Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:49:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716121.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_SRR9716121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:49:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,431,792
Mapped reads	1,215,416 / 84.89%
Unmapped reads	216,376 / 15.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,839 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	30,865 / 2.16%
Duplication rate	1.77%
Clipped reads	1,216,761 / 84.98%

2.2. ACGT Content

Number/percentage of A's	17,239,159 / 25.2%
Number/percentage of C's	13,666,585 / 19.98%
Number/percentage of T's	21,074,152 / 30.81%
Number/percentage of G's	16,420,022 / 24.01%
Number/percentage of N's	1,052 / 0%
GC Percentage	43.99%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2255

2.4. Mapping Quality

Mean Mapping Quality	42.07

2.5. Mismatches and indels

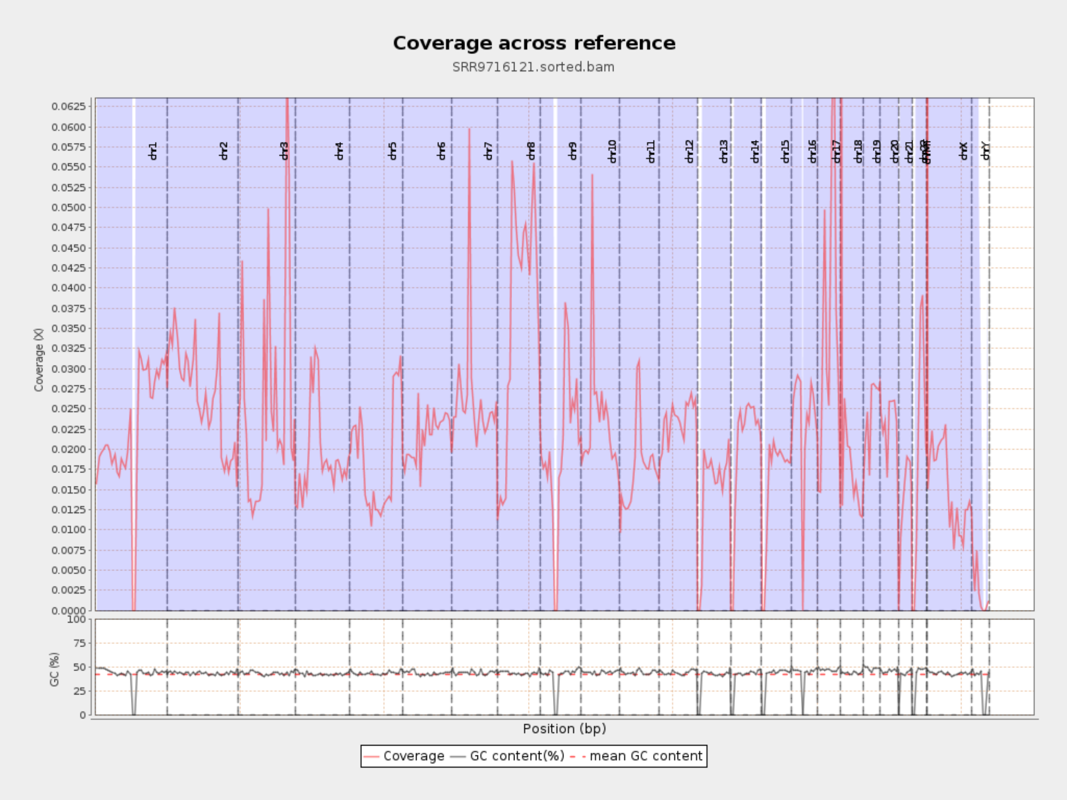
General error rate	0.53%
Mismatches	351,169
Insertions	5,490
Mapped reads with at least one insertion	0.45%
Deletions	12,495
Mapped reads with at least one deletion	1.02%
Homopolymer indels	38.67%

2.6. Chromosome stats

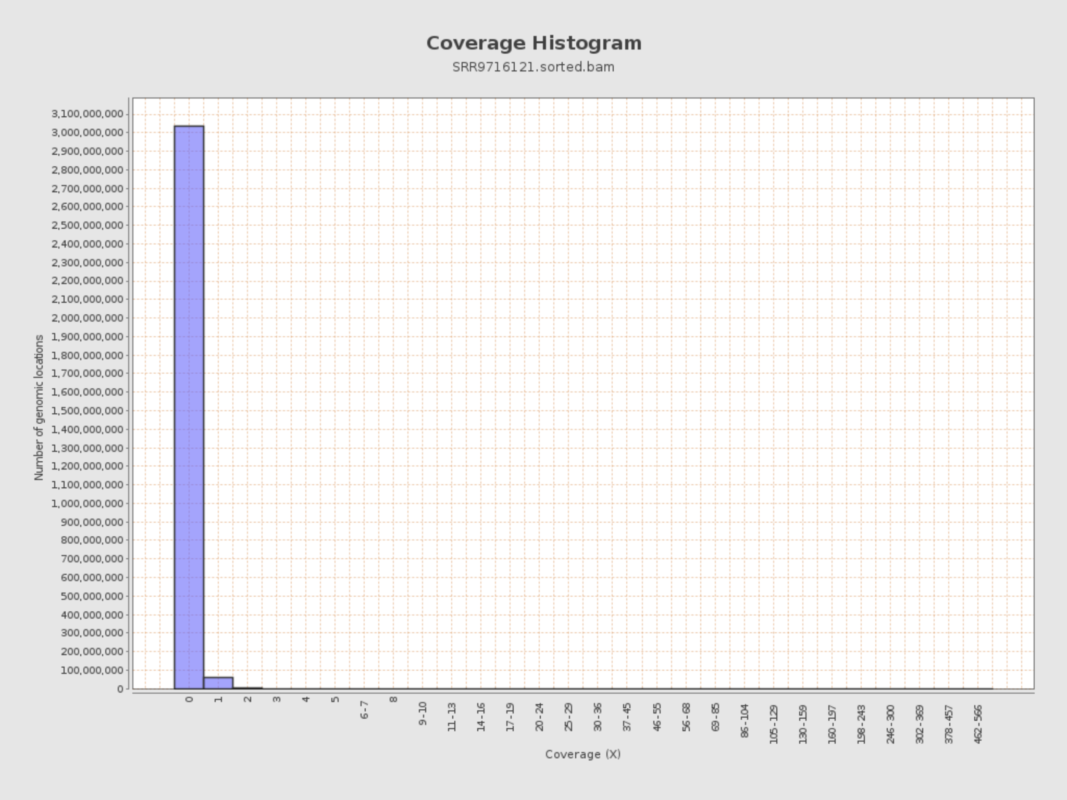
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5553849	0.0223	0.2479
chr2	243199373	6520874	0.0268	0.2906
chr3	198022430	5092109	0.0257	0.1822
chr4	191154276	3678655	0.0192	0.1524
chr5	180915260	3366966	0.0186	0.146
chr6	171115067	3697653	0.0216	0.1704
chr7	159138663	4201818	0.0264	0.5253

chr8	146364022	5486048	0.0375	0.2346
chr9	141213431	2796848	0.0198	0.1648
chr10	135534747	3206416	0.0237	0.2655
chr11	135006516	2423048	0.0179	0.1632
chr12	133851895	3144244	0.0235	0.1698
chr13	115169878	1704490	0.0148	0.1295
chr14	107349540	2160719	0.0201	0.1544
chr15	102531392	1608210	0.0157	0.1384
chr16	90354753	2100962	0.0233	0.1693
chr17	81195210	2885734	0.0355	0.2103
chr18	78077248	1561680	0.02	0.2311
chr19	59128983	1447853	0.0245	0.2364
chr20	63025520	1456695	0.0231	0.1677
chr21	48129895	665064	0.0138	0.1282
chr22	51304566	1033153	0.0201	0.1532
chrMT	16571	117535	7.0928	4.7443
chrX	155270560	2365995	0.0152	0.1482
chrY	59373566	144192	0.0024	0.0662

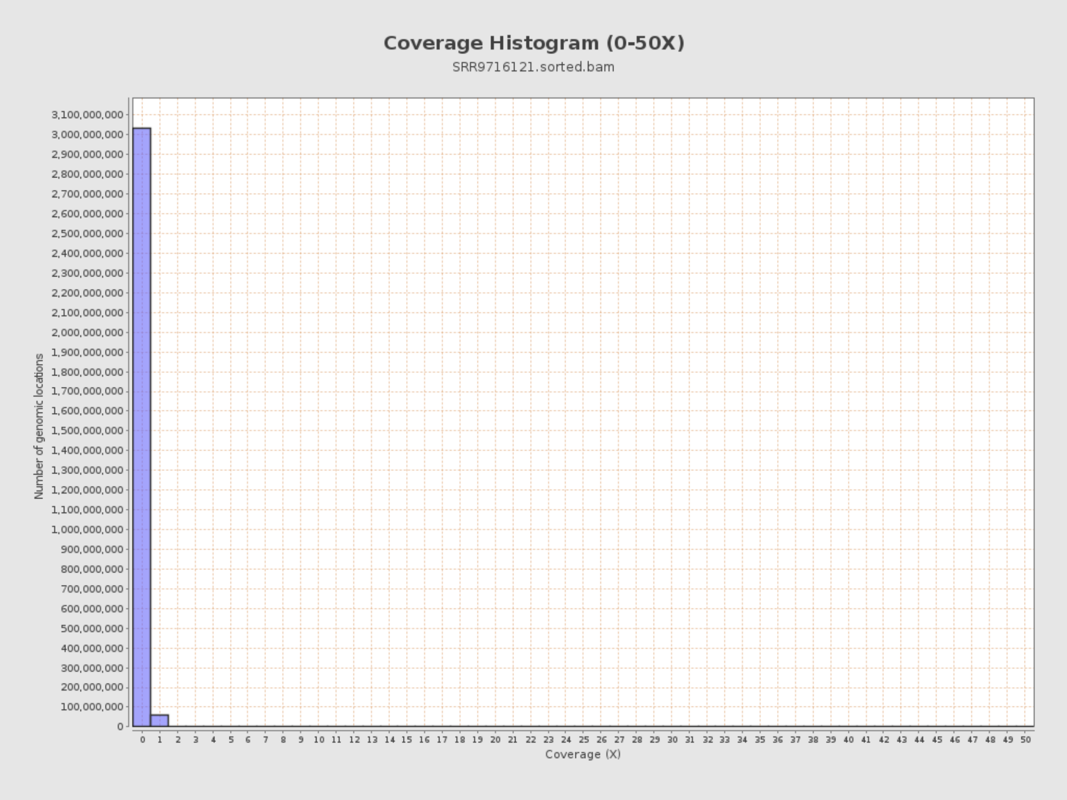
3. Results : Coverage across reference



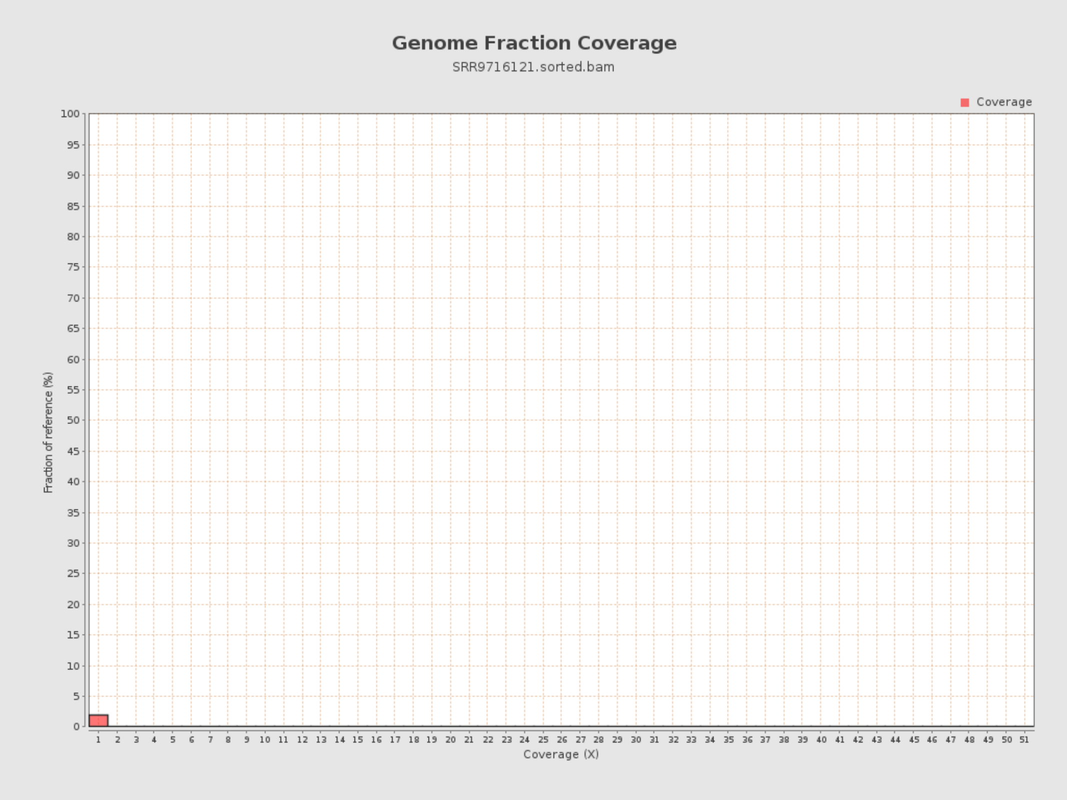
4. Results : Coverage Histogram



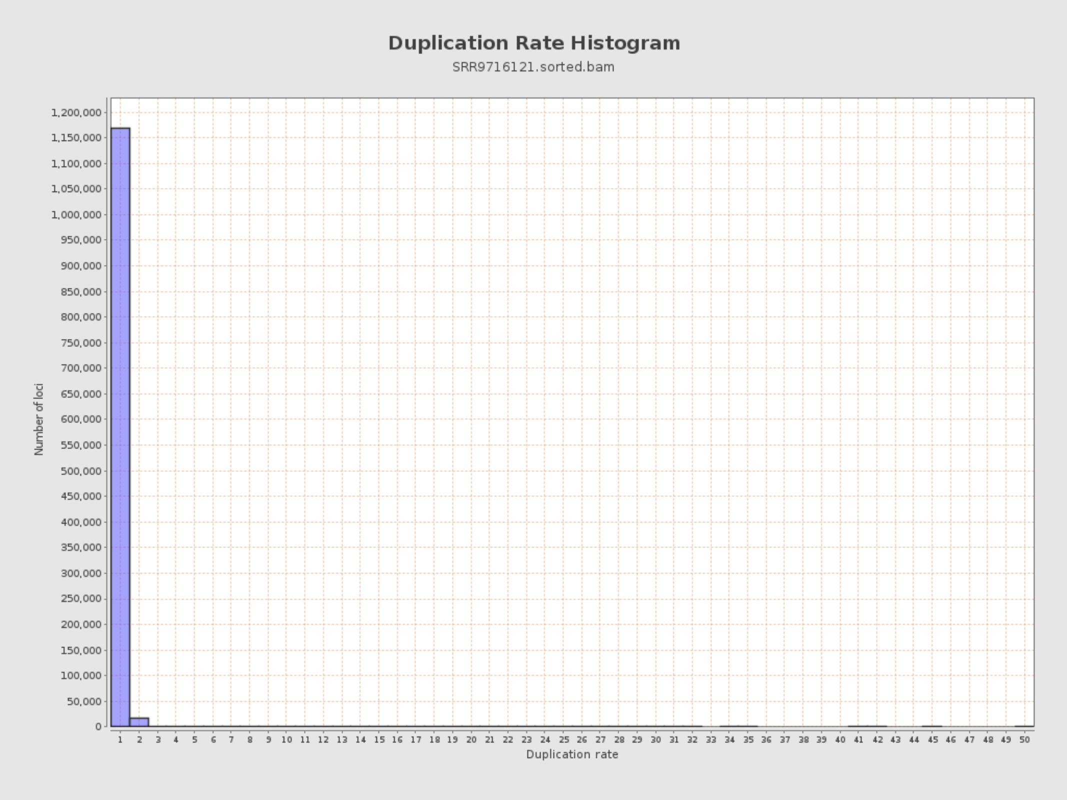
5. Results : Coverage Histogram (0-50X)



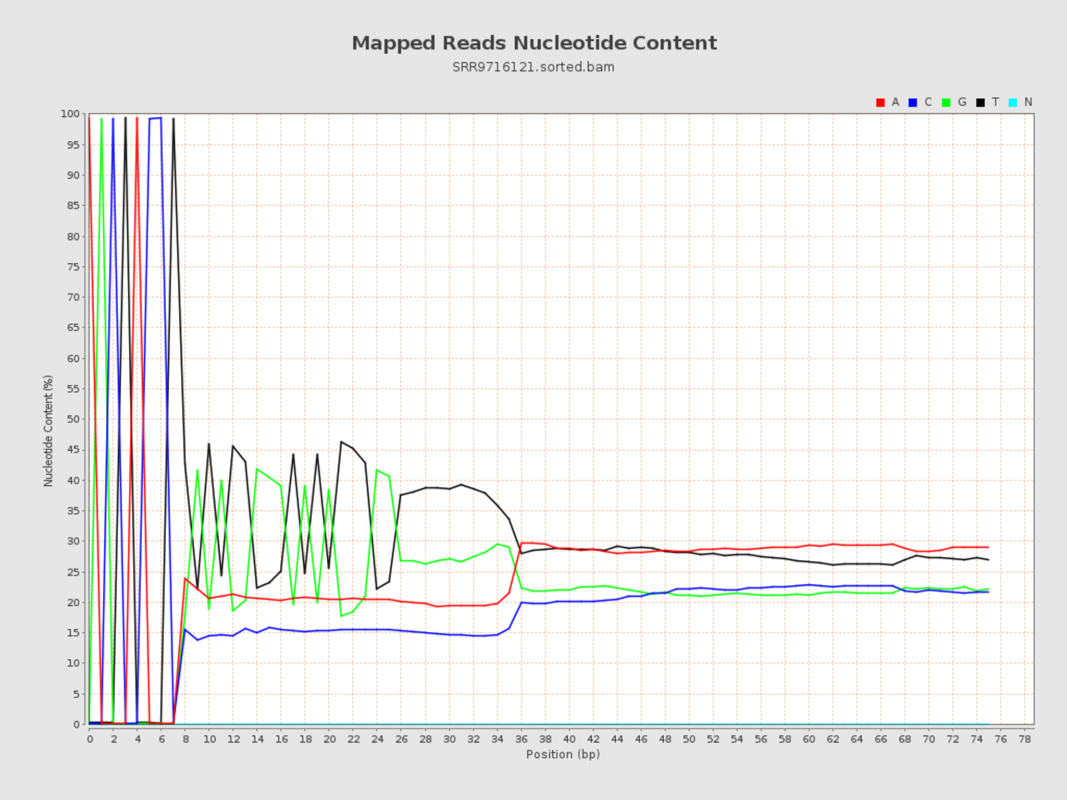
6. Results : Genome Fraction Coverage



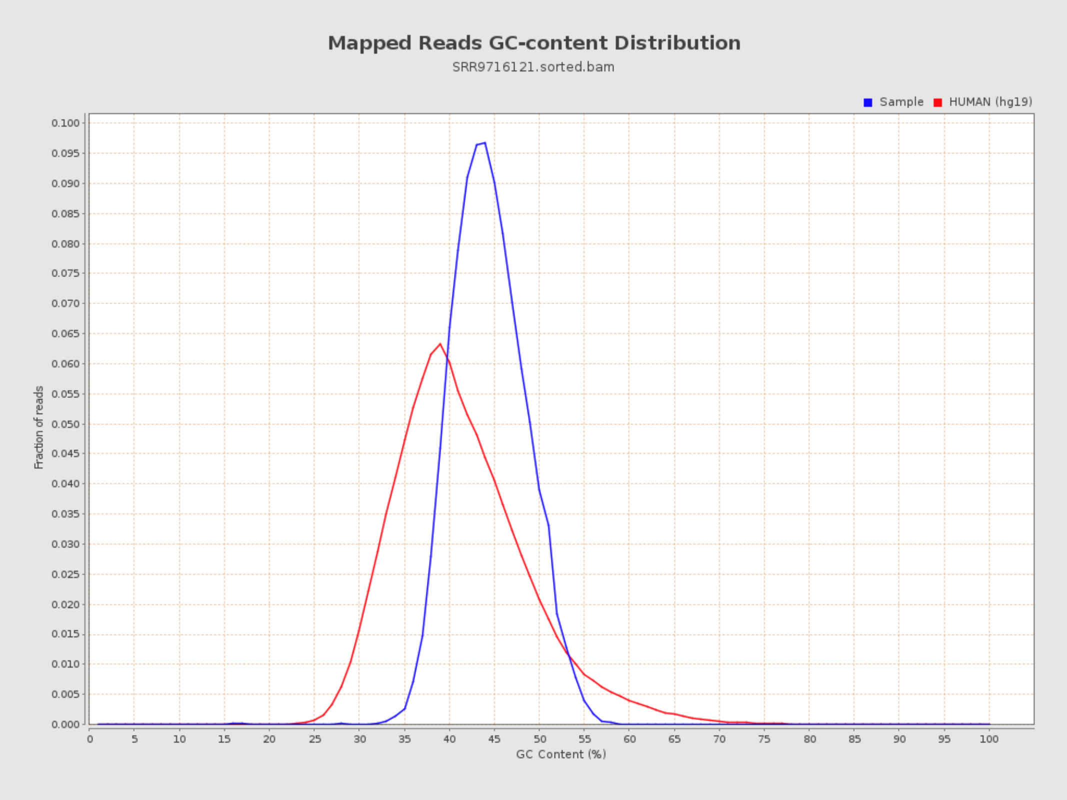
7. Results : Duplication Rate Histogram



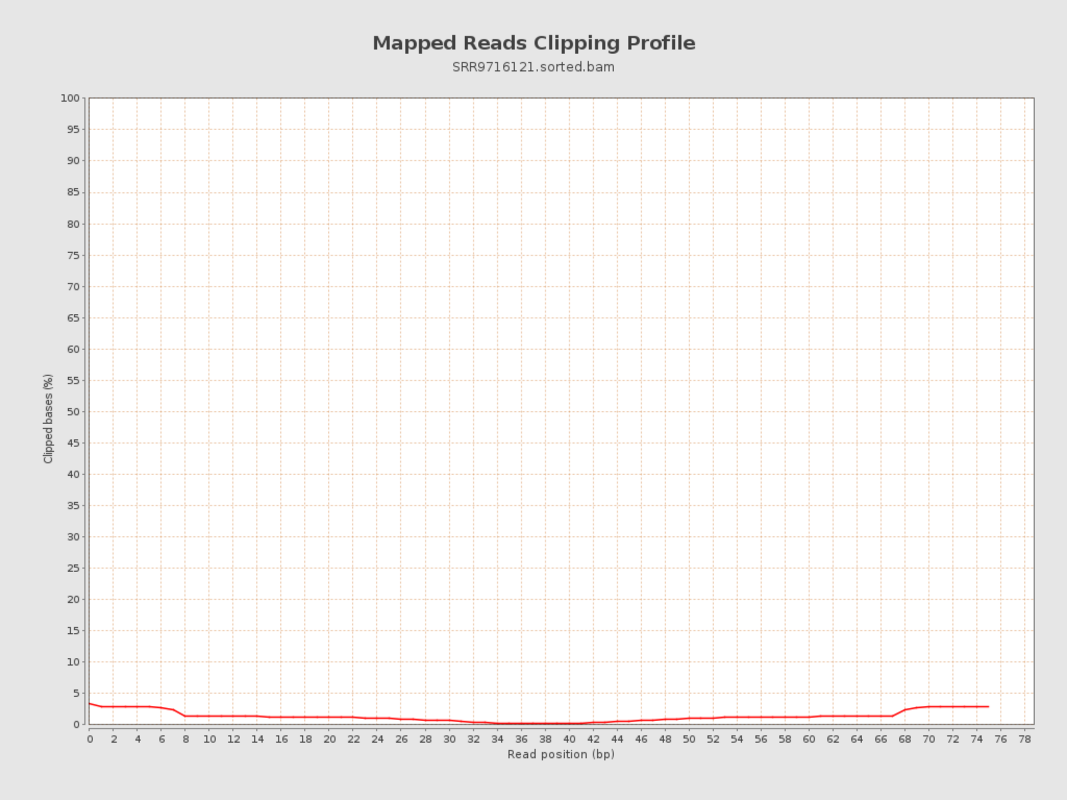
8. Results : Mapped Reads Nucleotide Content



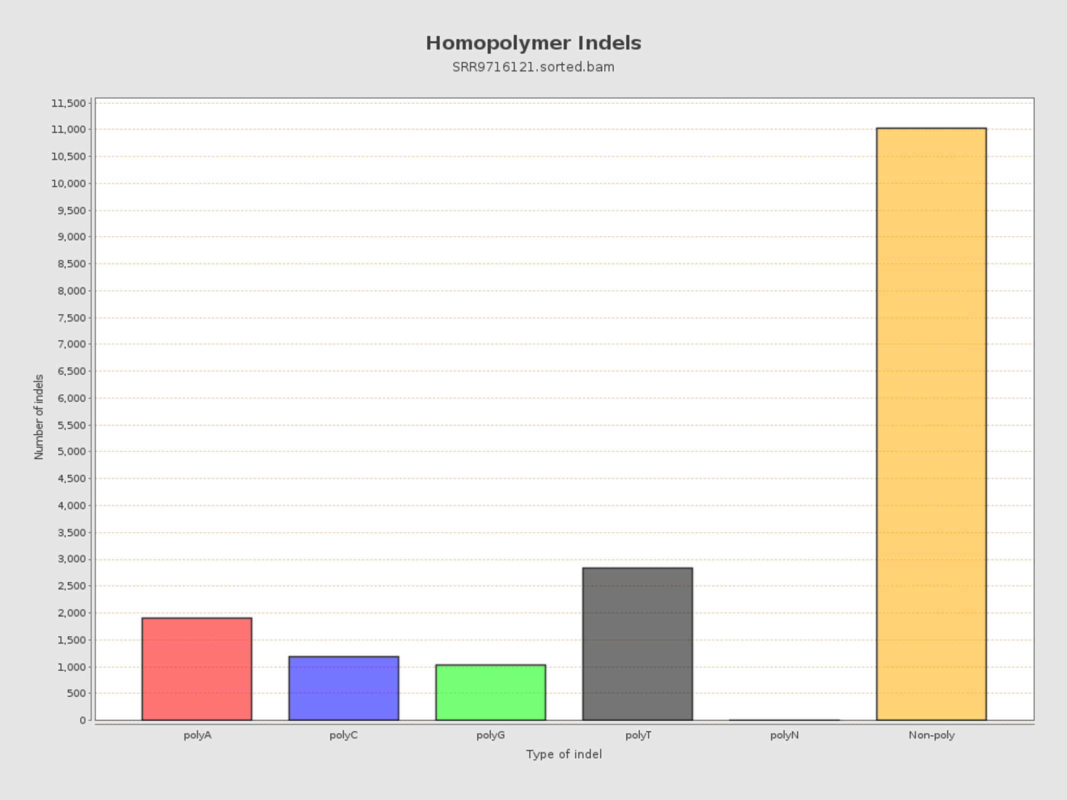
9. Results : Mapped Reads GC-content Distribution



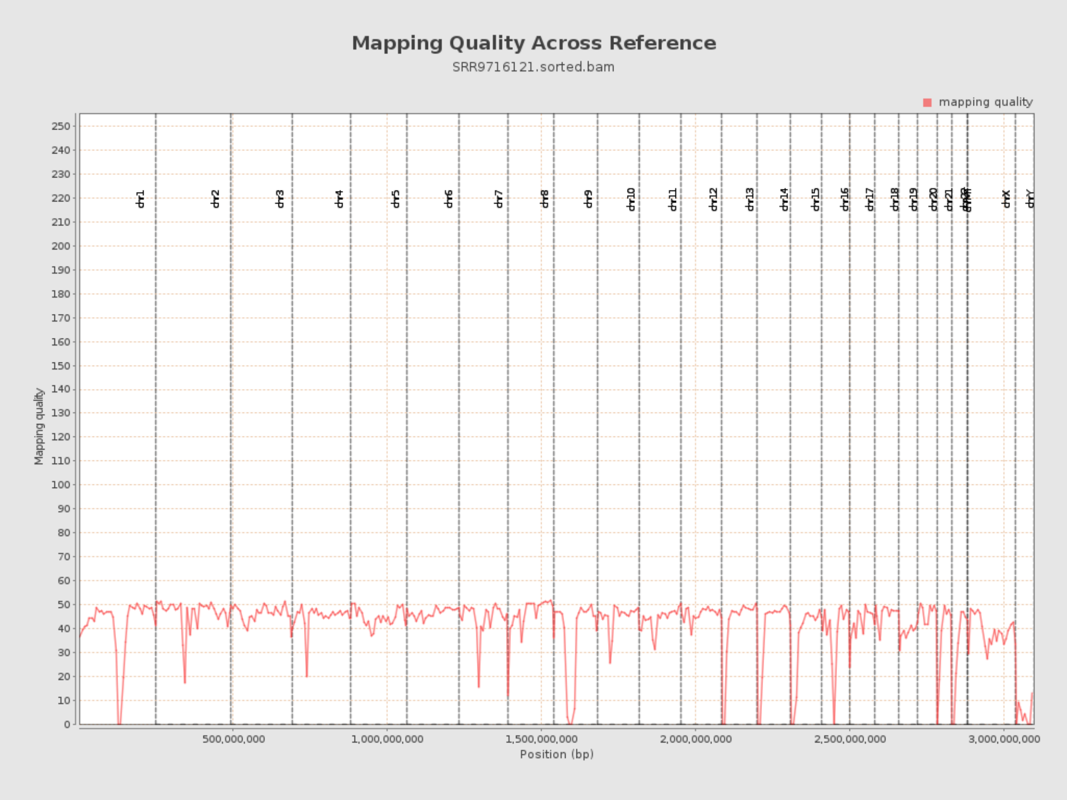
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram