Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:19:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716134.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_SRR9716134 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716134.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:19:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716134.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	469,968
Mapped reads	430,923 / 91.69%
Unmapped reads	39,045 / 8.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	939 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	7,505 / 1.6%
Duplication rate	1.32%
Clipped reads	431,382 / 91.79%

2.2. ACGT Content

Number/percentage of A's	5,896,643 / 23.69%
Number/percentage of C's	4,377,878 / 17.59%
Number/percentage of T's	8,301,123 / 33.35%
Number/percentage of G's	6,318,114 / 25.38%
Number/percentage of N's	269 / 0%
GC Percentage	42.97%

2.3. Coverage

Mean	0.008

Standard Deviation	0.1056

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Mismatches and indels

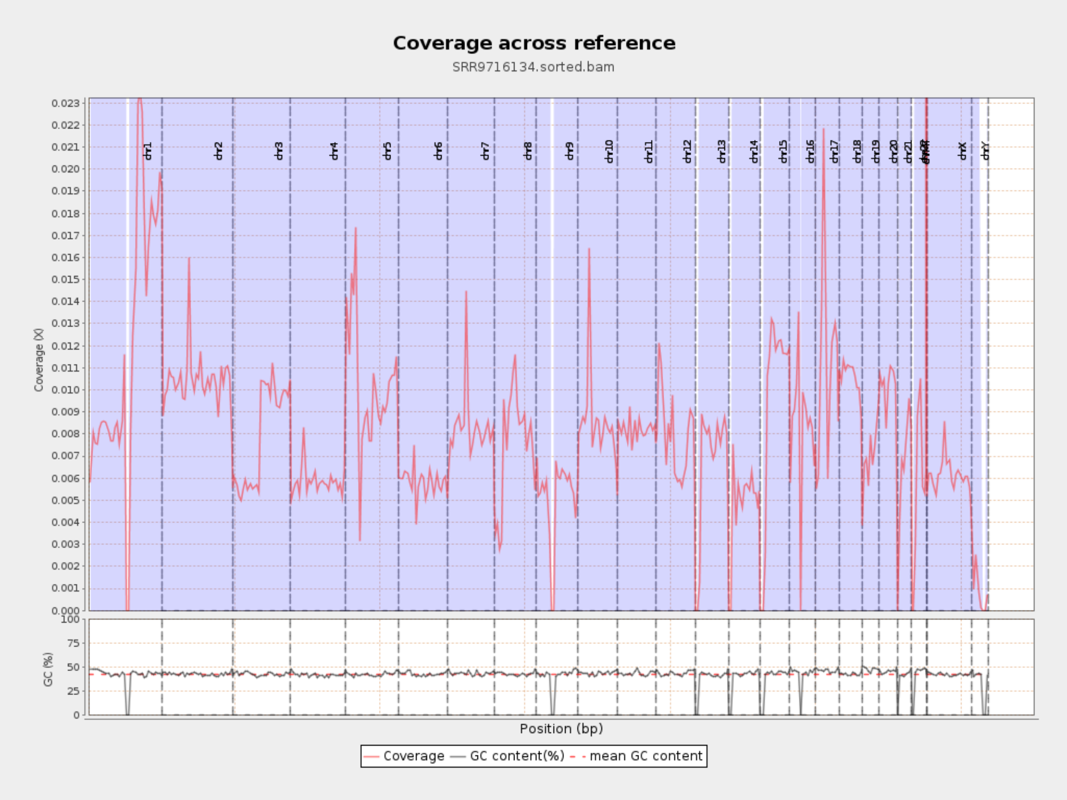
General error rate	0.5%
Mismatches	123,071
Insertions	1,419
Mapped reads with at least one insertion	0.33%
Deletions	4,967
Mapped reads with at least one deletion	1.14%
Homopolymer indels	45.8%

2.6. Chromosome stats

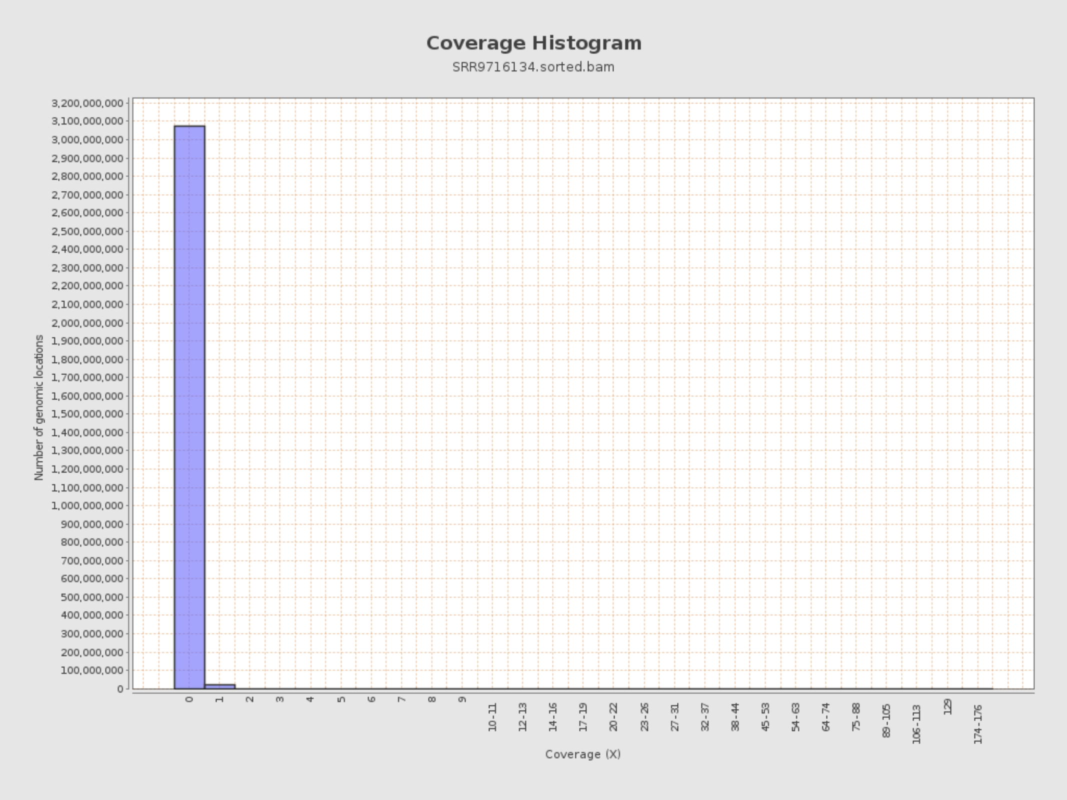
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2947174	0.0118	0.14
chr2	243199373	2551427	0.0105	0.1395
chr3	198022430	1559939	0.0079	0.0919
chr4	191154276	1116249	0.0058	0.0801
chr5	180915260	1855089	0.0103	0.1042
chr6	171115067	994155	0.0058	0.0827
chr7	159138663	1331932	0.0084	0.1274

chr8	146364022	1104351	0.0075	0.0964
chr9	141213431	706233	0.005	0.0874
chr10	135534747	1172736	0.0087	0.1221
chr11	135006516	1100638	0.0082	0.1039
chr12	133851895	1056817	0.0079	0.0918
chr13	115169878	764840	0.0066	0.0837
chr14	107349540	511202	0.0048	0.0723
chr15	102531392	978917	0.0095	0.1006
chr16	90354753	747482	0.0083	0.0982
chr17	81195210	920147	0.0113	0.1121
chr18	78077248	830419	0.0106	0.1491
chr19	59128983	419597	0.0071	0.1064
chr20	63025520	633622	0.0101	0.1033
chr21	48129895	314093	0.0065	0.0838
chr22	51304566	269377	0.0053	0.0748
chrMT	16571	3670	0.2215	0.5553
chrX	155270560	957368	0.0062	0.0863
chrY	59373566	54301	0.0009	0.0333

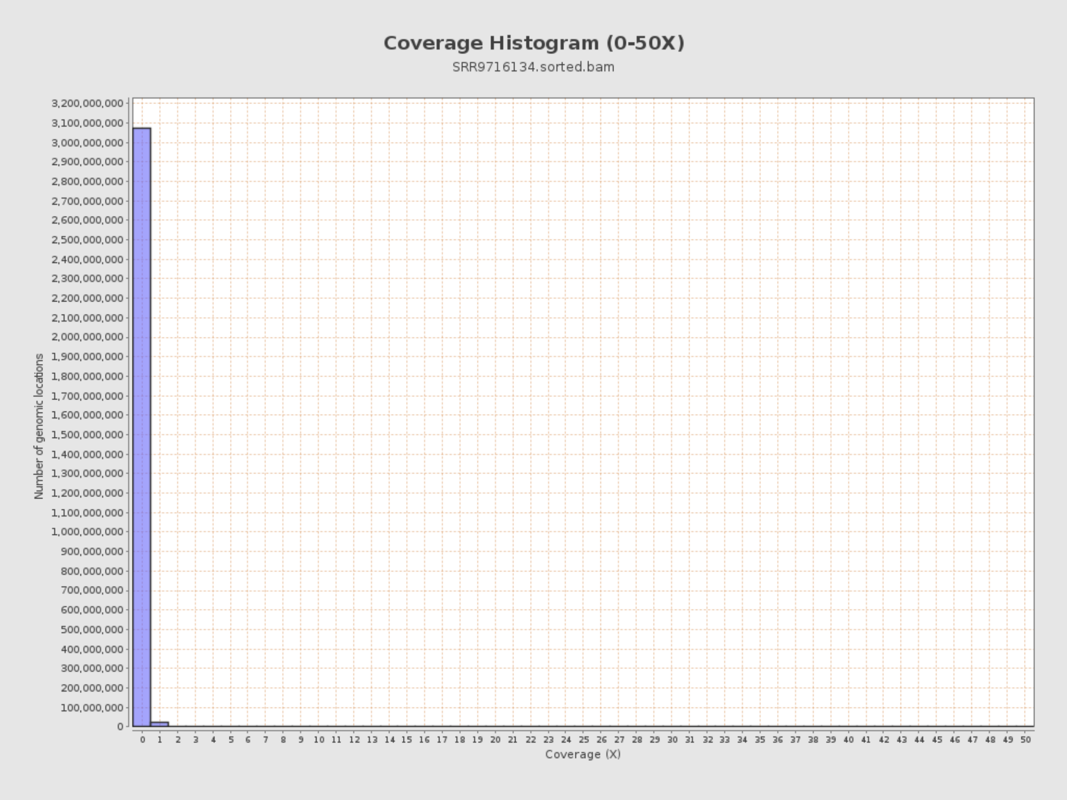
3. Results : Coverage across reference



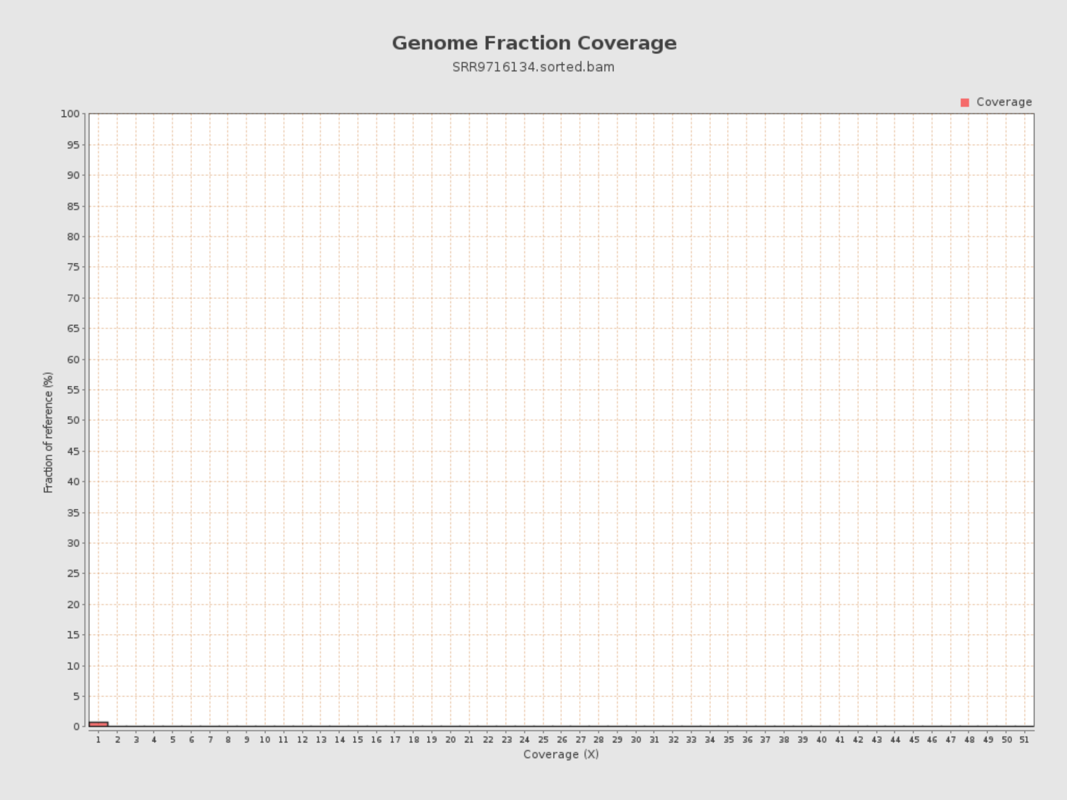
4. Results : Coverage Histogram



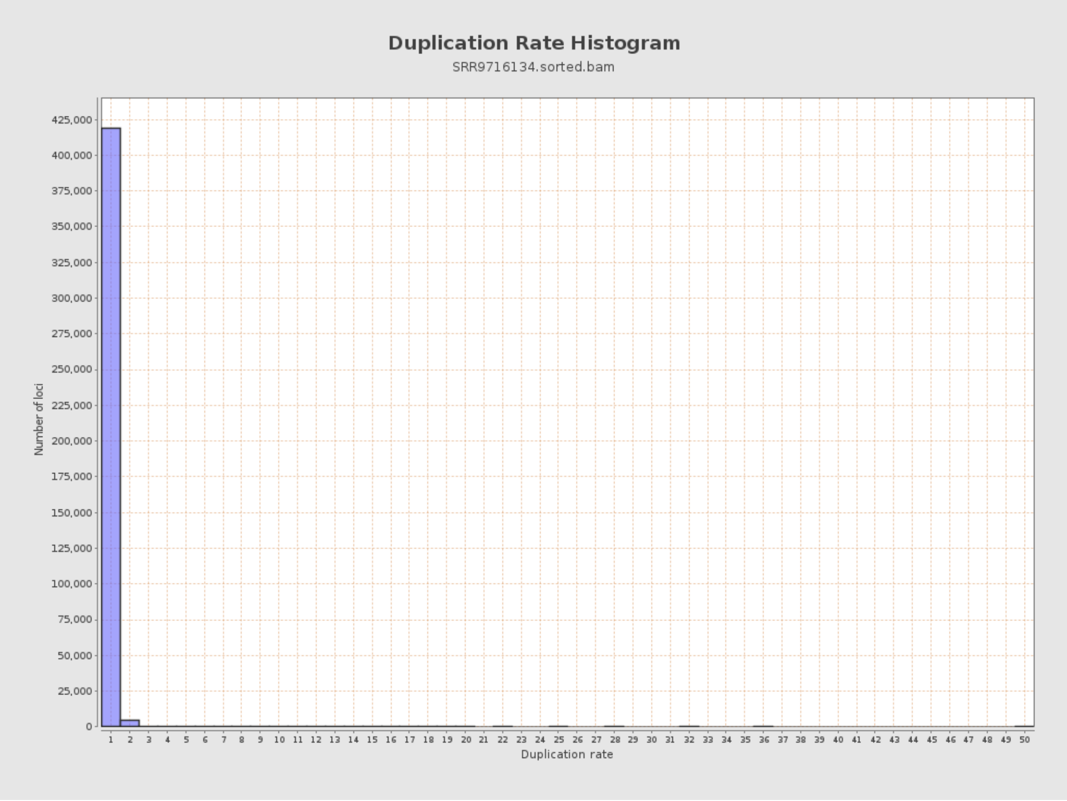
5. Results : Coverage Histogram (0-50X)



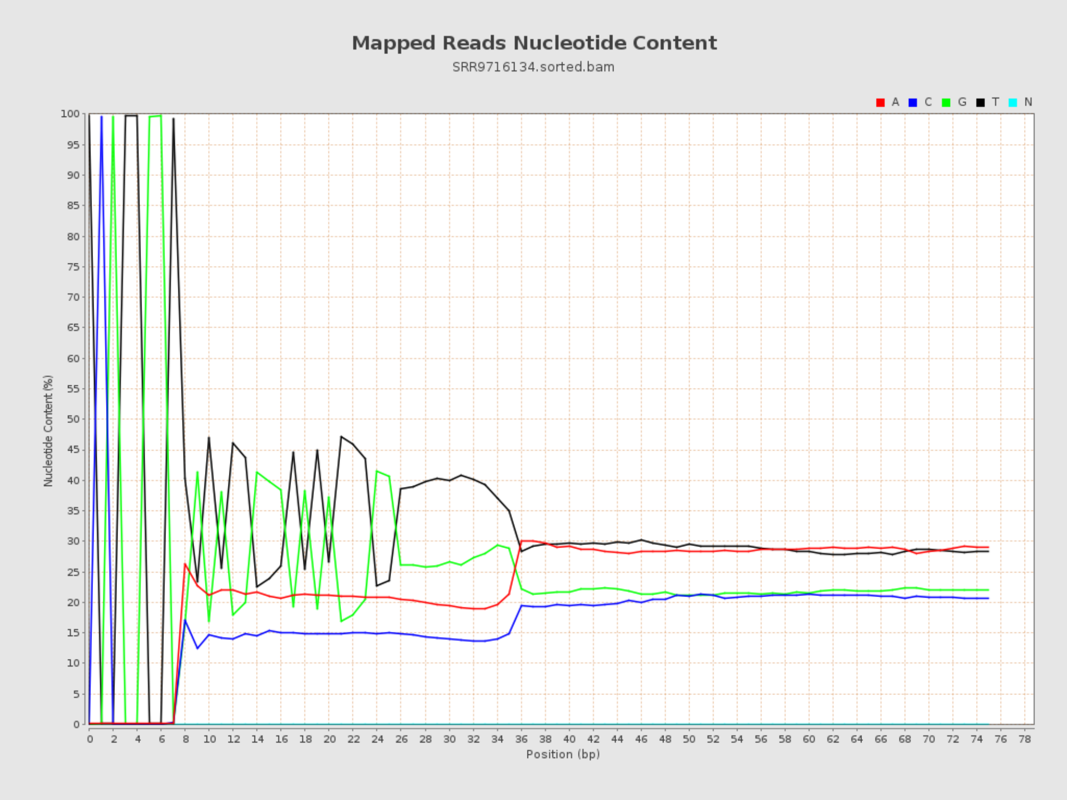
6. Results : Genome Fraction Coverage



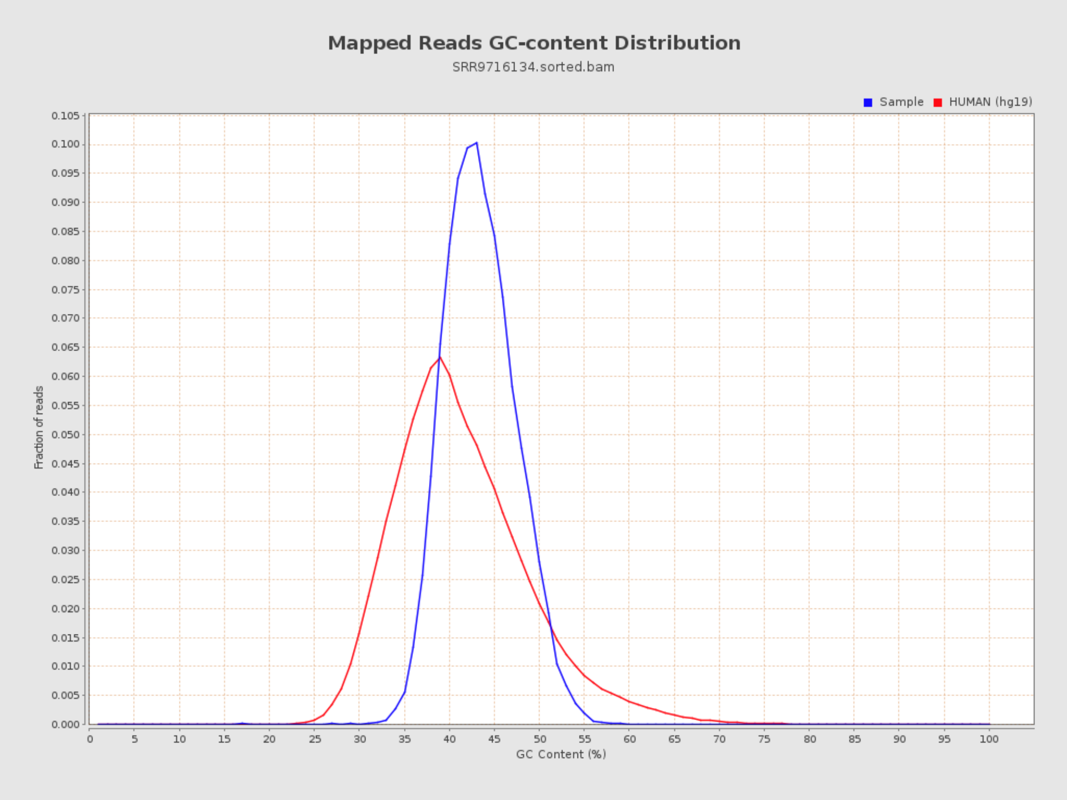
7. Results : Duplication Rate Histogram



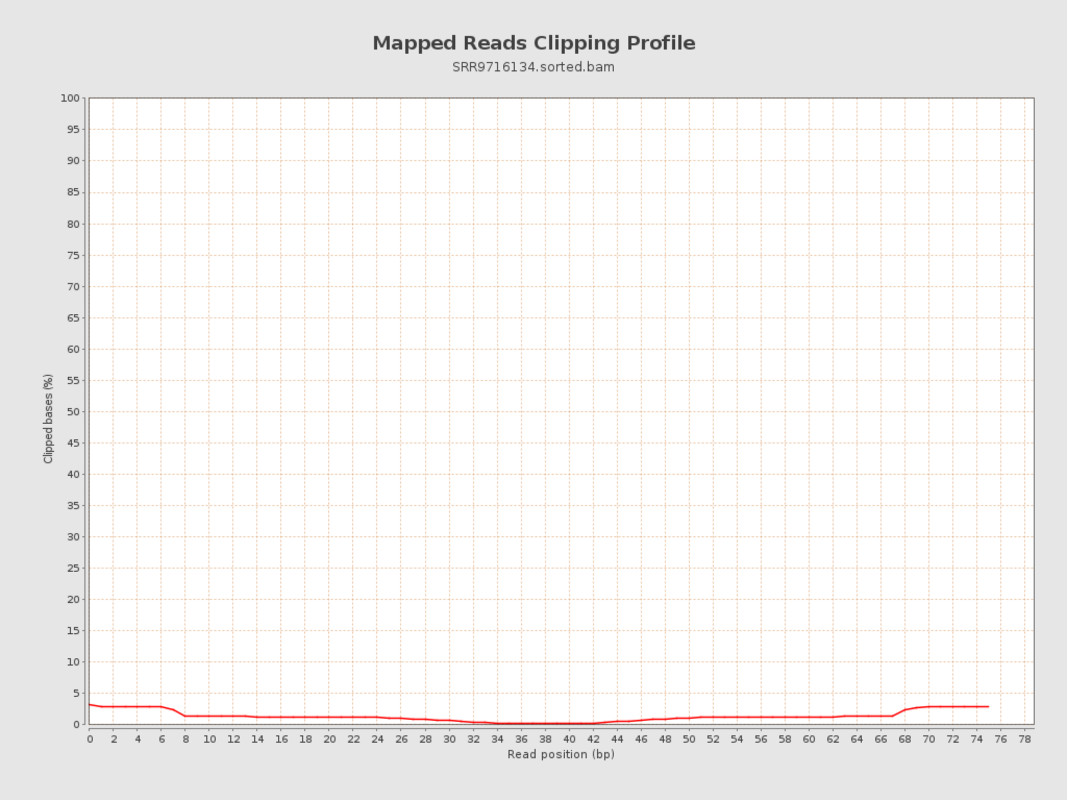
8. Results : Mapped Reads Nucleotide Content



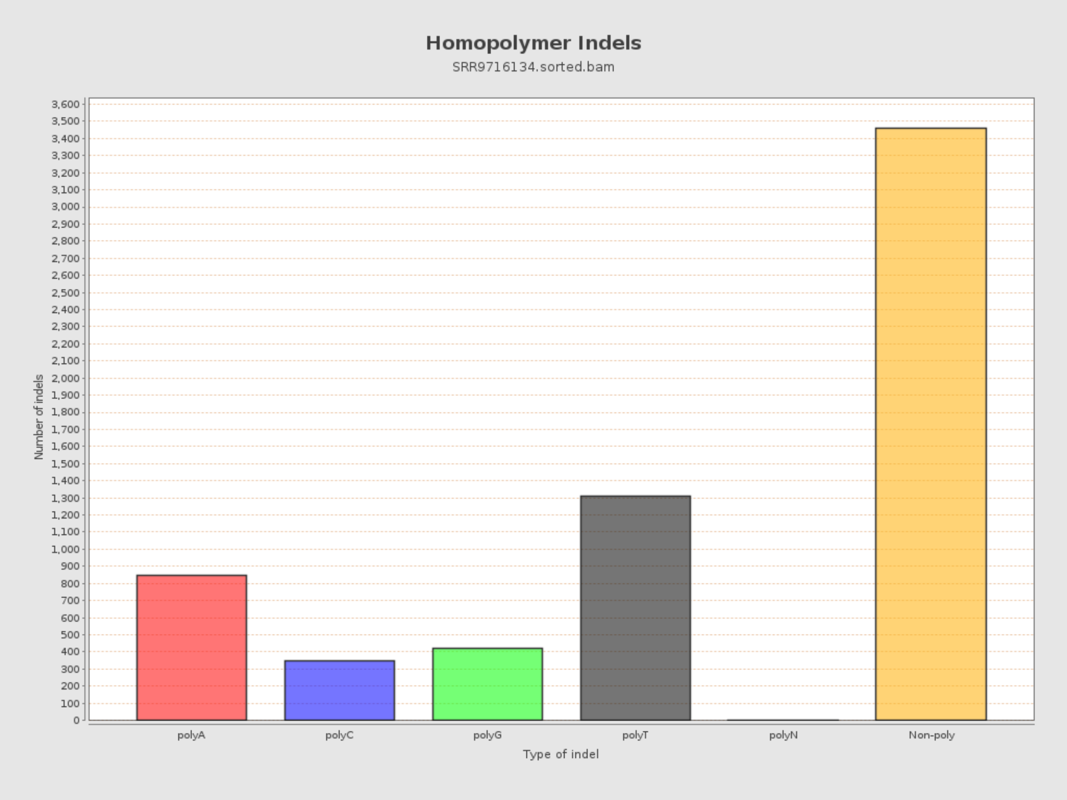
9. Results : Mapped Reads GC-content Distribution



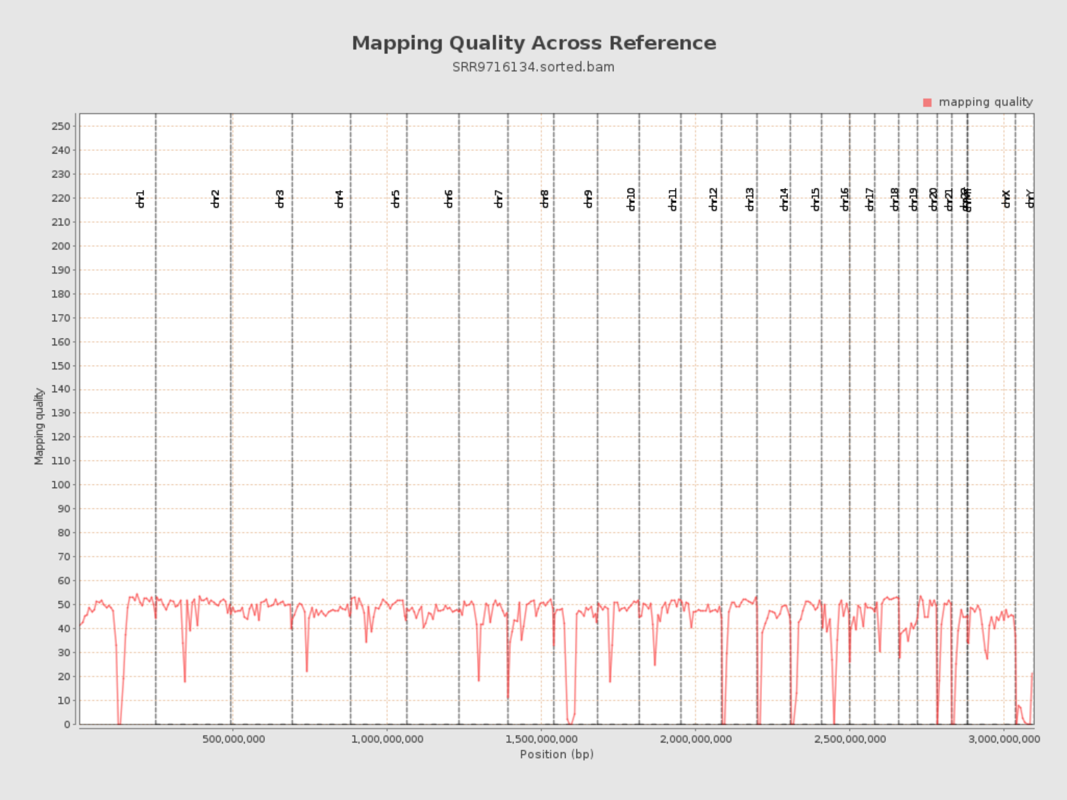
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram