Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:04:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716929.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_SRR9716929 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716929.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:04:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716929.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,521,302
Mapped reads	2,299,872 / 91.22%
Unmapped reads	221,430 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,646 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	96,011 / 3.81%
Duplication rate	3.12%
Clipped reads	2,310,968 / 91.66%

2.2. ACGT Content

Number/percentage of A's	33,373,797 / 24.95%
Number/percentage of C's	25,465,376 / 19.04%
Number/percentage of T's	42,505,169 / 31.78%
Number/percentage of G's	32,388,652 / 24.22%
Number/percentage of N's	3,759 / 0%
GC Percentage	43.26%

2.3. Coverage

Mean	0.0432

Standard Deviation	0.3864

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

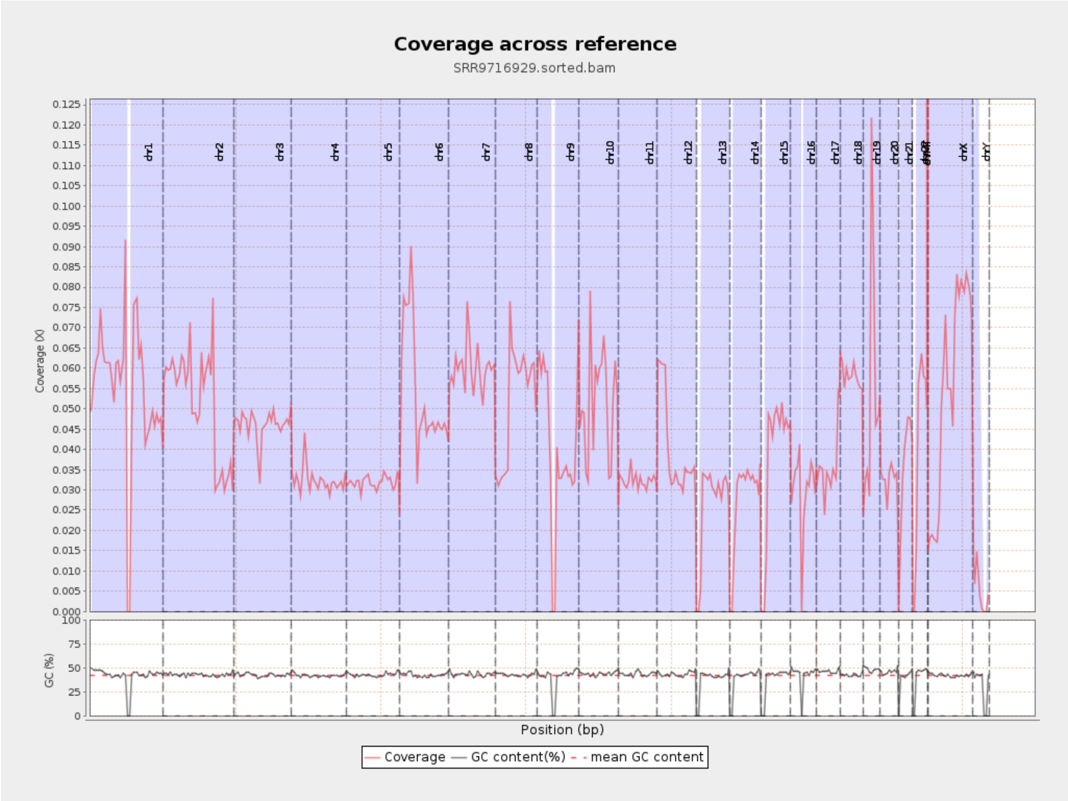
General error rate	0.5%
Mismatches	650,424
Insertions	7,275
Mapped reads with at least one insertion	0.31%
Deletions	22,290
Mapped reads with at least one deletion	0.96%
Homopolymer indels	42.85%

2.6. Chromosome stats

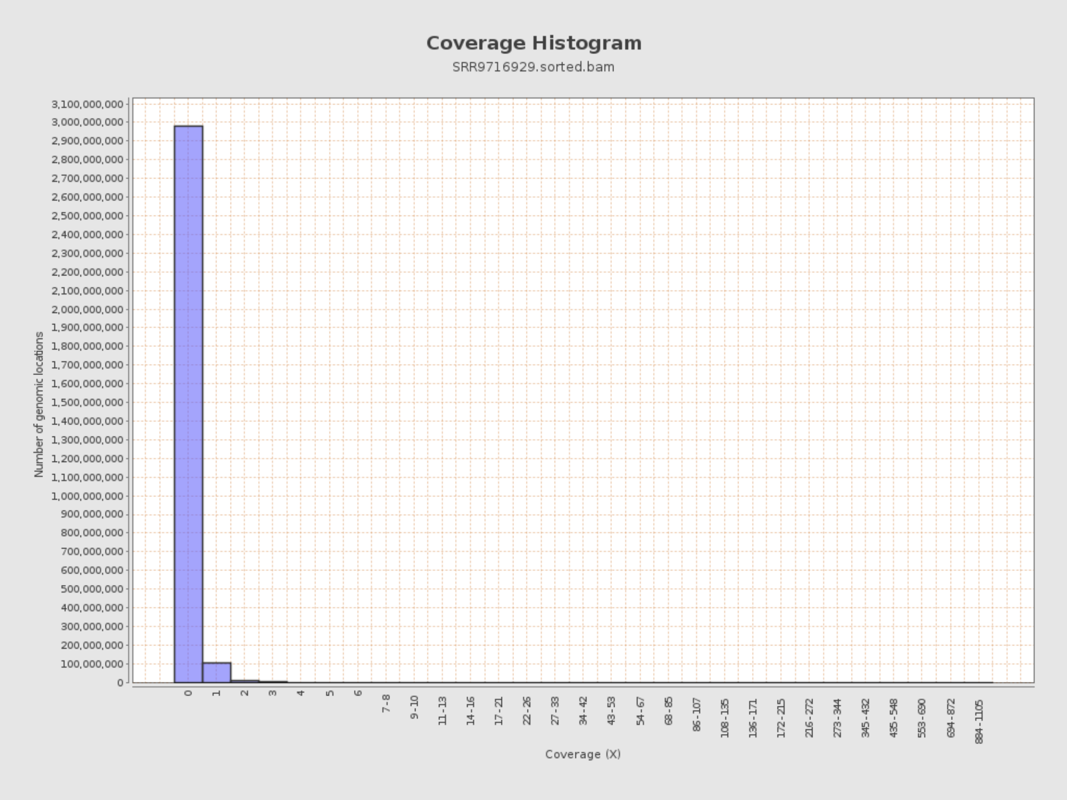
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13628524	0.0547	0.8386
chr2	243199373	12551700	0.0516	0.4574
chr3	198022430	9098758	0.0459	0.2444
chr4	191154276	6163981	0.0322	0.2159
chr5	180915260	5786333	0.032	0.2043
chr6	171115067	9130857	0.0534	0.3013
chr7	159138663	9571660	0.0601	0.4845

chr8	146364022	7631548	0.0521	0.3045
chr9	141213431	5489921	0.0389	0.3127
chr10	135534747	7006939	0.0517	0.3783
chr11	135006516	4346644	0.0322	0.2806
chr12	133851895	5362086	0.0401	0.2334
chr13	115169878	3027932	0.0263	0.1822
chr14	107349540	2920762	0.0272	0.2186
chr15	102531392	3898042	0.038	0.2226
chr16	90354753	2697677	0.0299	0.2182
chr17	81195210	2902080	0.0357	0.2244
chr18	78077248	4547832	0.0582	0.5436
chr19	59128983	3273315	0.0554	0.5733
chr20	63025520	2042891	0.0324	0.2051
chr21	48129895	1671288	0.0347	0.2366
chr22	51304566	2042165	0.0398	0.2252
chrMT	16571	107726	6.5009	3.8251
chrX	155270560	8572149	0.0552	0.3131
chrY	59373566	298860	0.005	0.1082

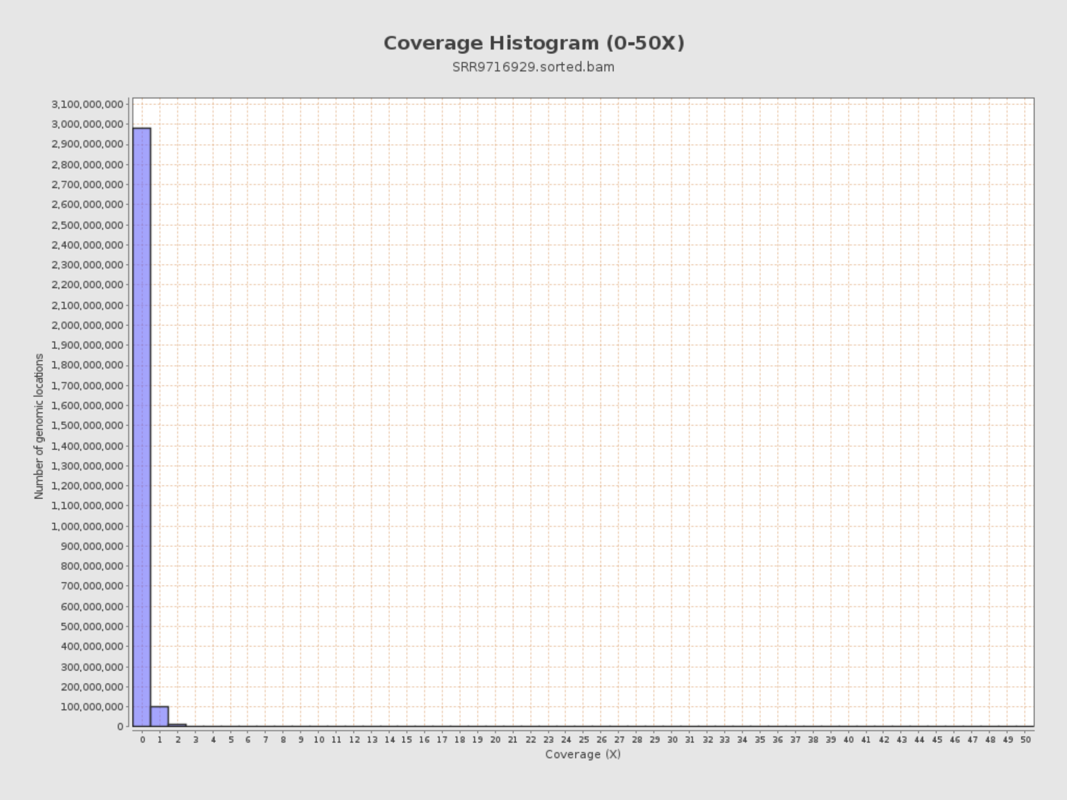
3. Results : Coverage across reference



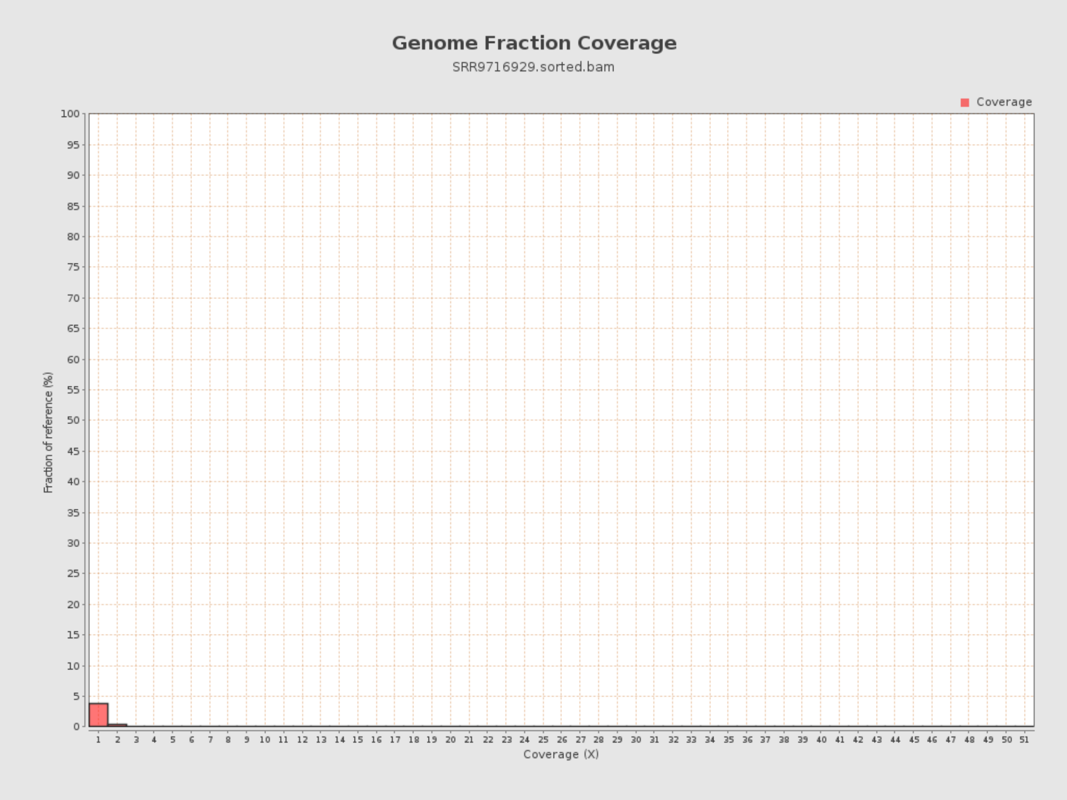
4. Results : Coverage Histogram



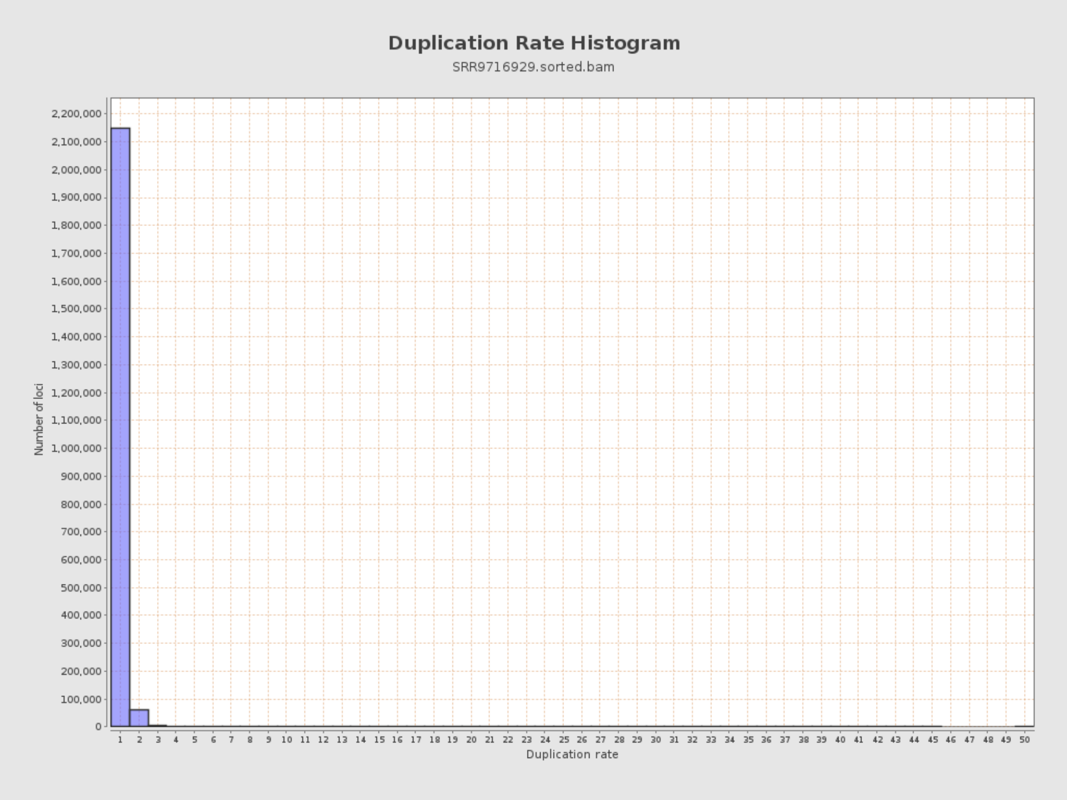
5. Results : Coverage Histogram (0-50X)



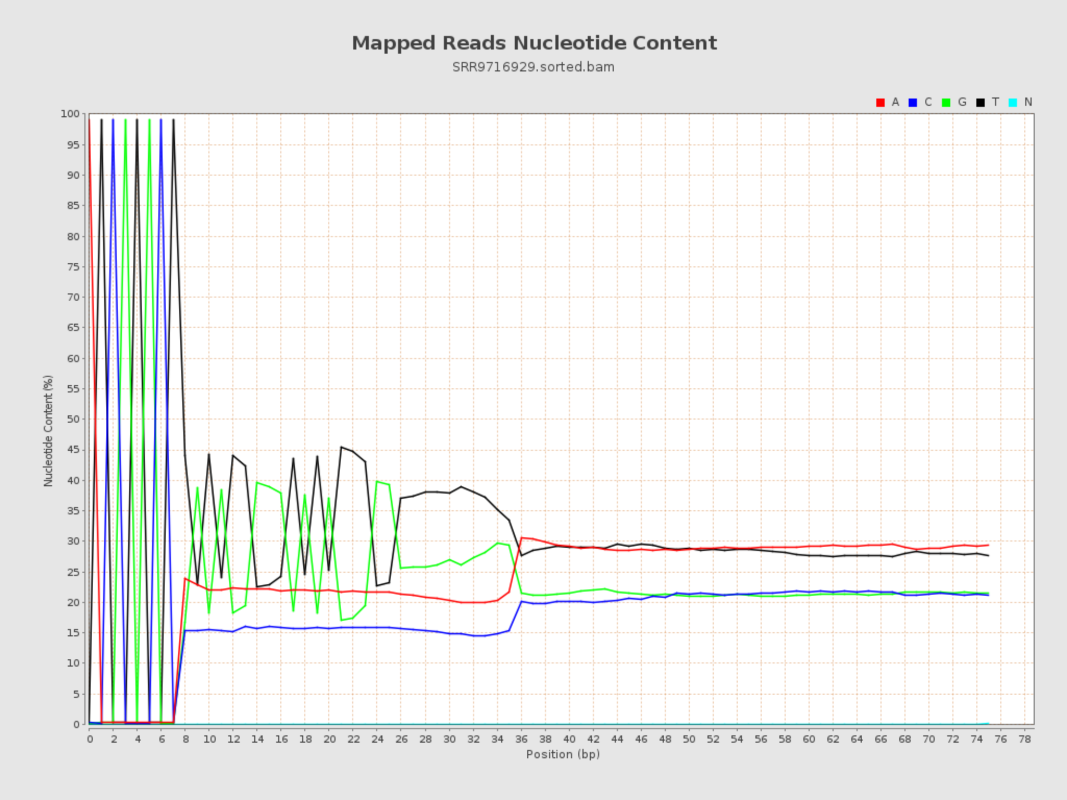
6. Results : Genome Fraction Coverage



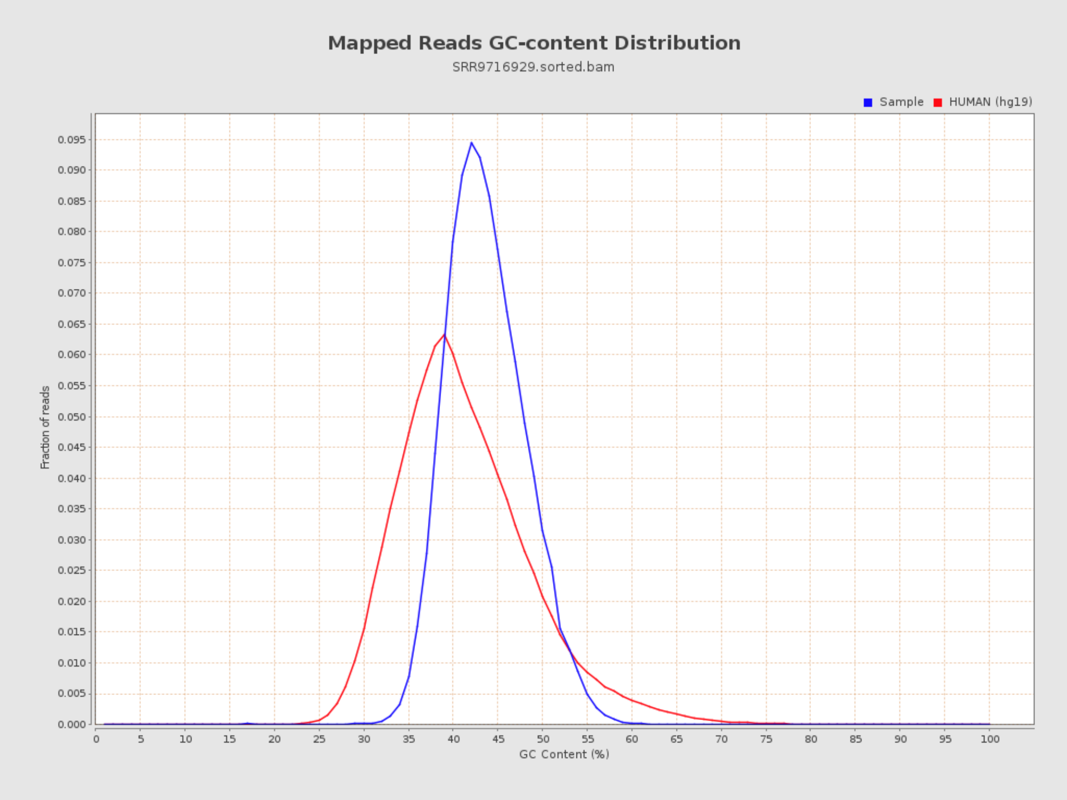
7. Results : Duplication Rate Histogram



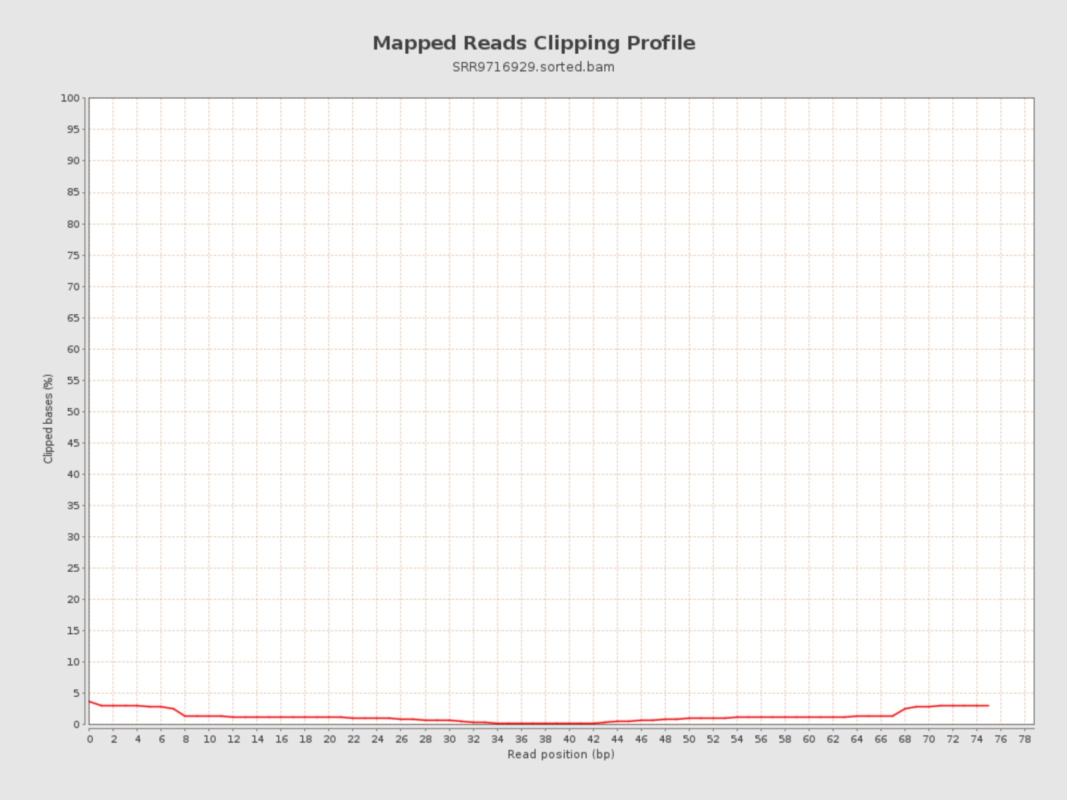
8. Results : Mapped Reads Nucleotide Content



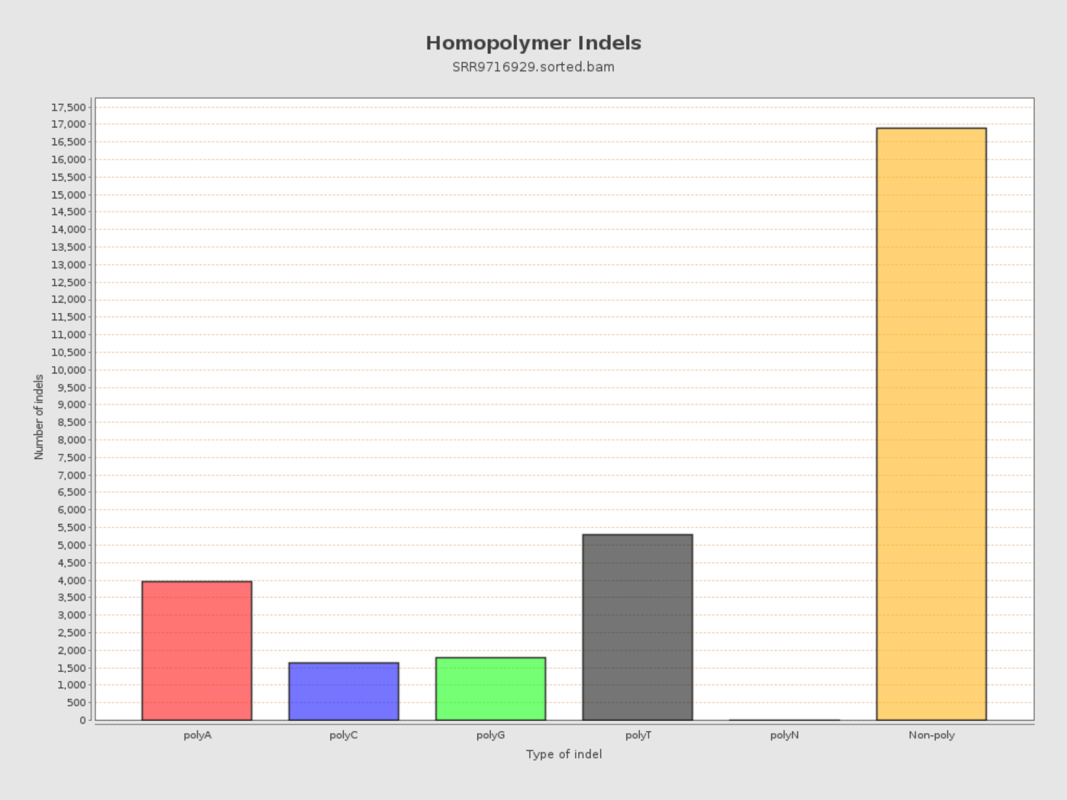
9. Results : Mapped Reads GC-content Distribution



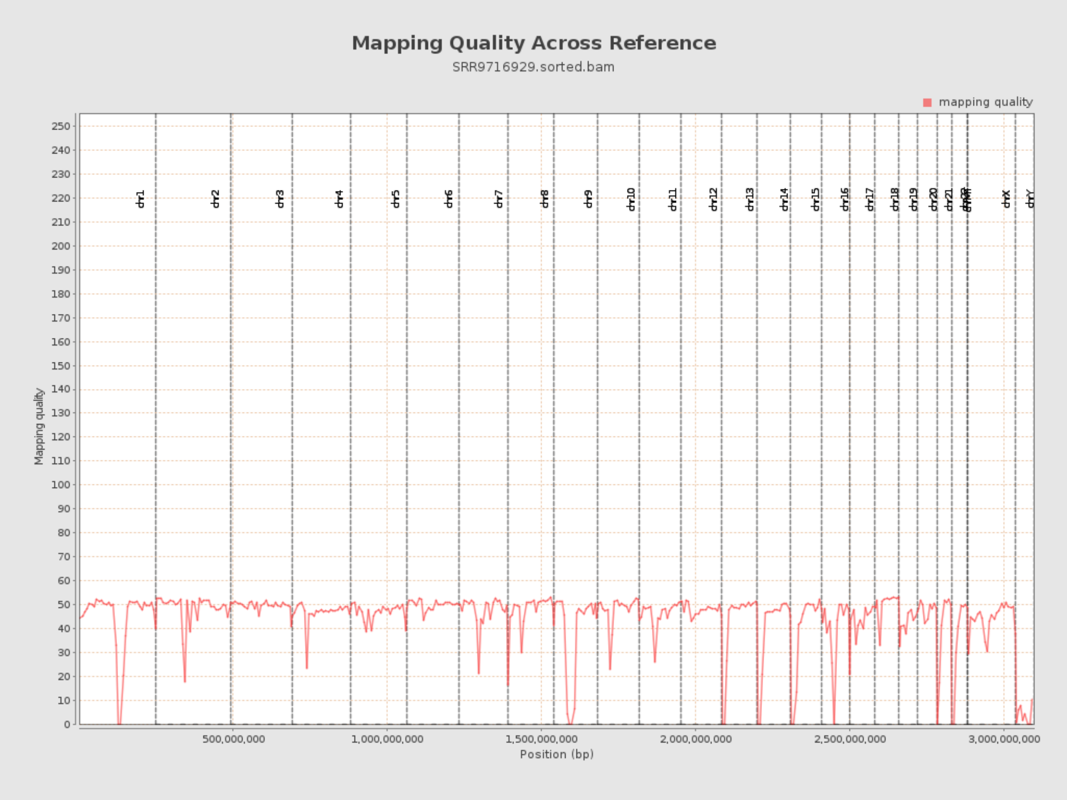
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram