Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:17:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716133.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_SRR9716133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:17:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	415,023
Mapped reads	355,863 / 85.75%
Unmapped reads	59,160 / 14.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	716 / 0.17%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	5,663 / 1.36%
Duplication rate	1.19%
Clipped reads	355,389 / 85.63%

2.2. ACGT Content

Number/percentage of A's	4,898,987 / 24.1%
Number/percentage of C's	4,038,785 / 19.87%
Number/percentage of T's	6,673,647 / 32.83%
Number/percentage of G's	4,718,997 / 23.21%
Number/percentage of N's	127 / 0%
GC Percentage	43.08%

2.3. Coverage

Mean	0.0066

Standard Deviation	0.0954

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

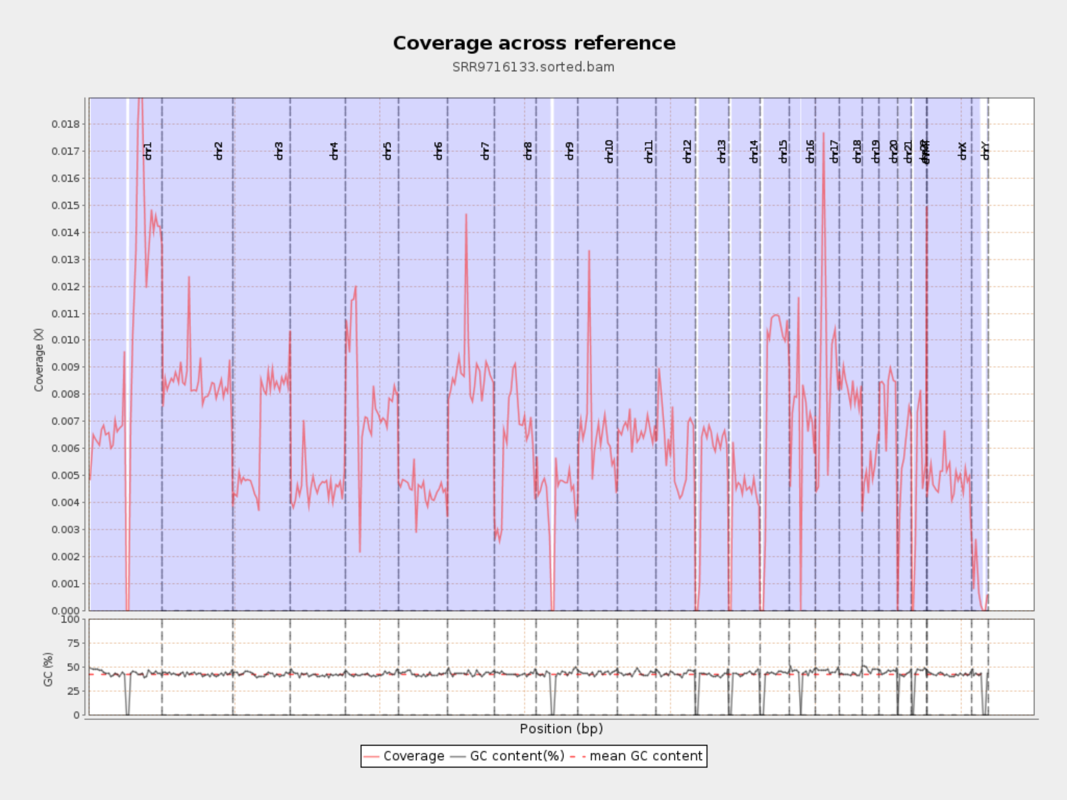
General error rate	0.52%
Mismatches	102,778
Insertions	1,678
Mapped reads with at least one insertion	0.47%
Deletions	4,299
Mapped reads with at least one deletion	1.2%
Homopolymer indels	41.29%

2.6. Chromosome stats

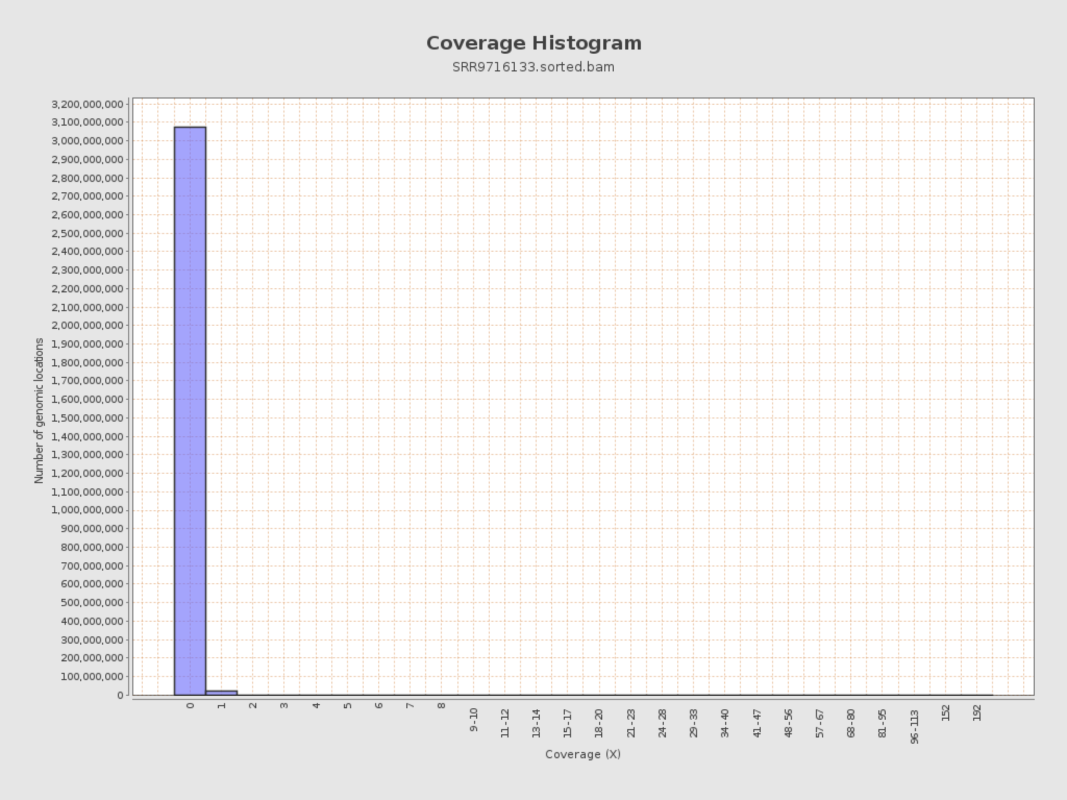
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2386691	0.0096	0.1248
chr2	243199373	2055792	0.0085	0.1278
chr3	198022430	1298850	0.0066	0.0841
chr4	191154276	877322	0.0046	0.0701
chr5	180915260	1430320	0.0079	0.0912
chr6	171115067	759638	0.0044	0.0718
chr7	159138663	1419267	0.0089	0.1375

chr8	146364022	906538	0.0062	0.0849
chr9	141213431	572852	0.0041	0.0728
chr10	135534747	901125	0.0066	0.1058
chr11	135006516	895022	0.0066	0.091
chr12	133851895	807586	0.006	0.0794
chr13	115169878	611769	0.0053	0.0749
chr14	107349540	436804	0.0041	0.0661
chr15	102531392	861138	0.0084	0.0943
chr16	90354753	624989	0.0069	0.0893
chr17	81195210	743954	0.0092	0.1001
chr18	78077248	639971	0.0082	0.1232
chr19	59128983	308623	0.0052	0.0932
chr20	63025520	507152	0.008	0.092
chr21	48129895	258128	0.0054	0.0757
chr22	51304566	224650	0.0044	0.068
chrMT	16571	248	0.015	0.1214
chrX	155270560	761159	0.0049	0.0774
chrY	59373566	47791	0.0008	0.0323

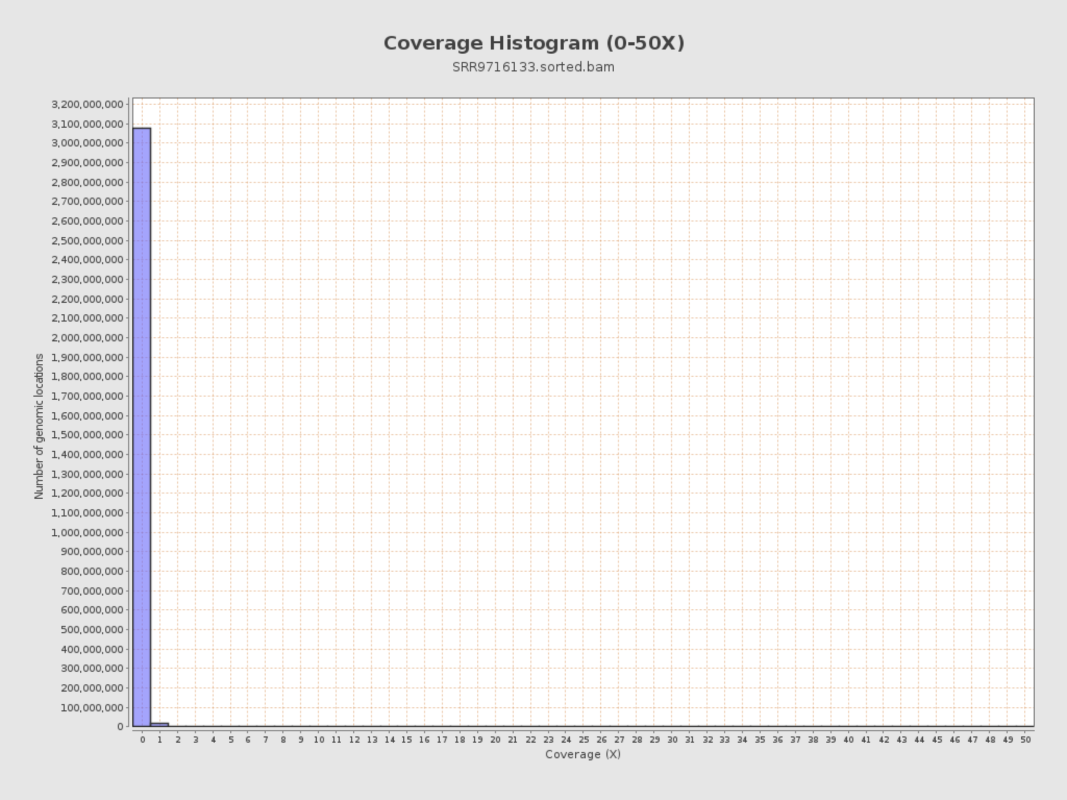
3. Results : Coverage across reference



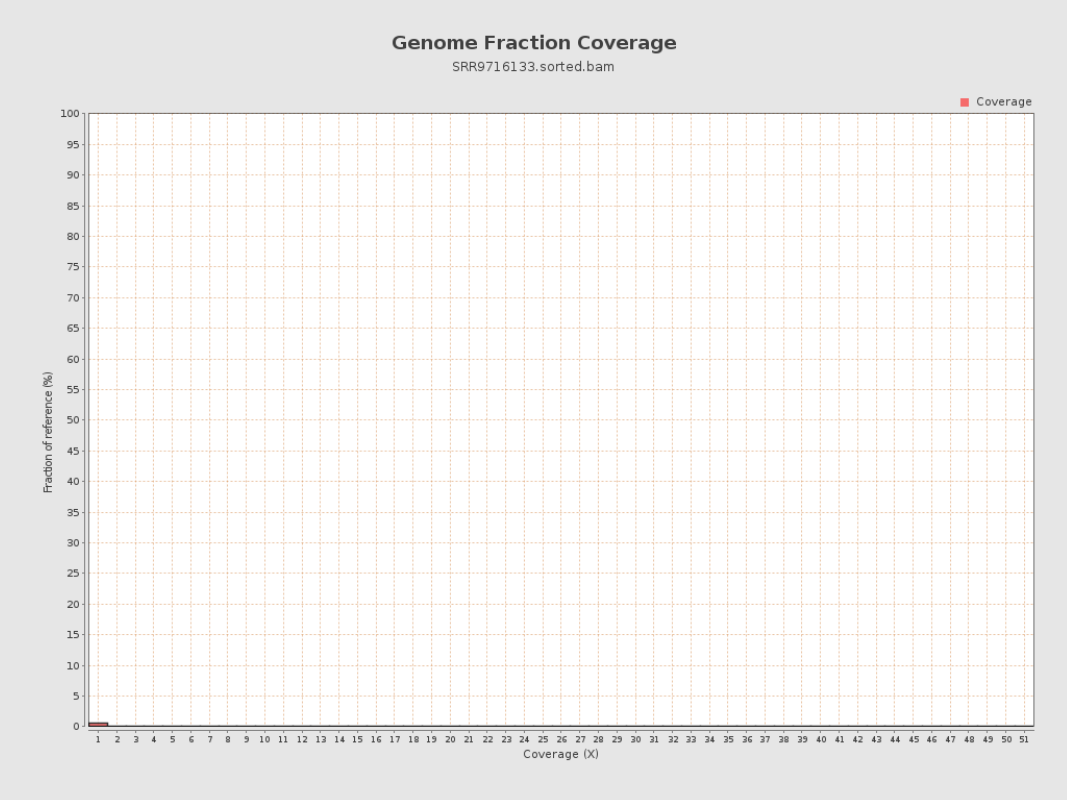
4. Results : Coverage Histogram



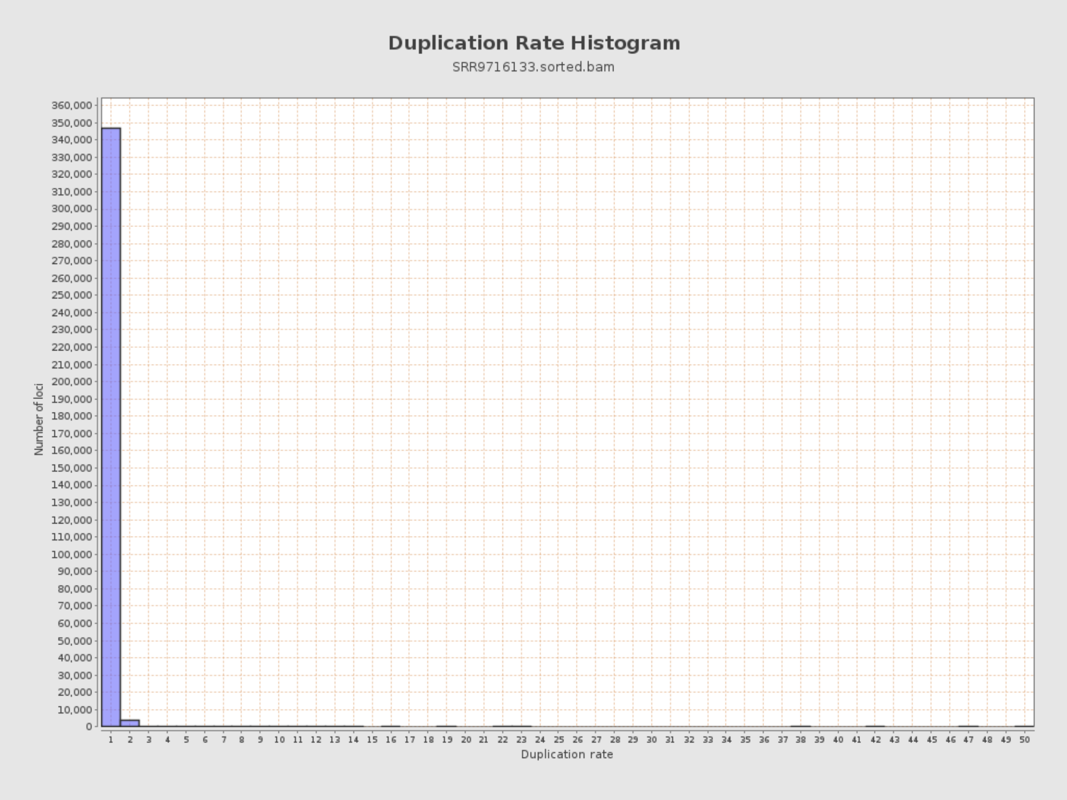
5. Results : Coverage Histogram (0-50X)



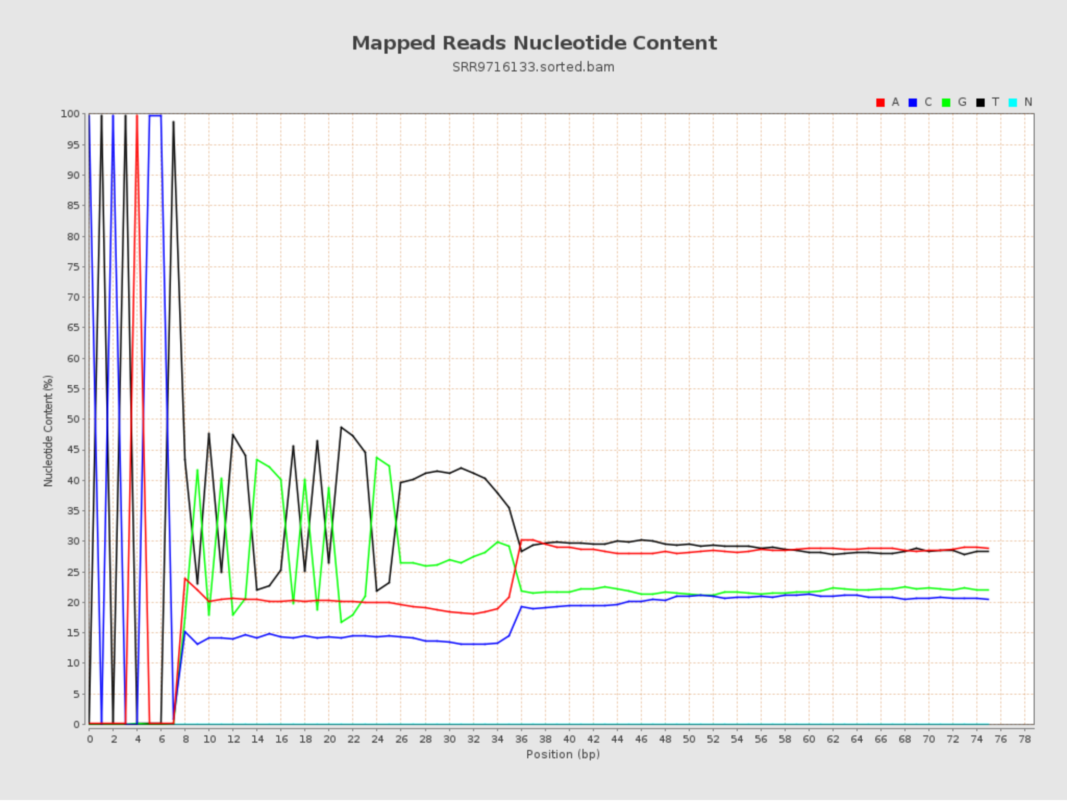
6. Results : Genome Fraction Coverage



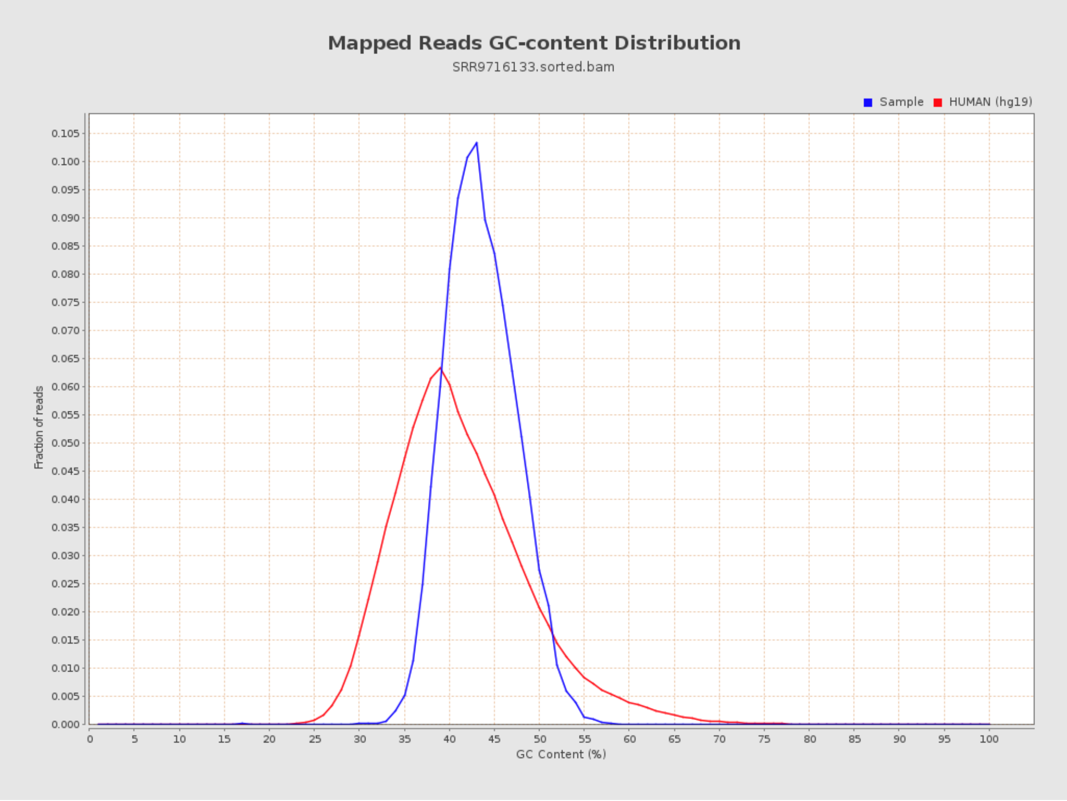
7. Results : Duplication Rate Histogram



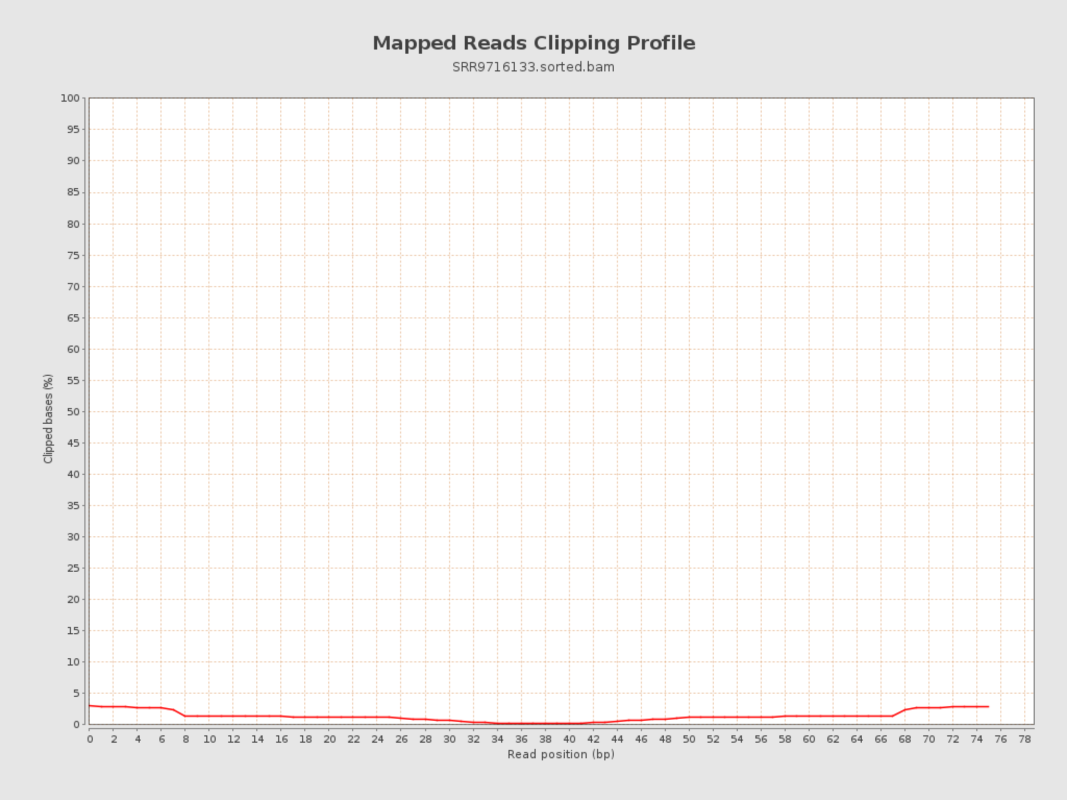
8. Results : Mapped Reads Nucleotide Content



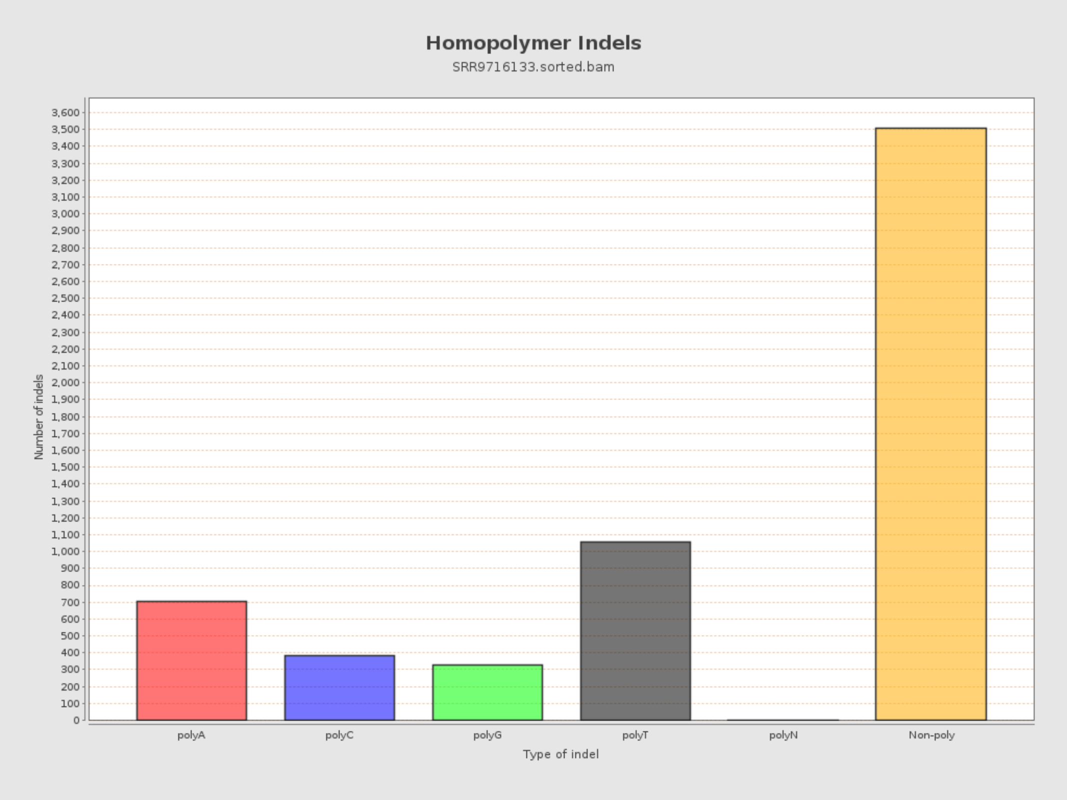
9. Results : Mapped Reads GC-content Distribution



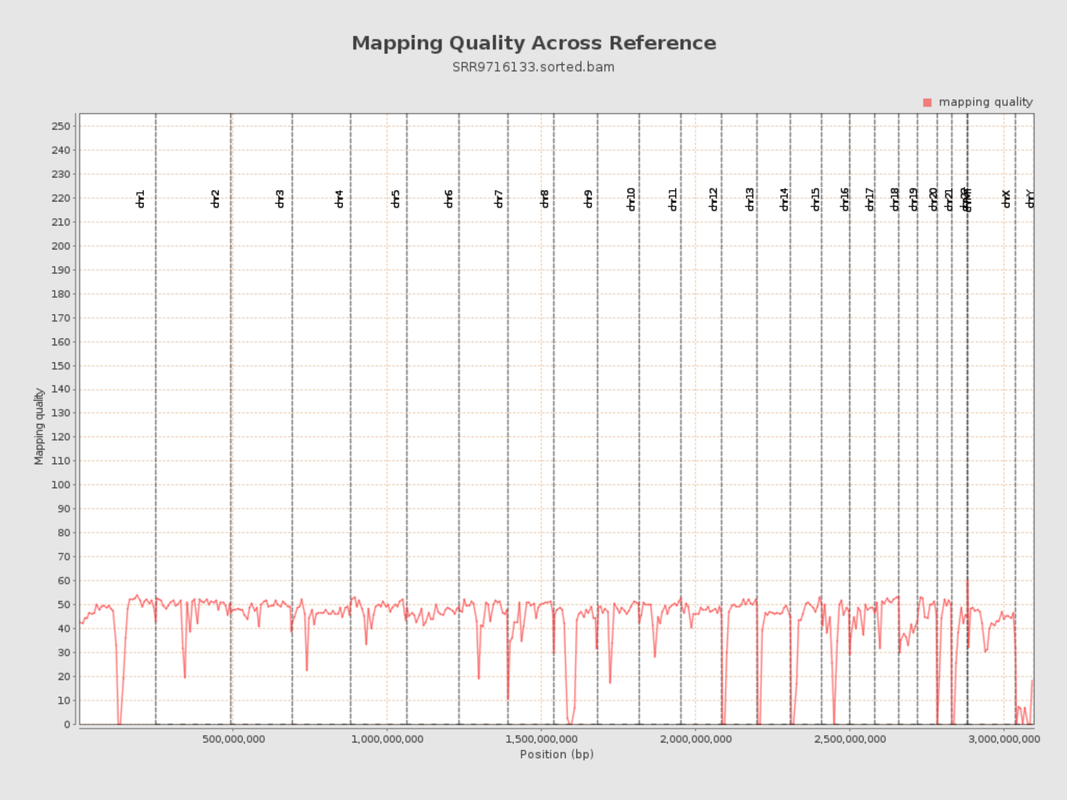
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram