Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:34:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716142.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_SRR9716142 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716142.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:34:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716142.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,747,978
Mapped reads	1,583,547 / 90.59%
Unmapped reads	164,431 / 9.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,017 / 0.52%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	65,314 / 3.74%
Duplication rate	3.25%
Clipped reads	1,586,868 / 90.78%

2.2. ACGT Content

Number/percentage of A's	22,929,573 / 24.87%
Number/percentage of C's	17,695,999 / 19.2%
Number/percentage of T's	29,135,564 / 31.61%
Number/percentage of G's	22,417,625 / 24.32%
Number/percentage of N's	663 / 0%
GC Percentage	43.52%

2.3. Coverage

Mean	0.0298

Standard Deviation	0.2579

2.4. Mapping Quality

Mean Mapping Quality	44.8

2.5. Mismatches and indels

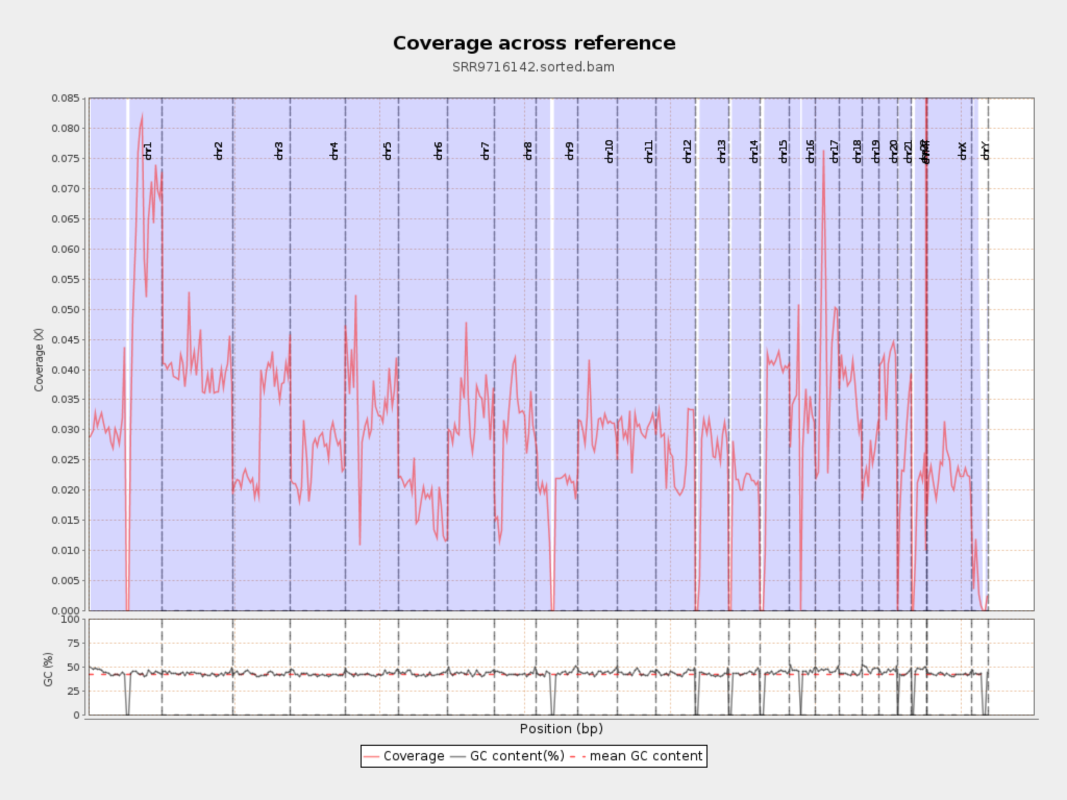
General error rate	0.51%
Mismatches	454,014
Insertions	7,205
Mapped reads with at least one insertion	0.45%
Deletions	16,386
Mapped reads with at least one deletion	1.03%
Homopolymer indels	39.6%

2.6. Chromosome stats

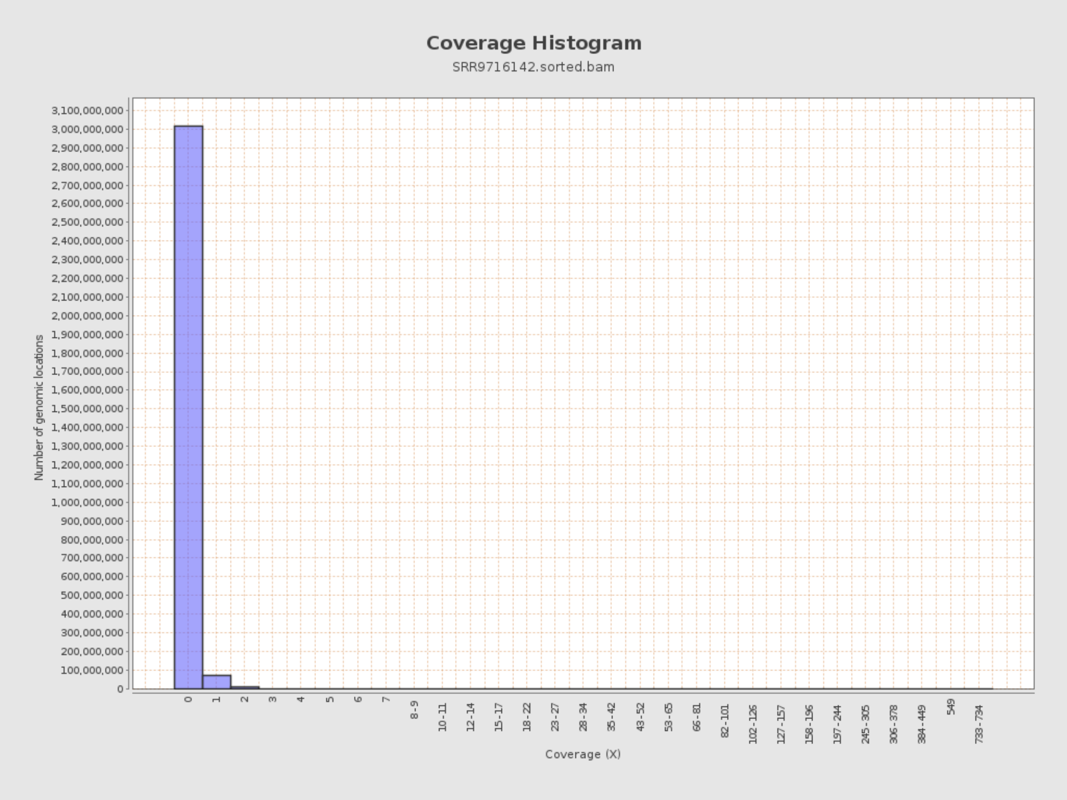
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10946209	0.0439	0.4056
chr2	243199373	9761149	0.0401	0.3839
chr3	198022430	6032086	0.0305	0.1937
chr4	191154276	4849299	0.0254	0.1935
chr5	180915260	6273835	0.0347	0.2063
chr6	171115067	3142244	0.0184	0.1684
chr7	159138663	5302050	0.0333	0.3653

chr8	146364022	4267050	0.0292	0.2453
chr9	141213431	2584825	0.0183	0.1933
chr10	135534747	4202958	0.031	0.2368
chr11	135006516	4056187	0.03	0.2368
chr12	133851895	3523776	0.0263	0.1814
chr13	115169878	2753675	0.0239	0.1726
chr14	107349540	2064235	0.0192	0.1626
chr15	102531392	3382379	0.033	0.2031
chr16	90354753	2836594	0.0314	0.2022
chr17	81195210	3532929	0.0435	0.2482
chr18	78077248	2913550	0.0373	0.3655
chr19	59128983	1478760	0.025	0.308
chr20	63025520	2550250	0.0405	0.2266
chr21	48129895	1199338	0.0249	0.1812
chr22	51304566	795186	0.0155	0.1366
chrMT	16571	8189	0.4942	0.7699
chrX	155270560	3540196	0.0228	0.1834
chrY	59373566	208395	0.0035	0.0946

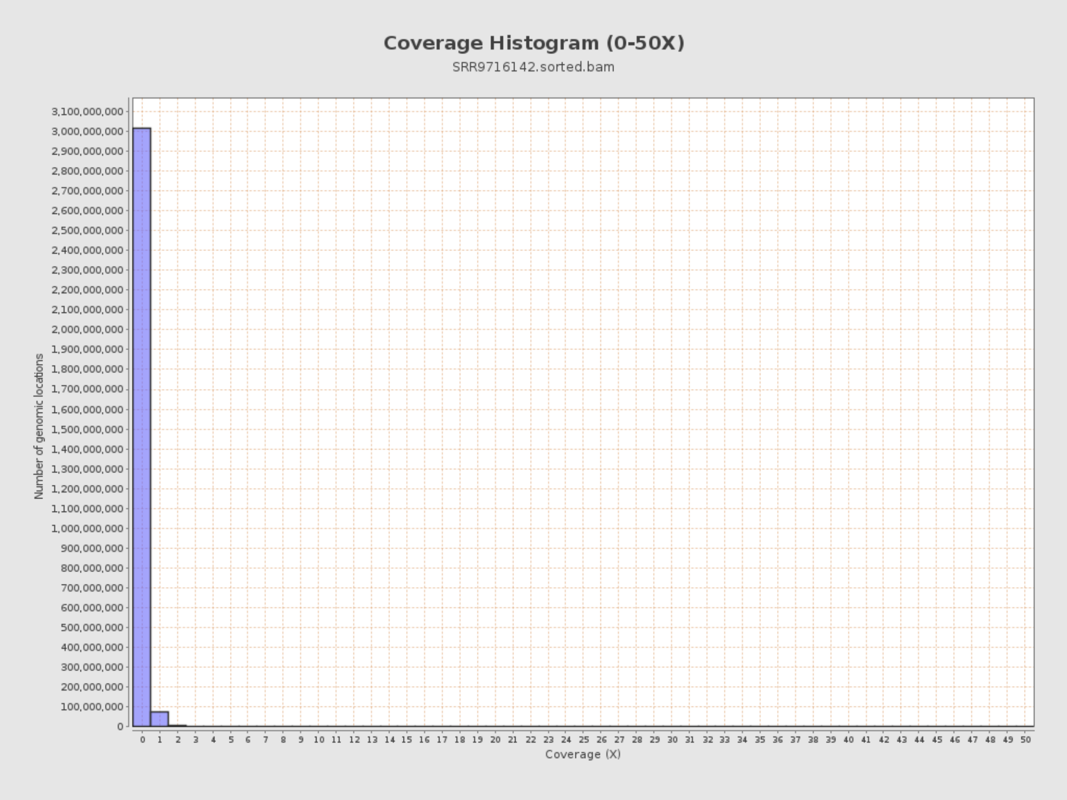
3. Results : Coverage across reference



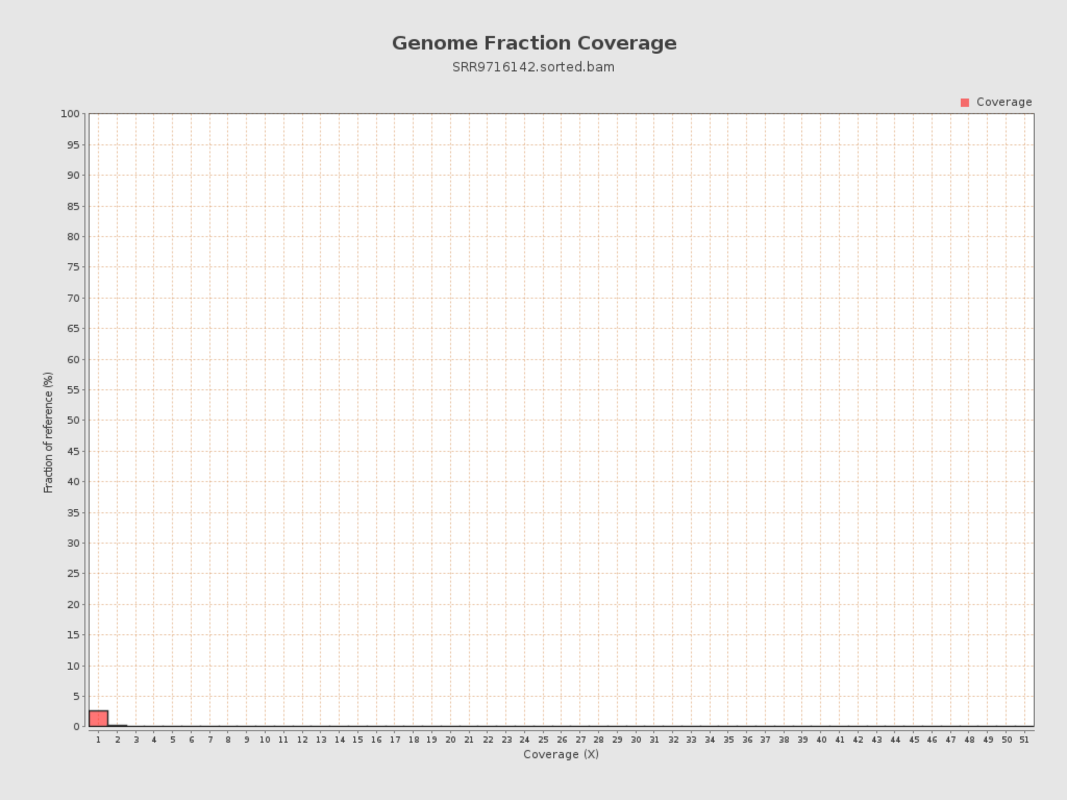
4. Results : Coverage Histogram



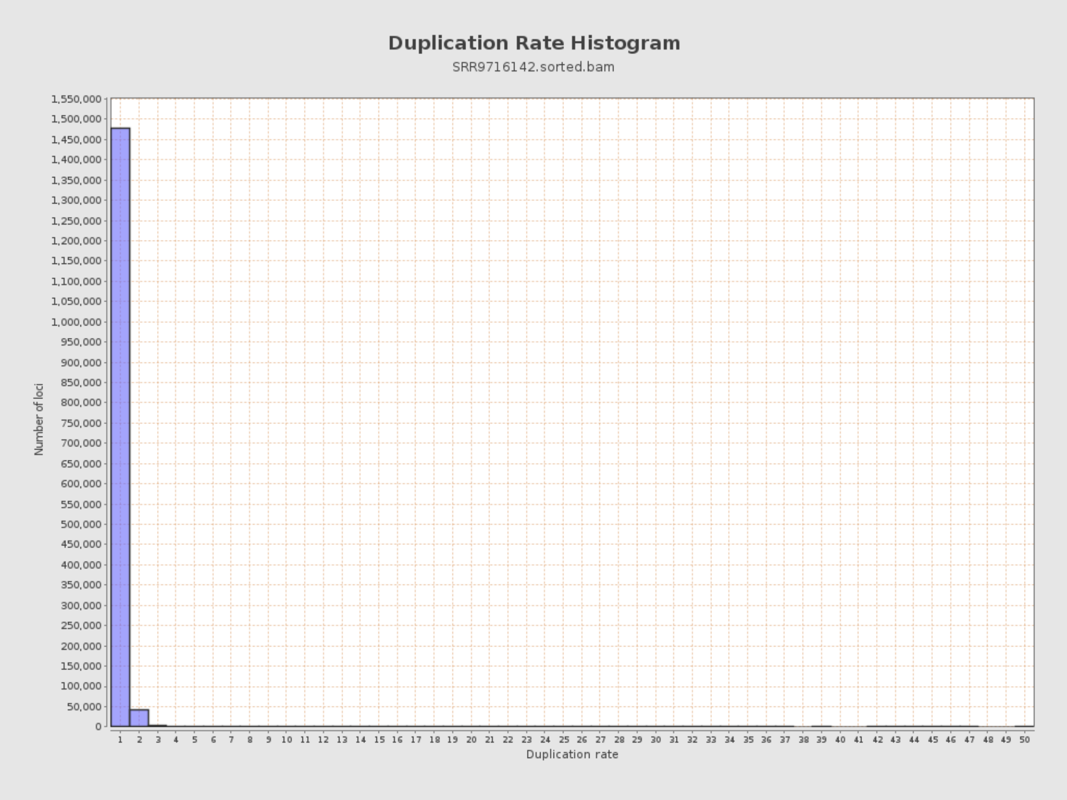
5. Results : Coverage Histogram (0-50X)



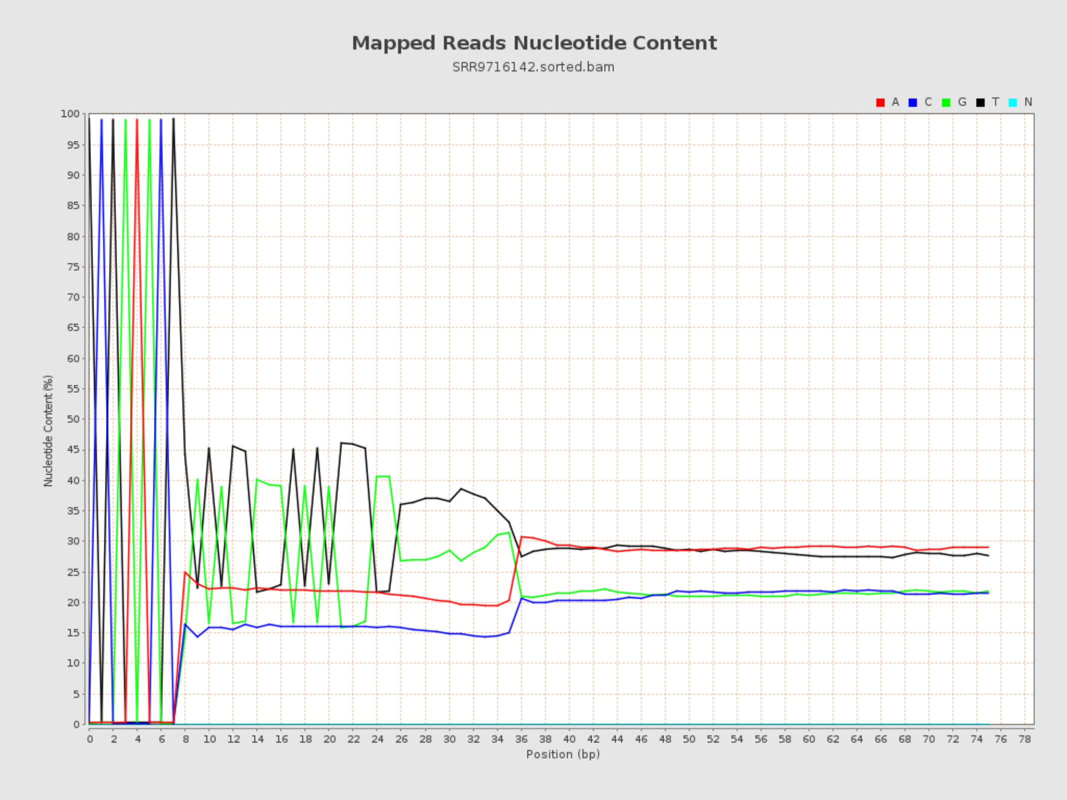
6. Results : Genome Fraction Coverage



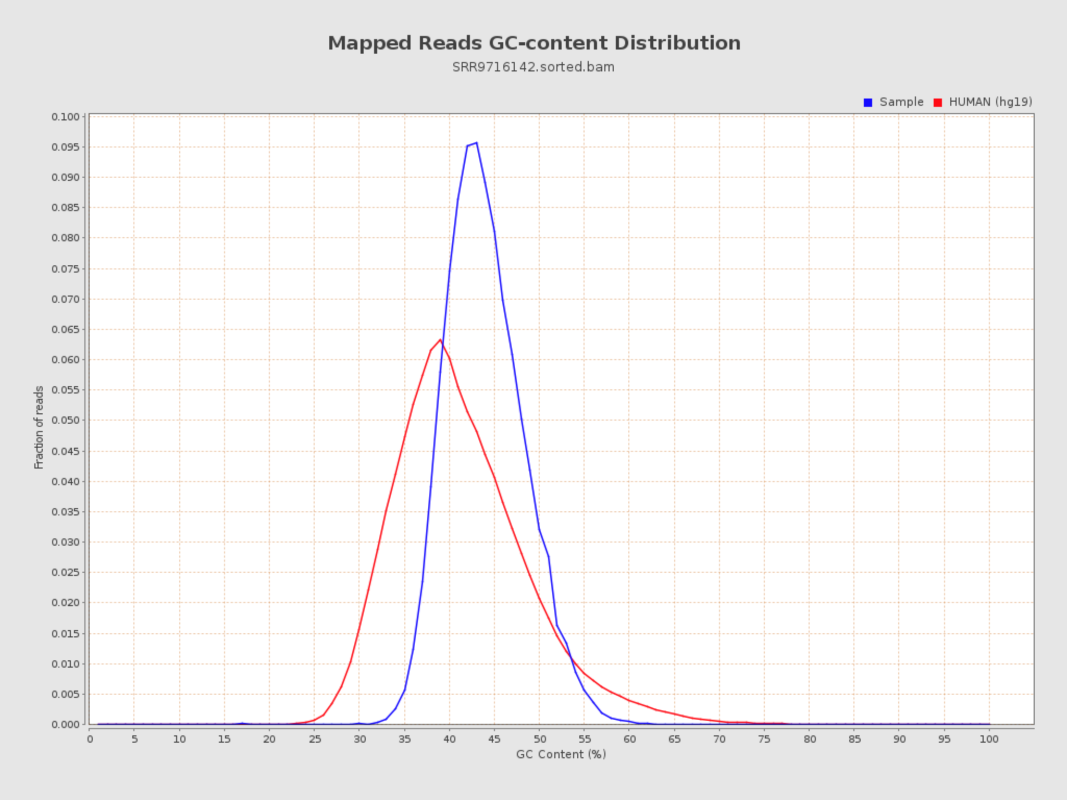
7. Results : Duplication Rate Histogram



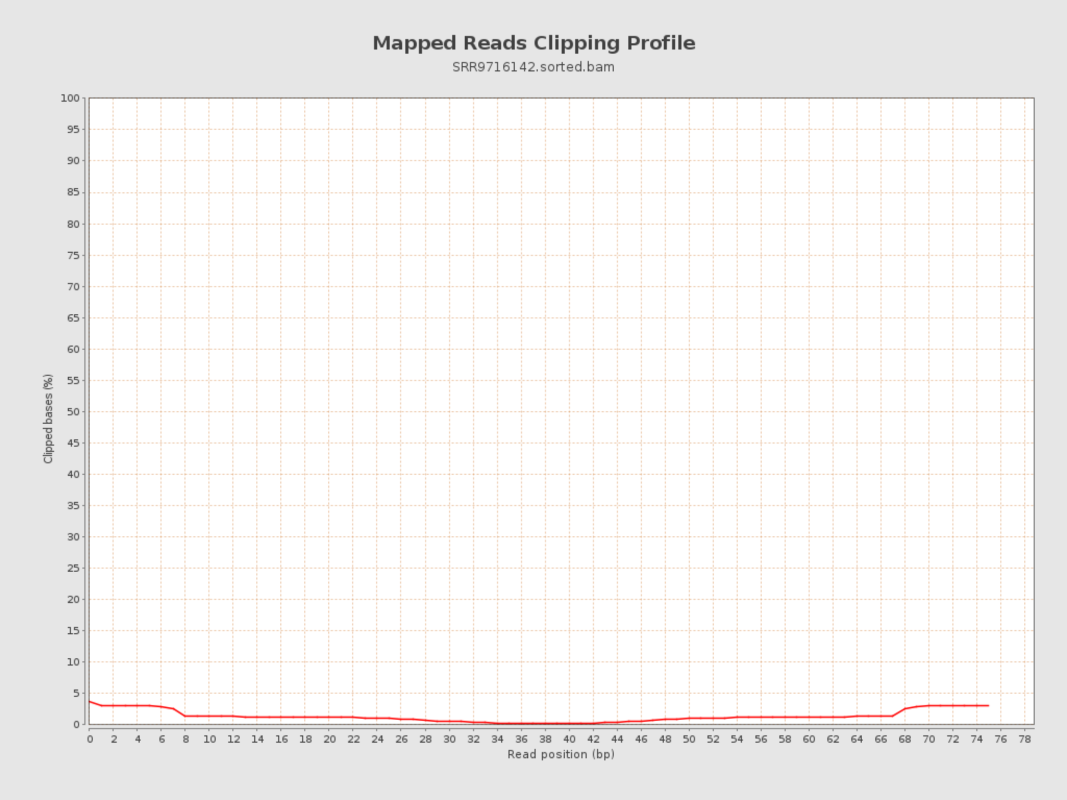
8. Results : Mapped Reads Nucleotide Content



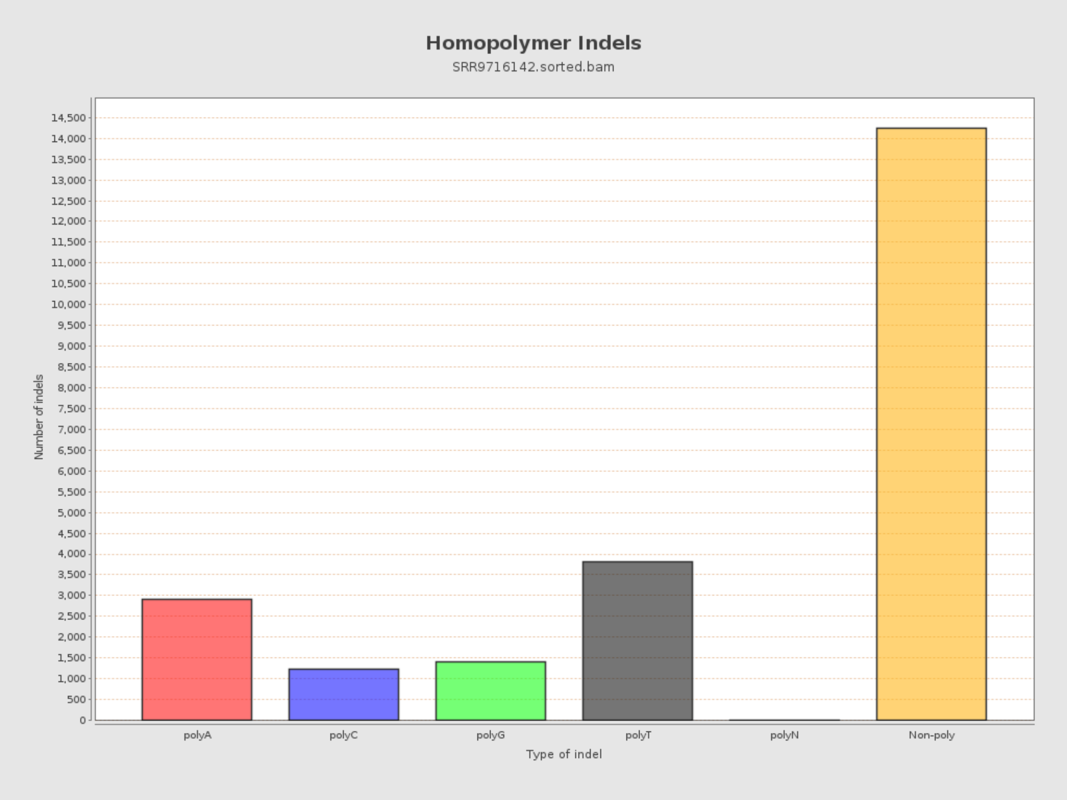
9. Results : Mapped Reads GC-content Distribution



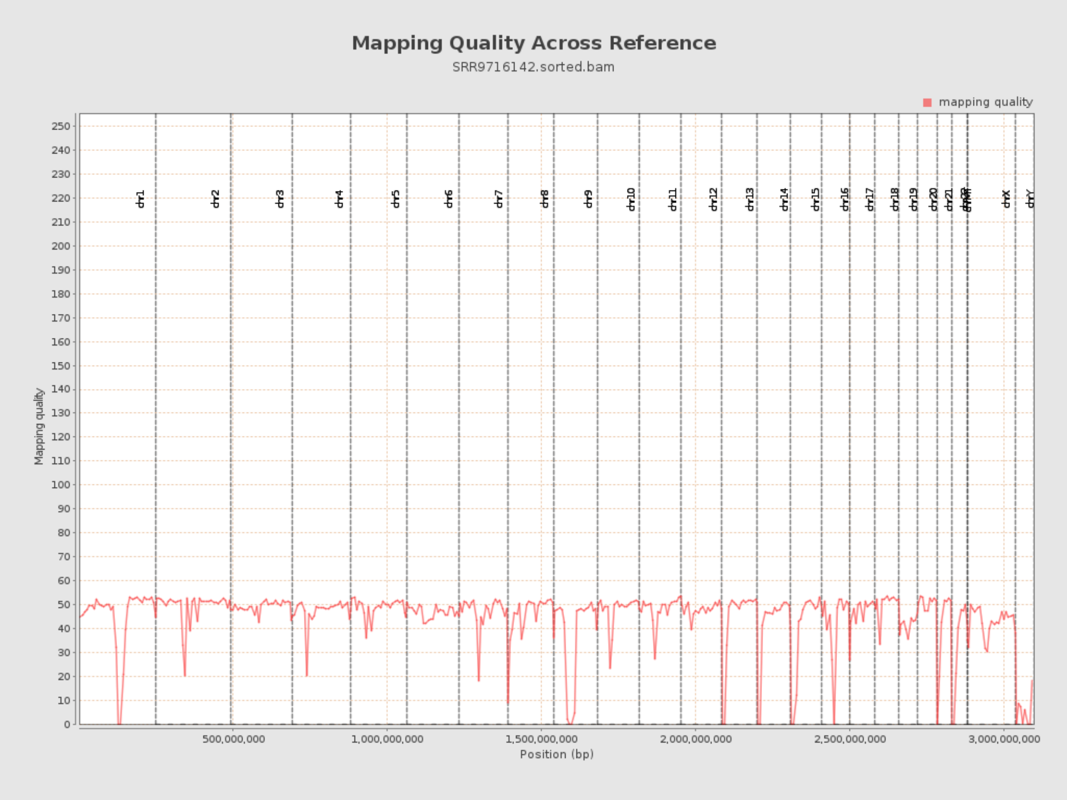
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram