Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:36:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716115.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_SRR9716115 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:36:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,112,909
Mapped reads	906,988 / 81.5%
Unmapped reads	205,921 / 18.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,960 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	15,928 / 1.43%
Duplication rate	1.24%
Clipped reads	907,821 / 81.57%

2.2. ACGT Content

Number/percentage of A's	12,593,296 / 24.75%
Number/percentage of C's	10,460,863 / 20.56%
Number/percentage of T's	15,352,627 / 30.18%
Number/percentage of G's	12,465,760 / 24.5%
Number/percentage of N's	1,558 / 0%
GC Percentage	45.07%

2.3. Coverage

Mean	0.0164

Standard Deviation	0.1582

2.4. Mapping Quality

Mean Mapping Quality	40.77

2.5. Mismatches and indels

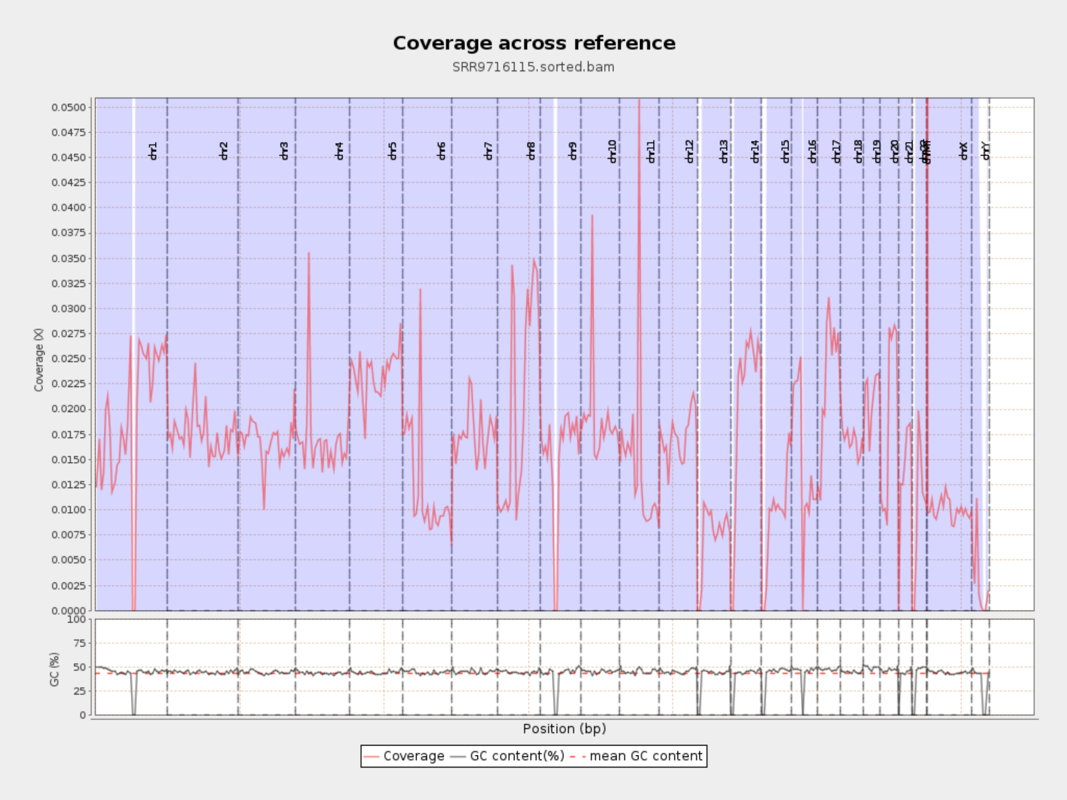
General error rate	0.54%
Mismatches	265,385
Insertions	4,145
Mapped reads with at least one insertion	0.45%
Deletions	8,570
Mapped reads with at least one deletion	0.94%
Homopolymer indels	35.46%

2.6. Chromosome stats

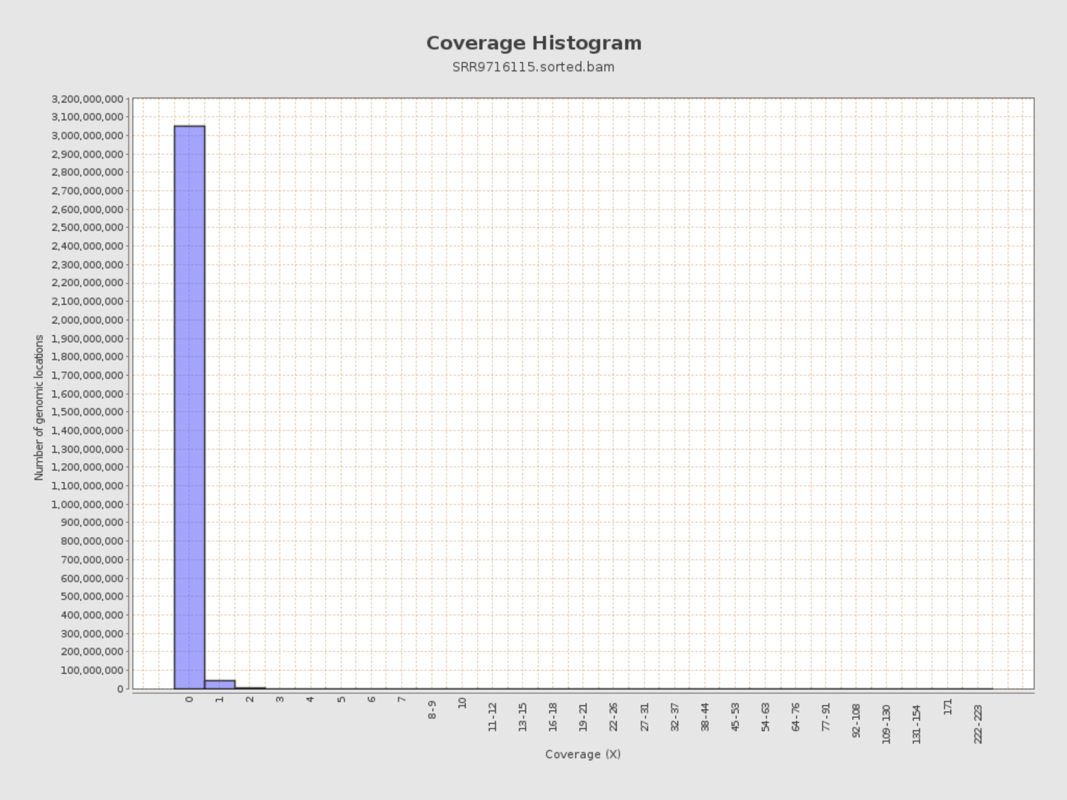
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4790789	0.0192	0.1964
chr2	243199373	4273667	0.0176	0.1881
chr3	198022430	3308151	0.0167	0.1392
chr4	191154276	3255312	0.017	0.1573
chr5	180915260	4285224	0.0237	0.1631
chr6	171115067	2113958	0.0124	0.1212
chr7	159138663	2804484	0.0176	0.1744

chr8	146364022	3051674	0.0208	0.1614
chr9	141213431	2147153	0.0152	0.1454
chr10	135534747	2592315	0.0191	0.2246
chr11	135006516	2030731	0.015	0.1558
chr12	133851895	2313847	0.0173	0.1396
chr13	115169878	849165	0.0074	0.0909
chr14	107349540	2231274	0.0208	0.1546
chr15	102531392	948733	0.0093	0.1027
chr16	90354753	1317965	0.0146	0.1389
chr17	81195210	1859180	0.0229	0.1682
chr18	78077248	1321529	0.0169	0.189
chr19	59128983	1246319	0.0211	0.1836
chr20	63025520	1207938	0.0192	0.1529
chr21	48129895	676384	0.0141	0.141
chr22	51304566	523534	0.0102	0.1081
chrMT	16571	13832	0.8347	1.193
chrX	155270560	1557557	0.01	0.1118
chrY	59373566	167347	0.0028	0.0967

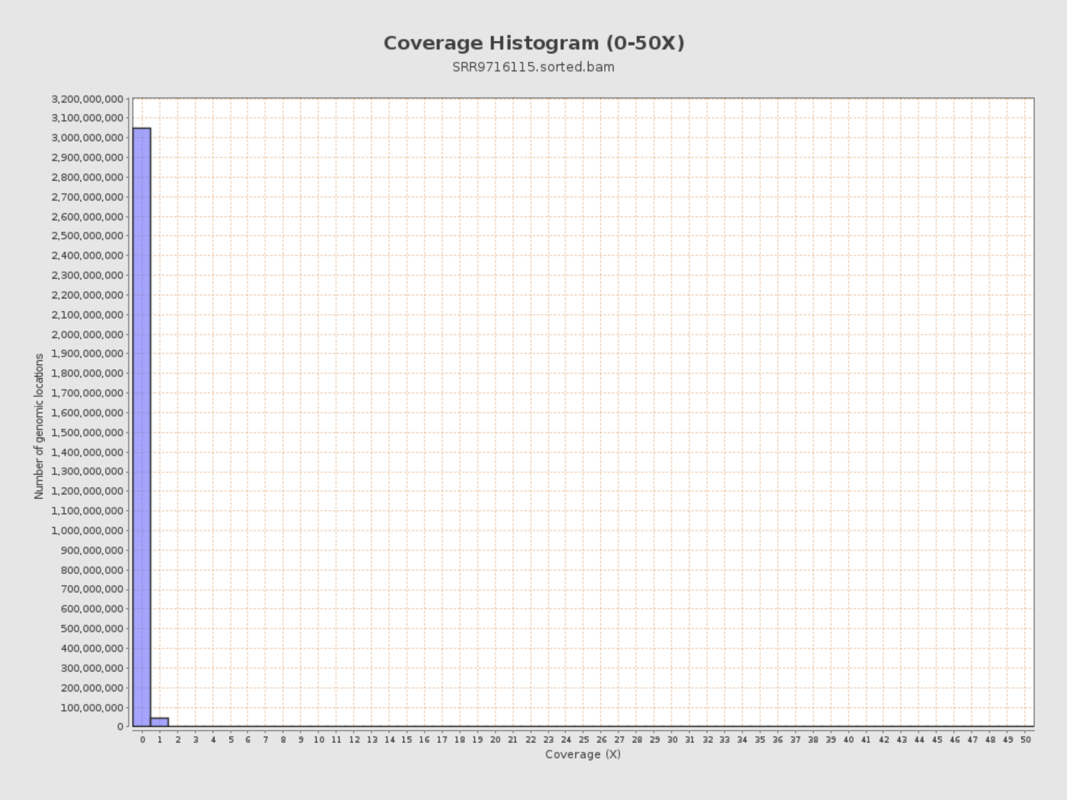
3. Results : Coverage across reference



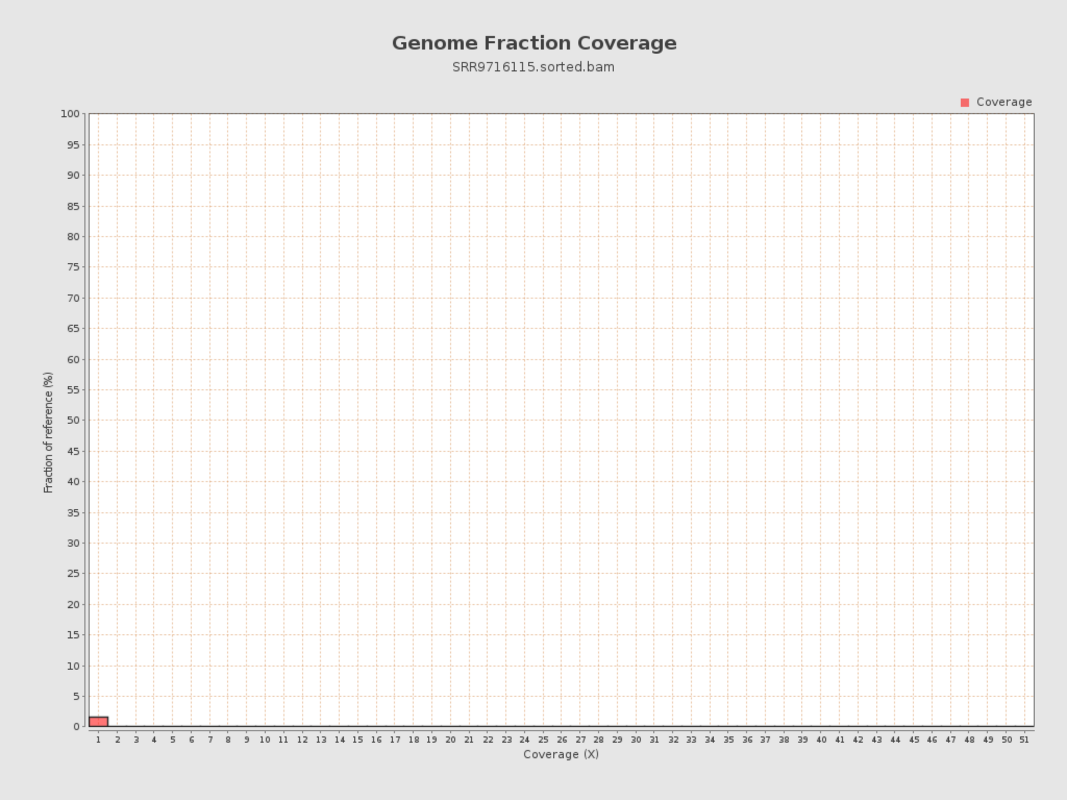
4. Results : Coverage Histogram



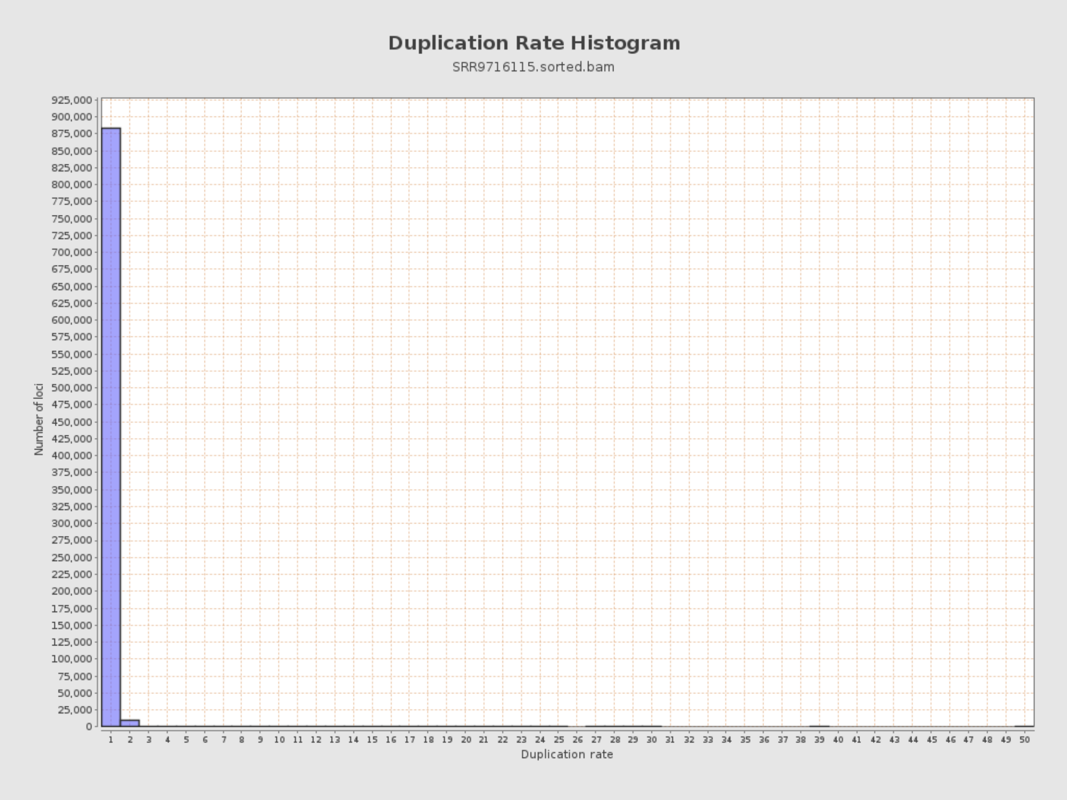
5. Results : Coverage Histogram (0-50X)



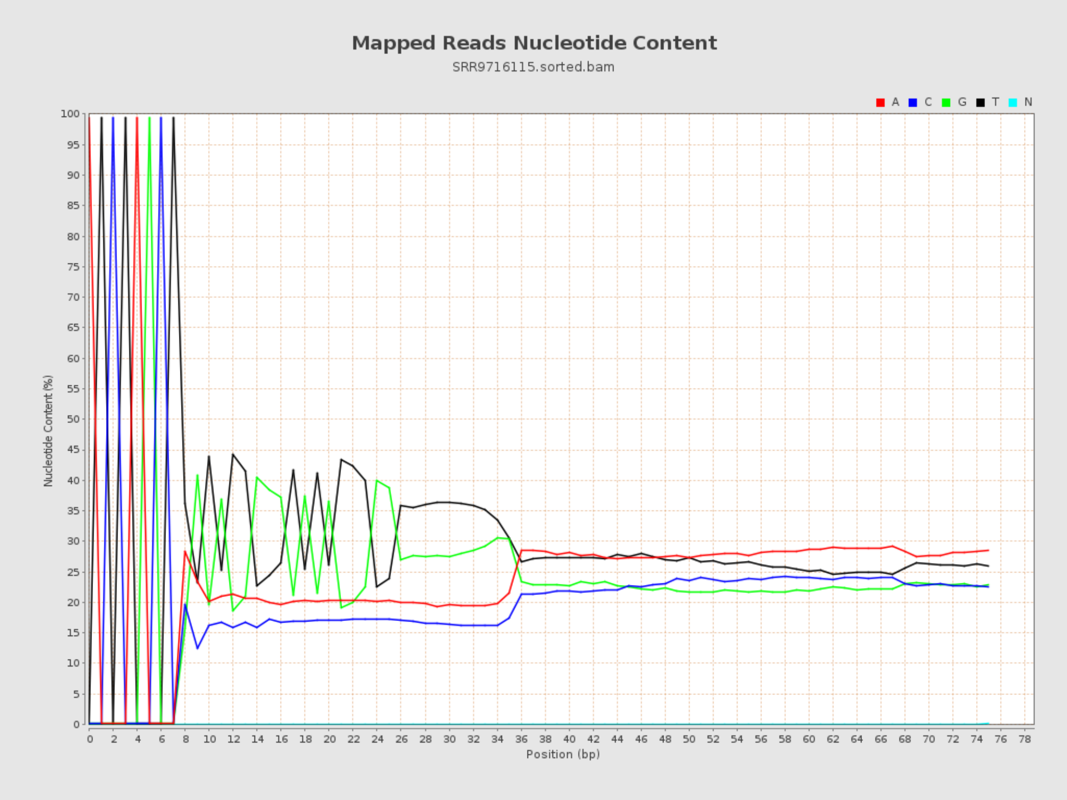
6. Results : Genome Fraction Coverage



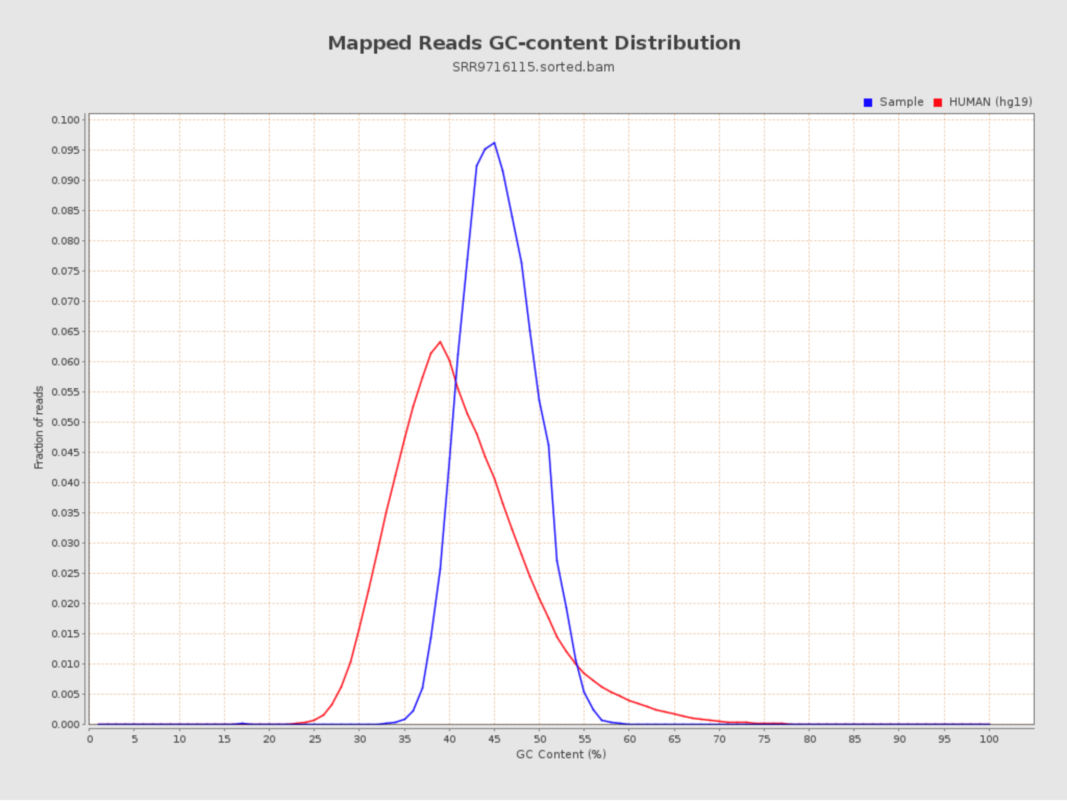
7. Results : Duplication Rate Histogram



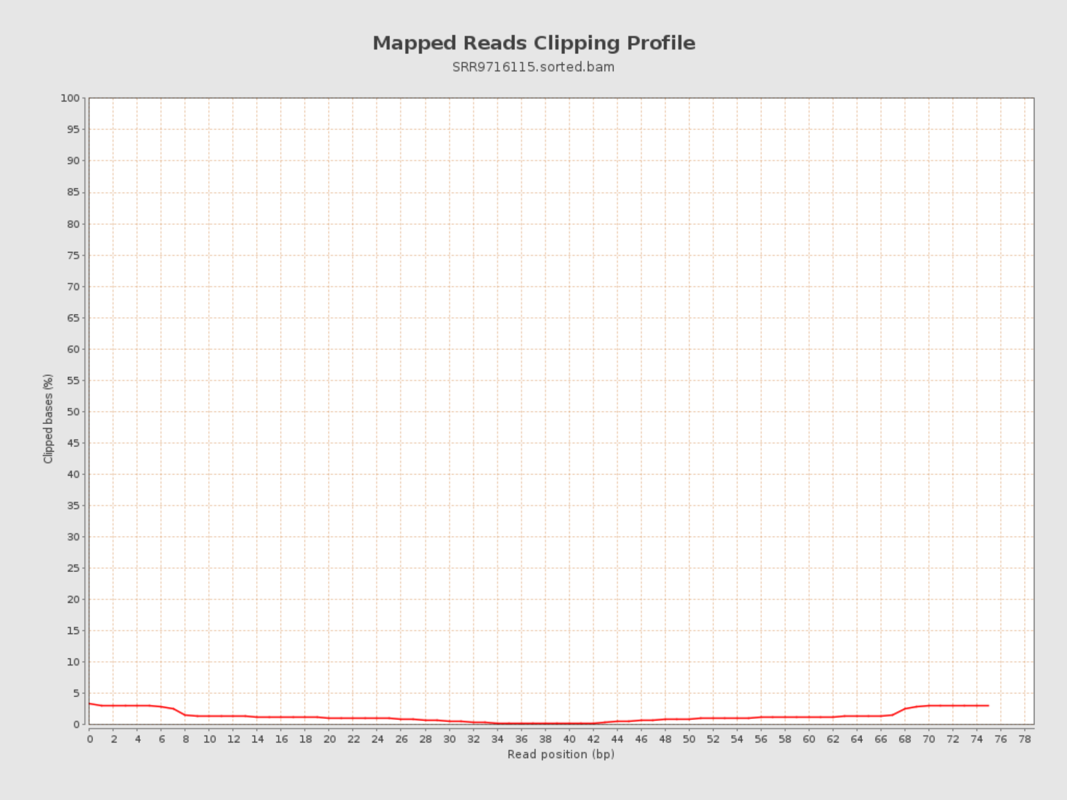
8. Results : Mapped Reads Nucleotide Content



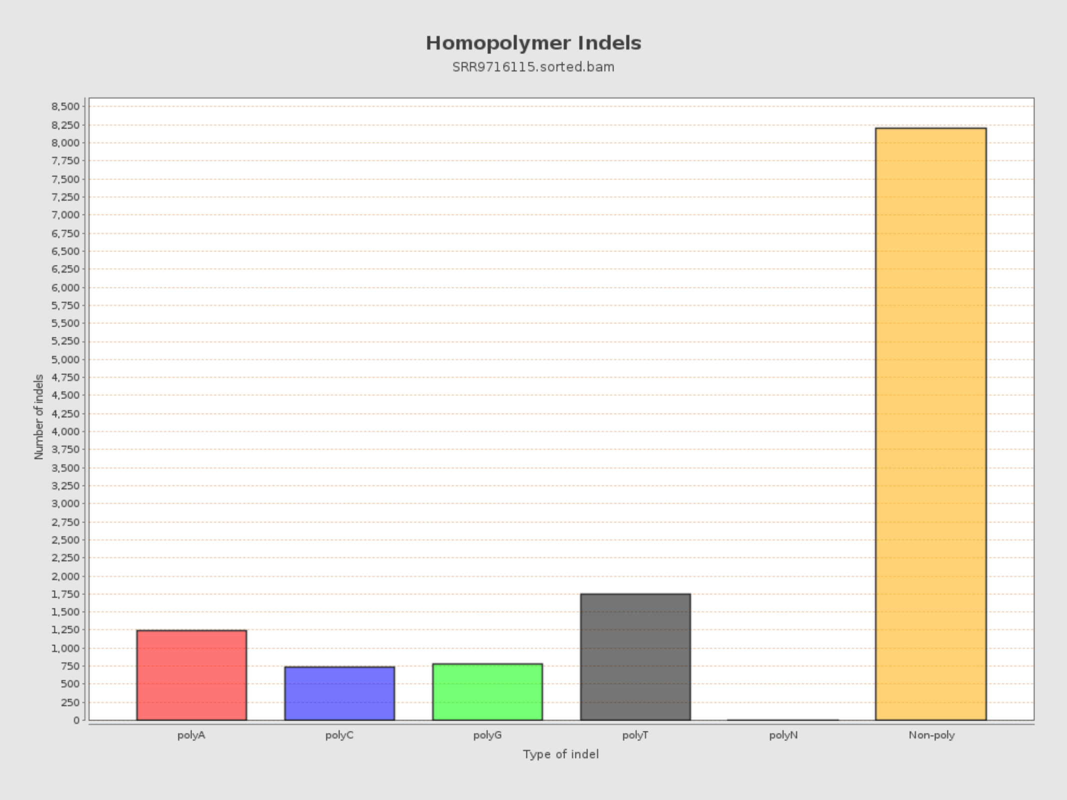
9. Results : Mapped Reads GC-content Distribution



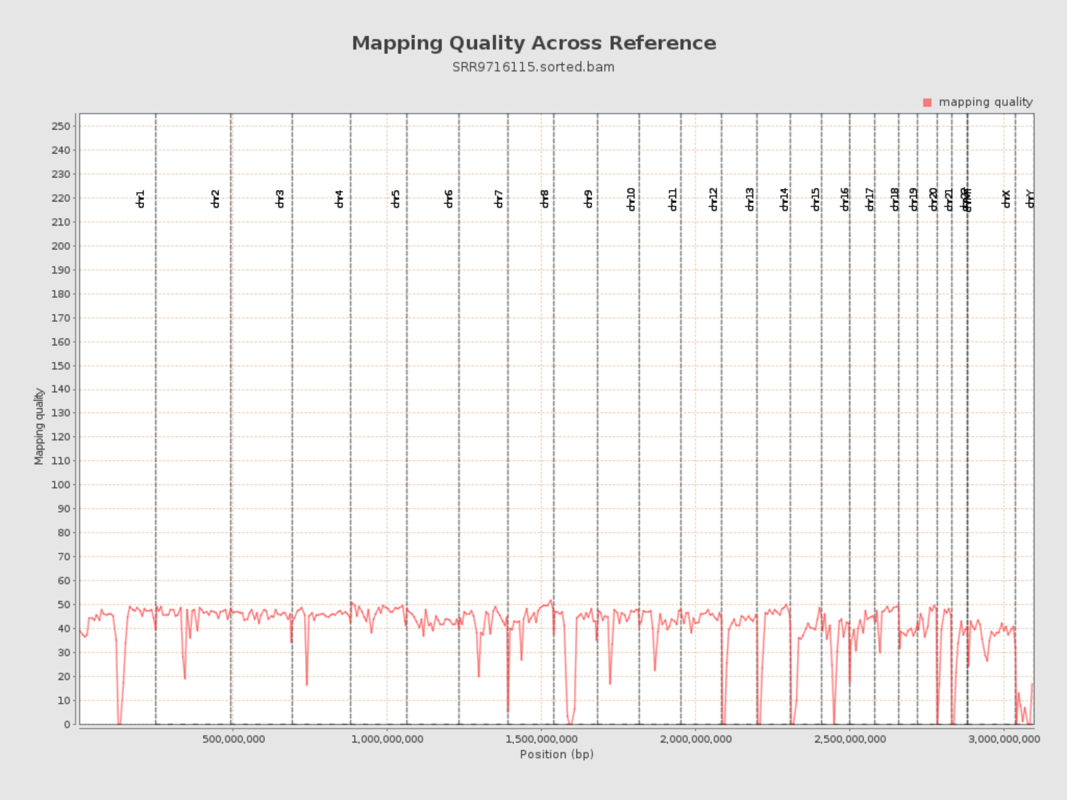
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram