Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:07:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716624.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_SRR9716624 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716624.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:07:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716624.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	546,411
Mapped reads	506,412 / 92.68%
Unmapped reads	39,999 / 7.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,093 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	11,277 / 2.06%
Duplication rate	1.75%
Clipped reads	507,875 / 92.95%

2.2. ACGT Content

Number/percentage of A's	7,281,911 / 24.71%
Number/percentage of C's	5,822,511 / 19.76%
Number/percentage of T's	9,135,995 / 31%
Number/percentage of G's	7,229,577 / 24.53%
Number/percentage of N's	821 / 0%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.1191

2.4. Mapping Quality

Mean Mapping Quality	45.23

2.5. Mismatches and indels

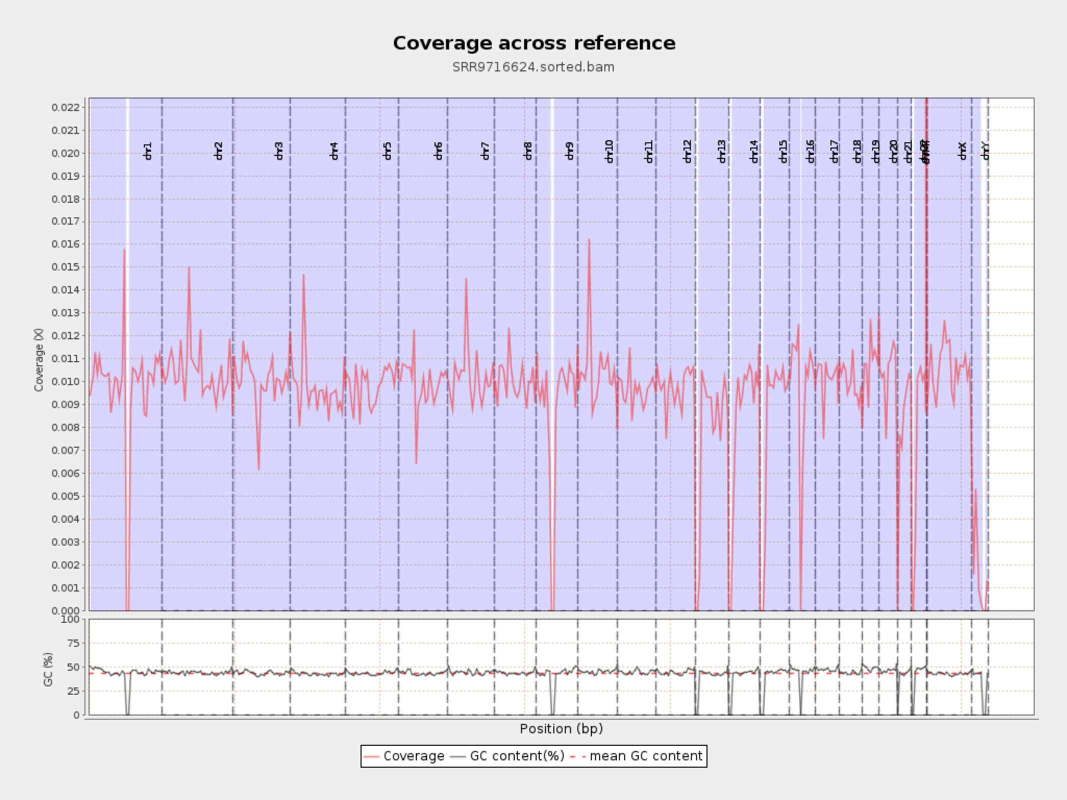
General error rate	0.5%
Mismatches	144,450
Insertions	1,773
Mapped reads with at least one insertion	0.35%
Deletions	5,521
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.57%

2.6. Chromosome stats

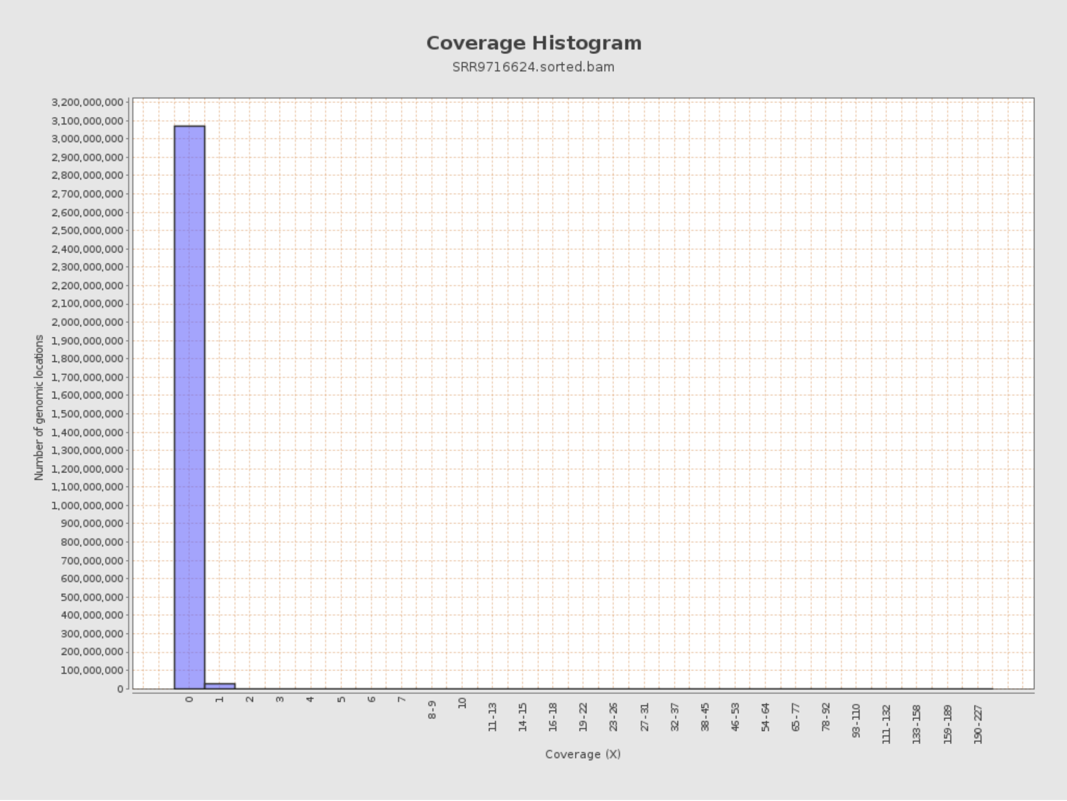
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2410118	0.0097	0.1758
chr2	243199373	2546919	0.0105	0.1444
chr3	198022430	1979673	0.01	0.104
chr4	191154276	1851797	0.0097	0.1058
chr5	180915260	1782048	0.0099	0.1035
chr6	171115067	1702942	0.01	0.1107
chr7	159138663	1627642	0.0102	0.133

chr8	146364022	1468286	0.01	0.1161
chr9	141213431	1217637	0.0086	0.1077
chr10	135534747	1419314	0.0105	0.1186
chr11	135006516	1299118	0.0096	0.1148
chr12	133851895	1309586	0.0098	0.1042
chr13	115169878	880683	0.0076	0.091
chr14	107349540	880360	0.0082	0.0957
chr15	102531392	834836	0.0081	0.0948
chr16	90354753	881374	0.0098	0.1053
chr17	81195210	821685	0.0101	0.1061
chr18	78077248	784979	0.0101	0.1467
chr19	59128983	640898	0.0108	0.1402
chr20	63025520	649376	0.0103	0.1064
chr21	48129895	388692	0.0081	0.0971
chr22	51304566	360407	0.007	0.0871
chrMT	16571	3637	0.2195	0.4867
chrX	155270560	1642444	0.0106	0.1096
chrY	59373566	95310	0.0016	0.0545

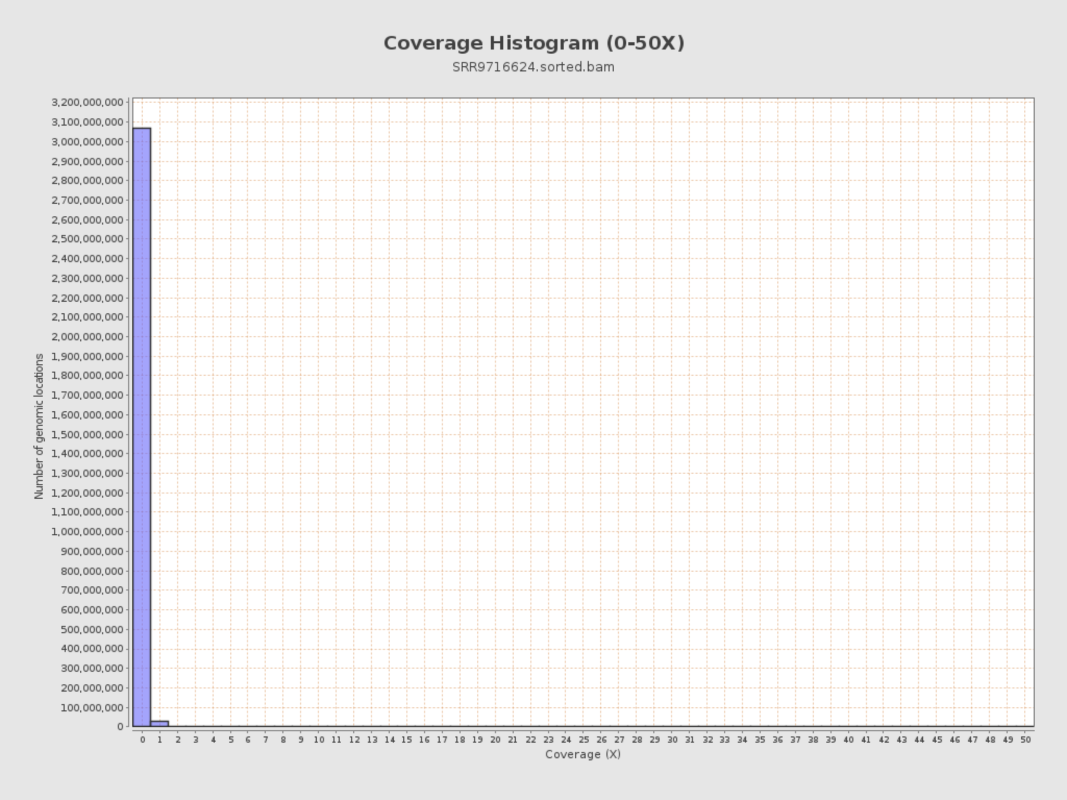
3. Results : Coverage across reference



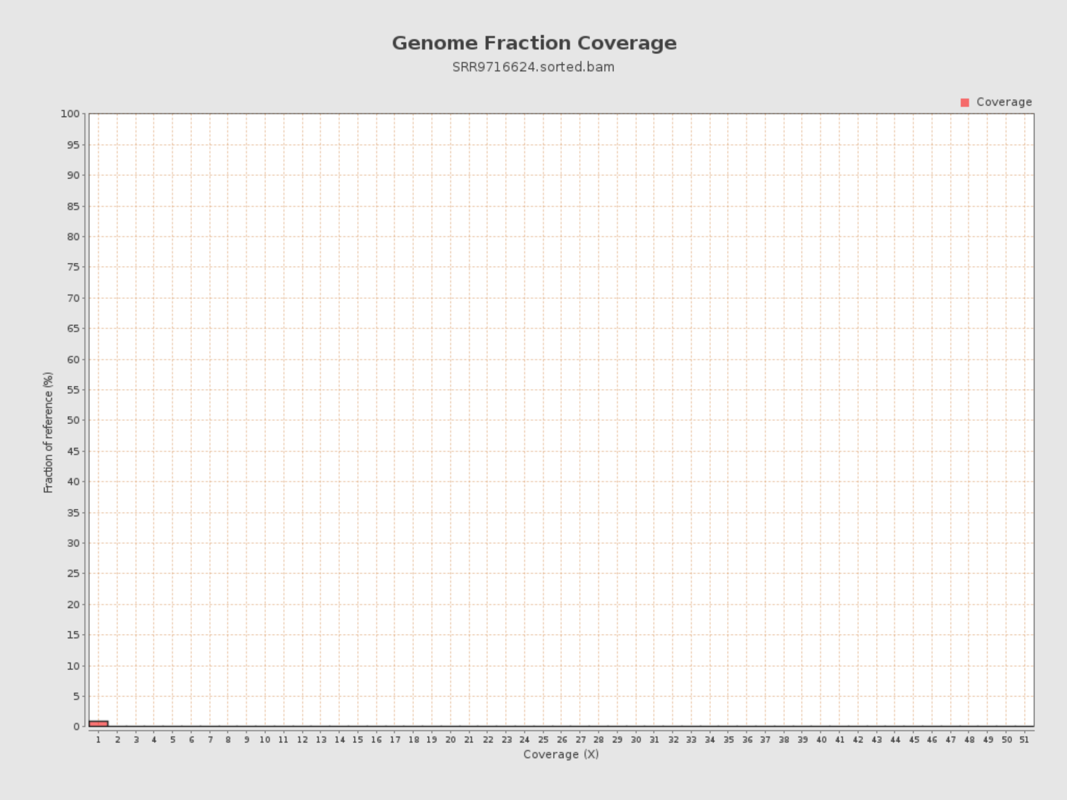
4. Results : Coverage Histogram



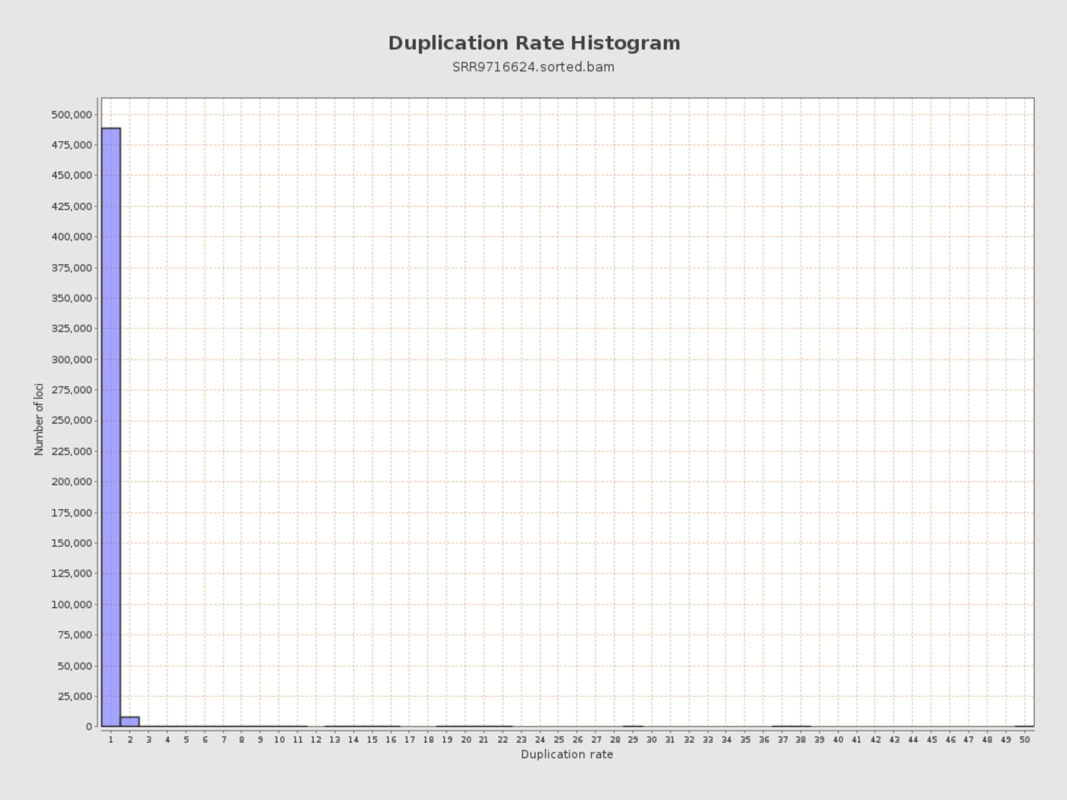
5. Results : Coverage Histogram (0-50X)



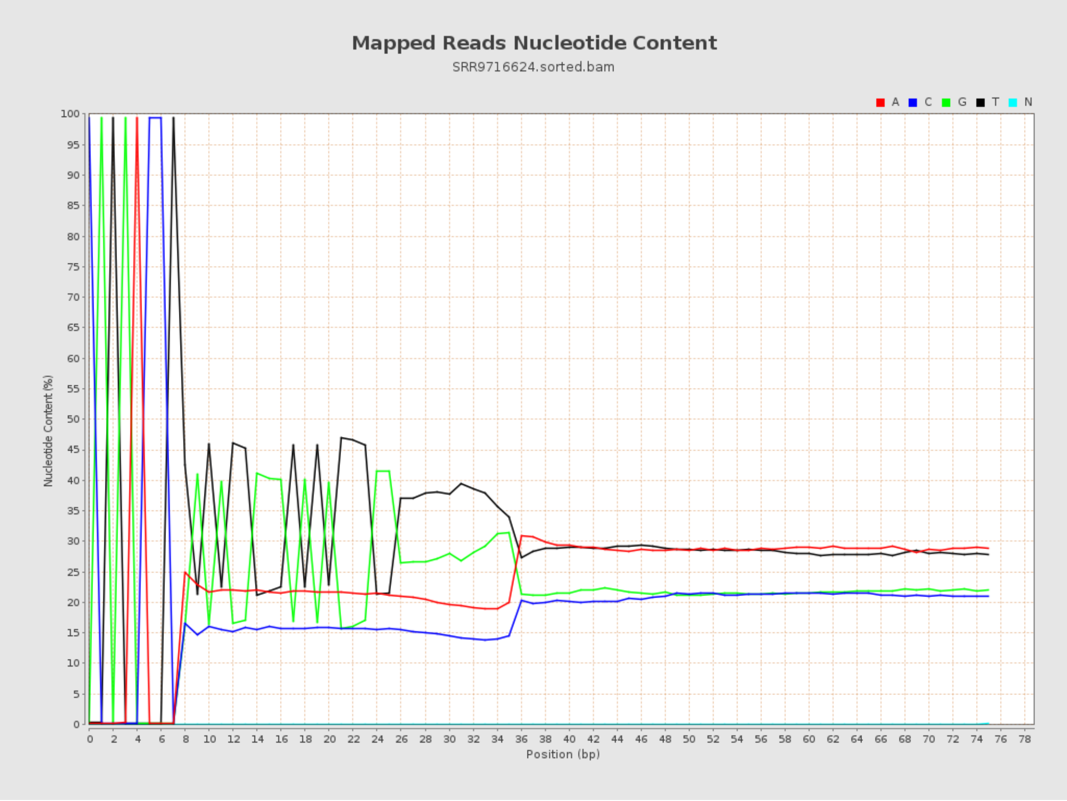
6. Results : Genome Fraction Coverage



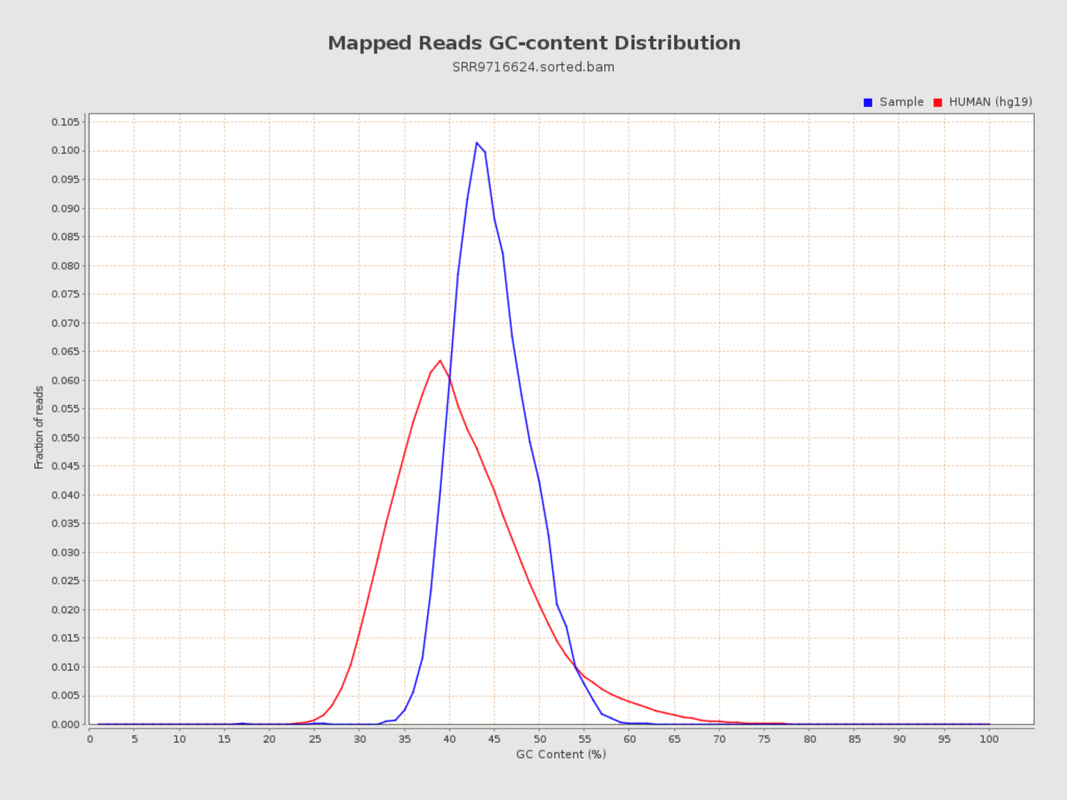
7. Results : Duplication Rate Histogram



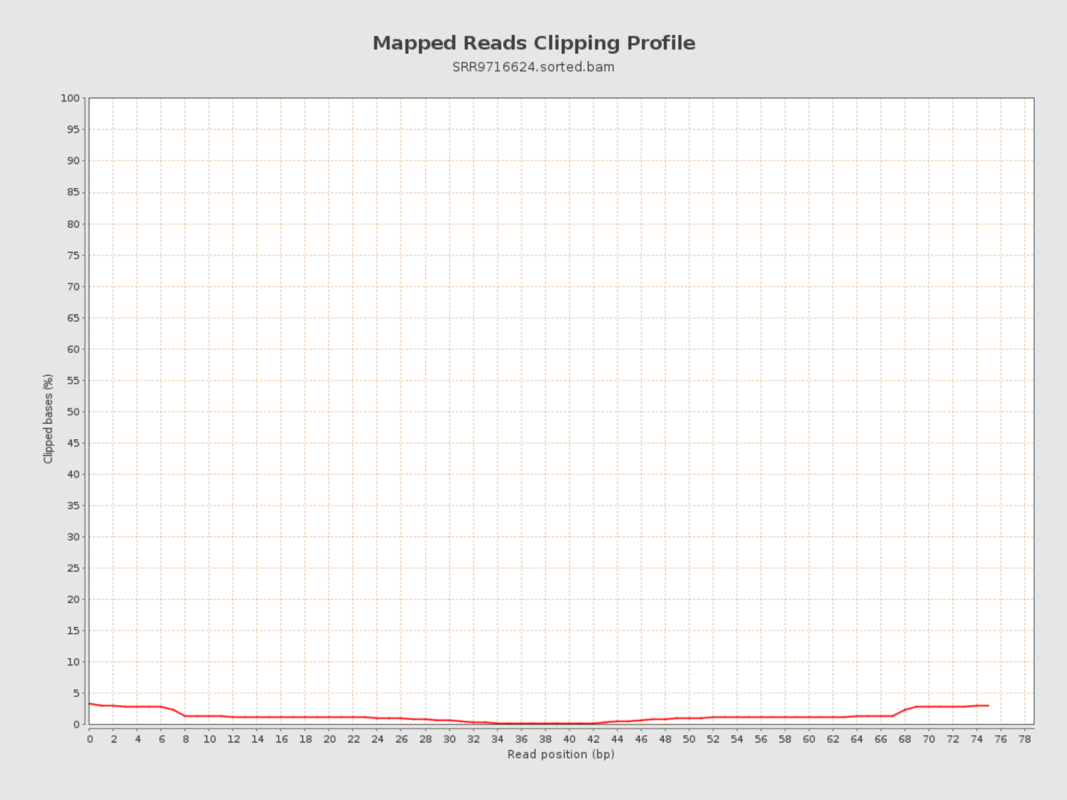
8. Results : Mapped Reads Nucleotide Content



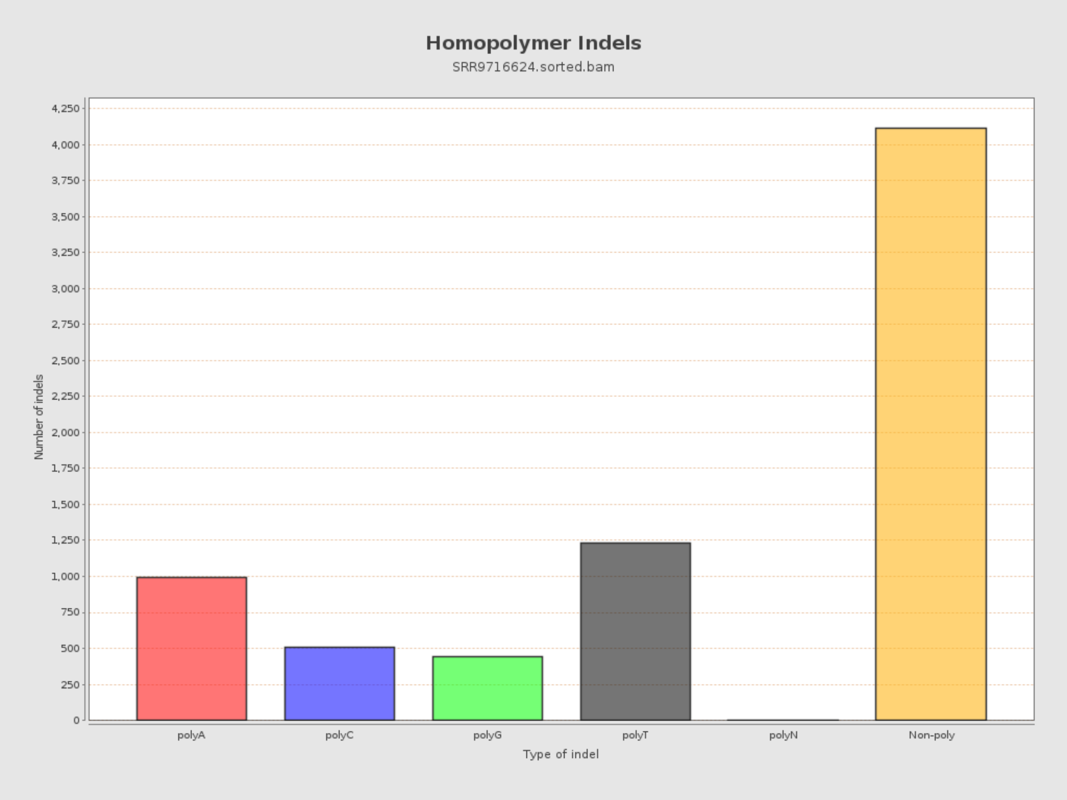
9. Results : Mapped Reads GC-content Distribution



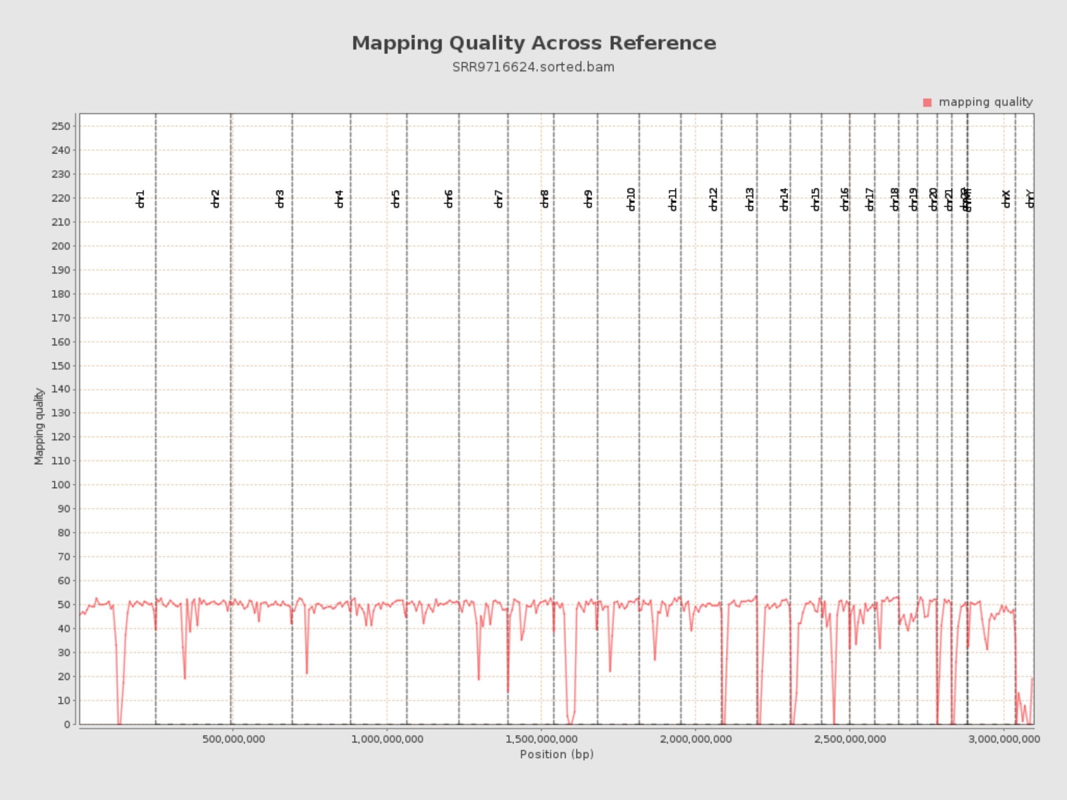
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram