

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:25:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818812.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_SRR1818812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818812.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:25:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818812.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,635,849
Mapped reads	2,401,477 / 91.11%
Unmapped reads	234,372 / 8.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,395 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	1,104,246 / 41.89%
Duplication rate	39.77%
Clipped reads	2,400,875 / 91.09%

2.2. ACGT Content

Number/percentage of A's	47,255,855 / 28.98%
Number/percentage of C's	34,448,128 / 21.12%
Number/percentage of T's	47,549,119 / 29.16%
Number/percentage of G's	33,823,974 / 20.74%
Number/percentage of N's	10,366 / 0.01%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0527

Standard Deviation	0.6306
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2.4. Mapping Quality

Mean Mapping Quality	47.61
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2.5. Mismatches and indels

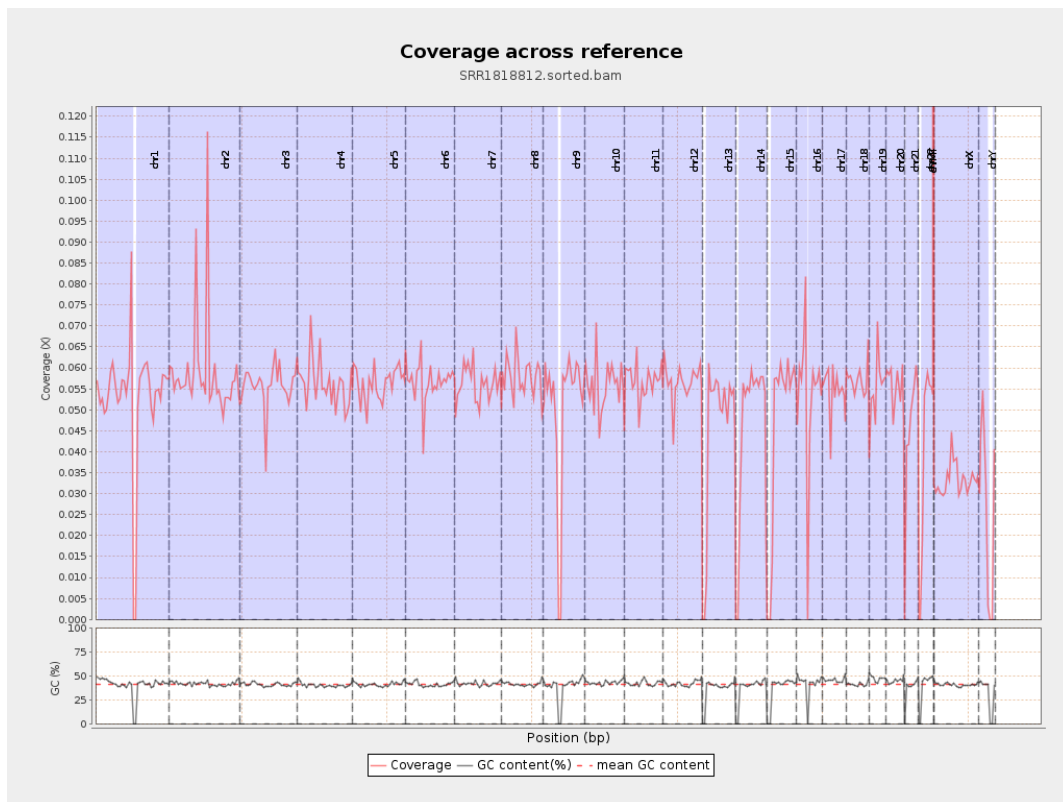
General error rate	0.54%
Mismatches	836,963
Insertions	20,730
Mapped reads with at least one insertion	0.85%
Deletions	42,375
Mapped reads with at least one deletion	1.75%
Homopolymer indels	39.23%

2.6. Chromosome stats

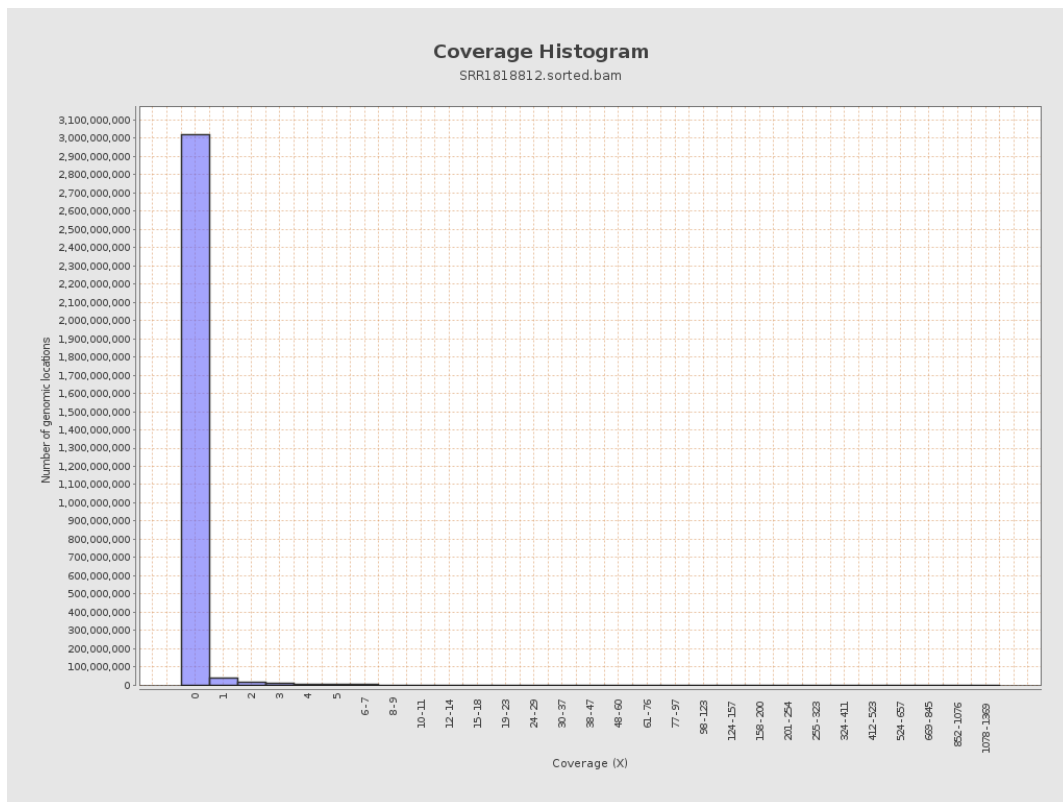
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13172069	0.0528	0.8956
chr2	243199373	14335731	0.0589	1.0598
chr3	198022430	11045422	0.0558	0.4335
chr4	191154276	10712142	0.056	0.5219
chr5	180915260	10171390	0.0562	0.4529
chr6	171115067	9728022	0.0569	0.5087
chr7	159138663	8952834	0.0563	0.5453

chr8	146364022	8504615	0.0581	0.5265
chr9	141213431	7105131	0.0503	0.5188
chr10	135534747	7570370	0.0559	0.6565
chr11	135006516	7679238	0.0569	0.517
chr12	133851895	7579137	0.0566	0.4704
chr13	115169878	5196781	0.0451	0.3877
chr14	107349540	5017838	0.0467	0.4686
chr15	102531392	4759136	0.0464	0.3991
chr16	90354753	4840830	0.0536	0.7502
chr17	81195210	4406480	0.0543	0.4567
chr18	78077248	4450846	0.057	0.7114
chr19	59128983	3300377	0.0558	0.7995
chr20	63025520	3510043	0.0557	0.4709
chr21	48129895	2193571	0.0456	0.4146
chr22	51304566	1983269	0.0387	0.4022
chrMT	16571	260276	15.7067	12.4867
chrX	155270560	5176238	0.0333	0.3912
chrY	59373566	1505150	0.0254	1.116

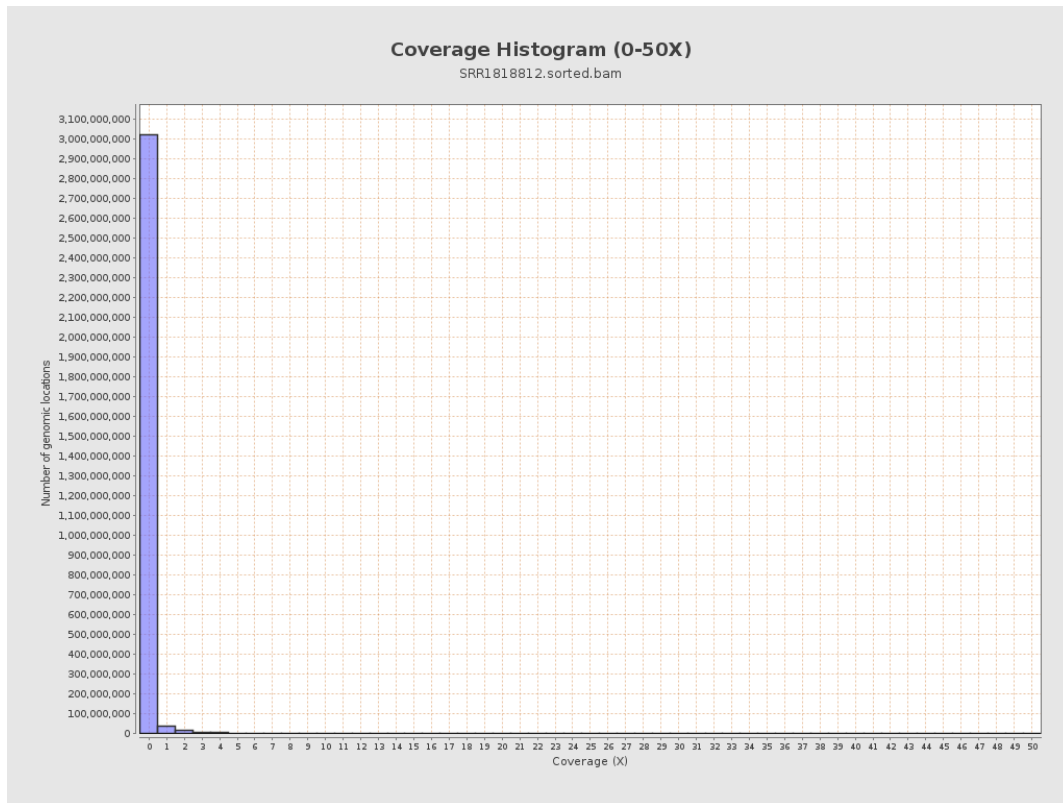
3. Results : Coverage across reference



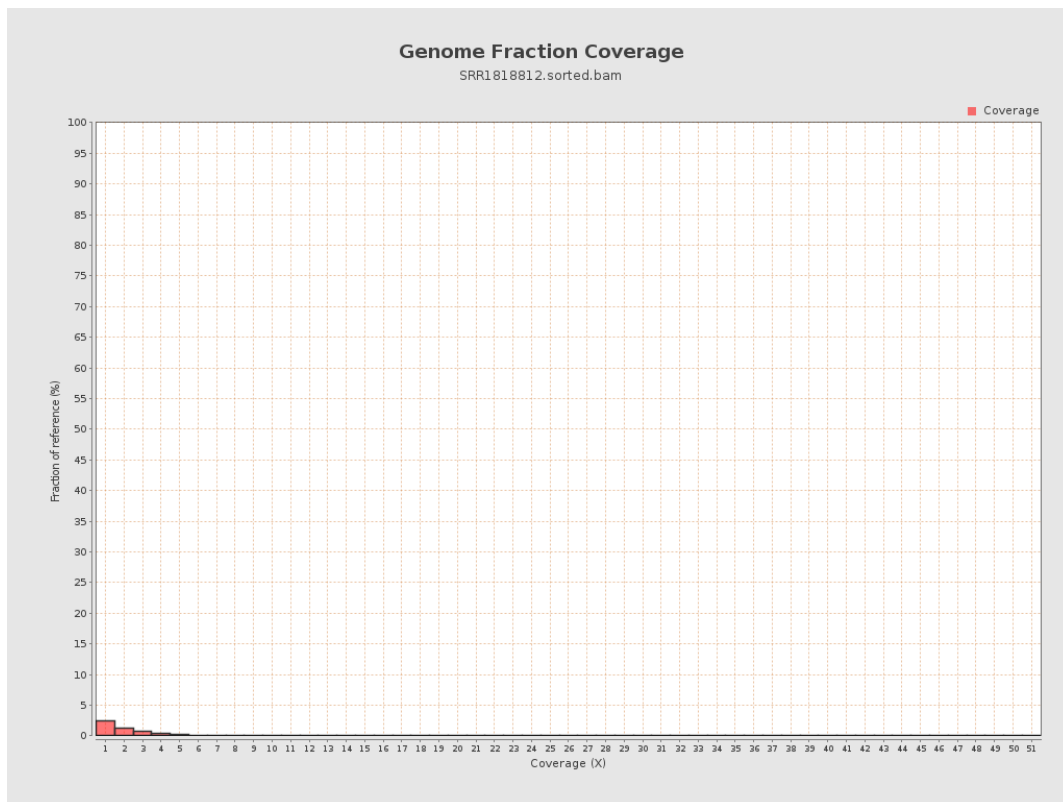
4. Results : Coverage Histogram



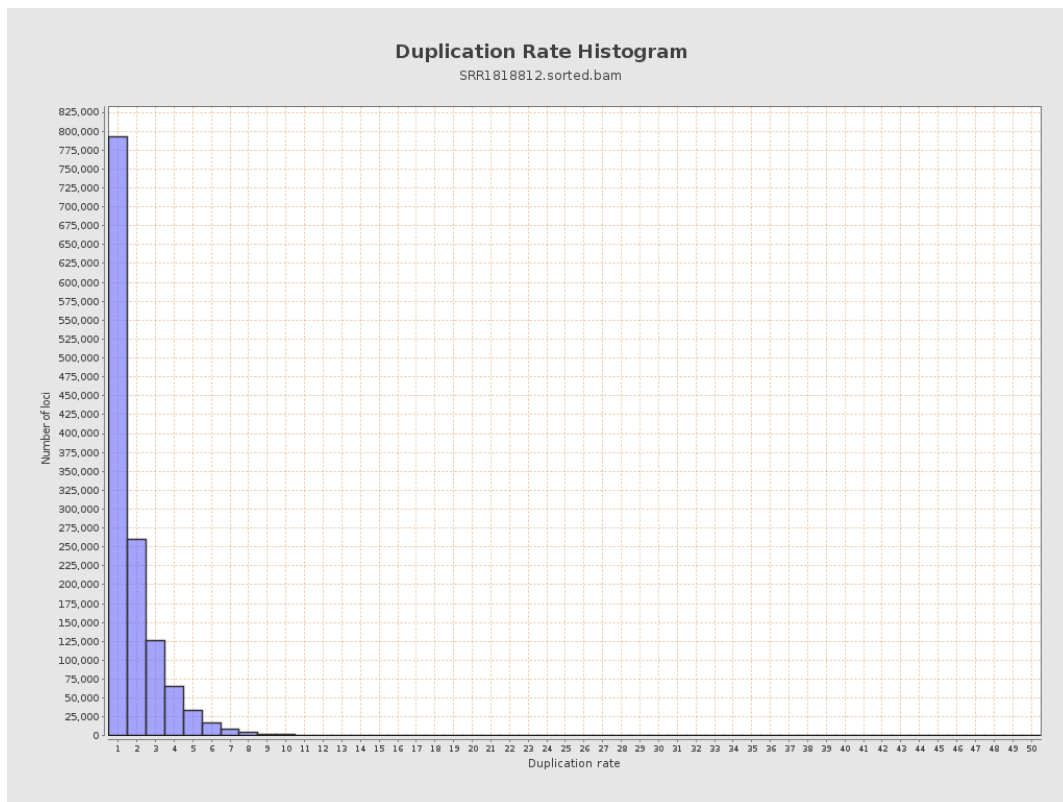
5. Results : Coverage Histogram (0-50X)



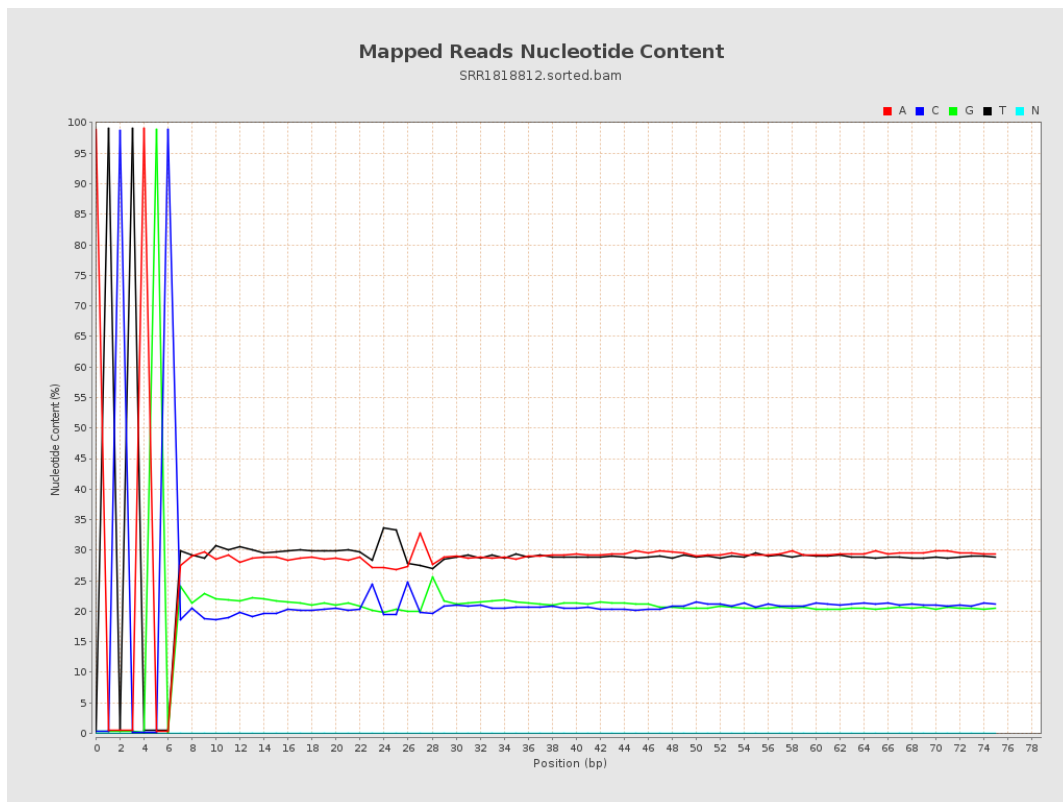
6. Results : Genome Fraction Coverage



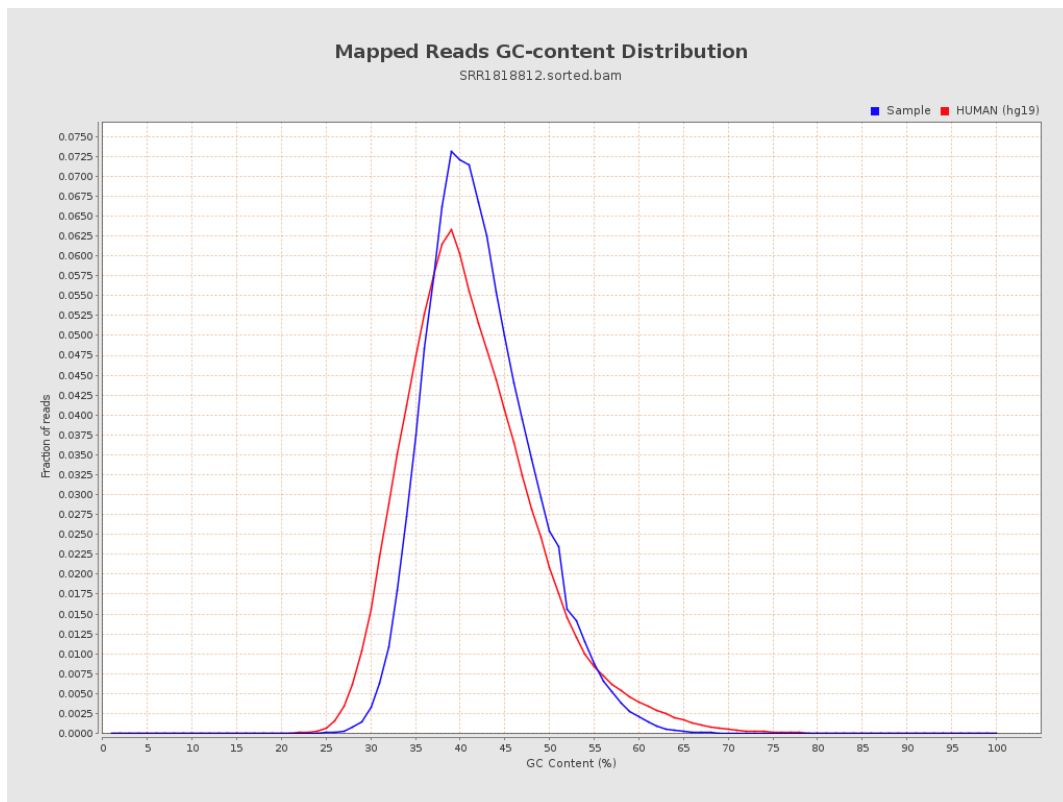
7. Results : Duplication Rate Histogram



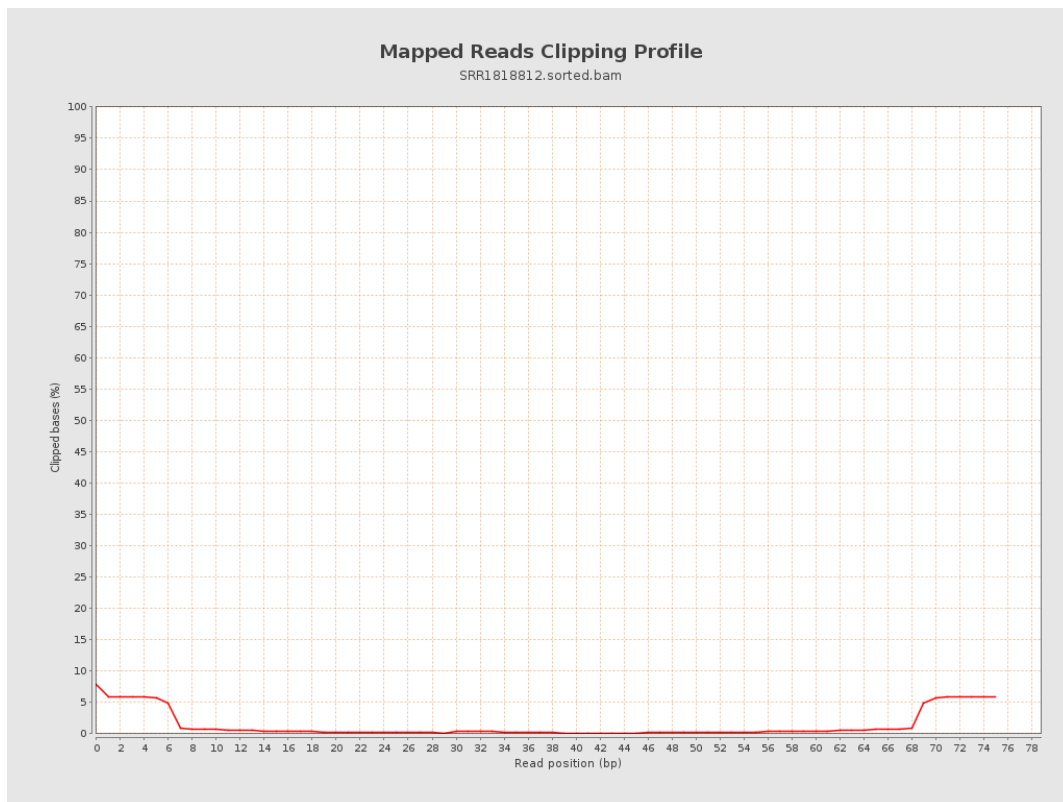
8. Results : Mapped Reads Nucleotide Content



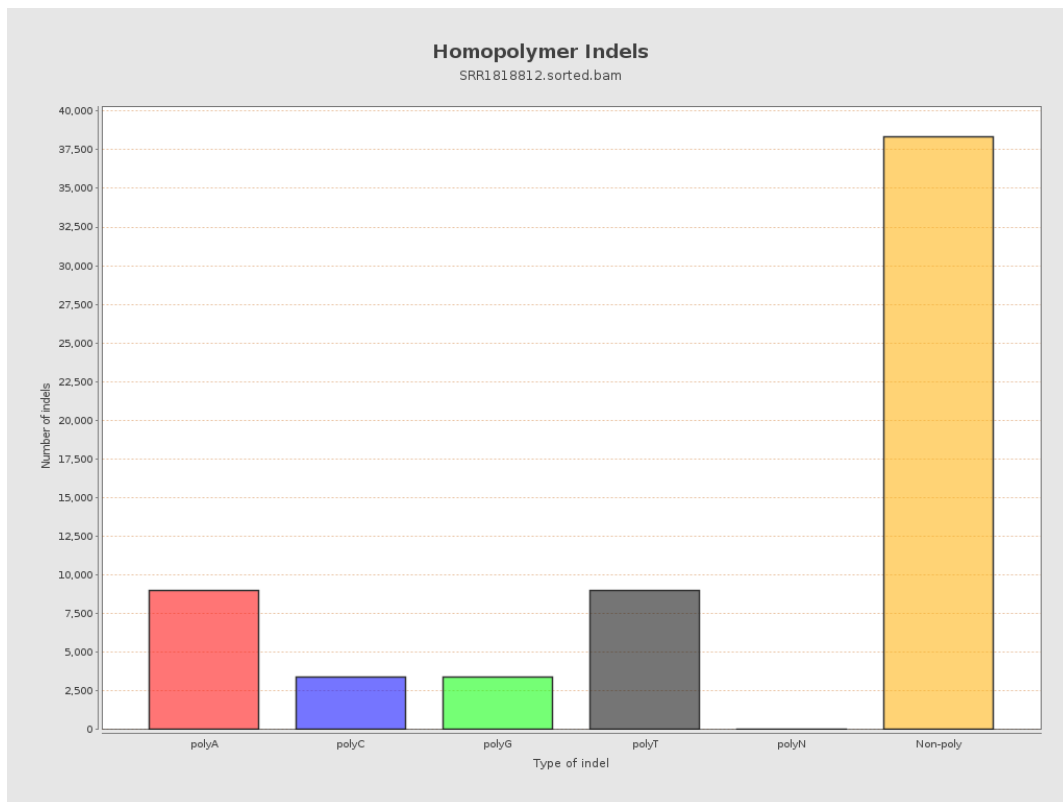
9. Results : Mapped Reads GC-content Distribution



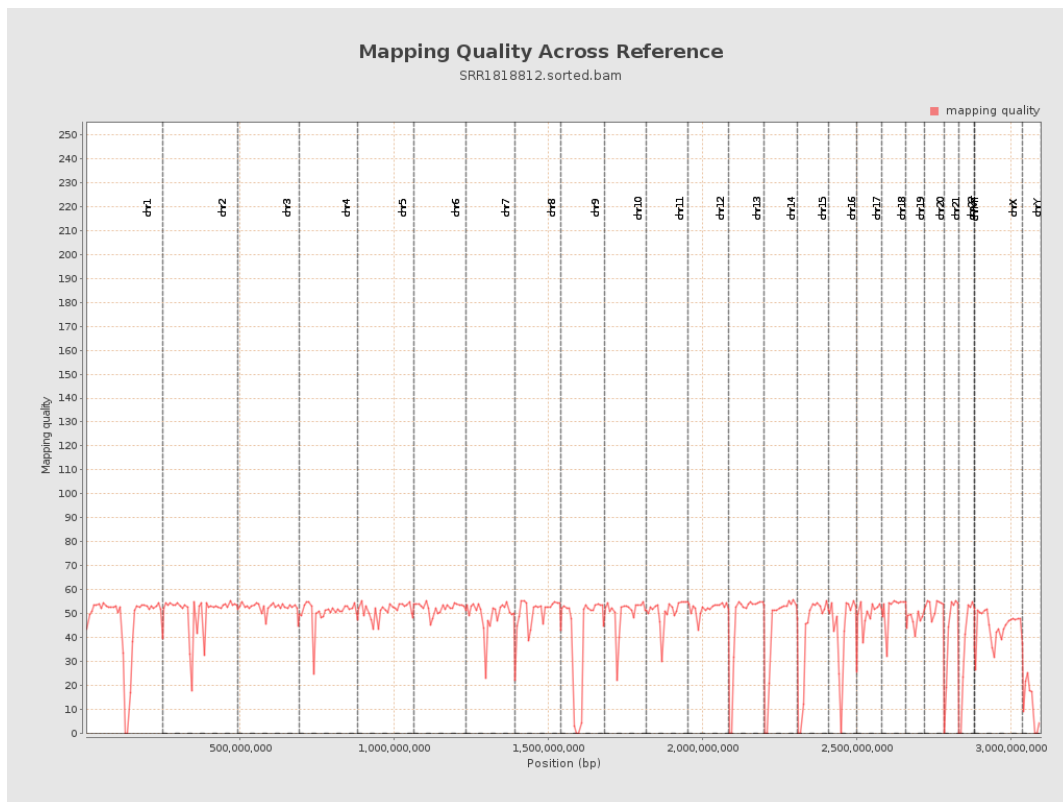
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

