

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:58:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716927.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_SRR9716927 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716927.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:58:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716927.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,055,137
Mapped reads	1,896,636 / 92.29%
Unmapped reads	158,501 / 7.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,906 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	84,375 / 4.11%
Duplication rate	3.37%
Clipped reads	1,904,242 / 92.66%

2.2. ACGT Content

Number/percentage of A's	26,552,056 / 23.95%
Number/percentage of C's	23,086,912 / 20.82%
Number/percentage of T's	35,020,196 / 31.59%
Number/percentage of G's	26,209,523 / 23.64%
Number/percentage of N's	1,502 / 0%
GC Percentage	44.46%

2.3. Coverage

Mean	0.0358

Standard Deviation	0.3265
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2.4. Mapping Quality

Mean Mapping Quality	44.65
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2.5. Mismatches and indels

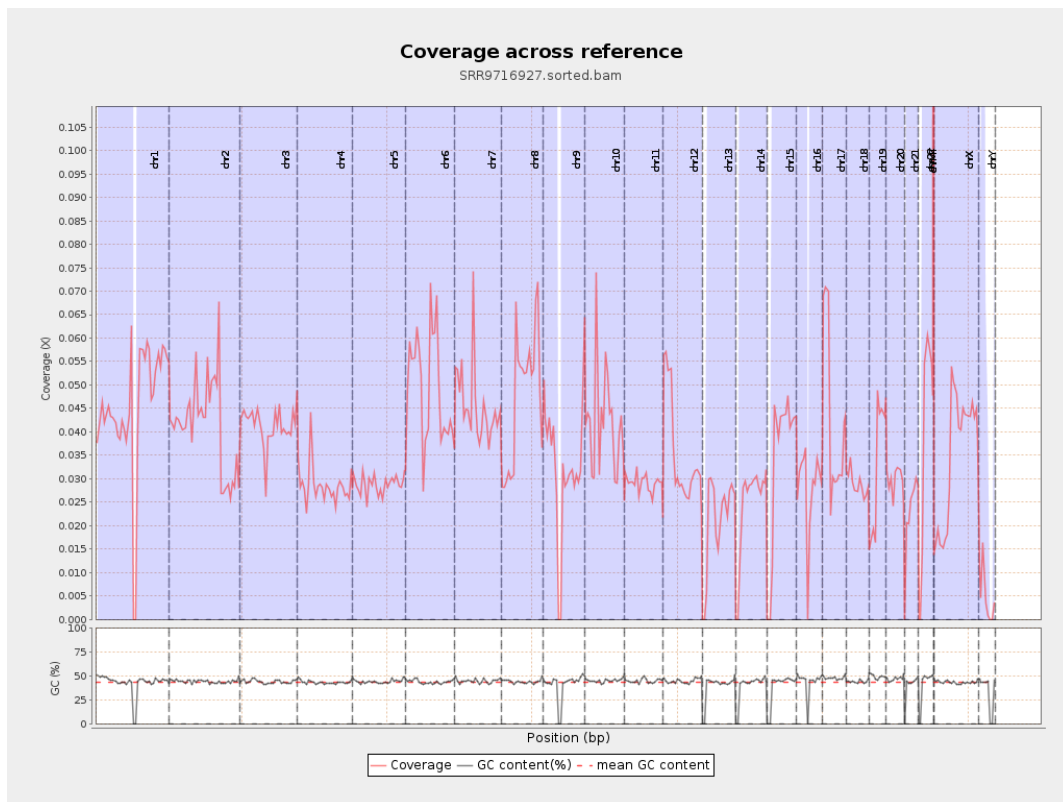
General error rate	0.5%
Mismatches	546,934
Insertions	6,353
Mapped reads with at least one insertion	0.33%
Deletions	19,810
Mapped reads with at least one deletion	1.04%
Homopolymer indels	44.47%

2.6. Chromosome stats

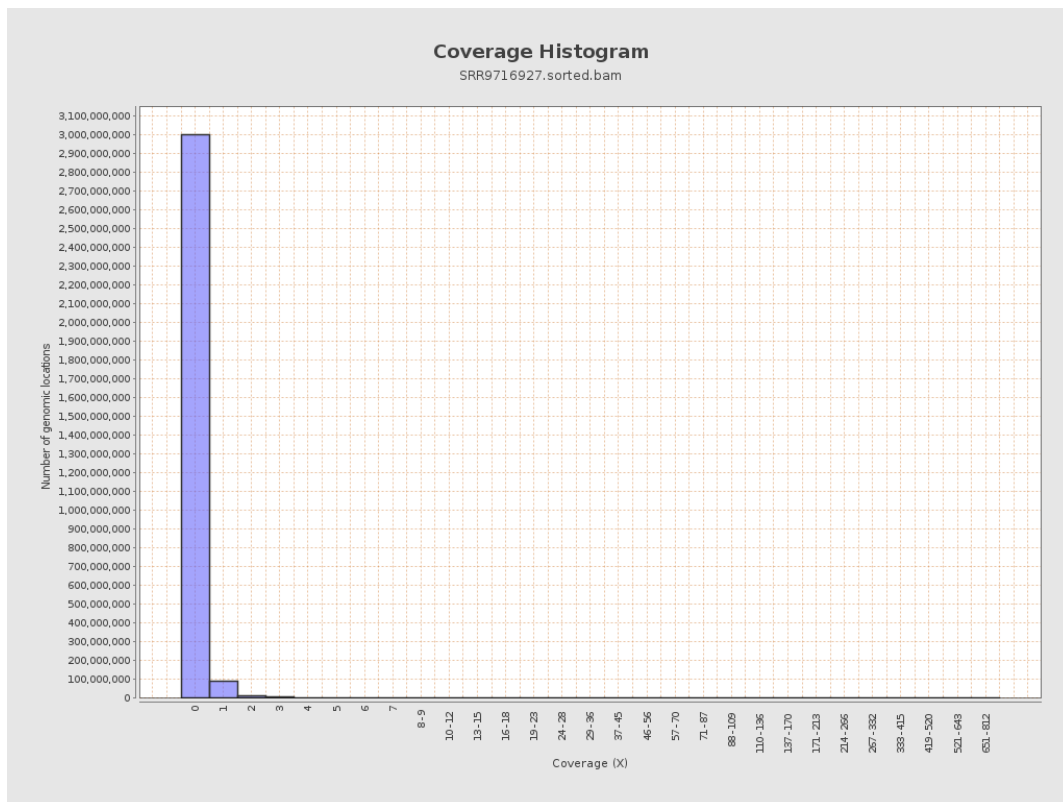
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11300472	0.0453	0.5735
chr2	243199373	10074134	0.0414	0.4084
chr3	198022430	8148472	0.0411	0.2267
chr4	191154276	5436551	0.0284	0.2091
chr5	180915260	5197619	0.0287	0.1907
chr6	171115067	8442538	0.0493	0.3079
chr7	159138663	7249442	0.0456	0.59

chr8	146364022	6954429	0.0475	0.2952
chr9	141213431	4380167	0.031	0.2544
chr10	135534747	5703704	0.0421	0.2981
chr11	135006516	3920933	0.029	0.269
chr12	133851895	4722077	0.0353	0.2125
chr13	115169878	2404404	0.0209	0.1625
chr14	107349540	2580099	0.024	0.1935
chr15	102531392	3551388	0.0346	0.2123
chr16	90354753	2542379	0.0281	0.2025
chr17	81195210	3446993	0.0425	0.2441
chr18	78077248	2259071	0.0289	0.4512
chr19	59128983	1954549	0.0331	0.378
chr20	63025520	1868308	0.0296	0.1971
chr21	48129895	1105731	0.023	0.1821
chr22	51304566	1974058	0.0385	0.2207
chrMT	16571	8600	0.519	0.8106
chrX	155270560	5394846	0.0347	0.2388
chrY	59373566	280293	0.0047	0.1147

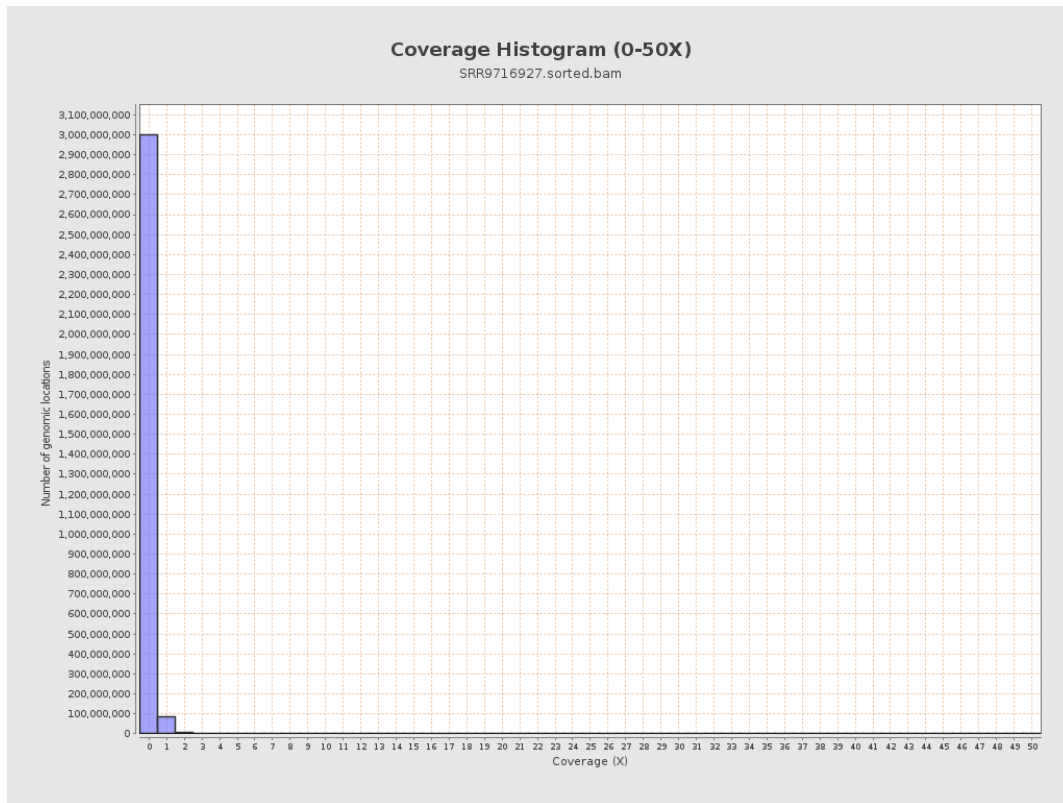
3. Results : Coverage across reference



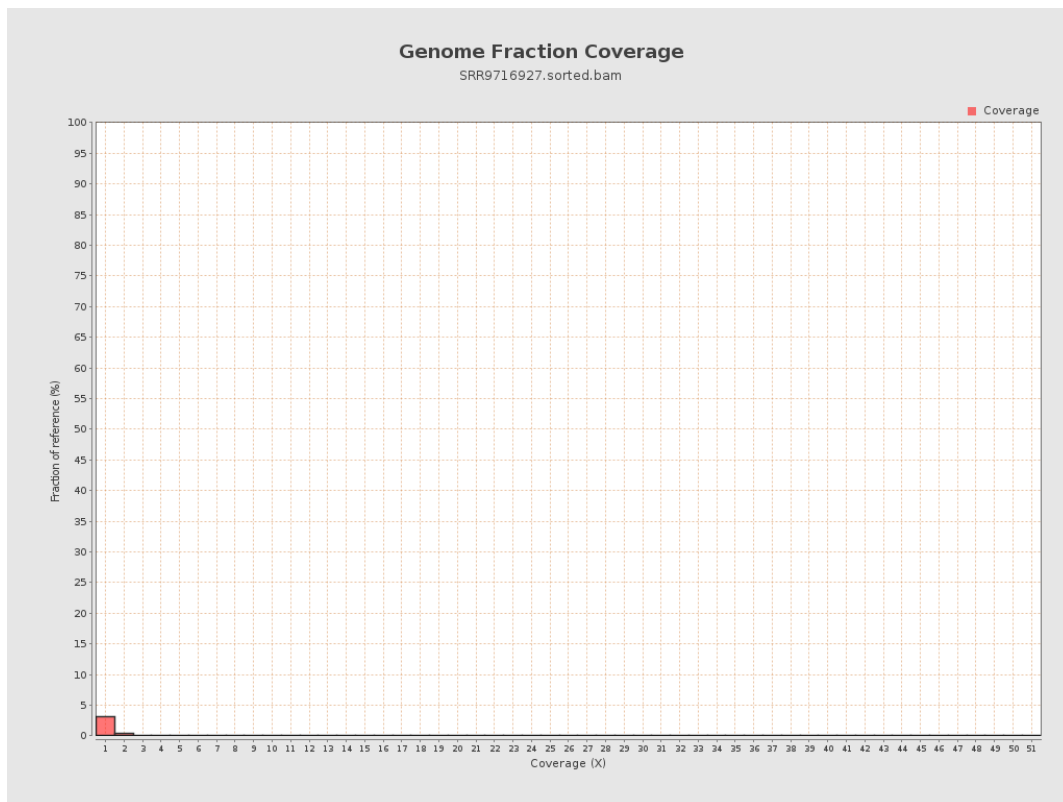
4. Results : Coverage Histogram



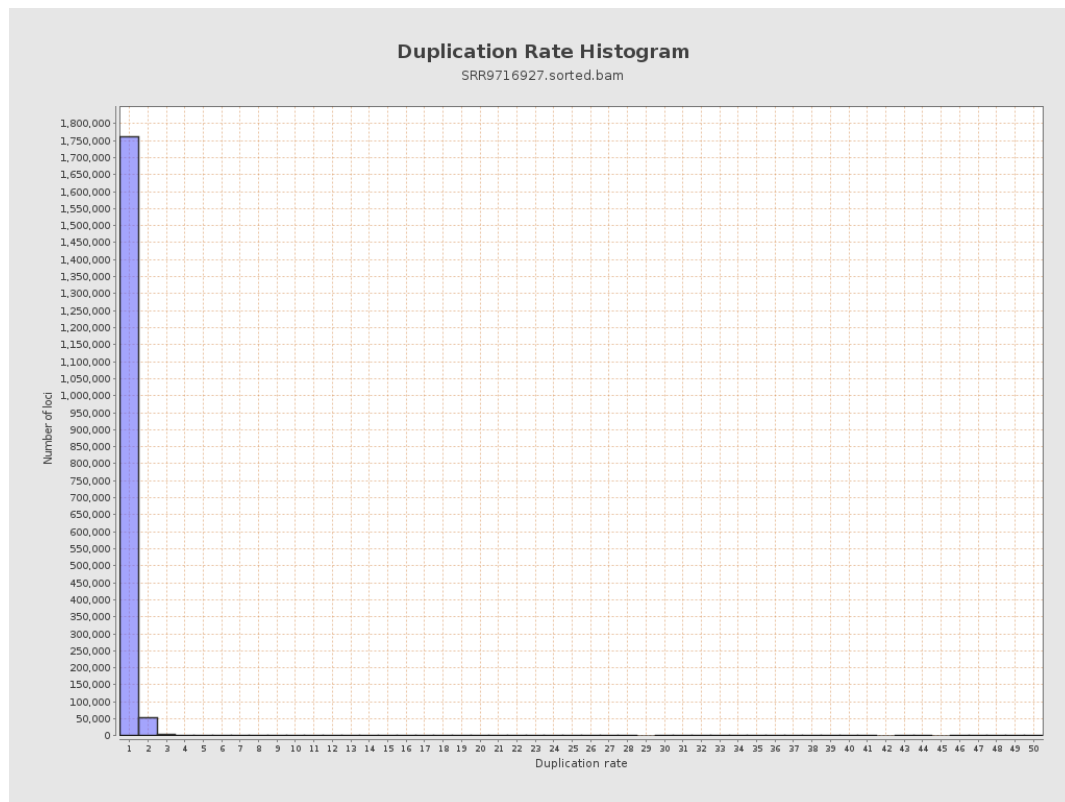
5. Results : Coverage Histogram (0-50X)



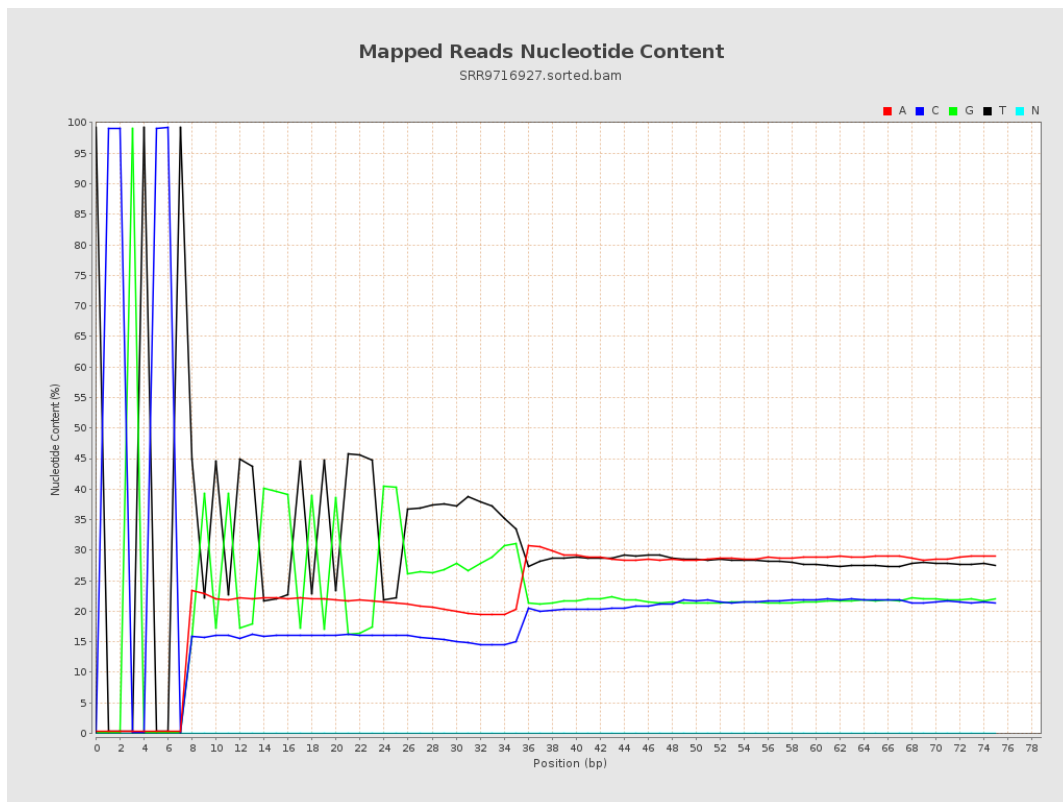
6. Results : Genome Fraction Coverage



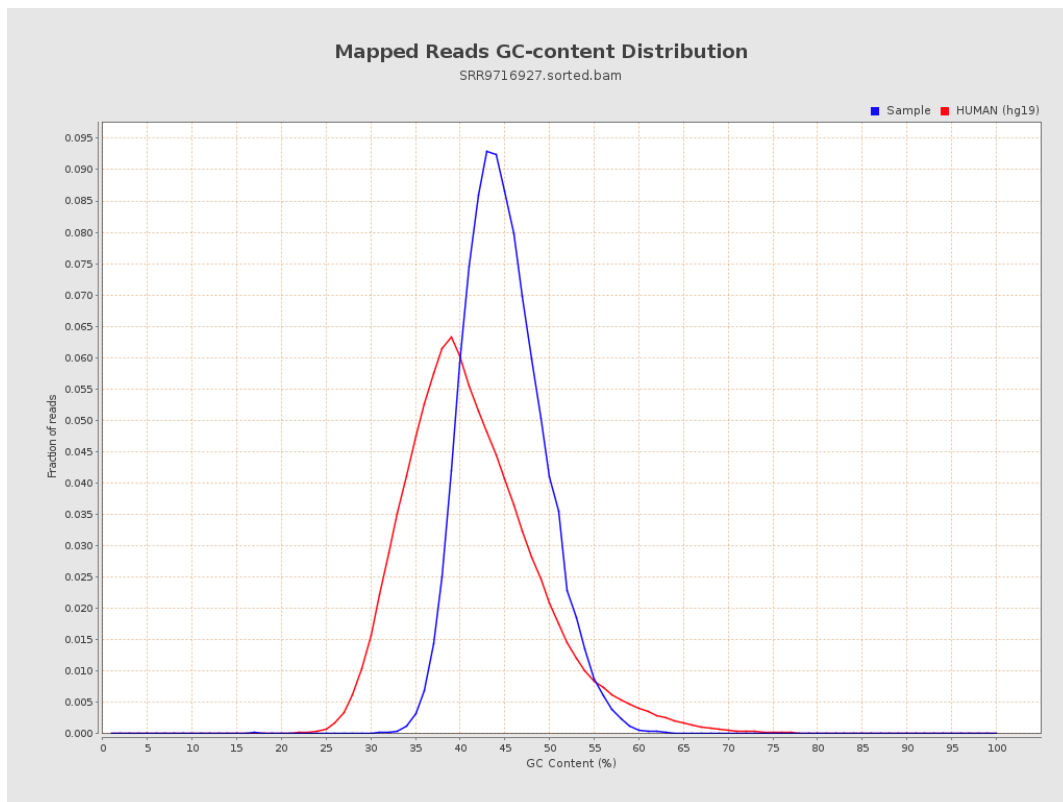
7. Results : Duplication Rate Histogram



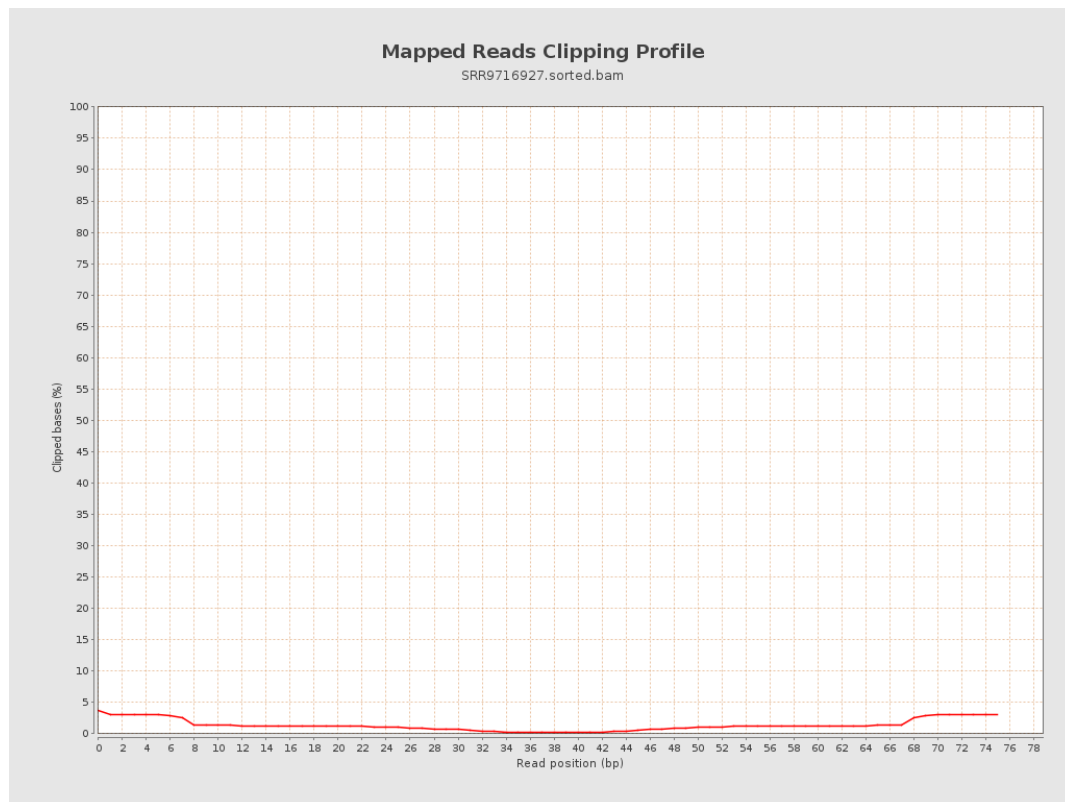
8. Results : Mapped Reads Nucleotide Content



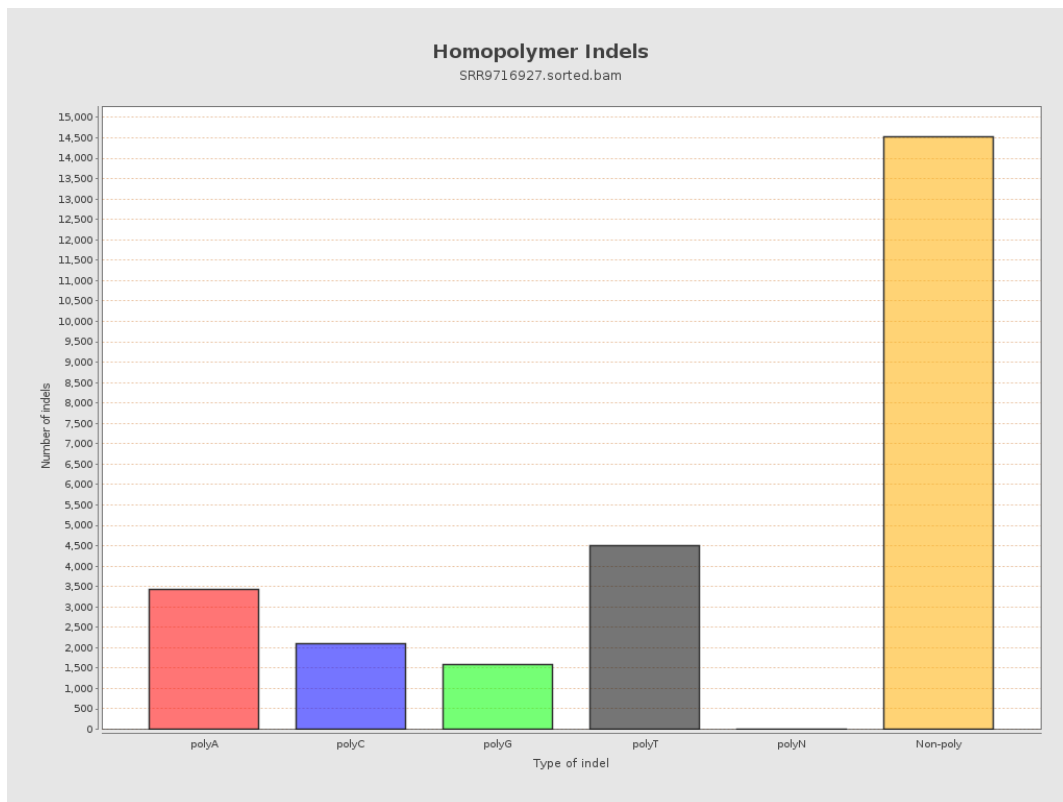
9. Results : Mapped Reads GC-content Distribution



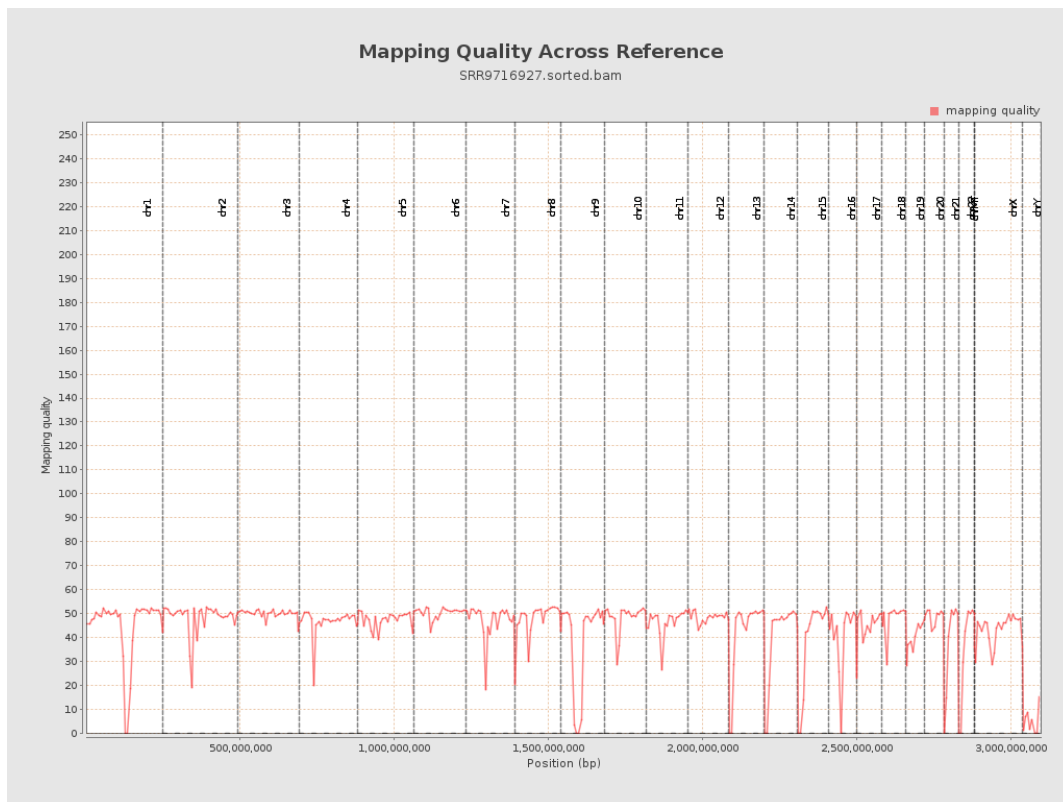
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

