

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 17:03:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234115.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_SRR6234115 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 17:03:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,560,353
Mapped reads	1,019,411 / 65.33%
Unmapped reads	540,942 / 34.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,006 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	53,664 / 3.44%
Duplication rate	4.39%
Clipped reads	698,926 / 44.79%

2.2. ACGT Content

Number/percentage of A's	15,989,742 / 25.78%
Number/percentage of C's	10,651,349 / 17.18%
Number/percentage of T's	19,934,596 / 32.14%
Number/percentage of G's	15,425,864 / 24.87%
Number/percentage of N's	14,013 / 0.02%
GC Percentage	42.05%

2.3. Coverage

Mean	0.02

Standard Deviation	0.2083
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2.4. Mapping Quality

Mean Mapping Quality	42.87
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2.5. Mismatches and indels

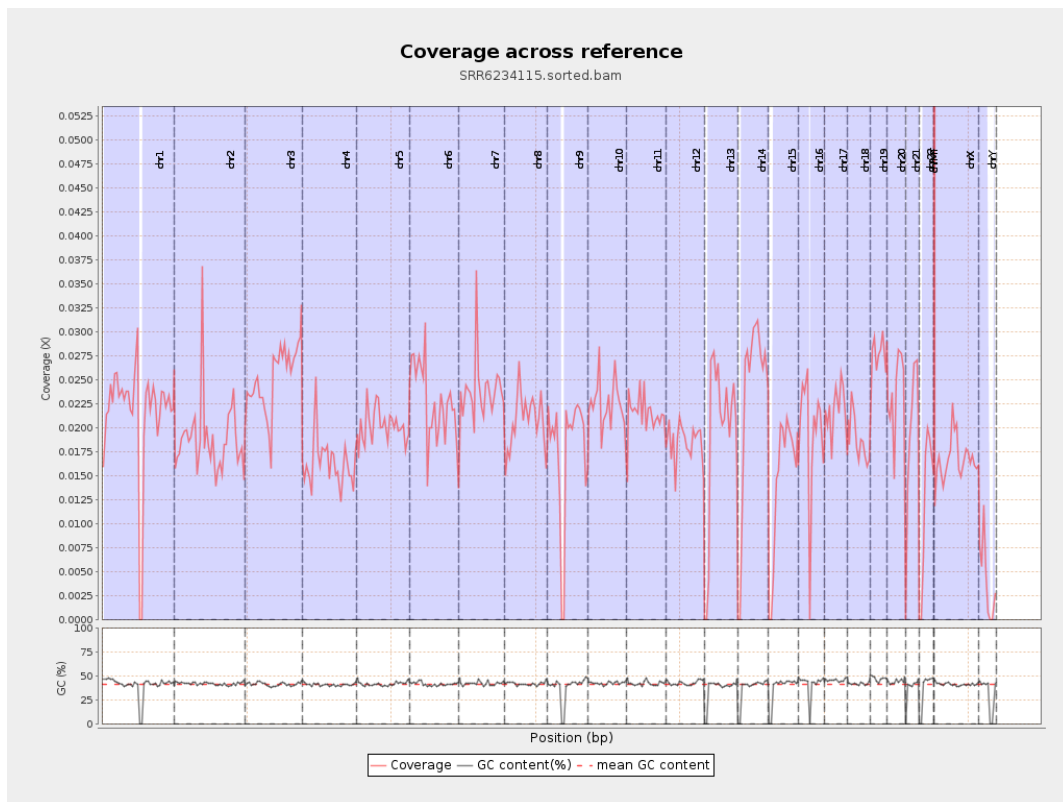
General error rate	0.95%
Mismatches	580,449
Insertions	5,219
Mapped reads with at least one insertion	0.51%
Deletions	24,712
Mapped reads with at least one deletion	2.39%
Homopolymer indels	46.17%

2.6. Chromosome stats

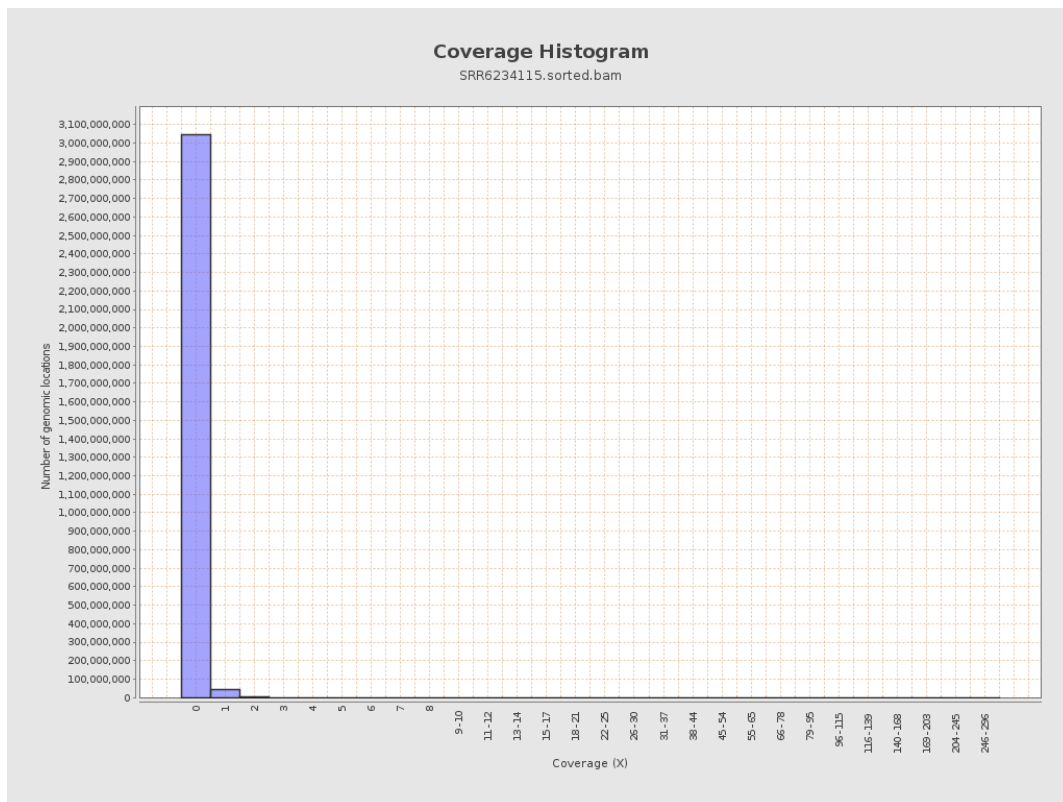
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5364109	0.0215	0.2793
chr2	243199373	4580980	0.0188	0.2368
chr3	198022430	4966957	0.0251	0.1843
chr4	191154276	3131732	0.0164	0.1561
chr5	180915260	3656645	0.0202	0.1662
chr6	171115067	3873044	0.0226	0.1995
chr7	159138663	3786317	0.0238	0.3047

chr8	146364022	3032139	0.0207	0.246
chr9	141213431	2496241	0.0177	0.1965
chr10	135534747	3036928	0.0224	0.1965
chr11	135006516	2920320	0.0216	0.222
chr12	133851895	2473575	0.0185	0.1588
chr13	115169878	2237610	0.0194	0.1733
chr14	107349540	2492897	0.0232	0.1837
chr15	102531392	1494709	0.0146	0.1462
chr16	90354753	1735298	0.0192	0.1684
chr17	81195210	1770029	0.0218	0.1863
chr18	78077248	1456193	0.0187	0.2877
chr19	59128983	1629569	0.0276	0.2373
chr20	63025520	1459356	0.0232	0.1859
chr21	48129895	947593	0.0197	0.1644
chr22	51304566	638314	0.0124	0.129
chrMT	16571	41332	2.4942	2.8359
chrX	155270560	2598188	0.0167	0.1641
chrY	59373566	239912	0.004	0.0832

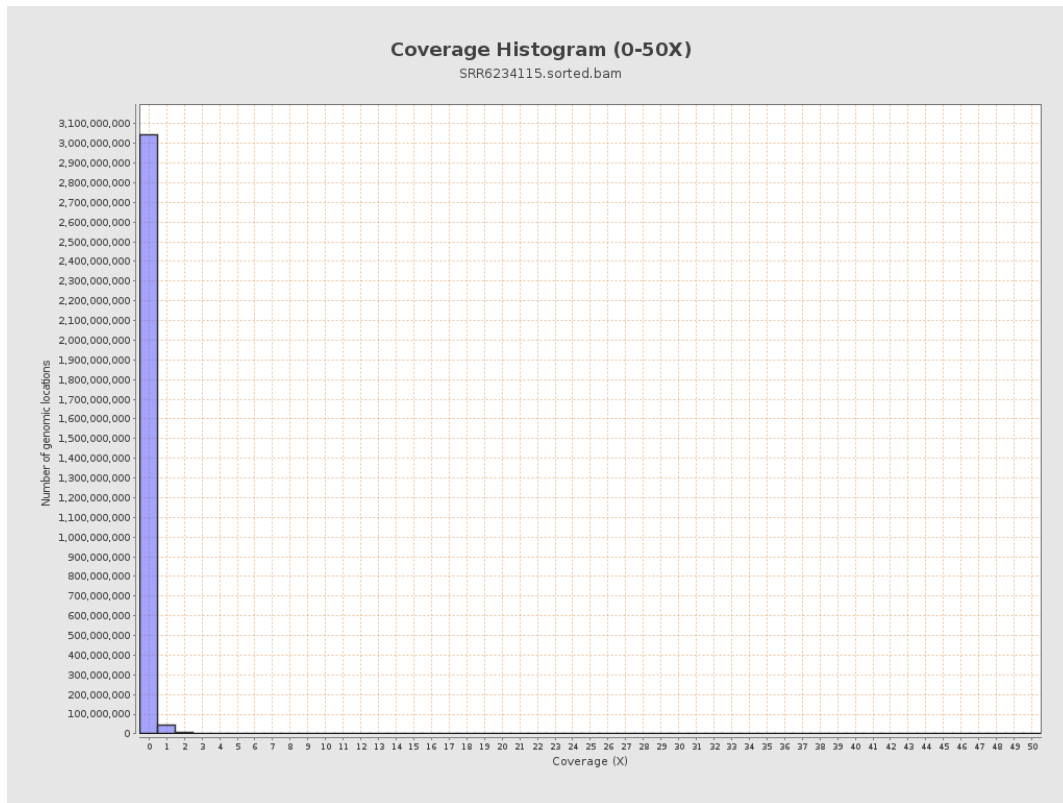
3. Results : Coverage across reference



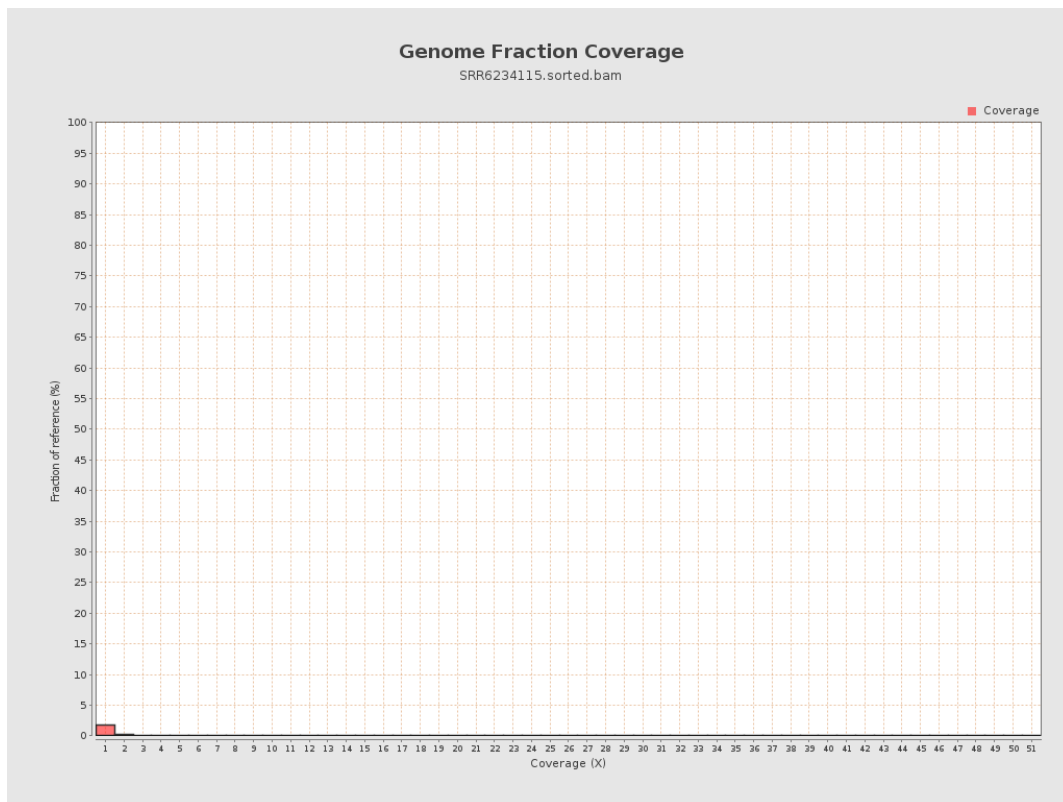
4. Results : Coverage Histogram



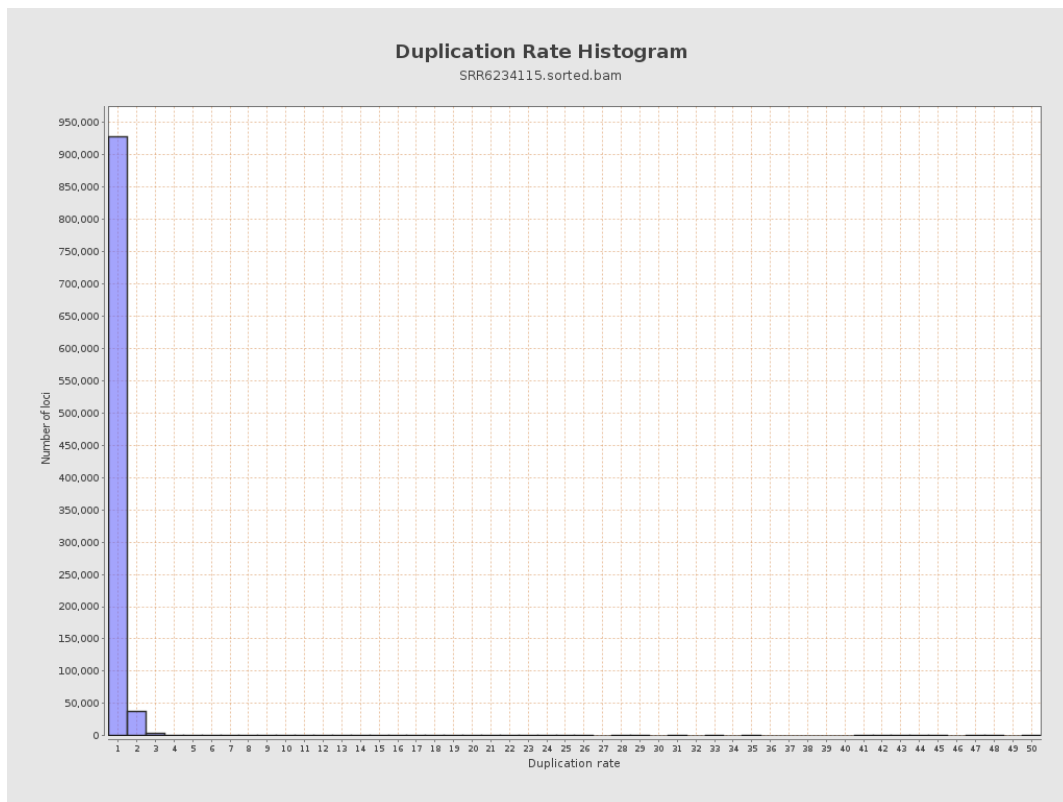
5. Results : Coverage Histogram (0-50X)



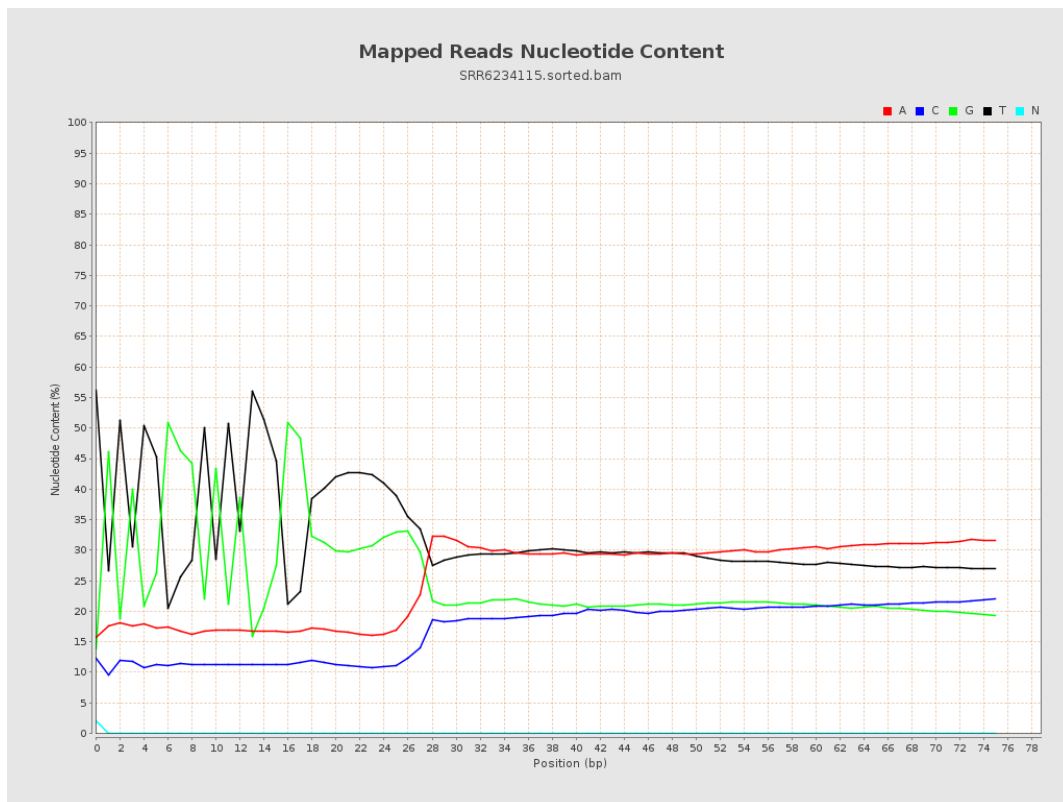
6. Results : Genome Fraction Coverage



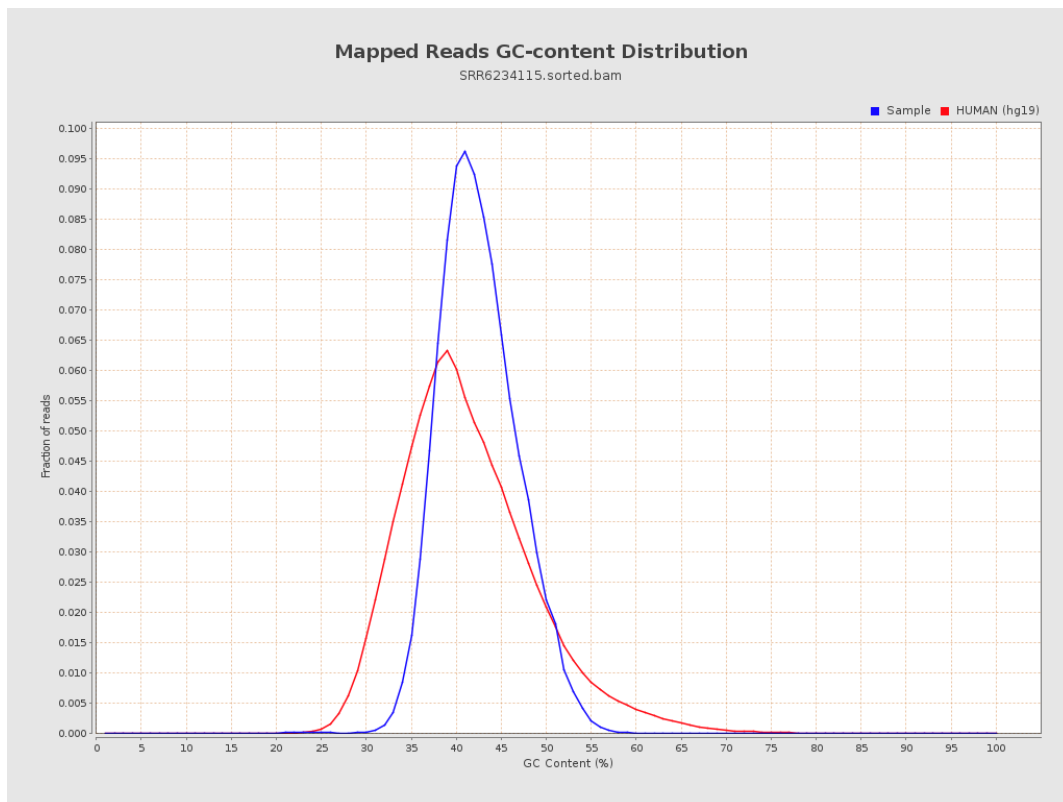
7. Results : Duplication Rate Histogram



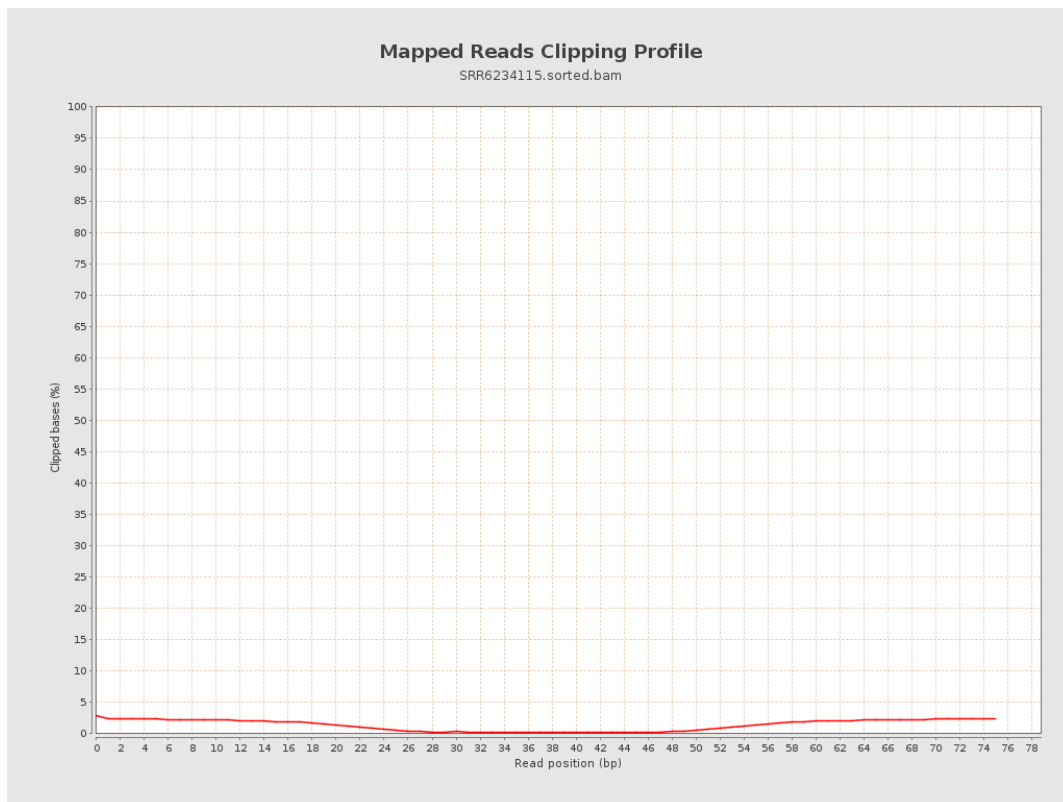
8. Results : Mapped Reads Nucleotide Content



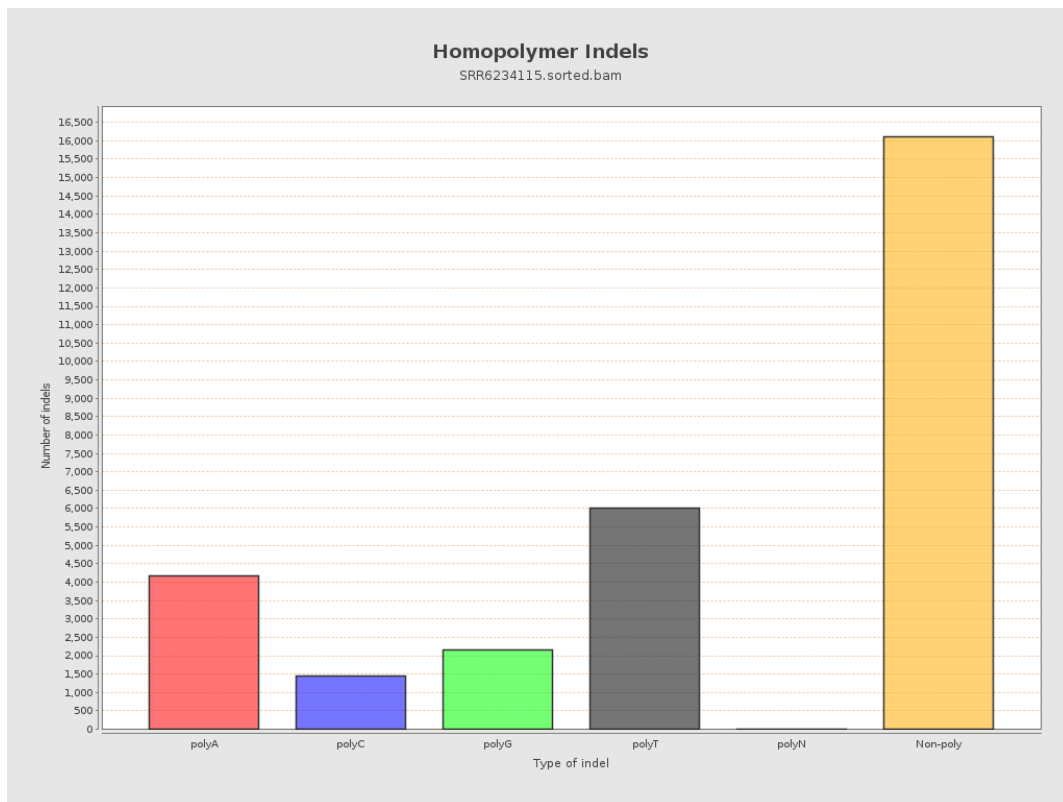
9. Results : Mapped Reads GC-content Distribution



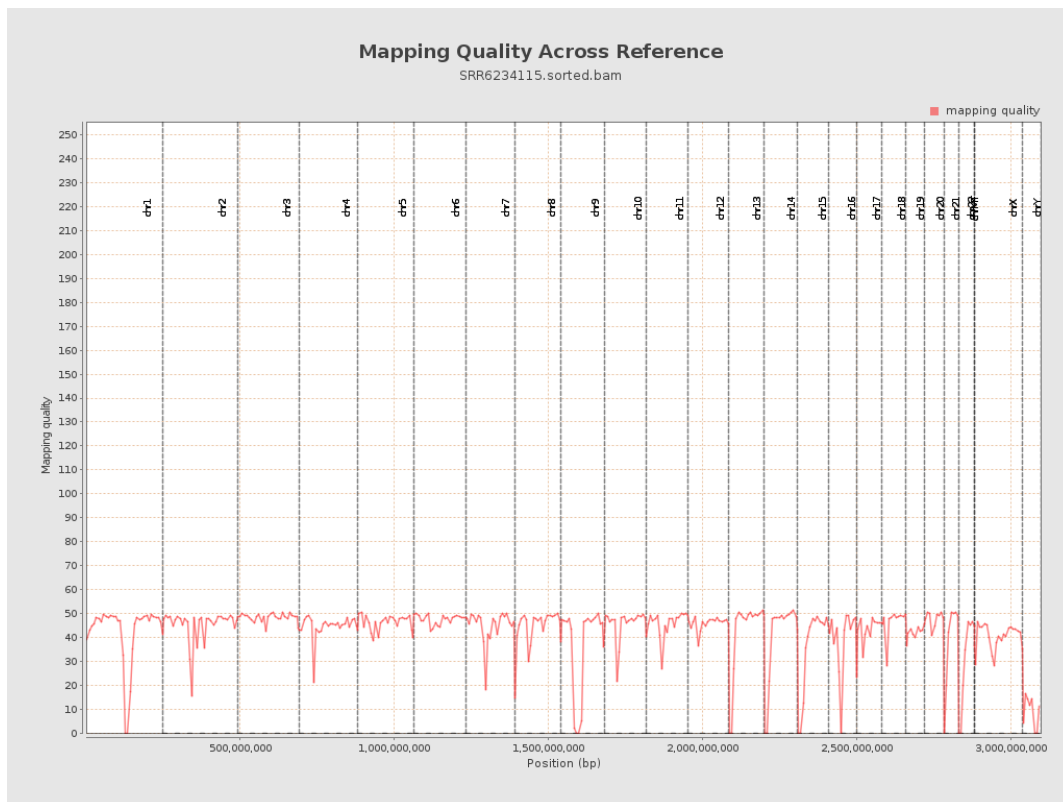
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

