7. Results : Duplication Rate Histogram



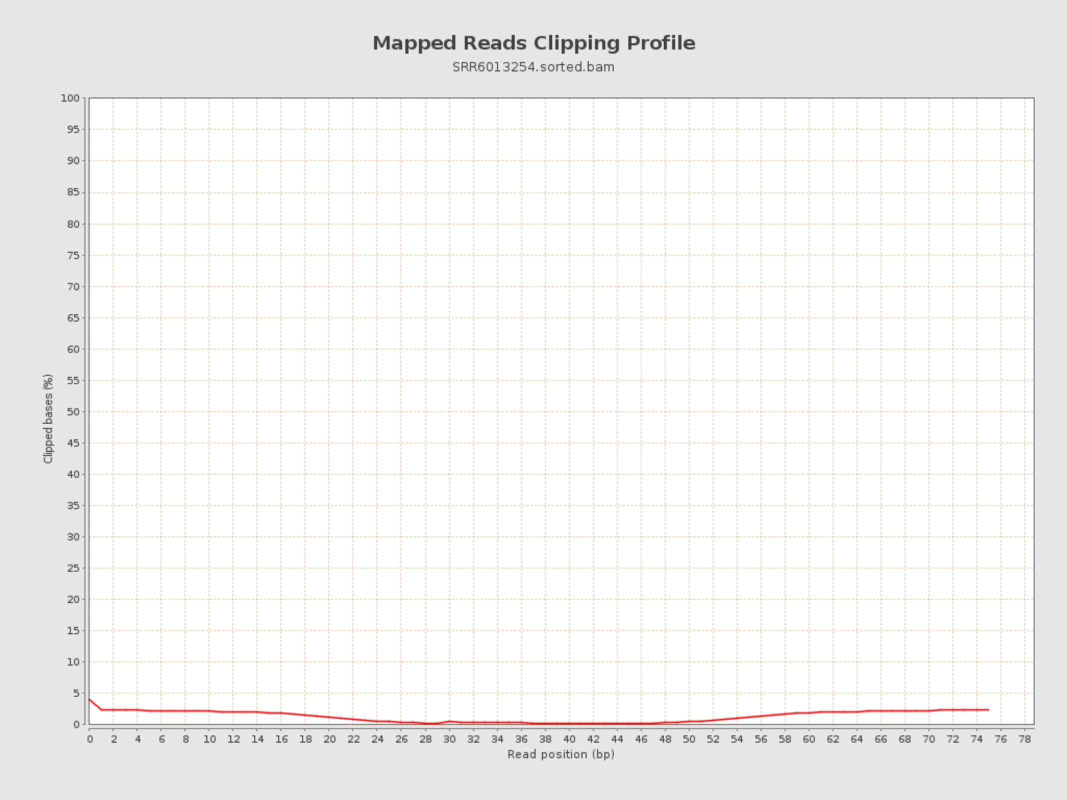
8. Results : Mapped Reads Nucleotide Content



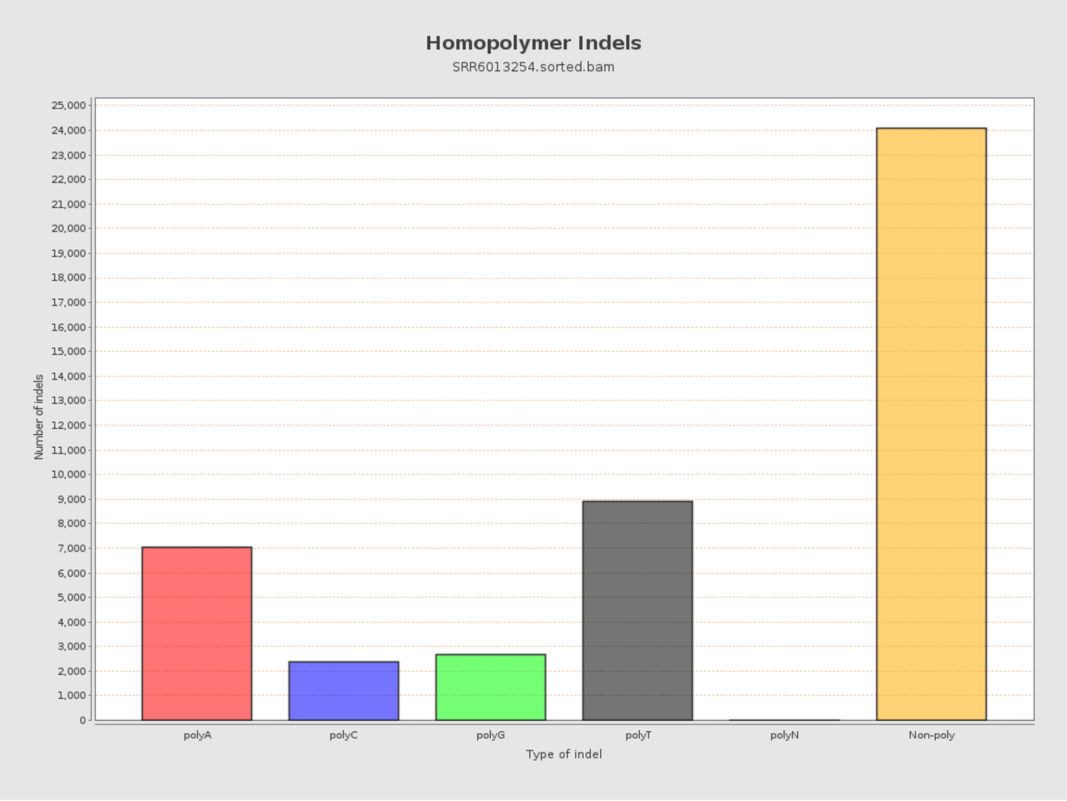
9. Results : Mapped Reads GC-content Distribution



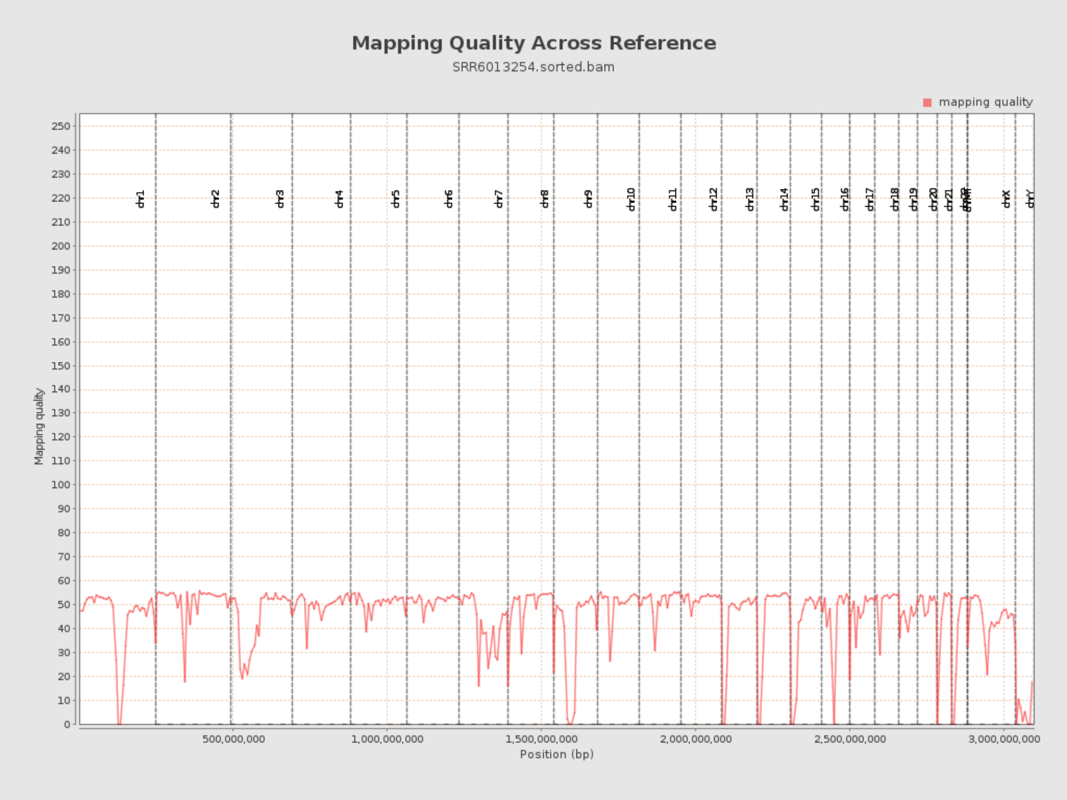
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram