

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:17:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716730.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_SRR9716730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716730.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:17:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716730.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,471,859
Mapped reads	2,836,580 / 81.7%
Unmapped reads	635,279 / 18.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,610 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	128,636 / 3.71%
Duplication rate	3.39%
Clipped reads	2,839,595 / 81.79%

2.2. ACGT Content

Number/percentage of A's	39,839,590 / 24.6%
Number/percentage of C's	32,001,087 / 19.76%
Number/percentage of T's	52,904,868 / 32.66%
Number/percentage of G's	37,221,599 / 22.98%
Number/percentage of N's	2,457 / 0%
GC Percentage	42.74%

2.3. Coverage

Mean	0.0523

Standard Deviation	0.3902
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2.4. Mapping Quality

Mean Mapping Quality	43.88
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2.5. Mismatches and indels

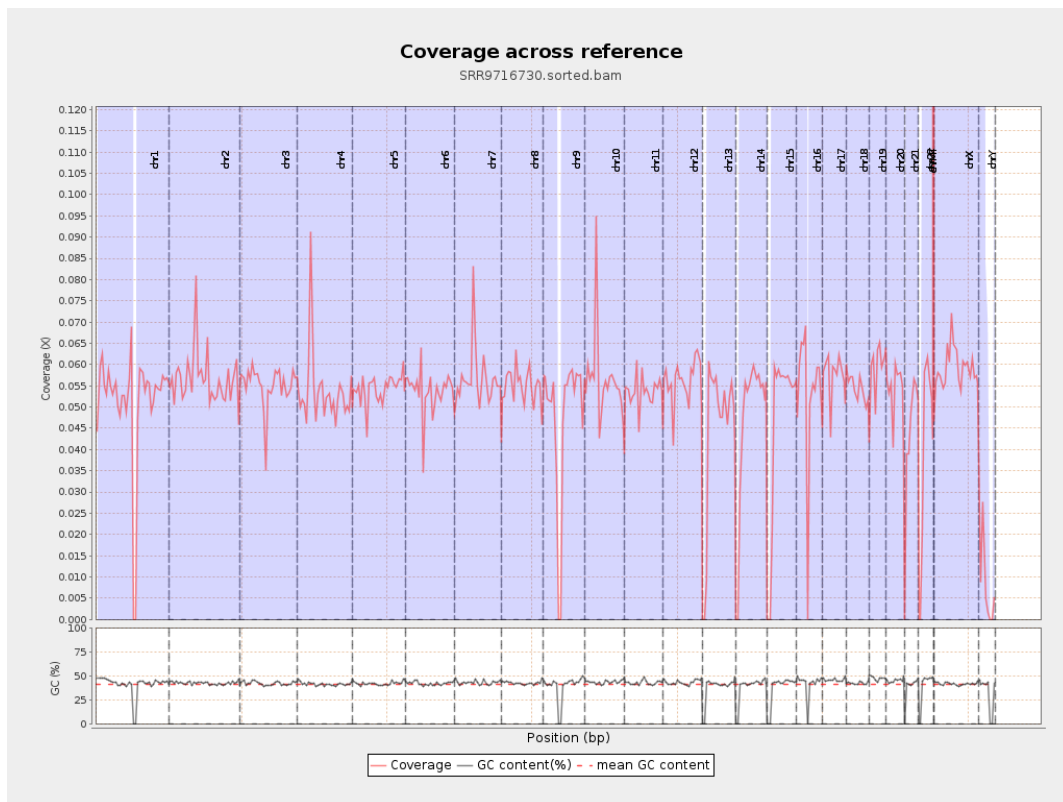
General error rate	0.54%
Mismatches	850,412
Insertions	11,013
Mapped reads with at least one insertion	0.39%
Deletions	32,177
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.62%

2.6. Chromosome stats

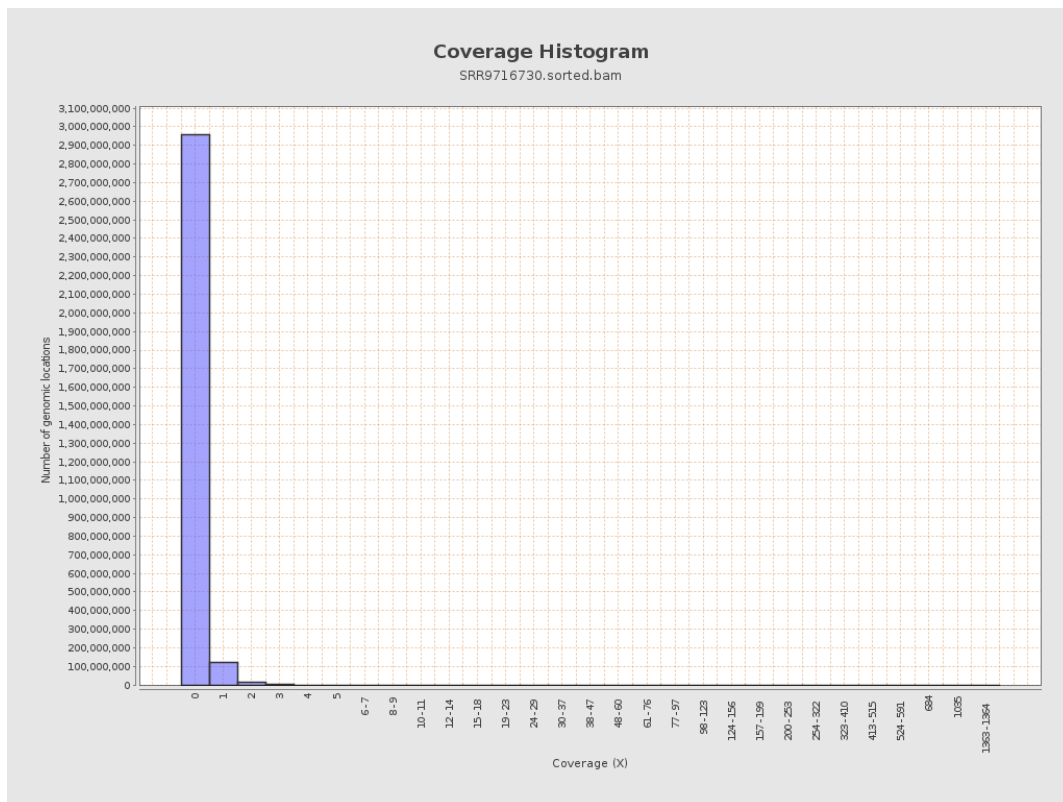
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12763392	0.0512	0.5286
chr2	243199373	13797356	0.0567	0.6448
chr3	198022430	10905812	0.0551	0.2734
chr4	191154276	10206178	0.0534	0.319
chr5	180915260	9825720	0.0543	0.2691
chr6	171115067	9178846	0.0536	0.3243
chr7	159138663	9053602	0.0569	0.5431

chr8	146364022	8038642	0.0549	0.3564
chr9	141213431	6655590	0.0471	0.3126
chr10	135534747	7642934	0.0564	0.4445
chr11	135006516	7210842	0.0534	0.3354
chr12	133851895	7526212	0.0562	0.2792
chr13	115169878	5074808	0.0441	0.2438
chr14	107349540	4982225	0.0464	0.2631
chr15	102531392	4746128	0.0463	0.2541
chr16	90354753	4805427	0.0532	0.3029
chr17	81195210	4652677	0.0573	0.306
chr18	78077248	4253906	0.0545	0.5704
chr19	59128983	3507752	0.0593	0.4442
chr20	63025520	3383237	0.0537	0.2782
chr21	48129895	2100213	0.0436	0.2757
chr22	51304566	2019032	0.0394	0.2307
chrMT	16571	29600	1.7863	1.7168
chrX	155270560	9166062	0.059	0.3153
chrY	59373566	494519	0.0083	0.2155

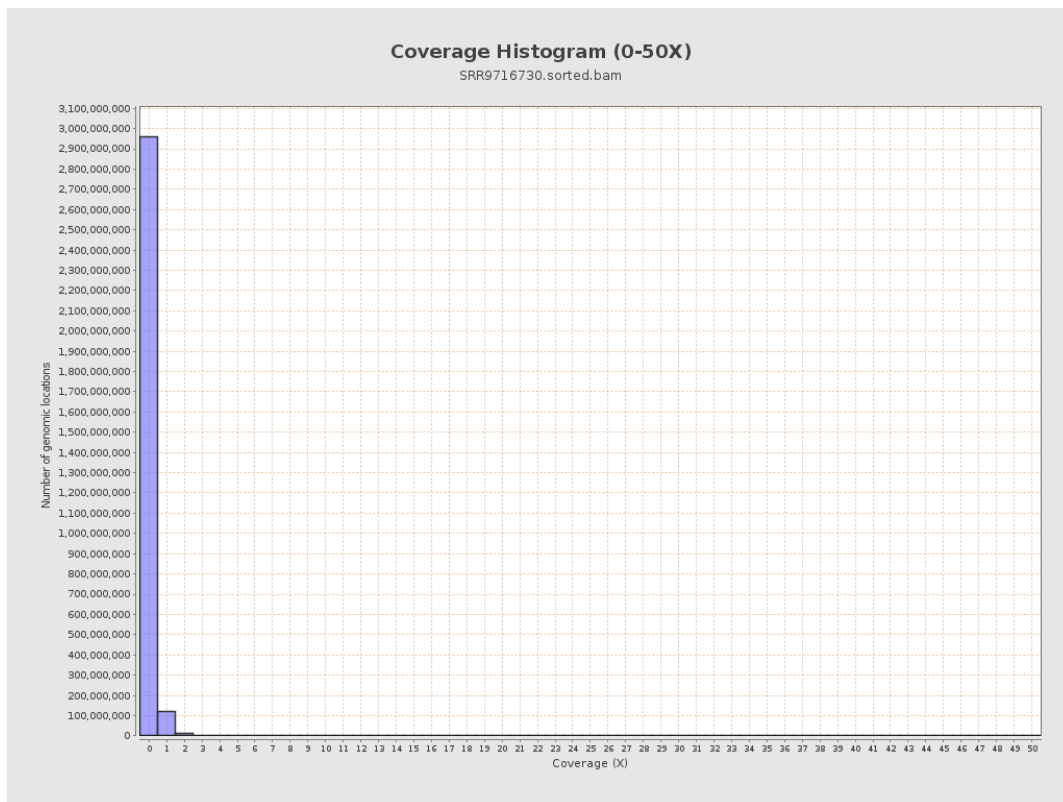
3. Results : Coverage across reference



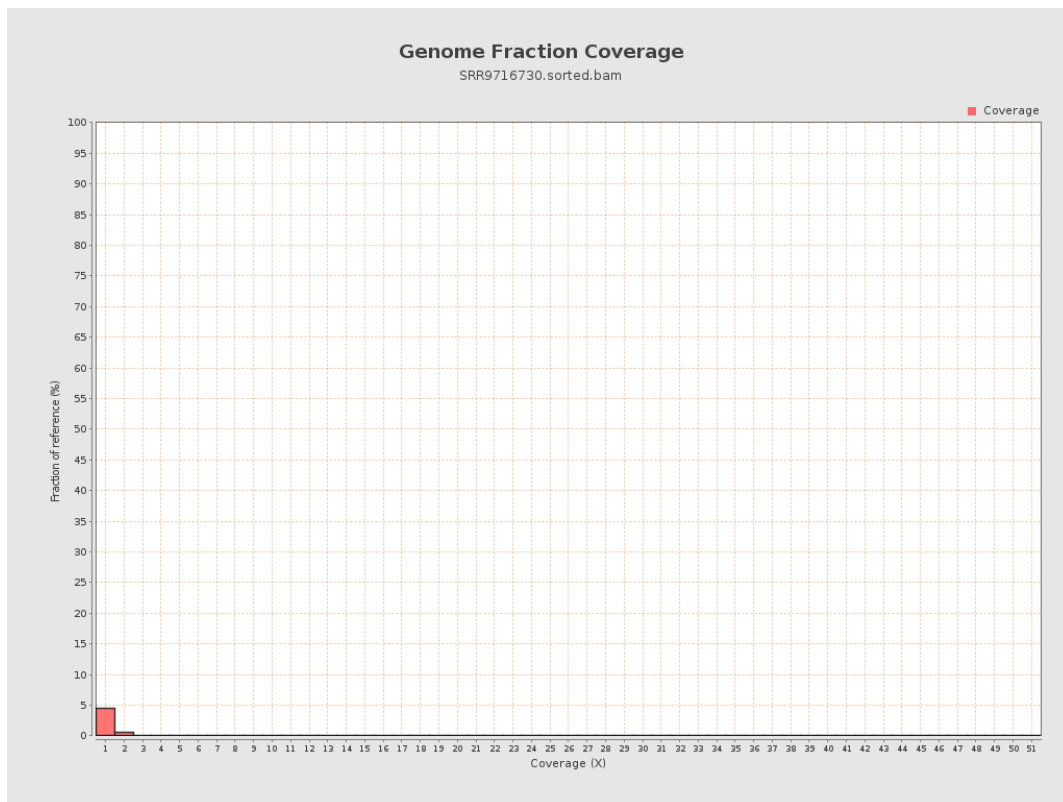
4. Results : Coverage Histogram



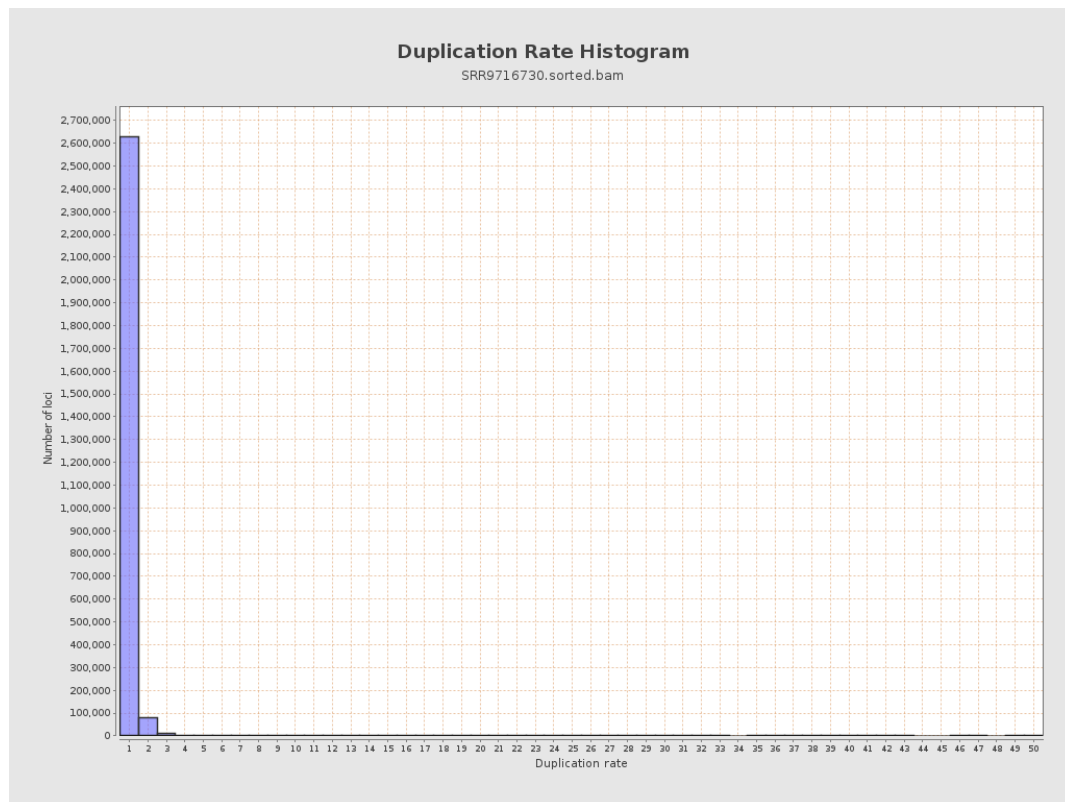
5. Results : Coverage Histogram (0-50X)



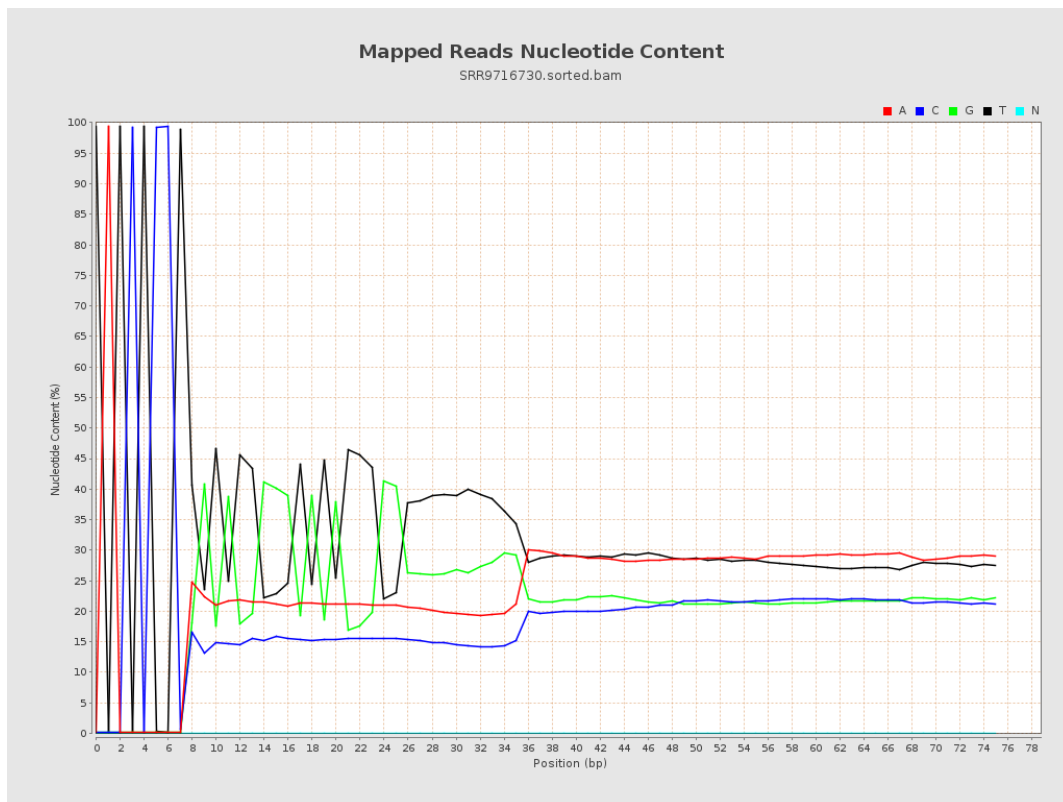
6. Results : Genome Fraction Coverage



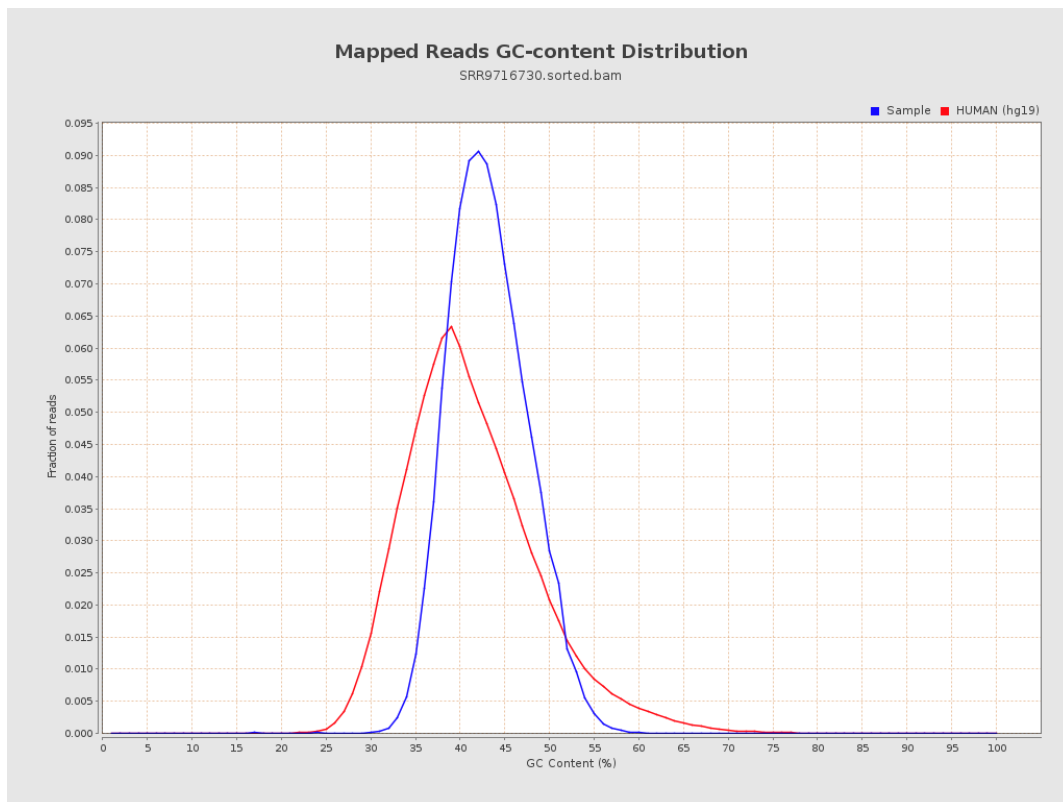
7. Results : Duplication Rate Histogram



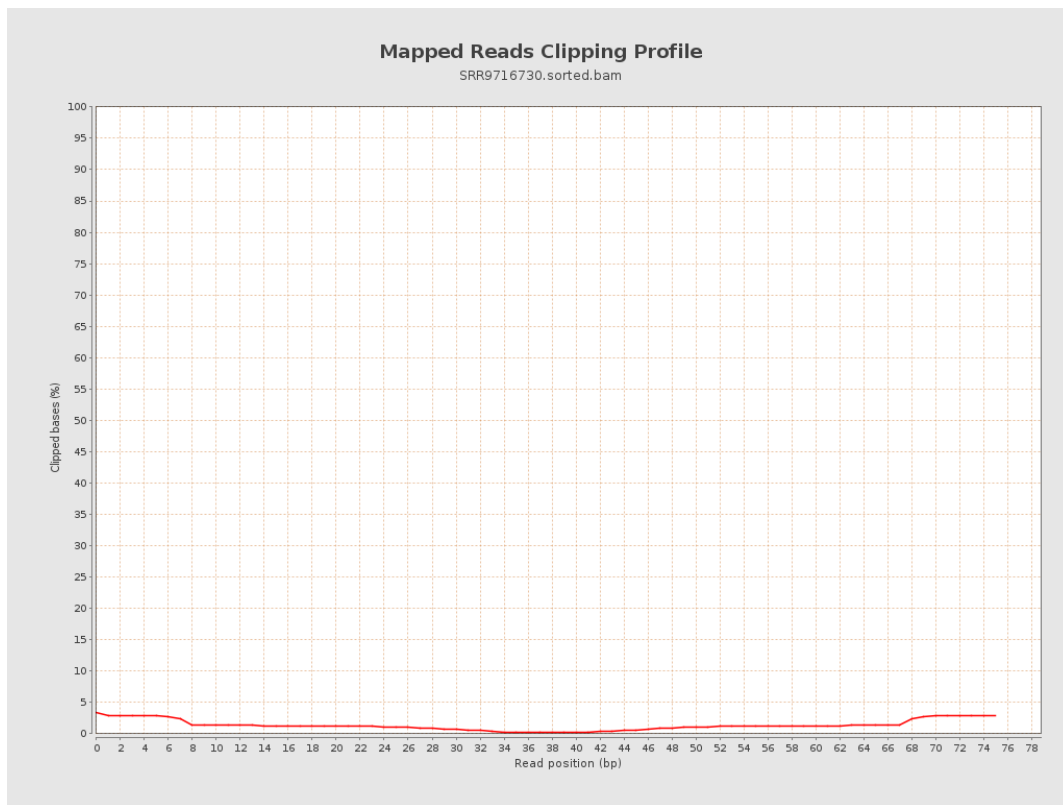
8. Results : Mapped Reads Nucleotide Content



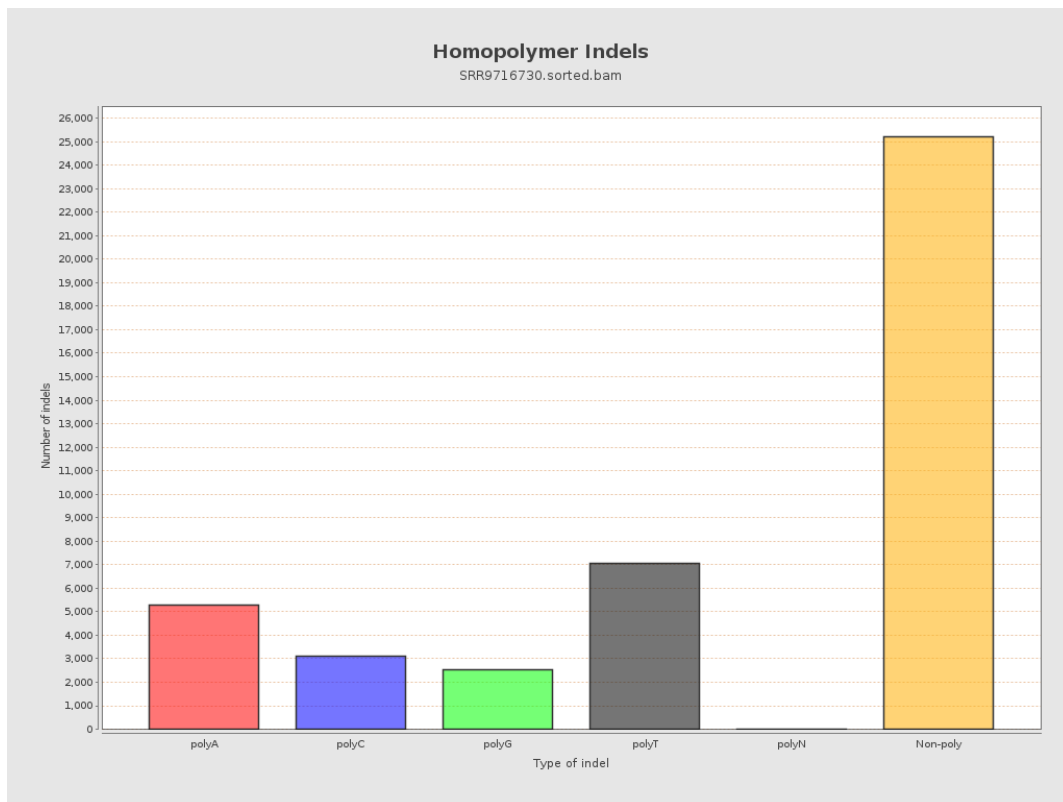
9. Results : Mapped Reads GC-content Distribution



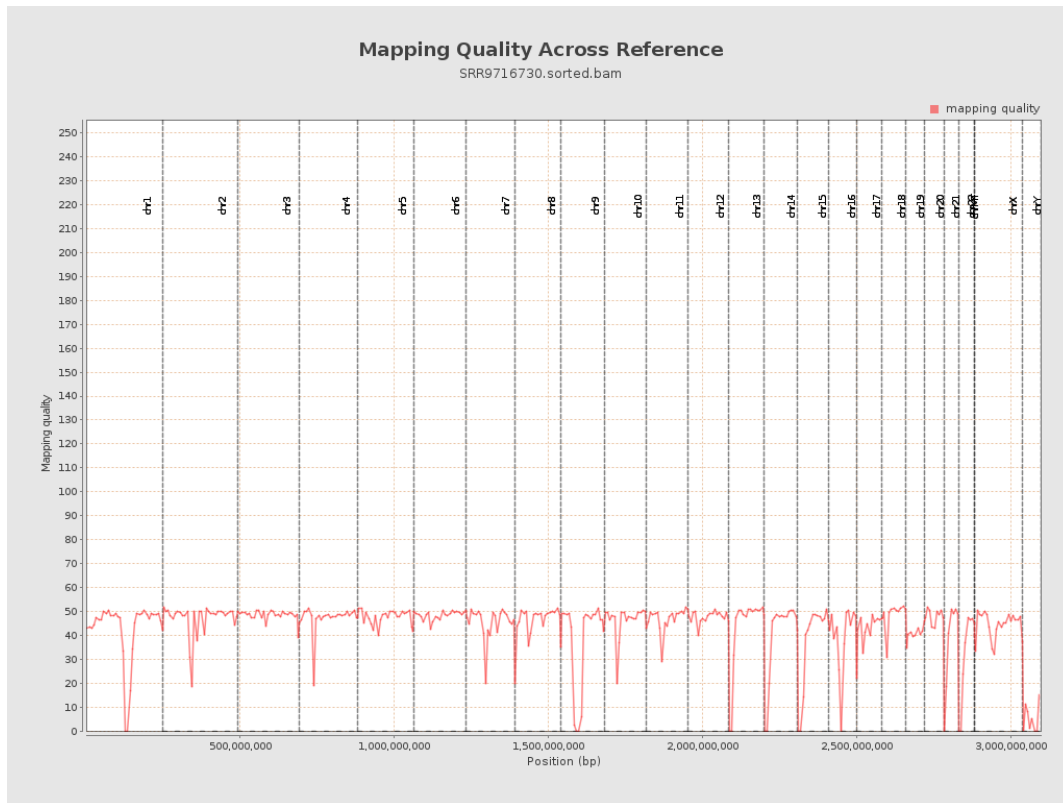
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

