Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:48:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716721.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_SRR9716721 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716721.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:48:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716721.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,251,767
Mapped reads	2,053,394 / 91.19%
Unmapped reads	198,373 / 8.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,691 / 0.52%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	77,525 / 3.44%
Duplication rate	2.66%
Clipped reads	2,059,257 / 91.45%

2.2. ACGT Content

Number/percentage of A's	31,349,693 / 26.34%
Number/percentage of C's	22,885,760 / 19.23%
Number/percentage of T's	35,716,916 / 30.01%
Number/percentage of G's	29,059,301 / 24.42%
Number/percentage of N's	1,446 / 0%
GC Percentage	43.65%

2.3. Coverage

Mean	0.0385

Standard Deviation	0.3542

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

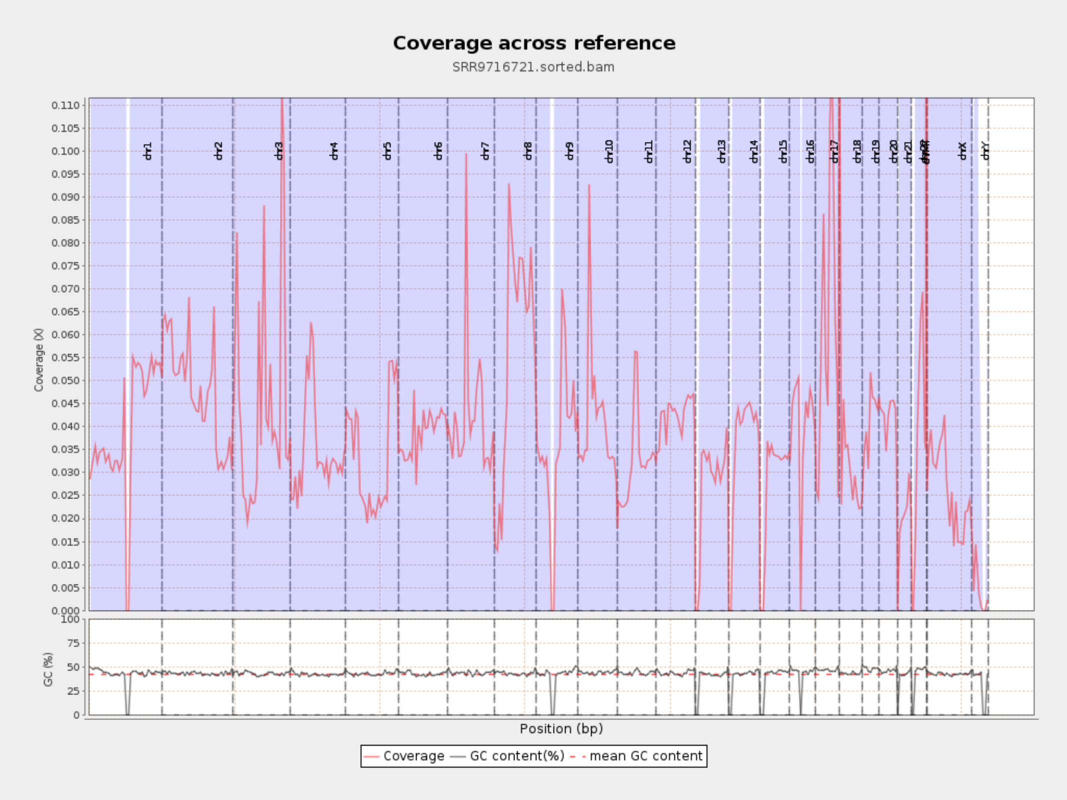
General error rate	0.52%
Mismatches	599,829
Insertions	8,845
Mapped reads with at least one insertion	0.43%
Deletions	21,262
Mapped reads with at least one deletion	1.03%
Homopolymer indels	39.88%

2.6. Chromosome stats

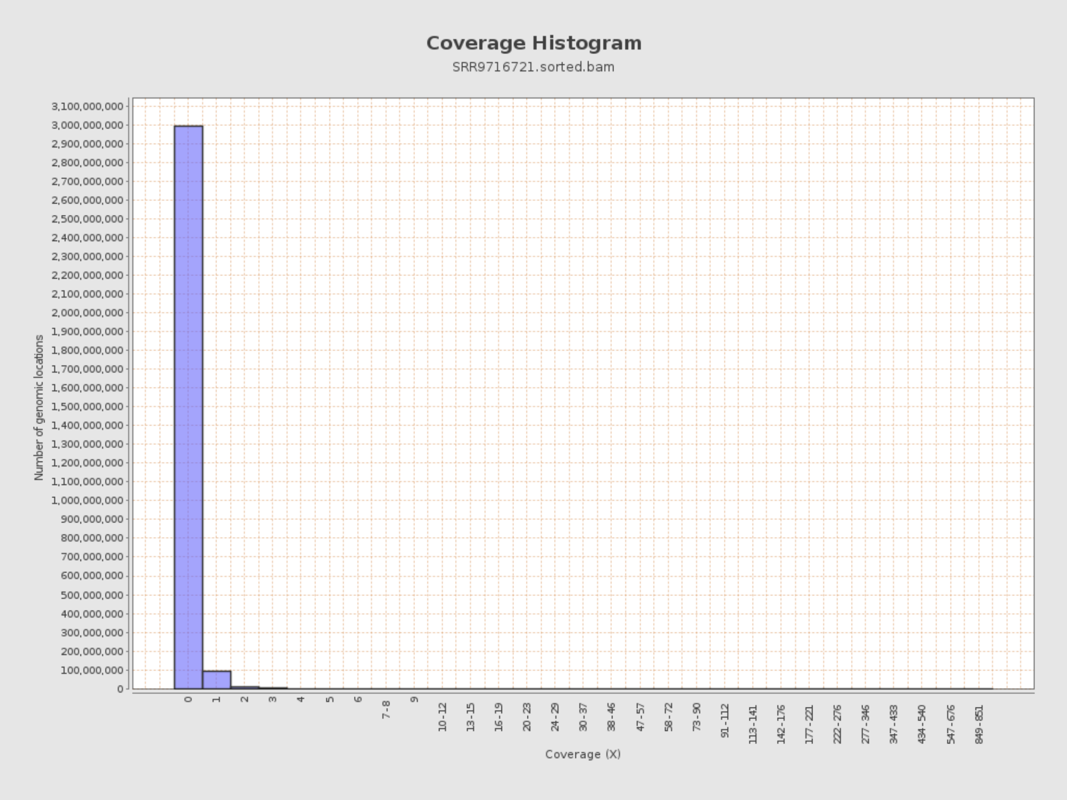
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9792639	0.0393	0.4686
chr2	243199373	11738204	0.0483	0.4368
chr3	198022430	8948778	0.0452	0.2531
chr4	191154276	6677942	0.0349	0.2268
chr5	180915260	6010953	0.0332	0.2037
chr6	171115067	6619447	0.0387	0.2398
chr7	159138663	6699355	0.0421	0.8511

chr8	146364022	8399747	0.0574	0.3552
chr9	141213431	4989574	0.0353	0.2502
chr10	135534747	5604102	0.0413	0.4304
chr11	135006516	4332243	0.0321	0.243
chr12	133851895	5659870	0.0423	0.2523
chr13	115169878	3108588	0.027	0.1837
chr14	107349540	3833289	0.0357	0.2144
chr15	102531392	2838394	0.0277	0.1987
chr16	90354753	3647927	0.0404	0.2355
chr17	81195210	5044493	0.0621	0.2931
chr18	78077248	2756245	0.0353	0.4004
chr19	59128983	2430996	0.0411	0.41
chr20	63025520	2664396	0.0423	0.2427
chr21	48129895	952512	0.0198	0.1685
chr22	51304566	1810413	0.0353	0.2081
chrMT	16571	57369	3.462	2.533
chrX	155270560	4162420	0.0268	0.2161
chrY	59373566	266835	0.0045	0.1129

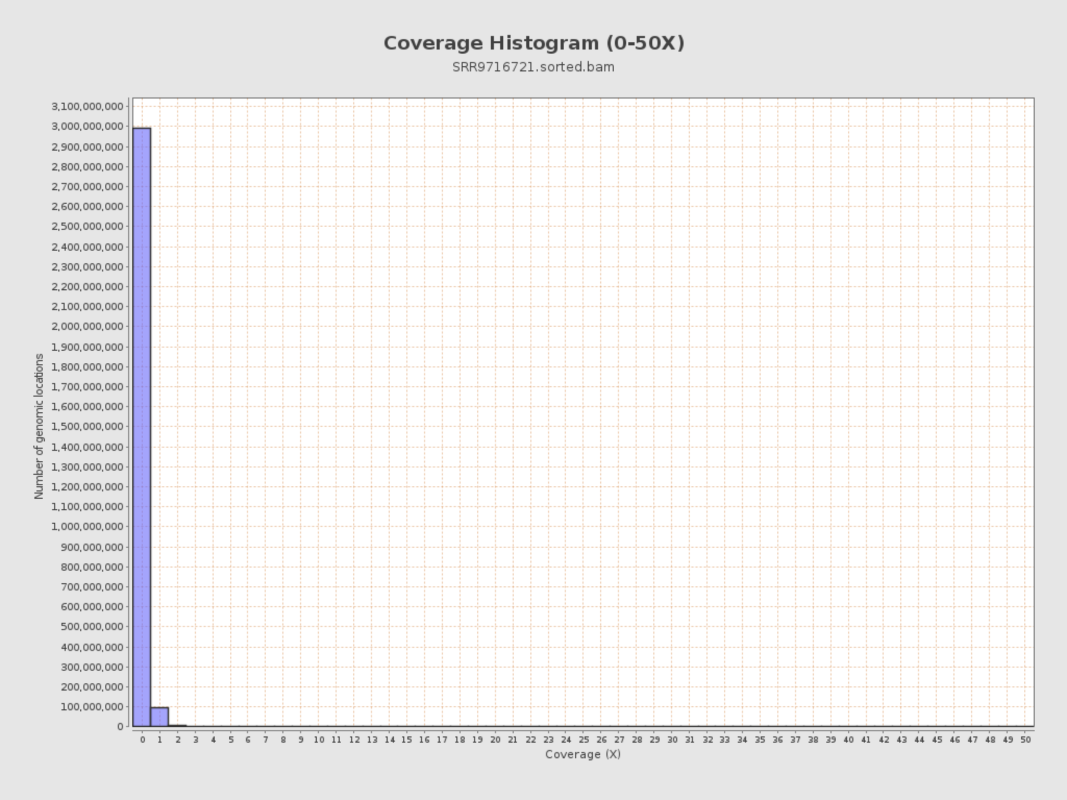
3. Results : Coverage across reference



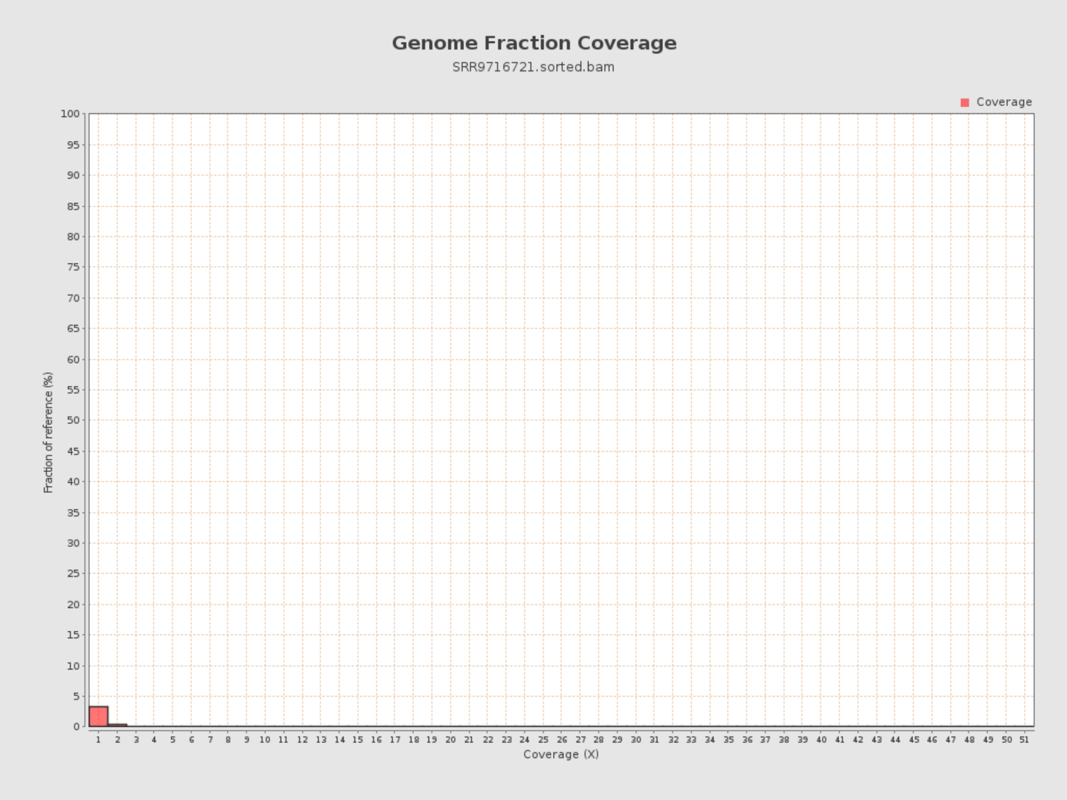
4. Results : Coverage Histogram



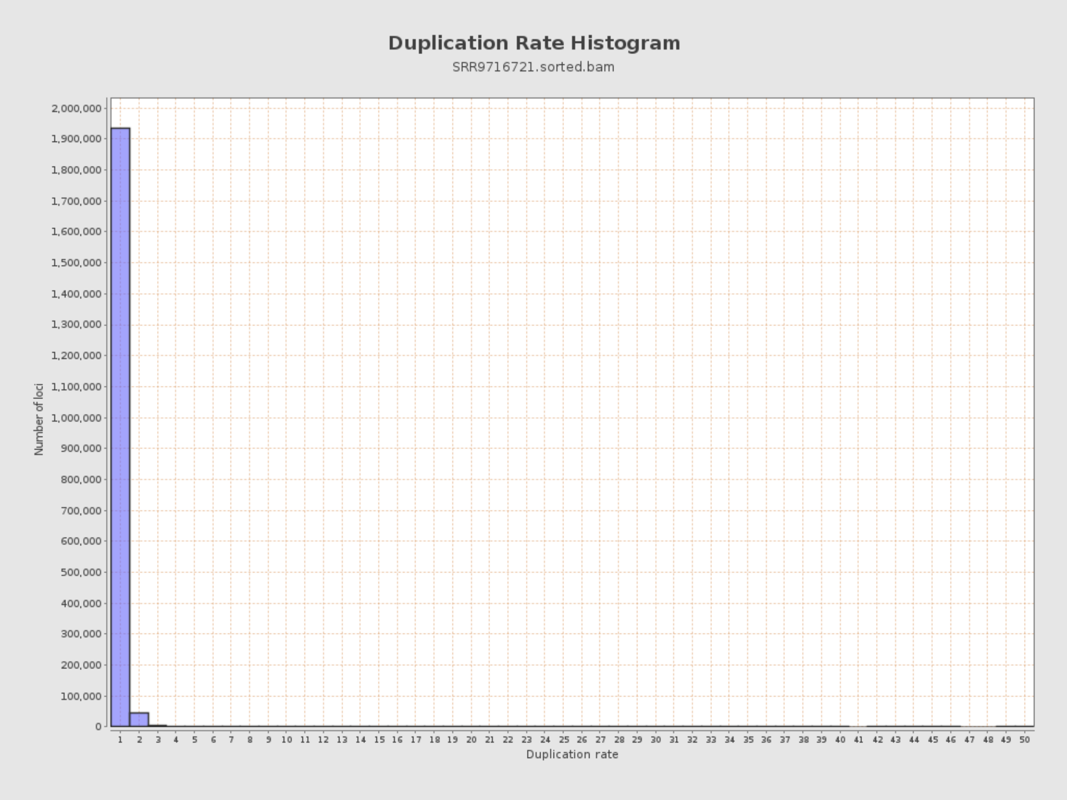
5. Results : Coverage Histogram (0-50X)



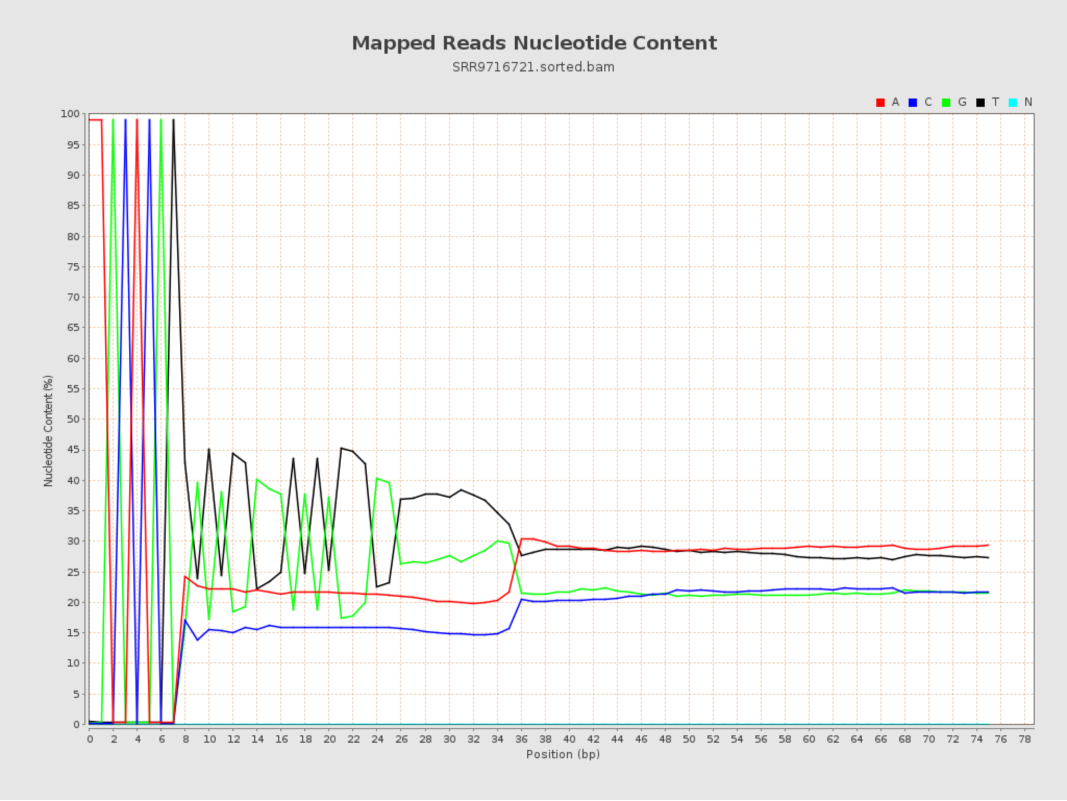
6. Results : Genome Fraction Coverage



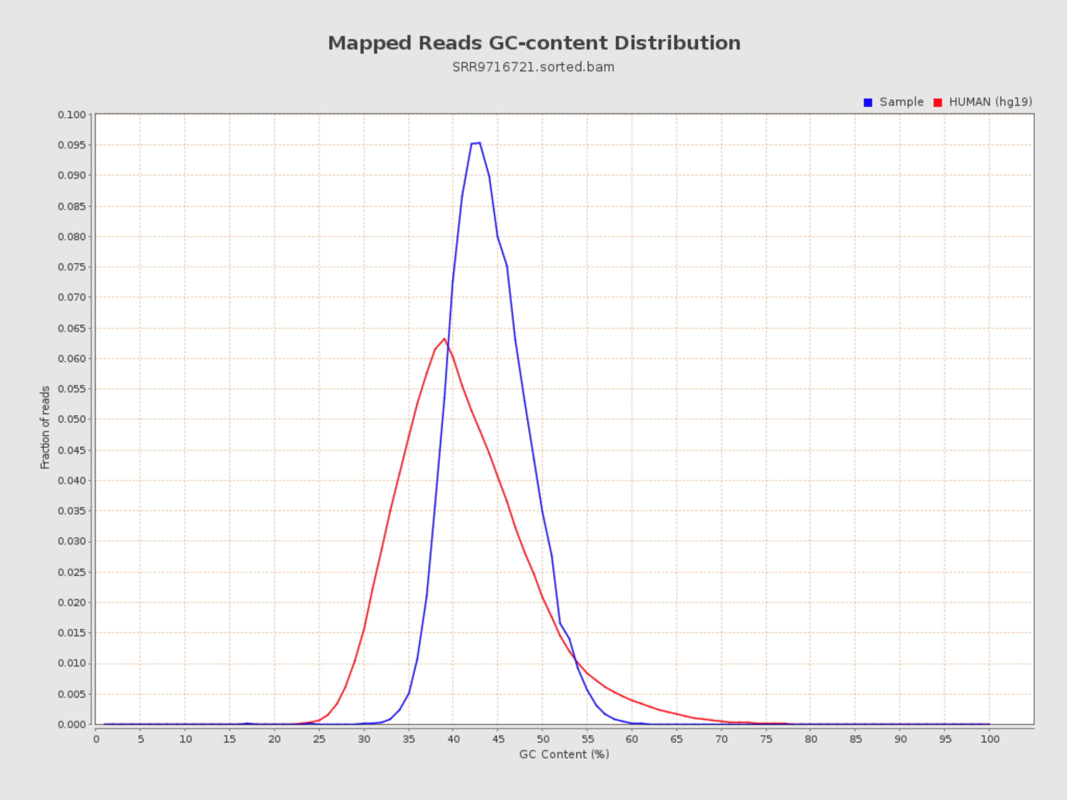
7. Results : Duplication Rate Histogram



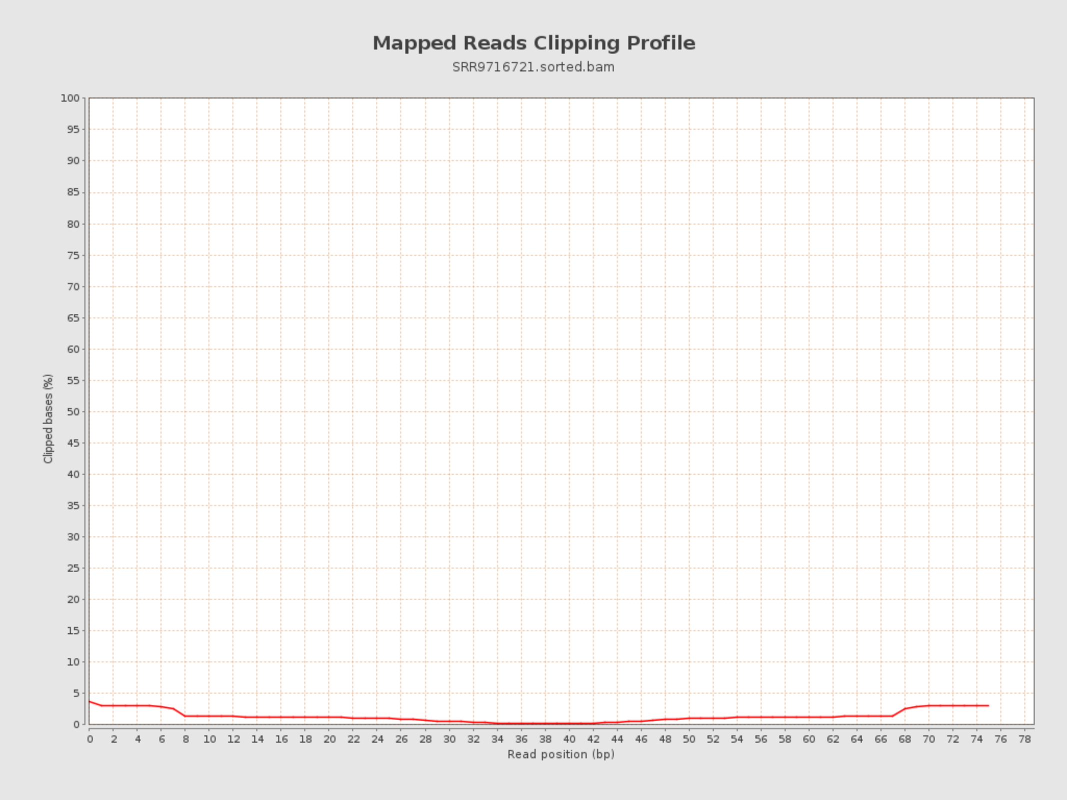
8. Results : Mapped Reads Nucleotide Content



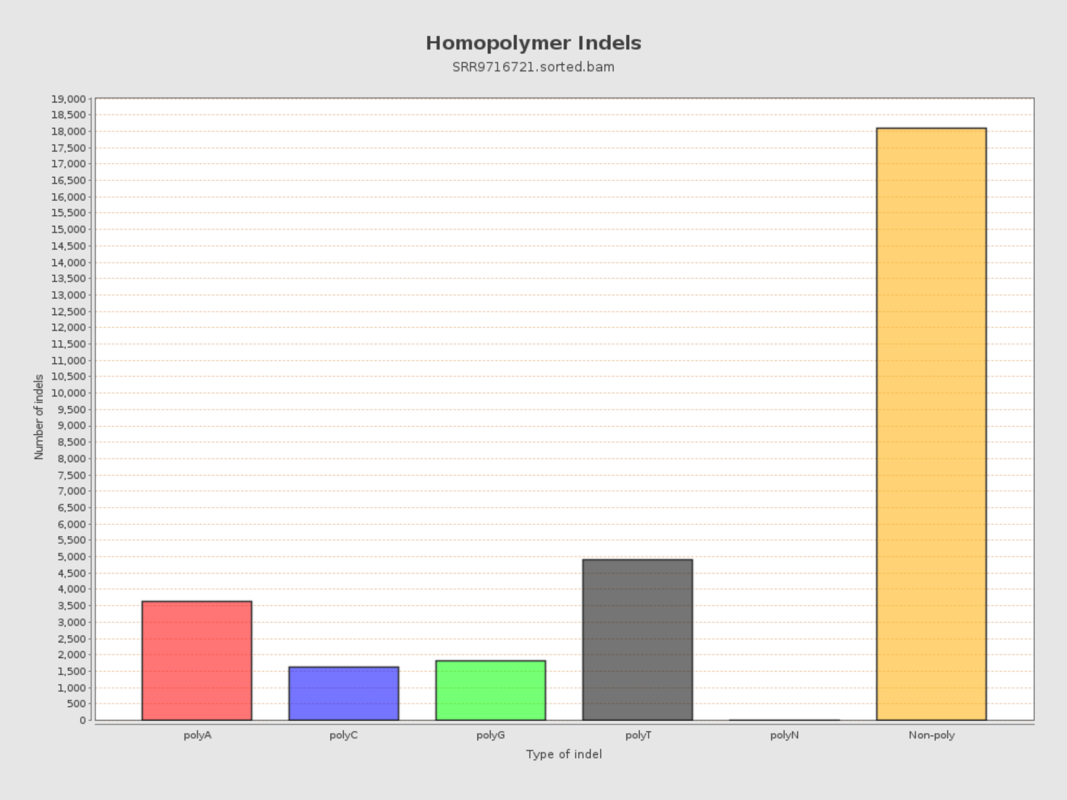
9. Results : Mapped Reads GC-content Distribution



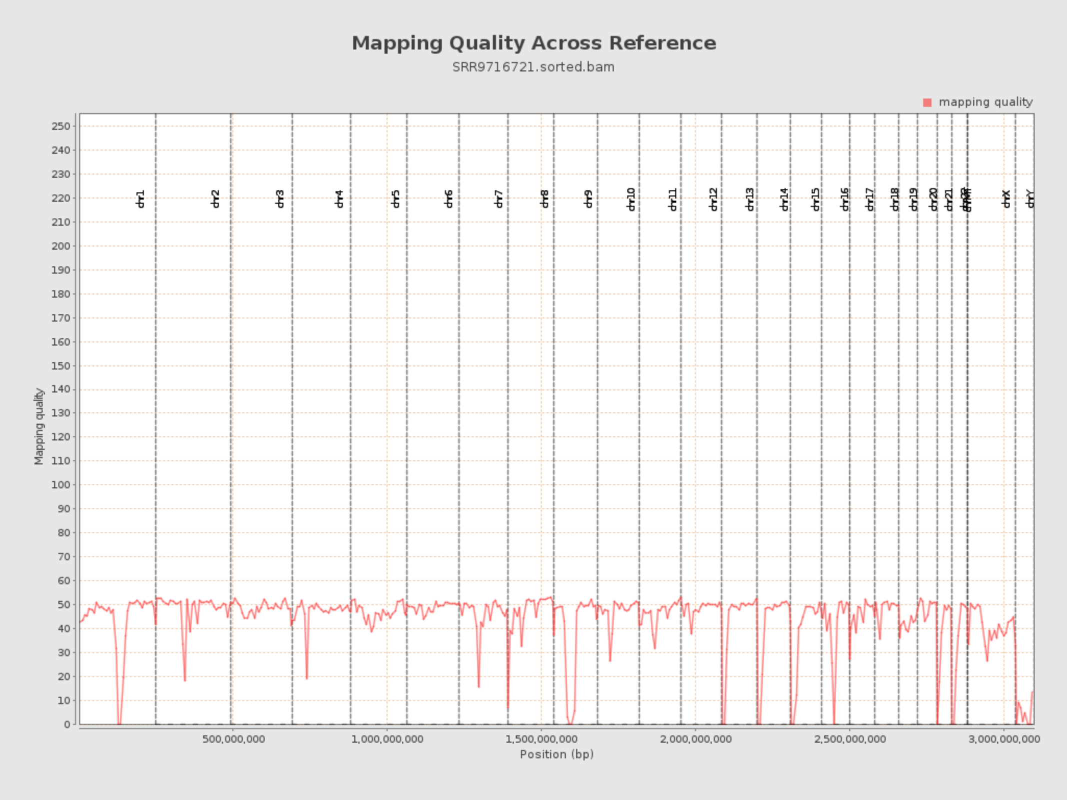
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram