Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:53:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716601.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_SRR9716601 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716601.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:53:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716601.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,360,915
Mapped reads	1,149,384 / 84.46%
Unmapped reads	211,531 / 15.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,385 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	35,697 / 2.62%
Duplication rate	2.39%
Clipped reads	1,151,578 / 84.62%

2.2. ACGT Content

Number/percentage of A's	16,810,419 / 25.28%
Number/percentage of C's	12,728,471 / 19.14%
Number/percentage of T's	21,059,818 / 31.67%
Number/percentage of G's	15,902,920 / 23.91%
Number/percentage of N's	813 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0215

Standard Deviation	0.2028

2.4. Mapping Quality

Mean Mapping Quality	44.76

2.5. Mismatches and indels

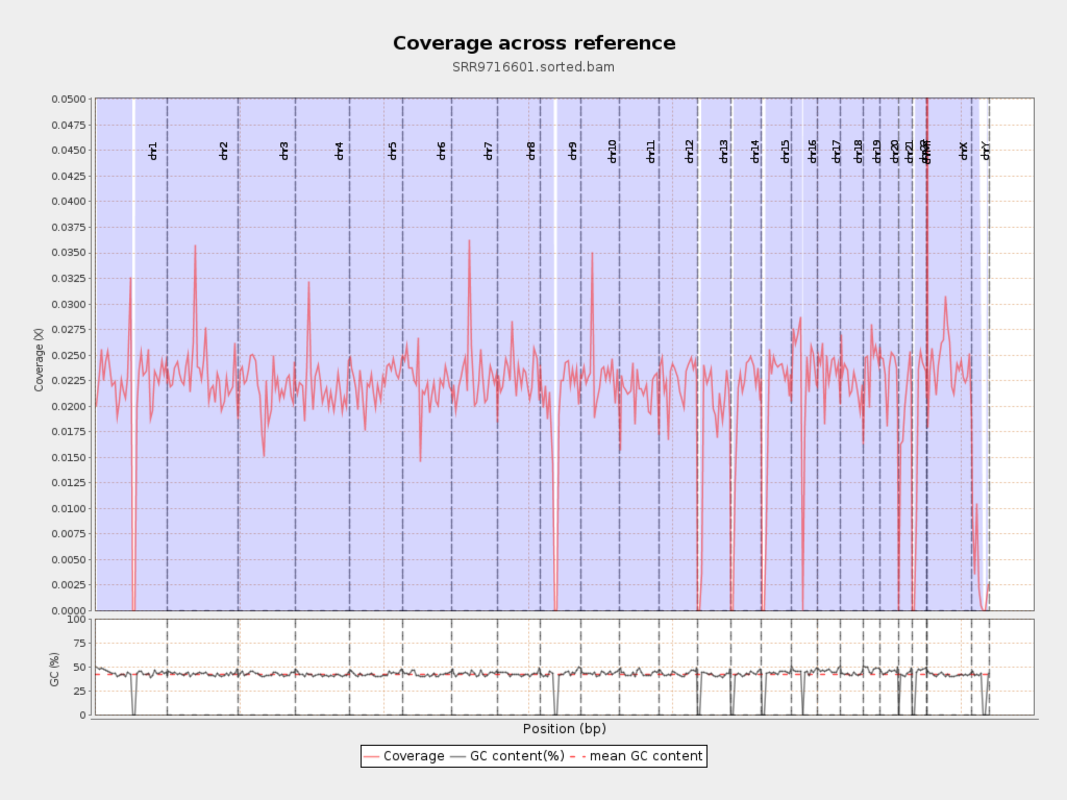
General error rate	0.51%
Mismatches	327,179
Insertions	5,363
Mapped reads with at least one insertion	0.47%
Deletions	12,022
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.51%

2.6. Chromosome stats

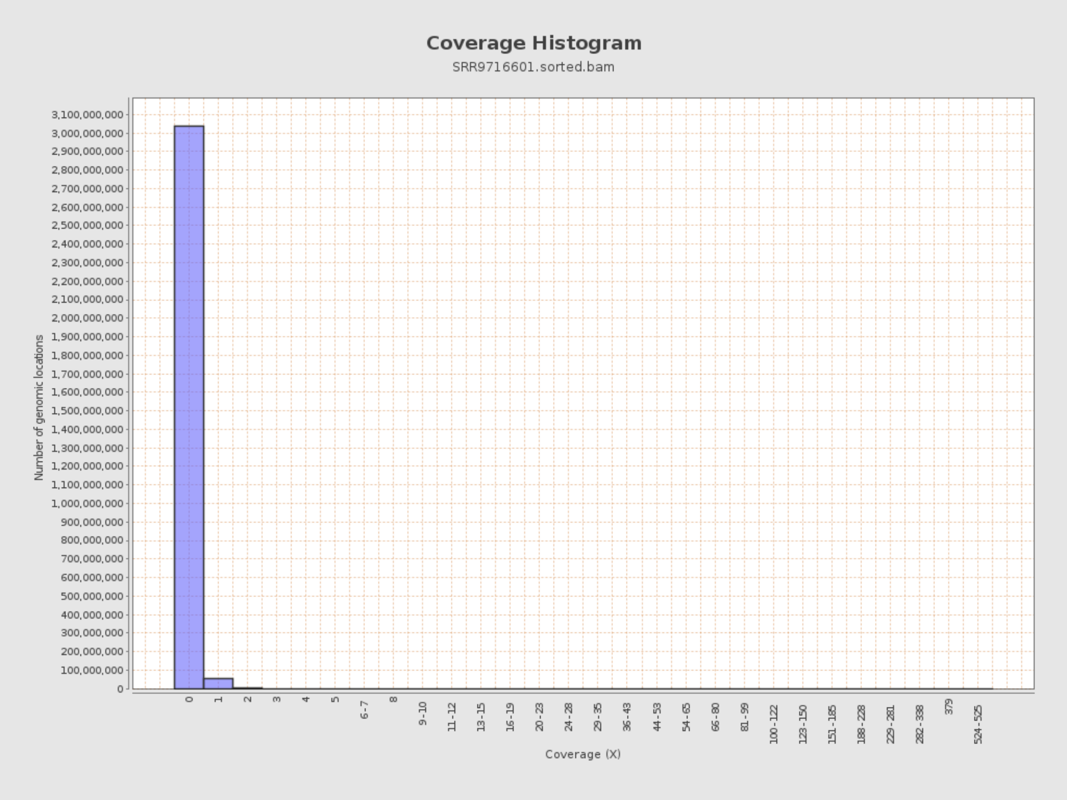
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5361802	0.0215	0.3001
chr2	243199373	5644816	0.0232	0.2788
chr3	198022430	4312894	0.0218	0.1584
chr4	191154276	4194684	0.0219	0.1706
chr5	180915260	4042920	0.0223	0.1603
chr6	171115067	3803207	0.0222	0.1721
chr7	159138663	3673780	0.0231	0.2689

chr8	146364022	3381388	0.0231	0.1939
chr9	141213431	2700552	0.0191	0.17
chr10	135534747	3133462	0.0231	0.2027
chr11	135006516	2913103	0.0216	0.1873
chr12	133851895	3036292	0.0227	0.163
chr13	115169878	2030976	0.0176	0.1432
chr14	107349540	2071950	0.0193	0.1546
chr15	102531392	1961404	0.0191	0.1547
chr16	90354753	2017411	0.0223	0.1662
chr17	81195210	1911780	0.0235	0.1726
chr18	78077248	1747836	0.0224	0.2677
chr19	59128983	1435048	0.0243	0.2434
chr20	63025520	1466269	0.0233	0.1655
chr21	48129895	883768	0.0184	0.1576
chr22	51304566	858338	0.0167	0.1395
chrMT	16571	7447	0.4494	0.7284
chrX	155270560	3734395	0.0241	0.178
chrY	59373566	195916	0.0033	0.0883

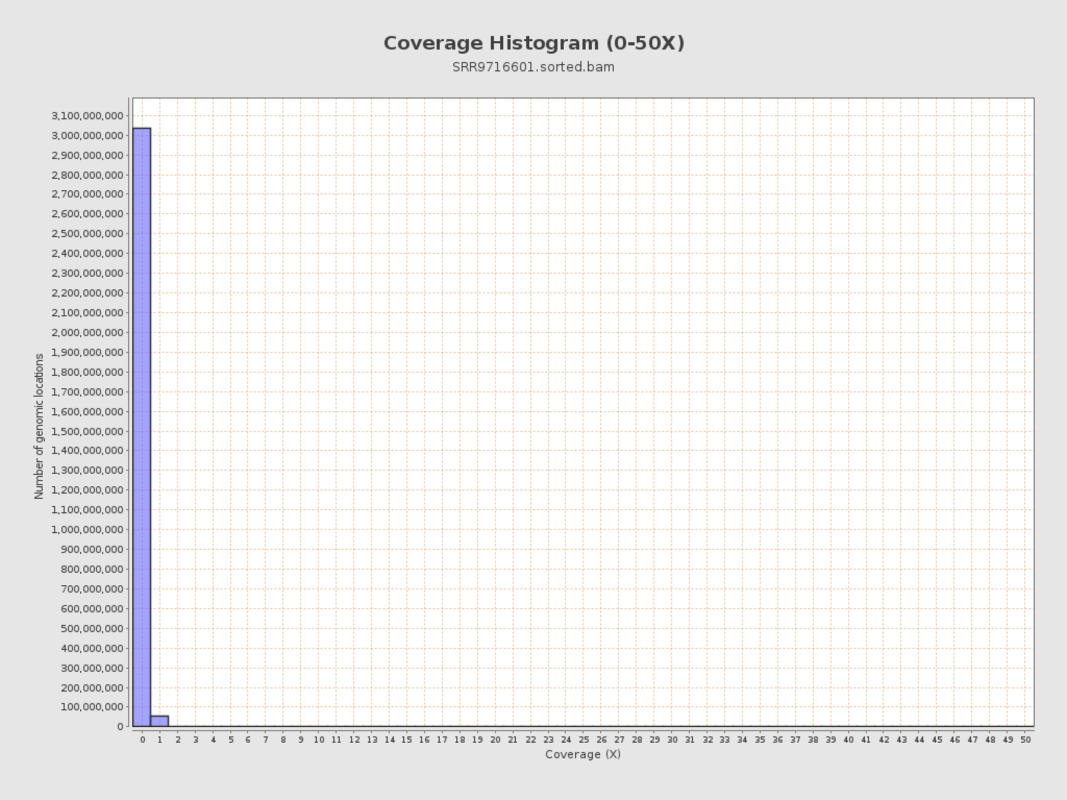
3. Results : Coverage across reference



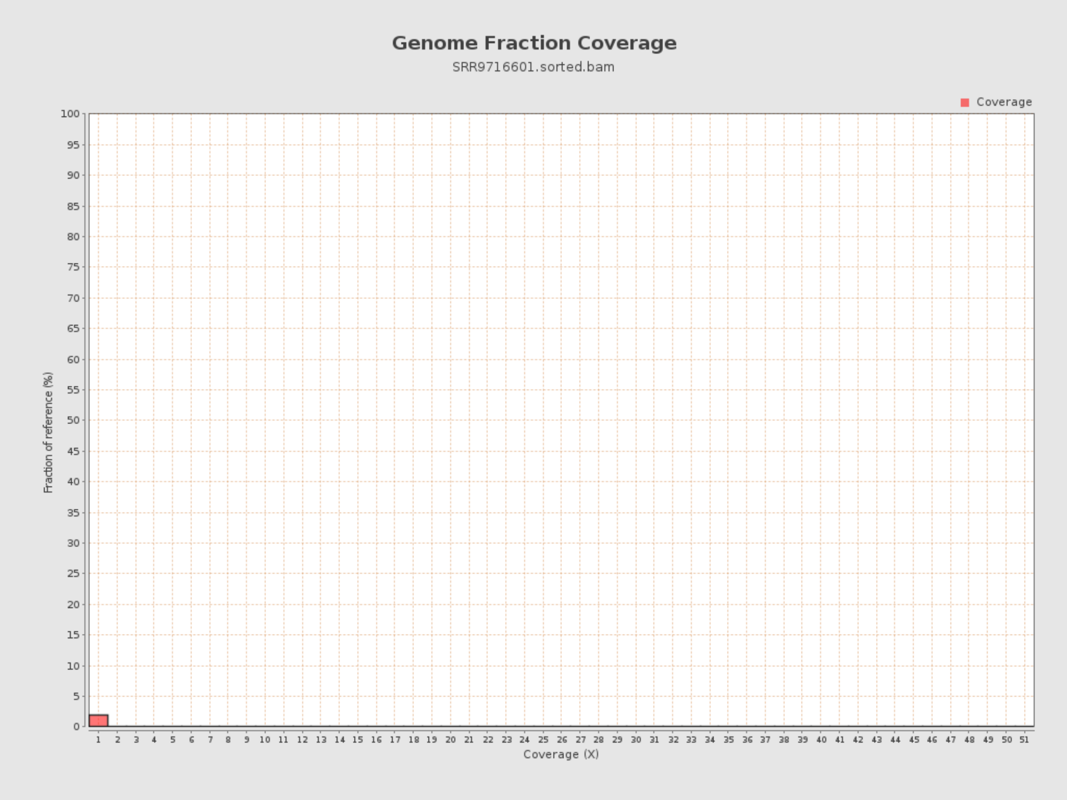
4. Results : Coverage Histogram



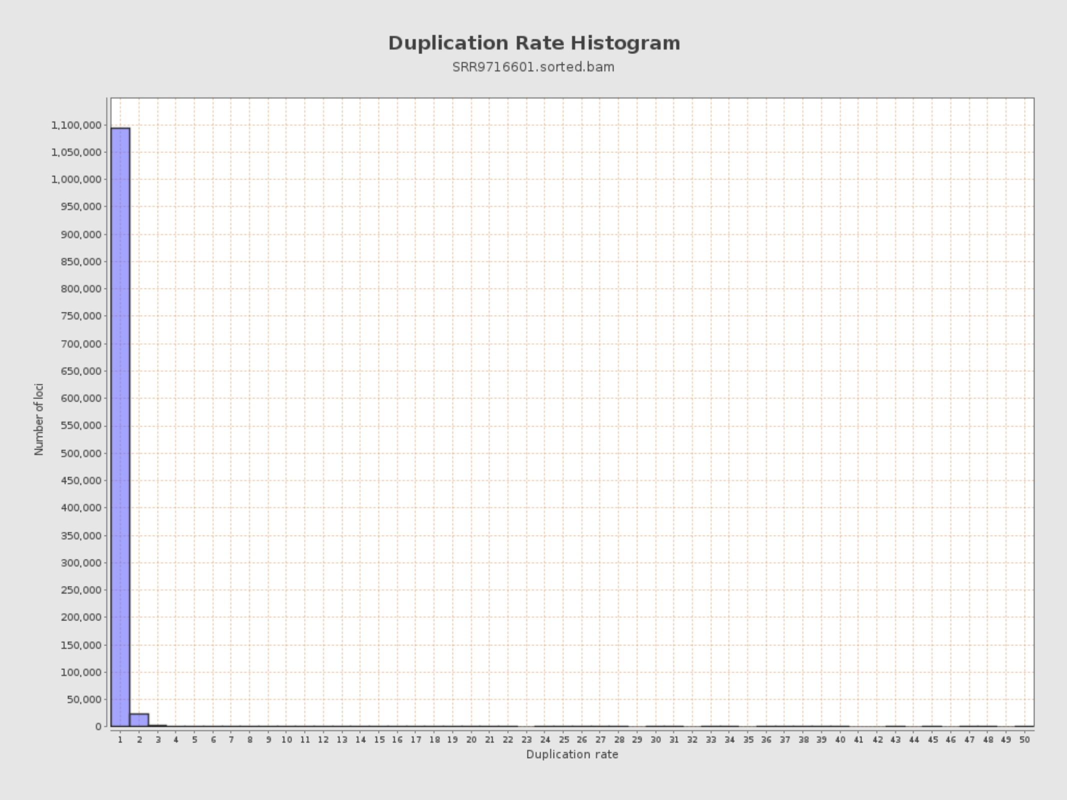
5. Results : Coverage Histogram (0-50X)



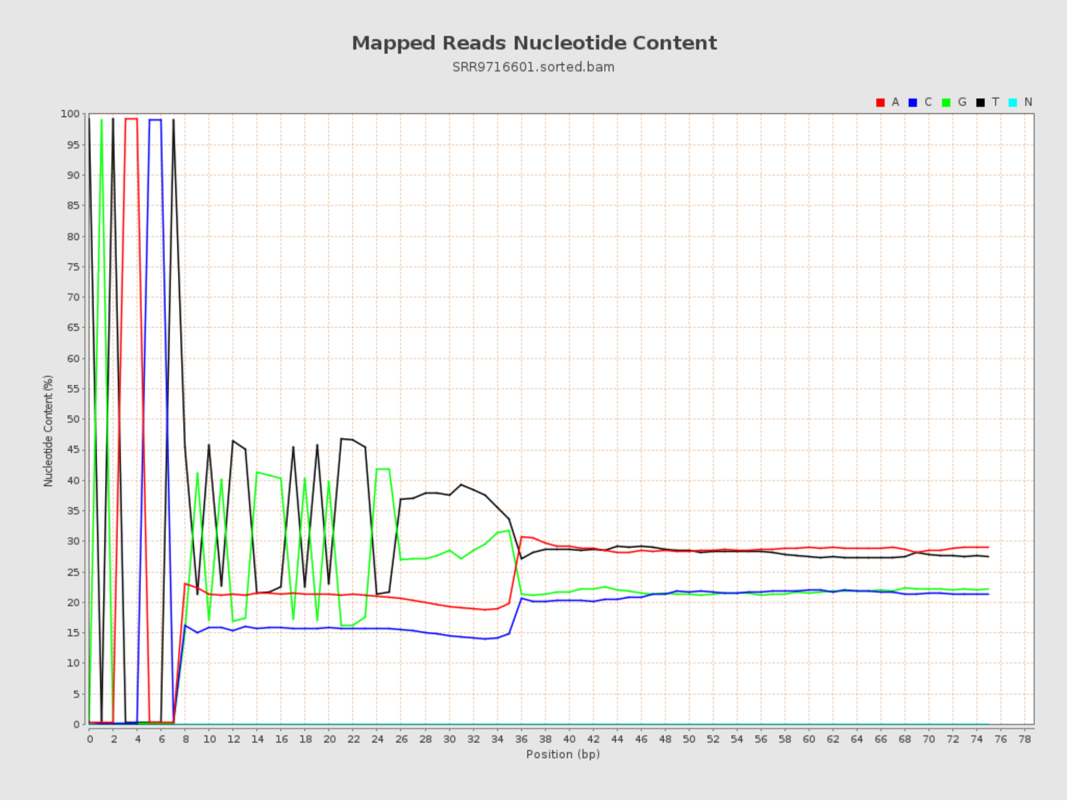
6. Results : Genome Fraction Coverage



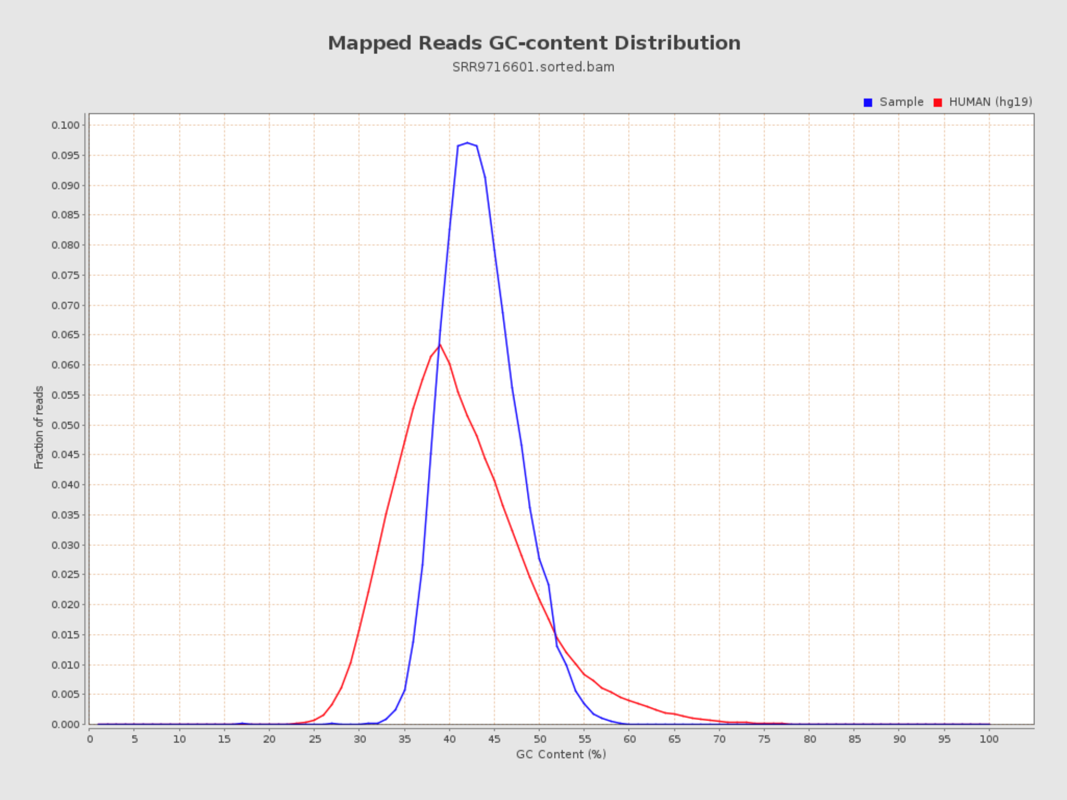
7. Results : Duplication Rate Histogram



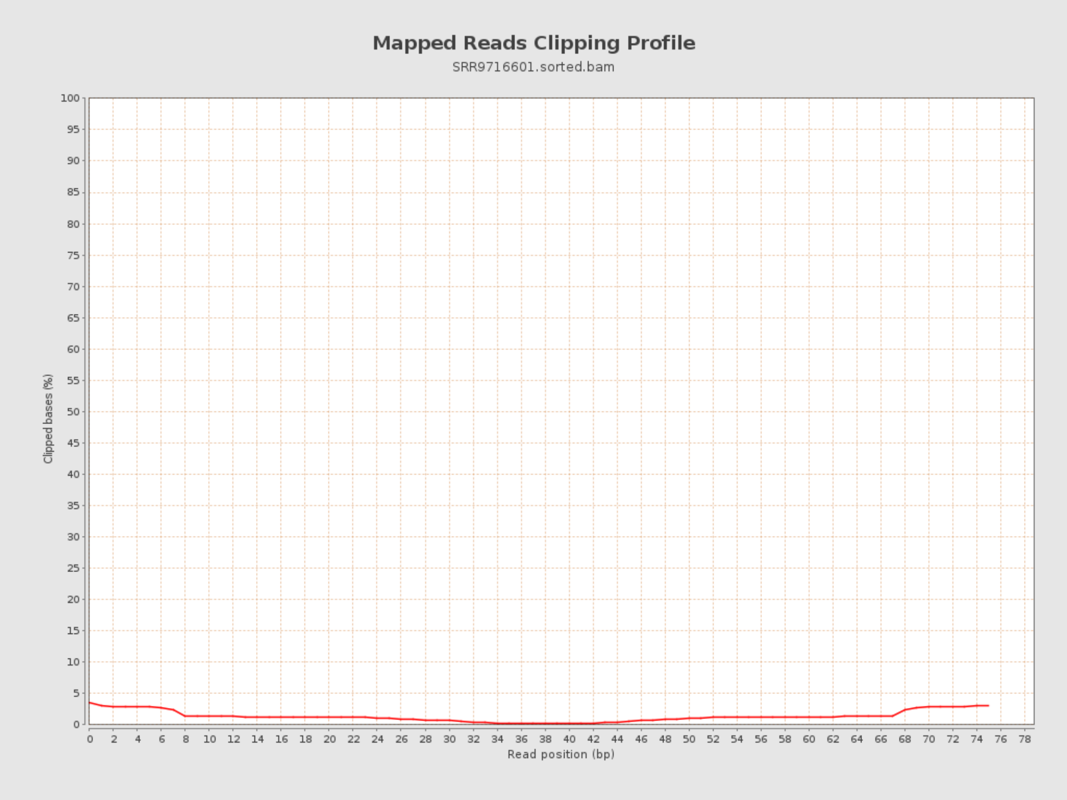
8. Results : Mapped Reads Nucleotide Content



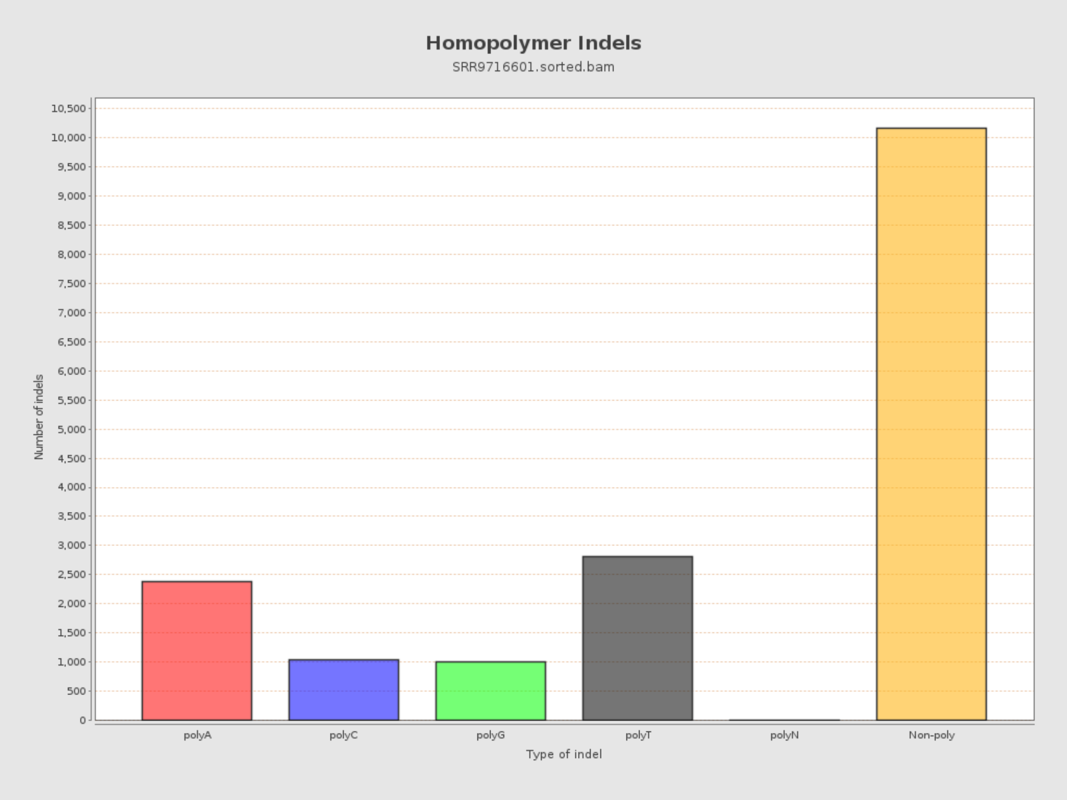
9. Results : Mapped Reads GC-content Distribution



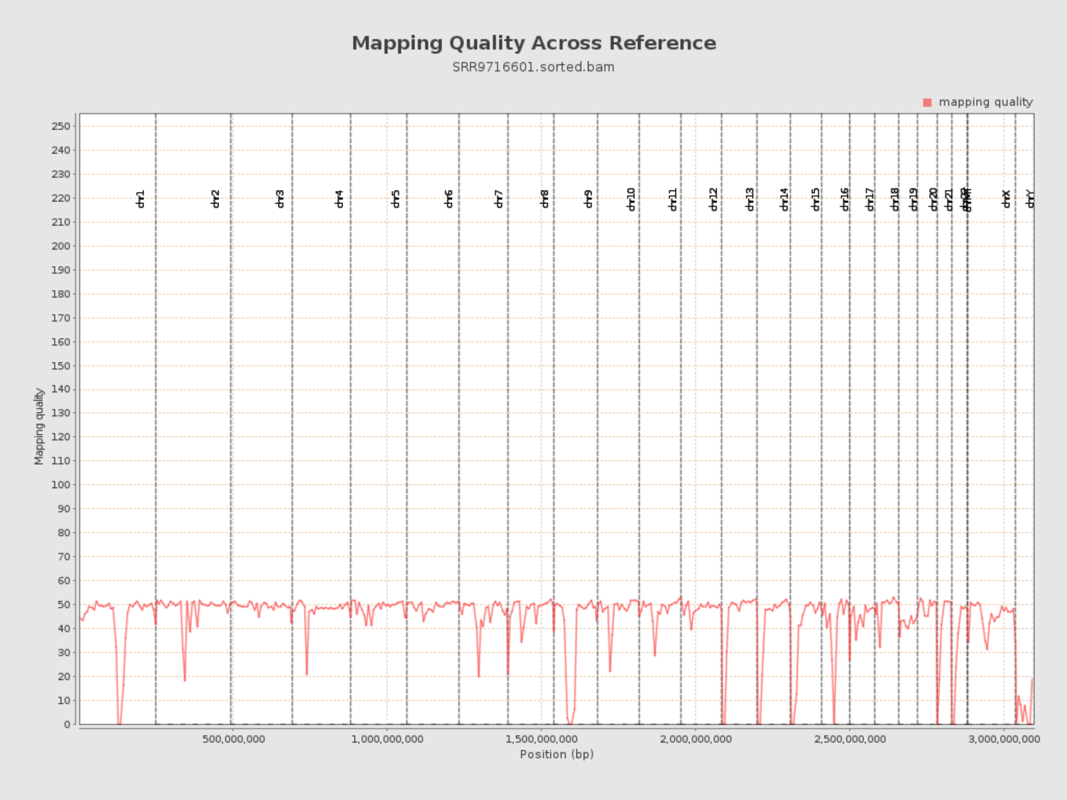
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram