Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:13:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716933.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_SRR9716933 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716933.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:13:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716933.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	500,650
Mapped reads	361,000 / 72.11%
Unmapped reads	139,650 / 27.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	417 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	16,807 / 3.36%
Duplication rate	4.05%
Clipped reads	360,510 / 72.01%

2.2. ACGT Content

Number/percentage of A's	4,109,732 / 21.48%
Number/percentage of C's	3,728,801 / 19.49%
Number/percentage of T's	6,374,424 / 33.32%
Number/percentage of G's	4,919,220 / 25.71%
Number/percentage of N's	364 / 0%
GC Percentage	45.2%

2.3. Coverage

Mean	0.0062

Standard Deviation	0.0911

2.4. Mapping Quality

Mean Mapping Quality	43.42

2.5. Mismatches and indels

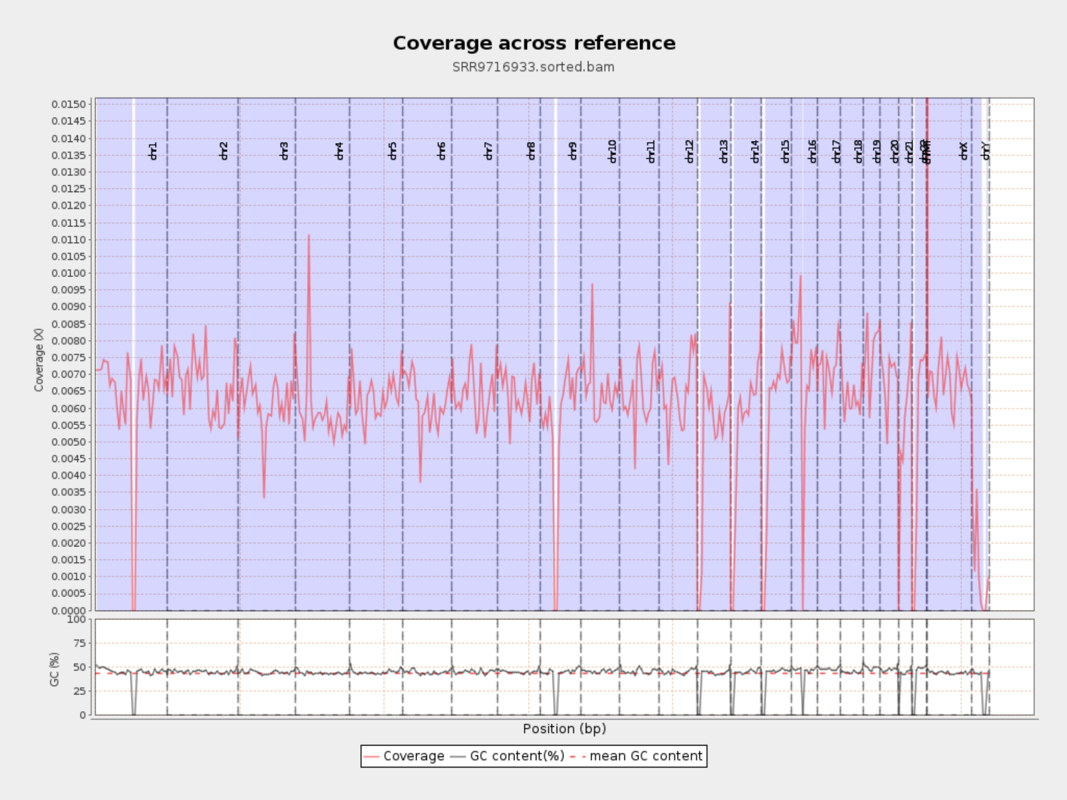
General error rate	0.74%
Mismatches	138,131
Insertions	1,426
Mapped reads with at least one insertion	0.39%
Deletions	3,099
Mapped reads with at least one deletion	0.85%
Homopolymer indels	38.72%

2.6. Chromosome stats

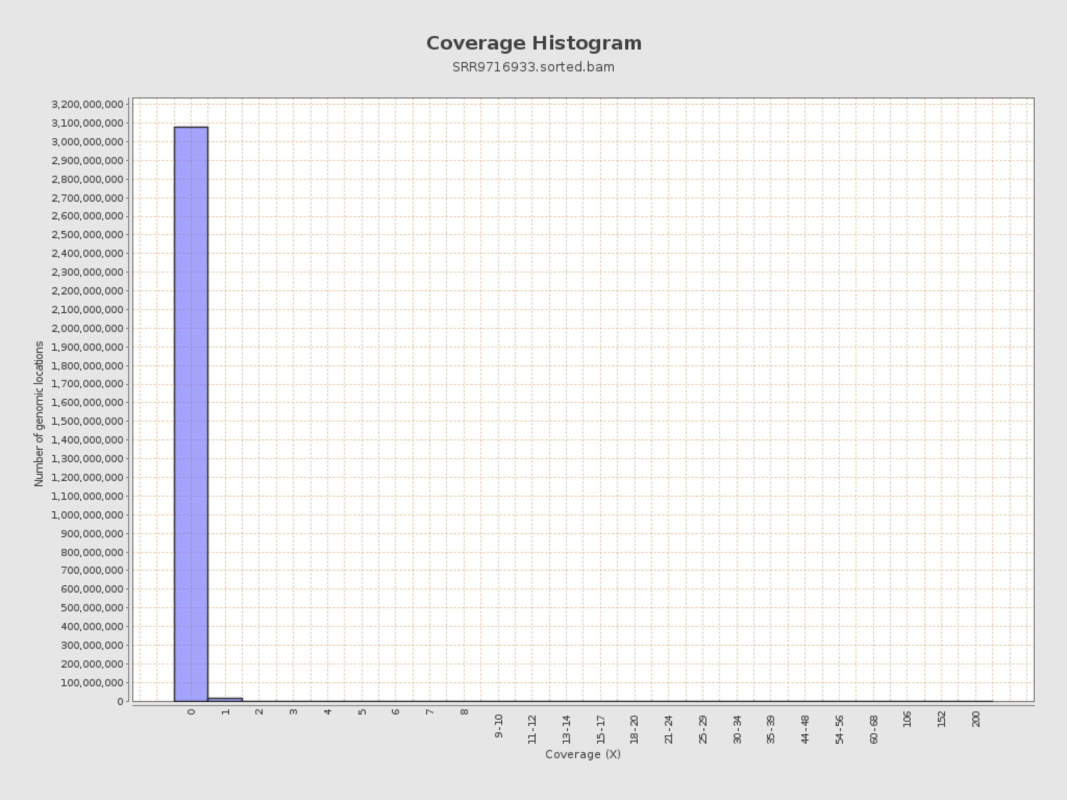
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1562278	0.0063	0.0907
chr2	243199373	1629854	0.0067	0.1207
chr3	198022430	1218320	0.0062	0.0841
chr4	191154276	1155648	0.006	0.086
chr5	180915260	1152441	0.0064	0.0865
chr6	171115067	1058601	0.0062	0.0903
chr7	159138663	1027348	0.0065	0.0936

chr8	146364022	951158	0.0065	0.0895
chr9	141213431	779710	0.0055	0.0838
chr10	135534747	897653	0.0066	0.0946
chr11	135006516	871951	0.0065	0.0915
chr12	133851895	870334	0.0065	0.0889
chr13	115169878	580393	0.005	0.0767
chr14	107349540	570144	0.0053	0.0795
chr15	102531392	570043	0.0056	0.0803
chr16	90354753	625424	0.0069	0.0963
chr17	81195210	585667	0.0072	0.0994
chr18	78077248	494538	0.0063	0.0941
chr19	59128983	450088	0.0076	0.1013
chr20	63025520	431834	0.0069	0.0946
chr21	48129895	264592	0.0055	0.0878
chr22	51304566	260185	0.0051	0.0791
chrMT	16571	4910	0.2963	0.6369
chrX	155270560	1055885	0.0068	0.0892
chrY	59373566	68920	0.0012	0.045

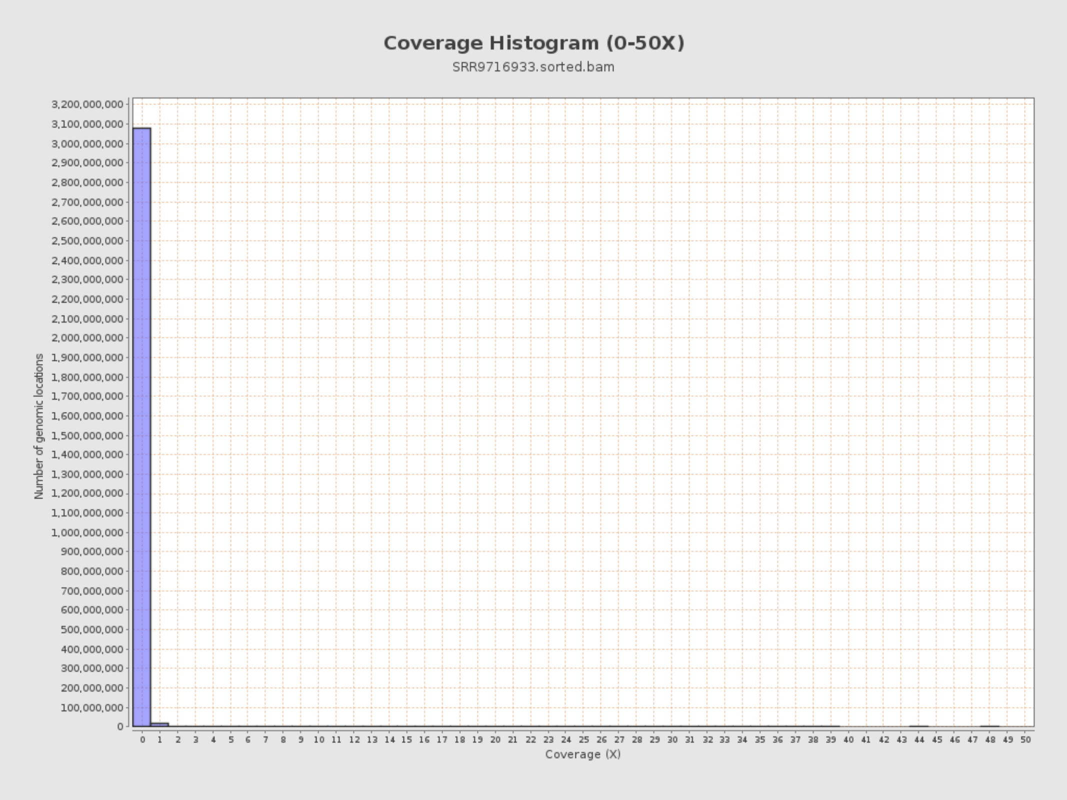
3. Results : Coverage across reference



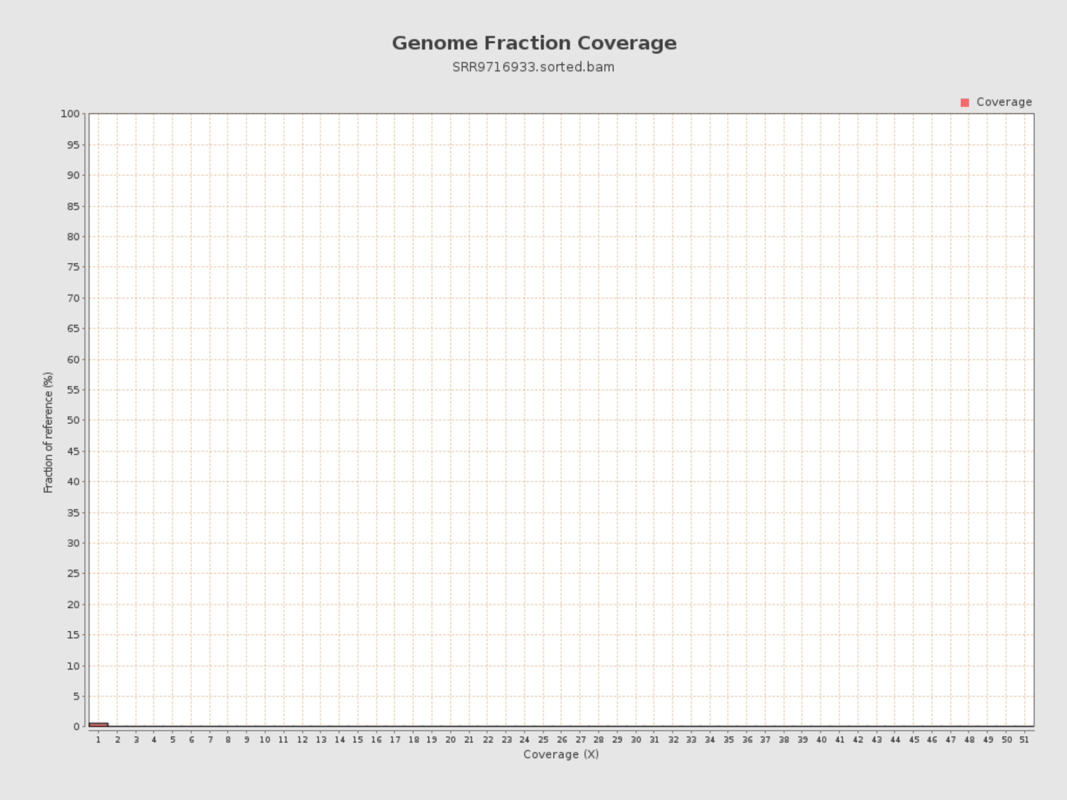
4. Results : Coverage Histogram



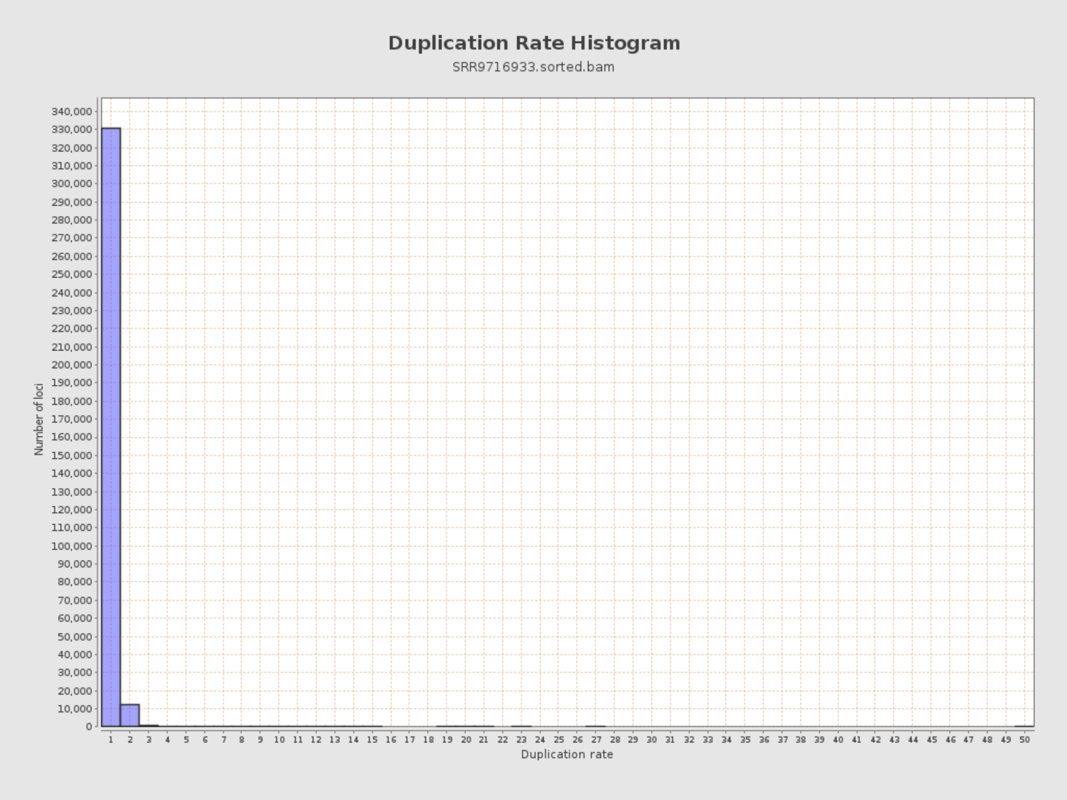
5. Results : Coverage Histogram (0-50X)



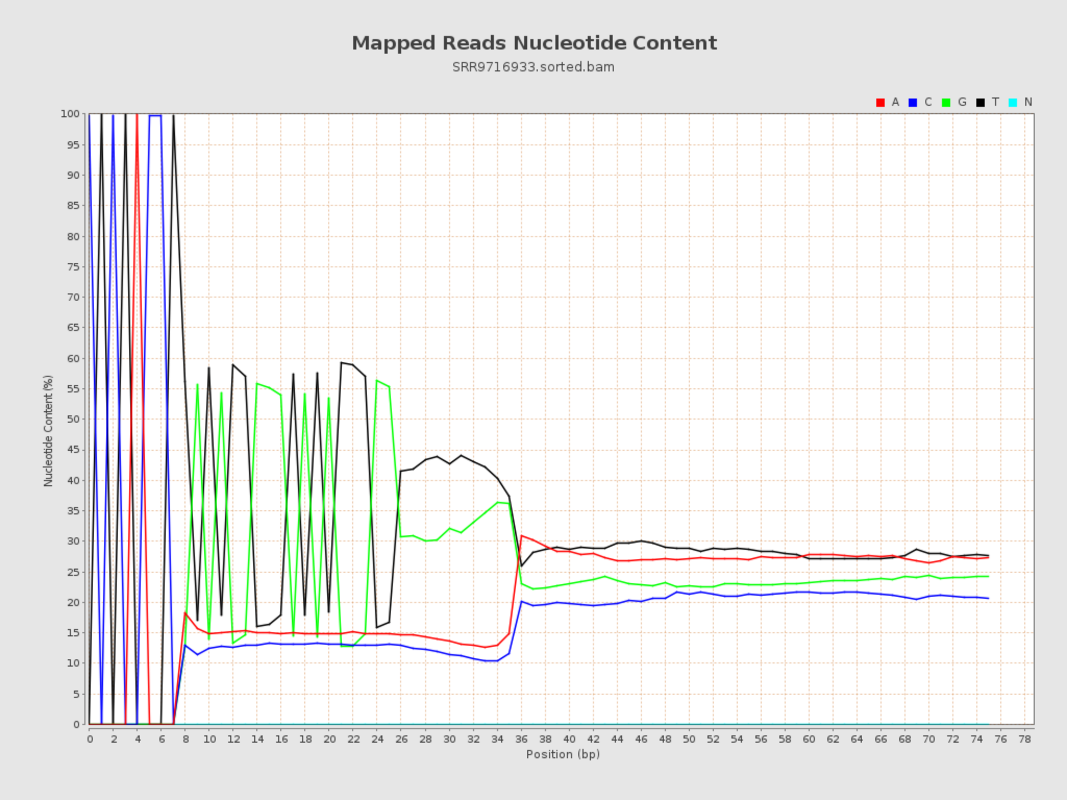
6. Results : Genome Fraction Coverage



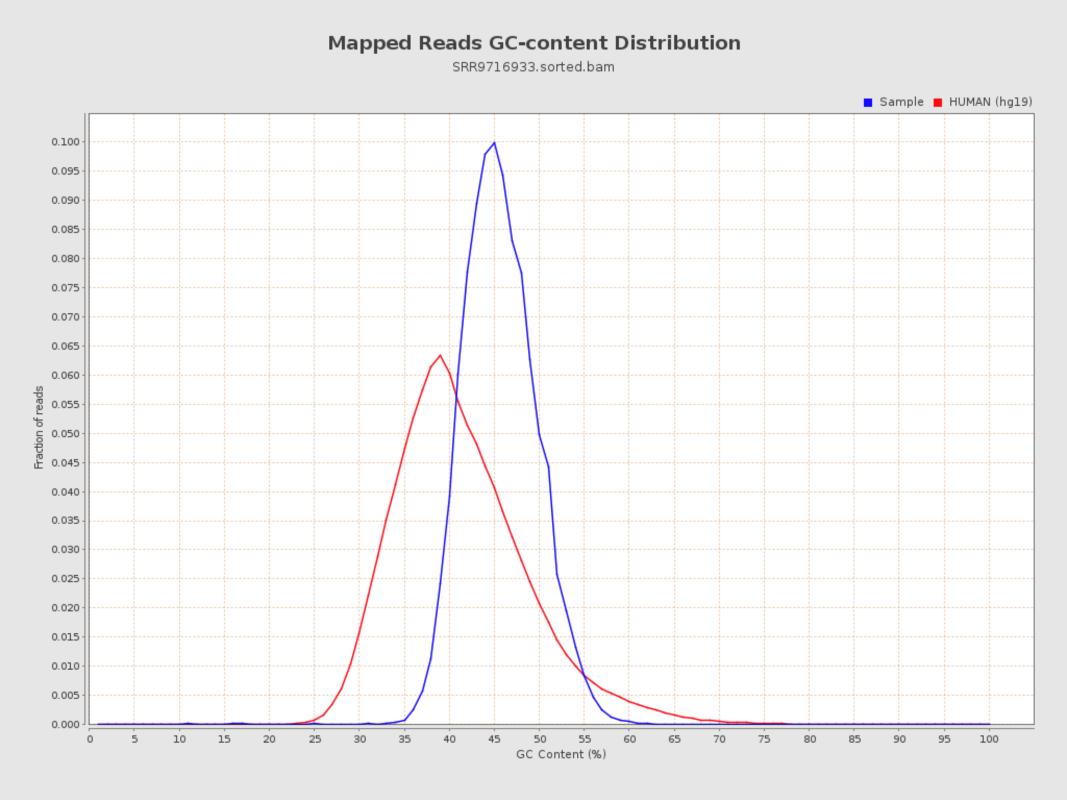
7. Results : Duplication Rate Histogram



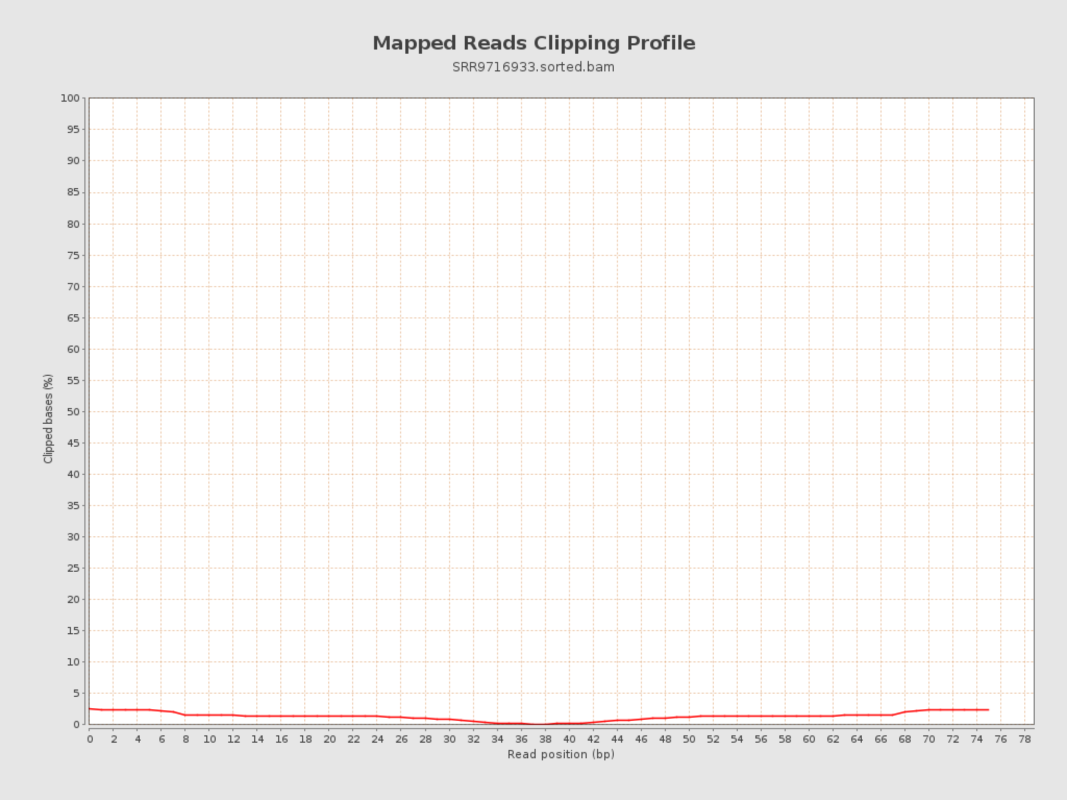
8. Results : Mapped Reads Nucleotide Content



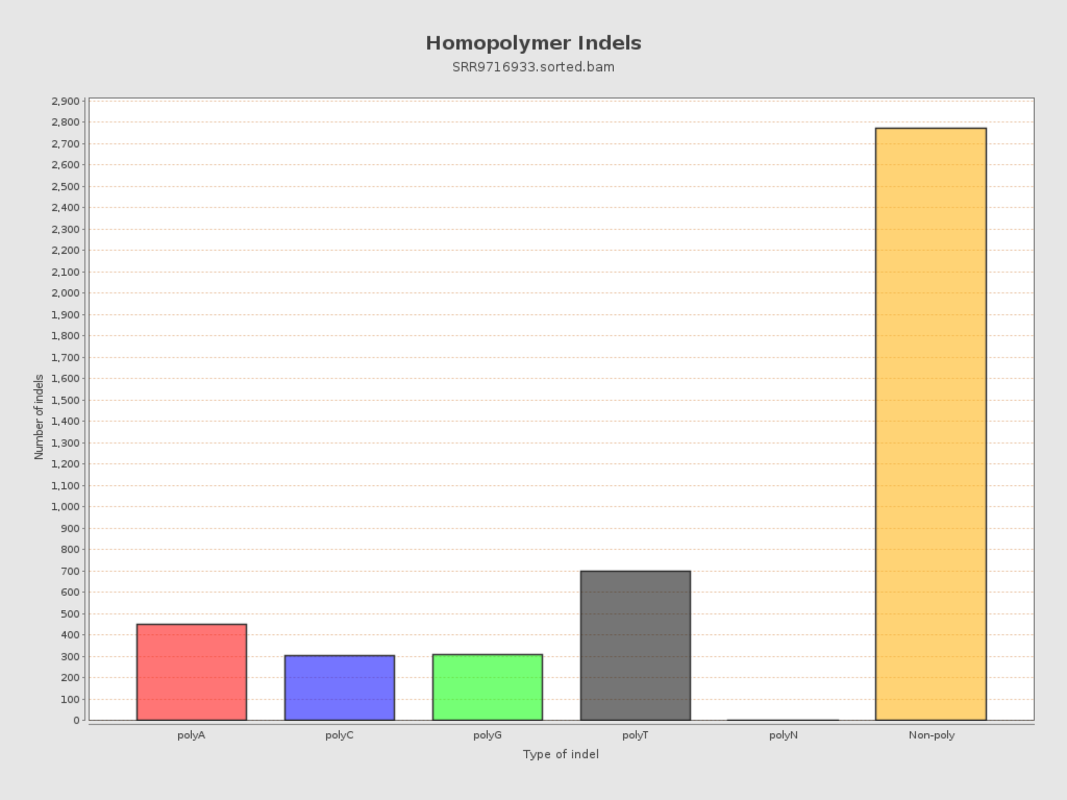
9. Results : Mapped Reads GC-content Distribution



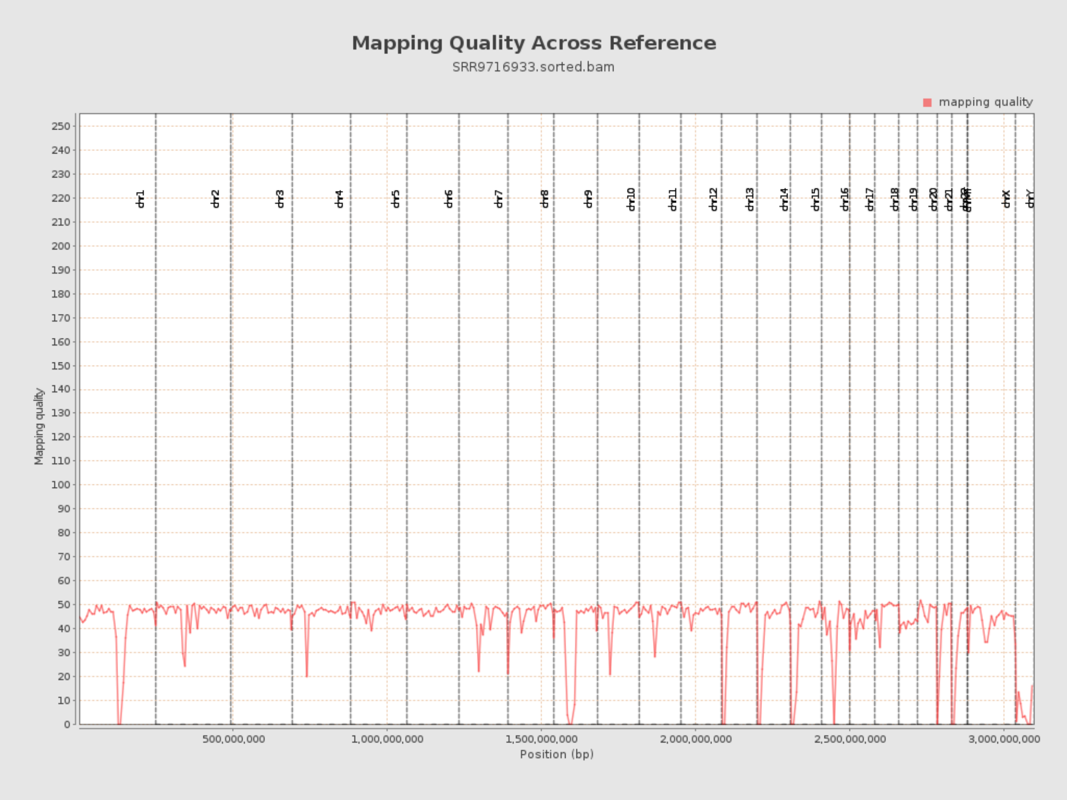
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram