Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 06:43:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212175.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_SRR3212175 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212175.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 06:43:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212175.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,714,736
Mapped reads	5,526,743 / 82.31%
Unmapped reads	1,187,993 / 17.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,412 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	349,823 / 5.21%
Duplication rate	4.49%
Clipped reads	2,960,877 / 44.1%

2.2. ACGT Content

Number/percentage of A's	100,397,228 / 28.18%
Number/percentage of C's	69,406,786 / 19.48%
Number/percentage of T's	109,300,055 / 30.68%
Number/percentage of G's	77,092,155 / 21.64%
Number/percentage of N's	86,544 / 0.02%
GC Percentage	41.12%

2.3. Coverage

Mean	0.1151

Standard Deviation	1.1017

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

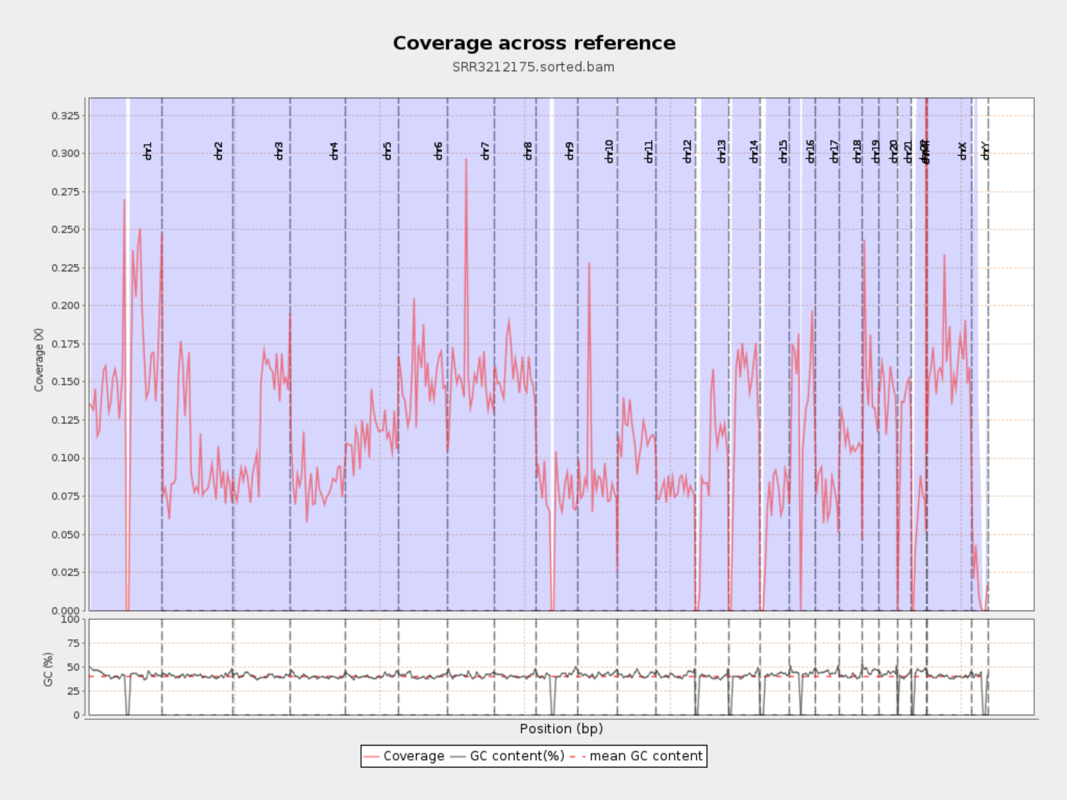
General error rate	1.12%
Mismatches	3,932,851
Insertions	26,651
Mapped reads with at least one insertion	0.48%
Deletions	79,695
Mapped reads with at least one deletion	1.43%
Homopolymer indels	45.91%

2.6. Chromosome stats

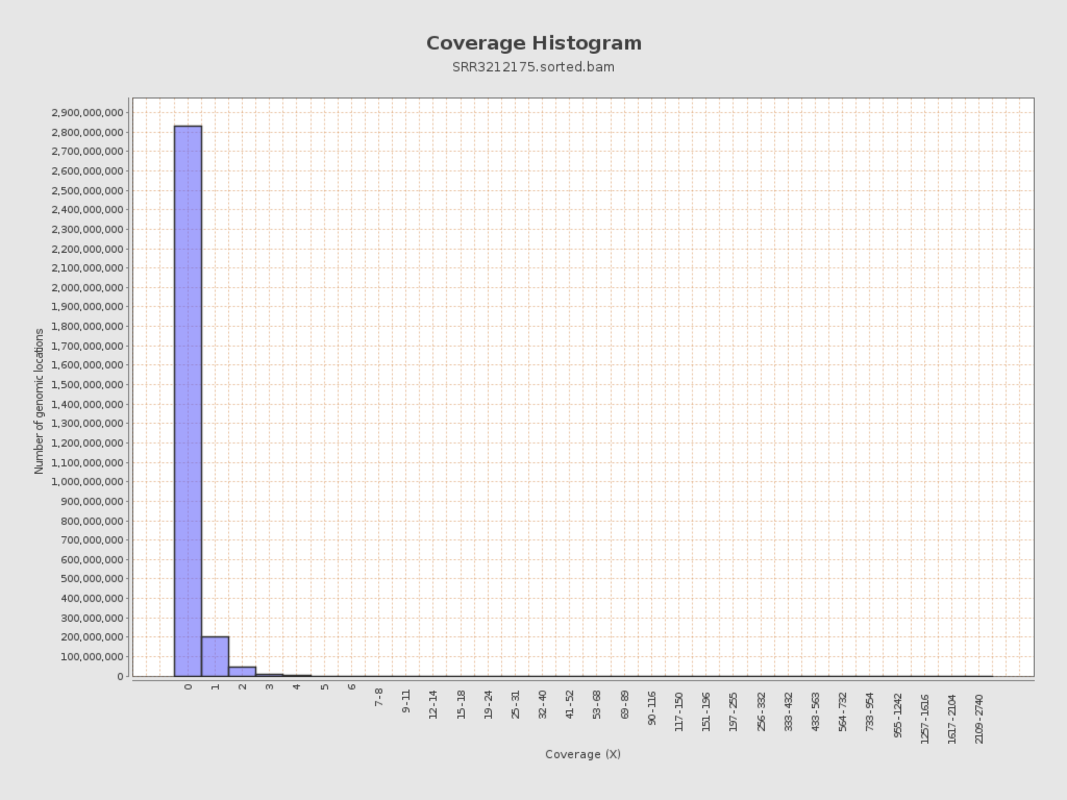
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38651322	0.1551	2.4159
chr2	243199373	23631371	0.0972	0.734
chr3	198022430	24260094	0.1225	0.4707
chr4	191154276	15858664	0.083	0.3825
chr5	180915260	20876607	0.1154	0.433
chr6	171115067	26118276	0.1526	0.7079
chr7	159138663	24721284	0.1553	2.0842

chr8	146364022	22872236	0.1563	1.5773
chr9	141213431	10068133	0.0713	0.6326
chr10	135534747	12125705	0.0895	1.271
chr11	135006516	15314913	0.1134	0.8391
chr12	133851895	10690192	0.0799	0.3856
chr13	115169878	10573502	0.0918	0.3796
chr14	107349540	14158738	0.1319	0.7418
chr15	102531392	6498959	0.0634	0.3099
chr16	90354753	12454177	0.1378	0.5353
chr17	81195210	6104957	0.0752	0.4639
chr18	78077248	8740060	0.1119	1.2518
chr19	59128983	8913593	0.1507	1.7562
chr20	63025520	9035218	0.1434	0.498
chr21	48129895	5677257	0.118	0.4719
chr22	51304566	2717515	0.053	0.2845
chrMT	16571	299976	18.1025	10.9106
chrX	155270560	25076508	0.1615	0.6
chrY	59373566	969294	0.0163	0.2339

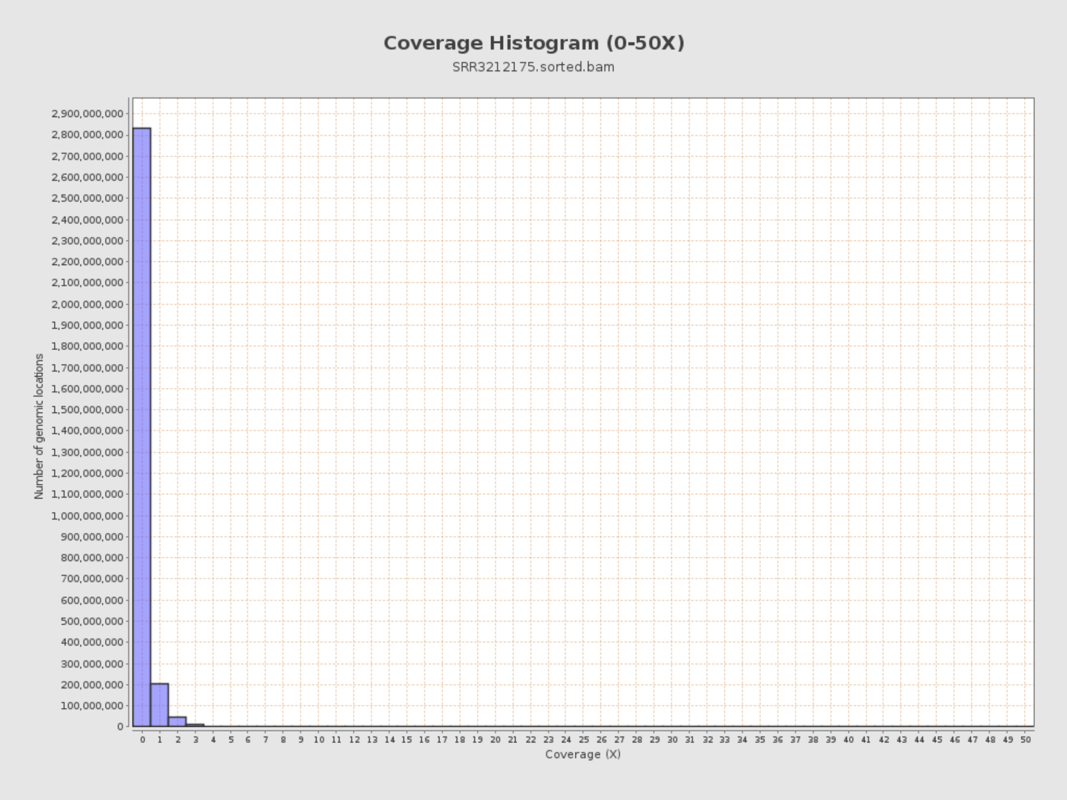
3. Results : Coverage across reference



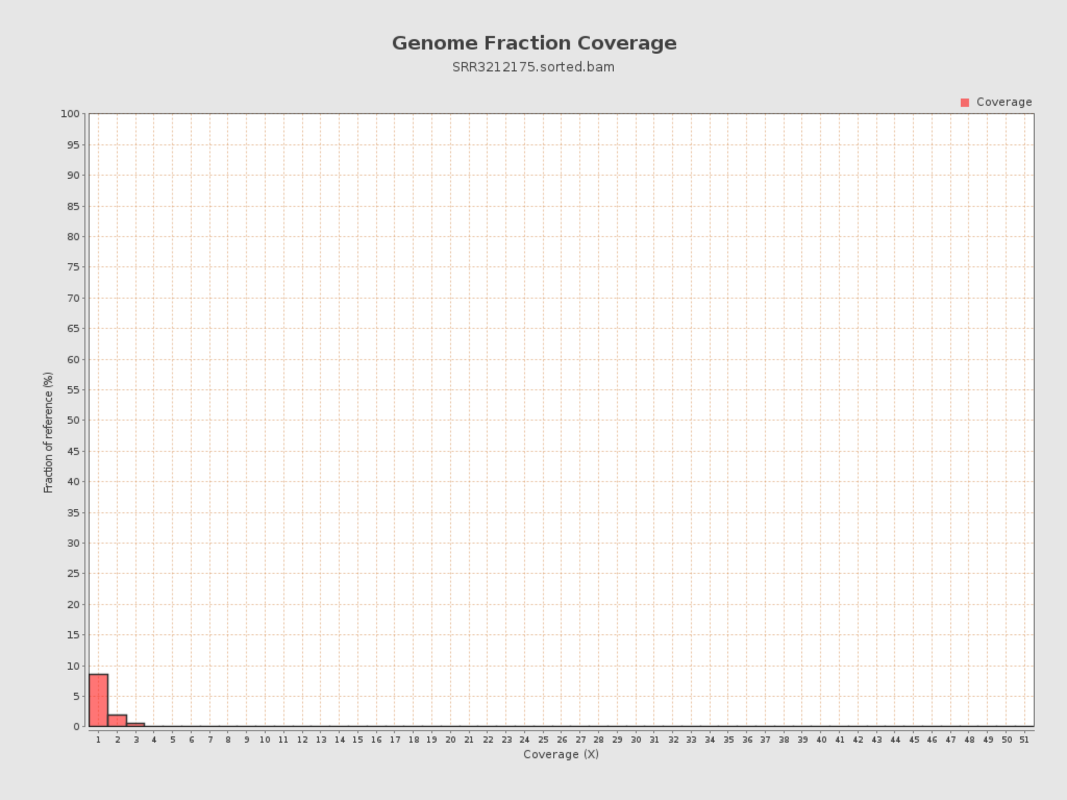
4. Results : Coverage Histogram



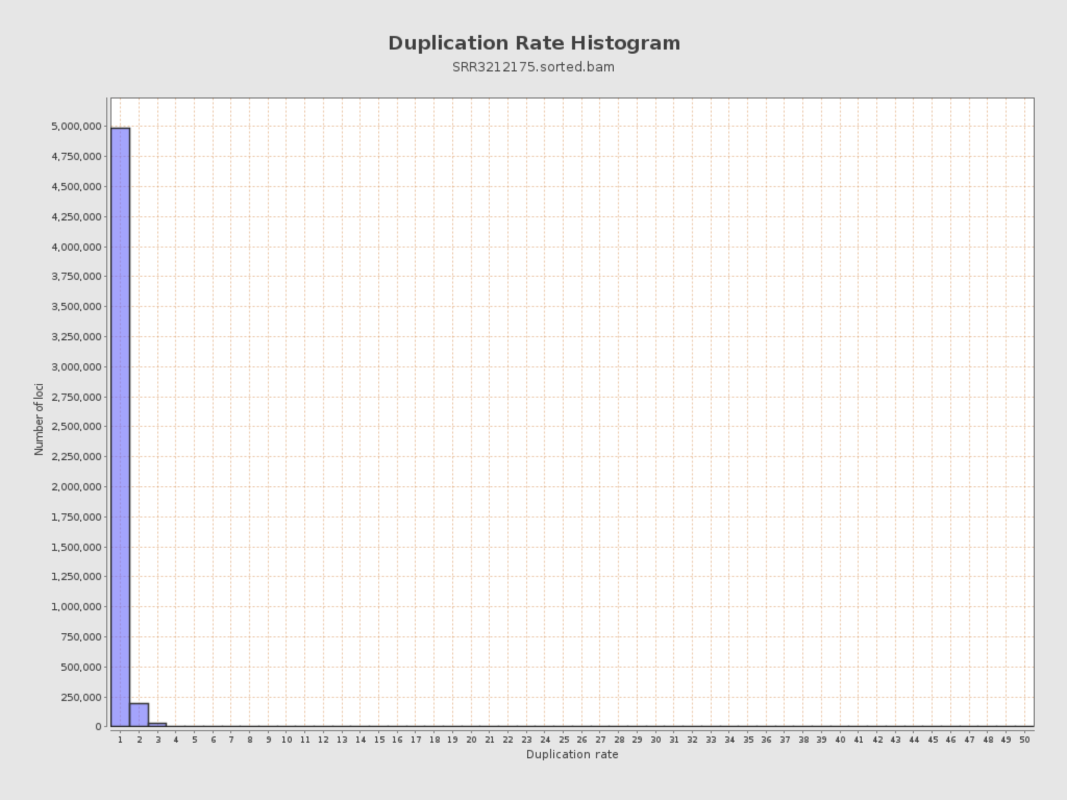
5. Results : Coverage Histogram (0-50X)



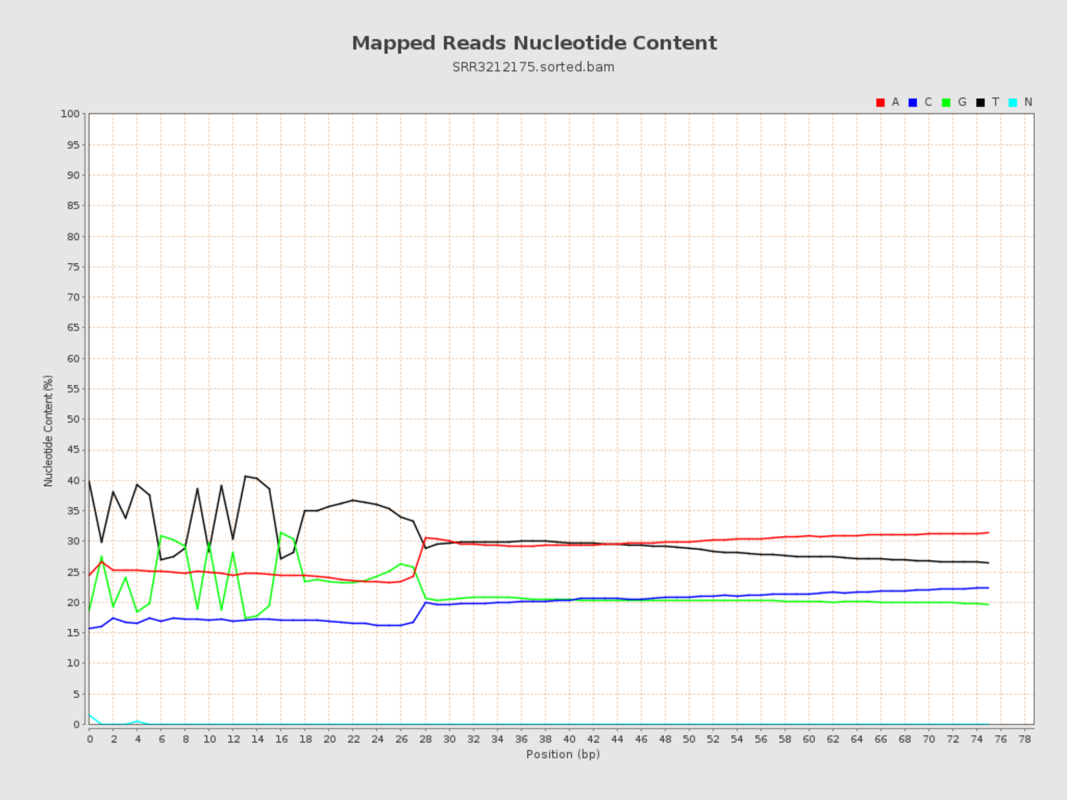
6. Results : Genome Fraction Coverage



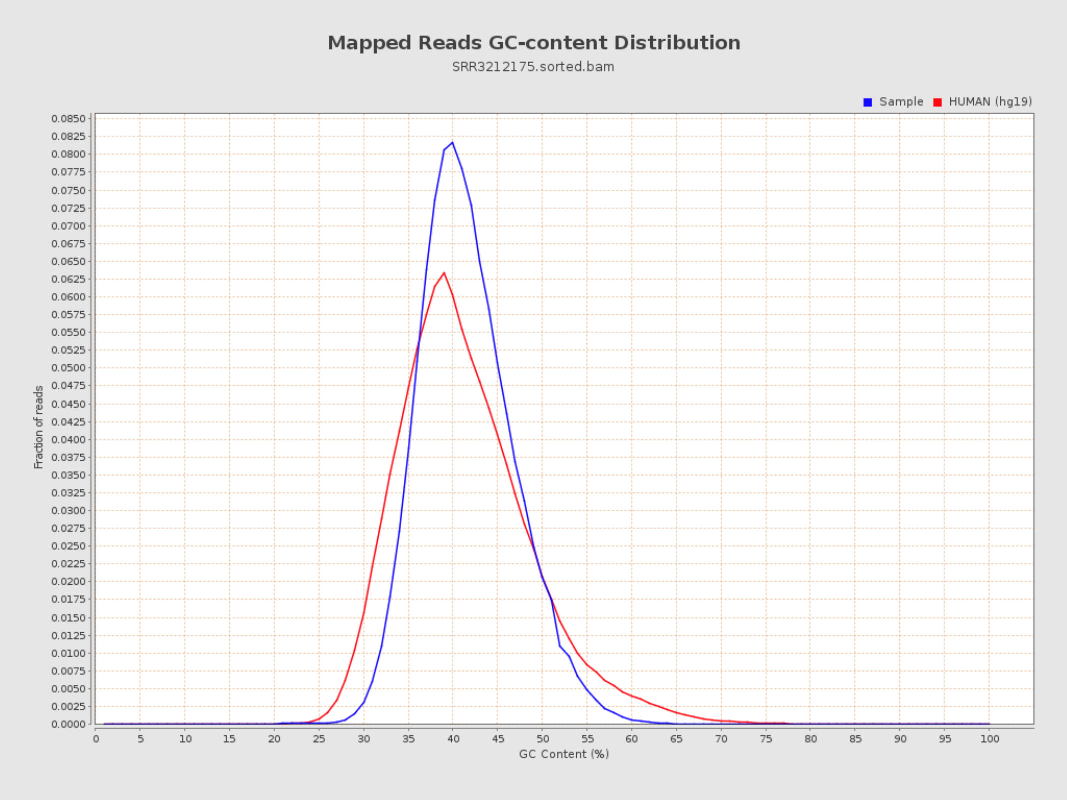
7. Results : Duplication Rate Histogram



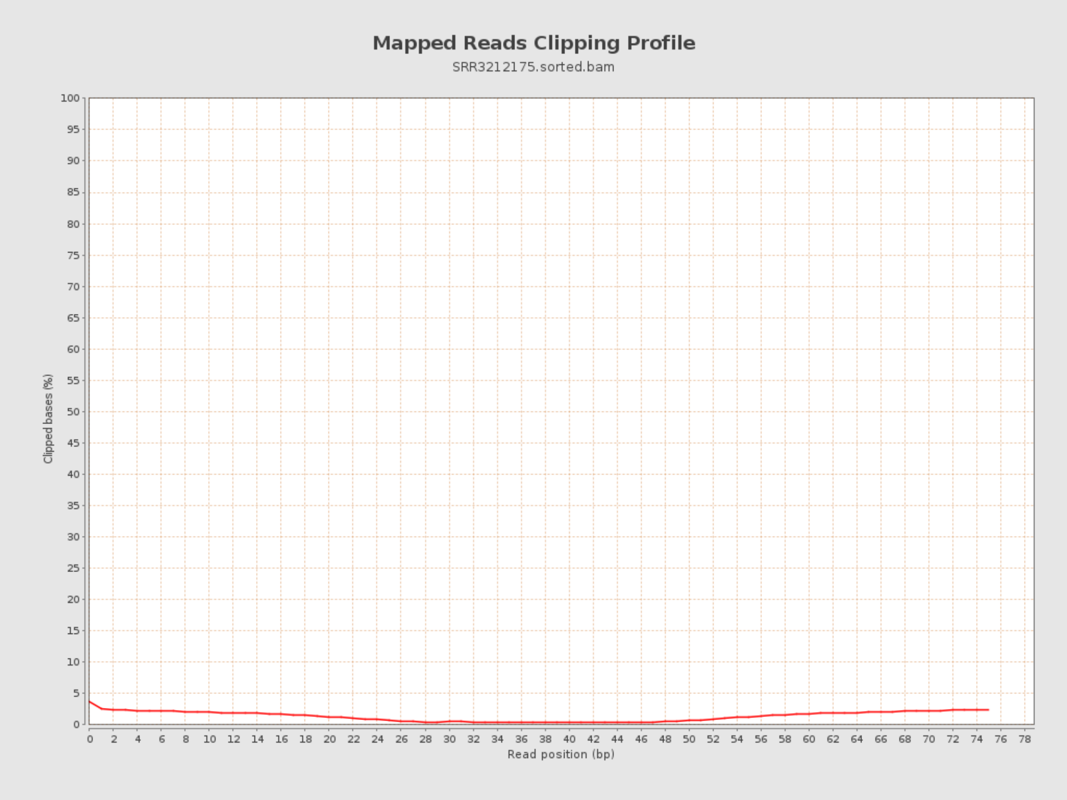
8. Results : Mapped Reads Nucleotide Content



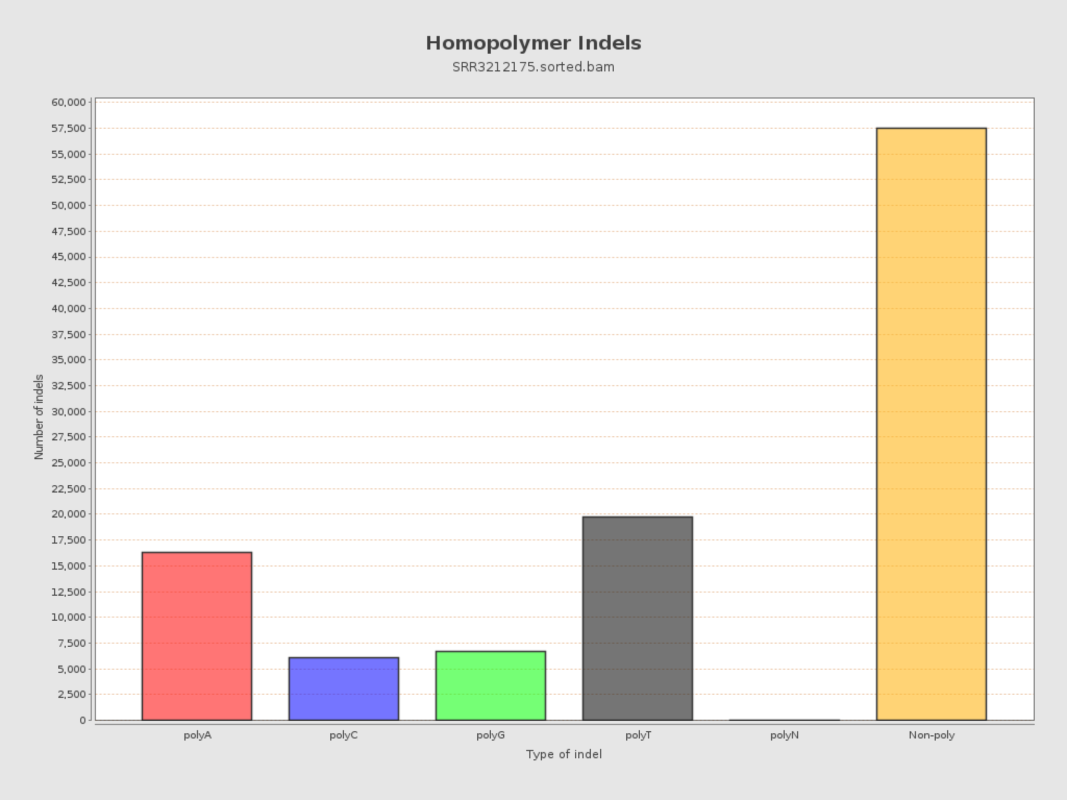
9. Results : Mapped Reads GC-content Distribution



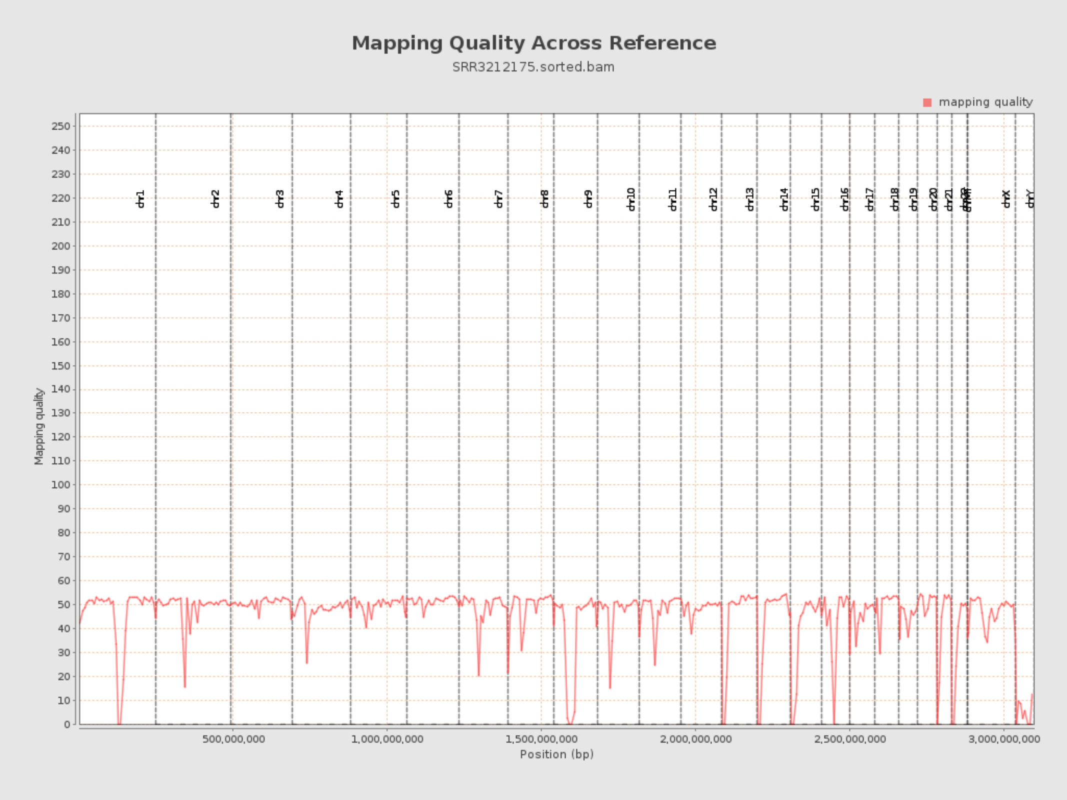
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram