Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 21:17:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236115.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_SRR6236115 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 21:17:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6236115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,305,841
Mapped reads	1,096,025 / 83.93%
Unmapped reads	209,816 / 16.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,262 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	73,659 / 5.64%
Duplication rate	5.19%
Clipped reads	444,212 / 34.02%

2.2. ACGT Content

Number/percentage of A's	20,743,935 / 28.11%
Number/percentage of C's	13,392,390 / 18.15%
Number/percentage of T's	23,547,032 / 31.9%
Number/percentage of G's	16,078,634 / 21.78%
Number/percentage of N's	45,109 / 0.06%
GC Percentage	39.93%

2.3. Coverage

Mean	0.0239

Standard Deviation	0.3607

2.4. Mapping Quality

Mean Mapping Quality	40.3

2.5. Mismatches and indels

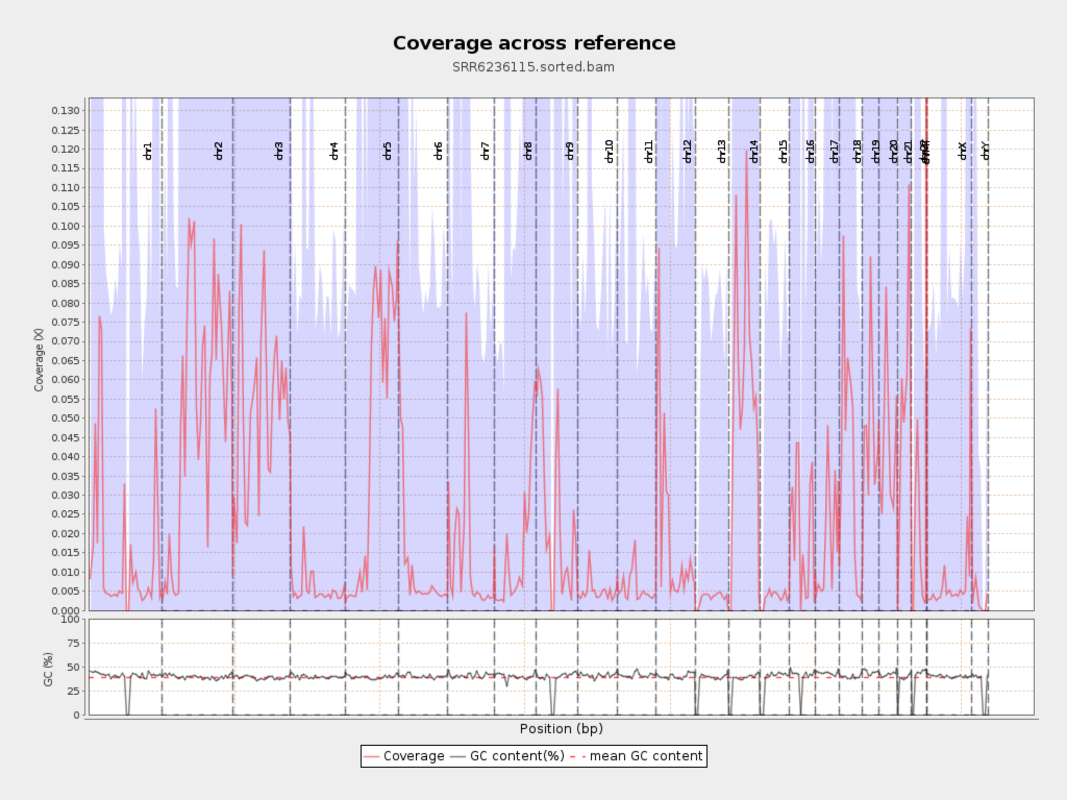
General error rate	0.85%
Mismatches	620,011
Insertions	5,539
Mapped reads with at least one insertion	0.5%
Deletions	20,964
Mapped reads with at least one deletion	1.89%
Homopolymer indels	47.1%

2.6. Chromosome stats

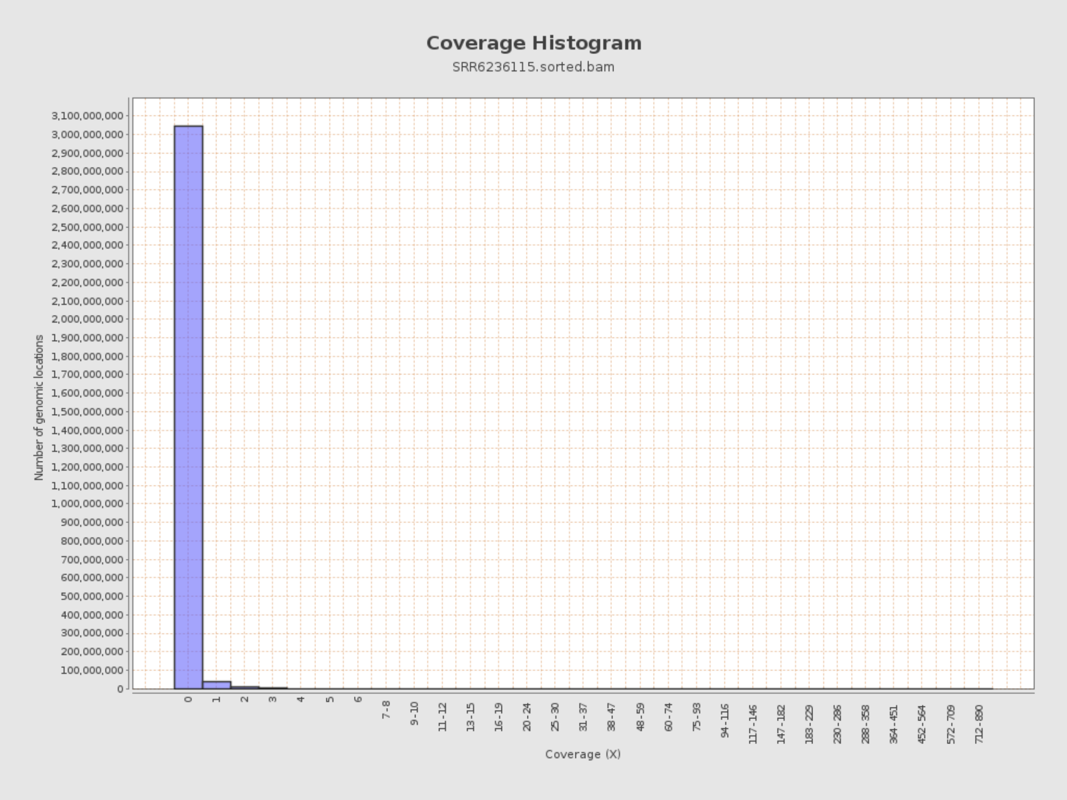
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3683503	0.0148	0.7374
chr2	243199373	12538322	0.0516	0.5285
chr3	198022430	10608169	0.0536	0.309
chr4	191154276	1054426	0.0055	0.1044
chr5	180915260	8107344	0.0448	0.2872
chr6	171115067	2075356	0.0121	0.1482
chr7	159138663	2328968	0.0146	0.4834

chr8	146364022	2326712	0.0159	0.4404
chr9	141213431	3500717	0.0248	0.34
chr10	135534747	668731	0.0049	0.135
chr11	135006516	784954	0.0058	0.1891
chr12	133851895	2716782	0.0203	0.1945
chr13	115169878	378048	0.0033	0.0716
chr14	107349540	6133333	0.0571	0.3207
chr15	102531392	349994	0.0034	0.0773
chr16	90354753	1880347	0.0208	0.2173
chr17	81195210	1506526	0.0186	0.1775
chr18	78077248	2996398	0.0384	0.4662
chr19	59128983	2861239	0.0484	0.467
chr20	63025520	2811386	0.0446	0.2842
chr21	48129895	2531370	0.0526	0.3109
chr22	51304566	772741	0.0151	0.1599
chrMT	16571	15155	0.9145	1.3189
chrX	155270560	1054943	0.0068	0.1587
chrY	59373566	158496	0.0027	0.0836

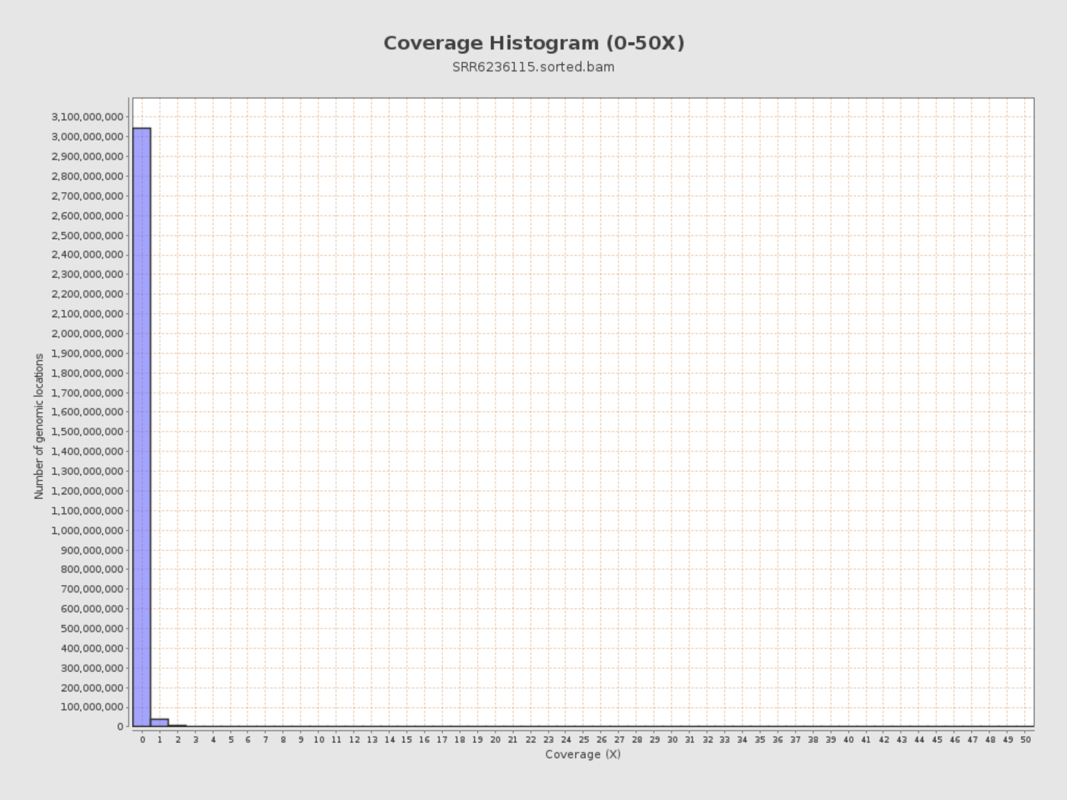
3. Results : Coverage across reference



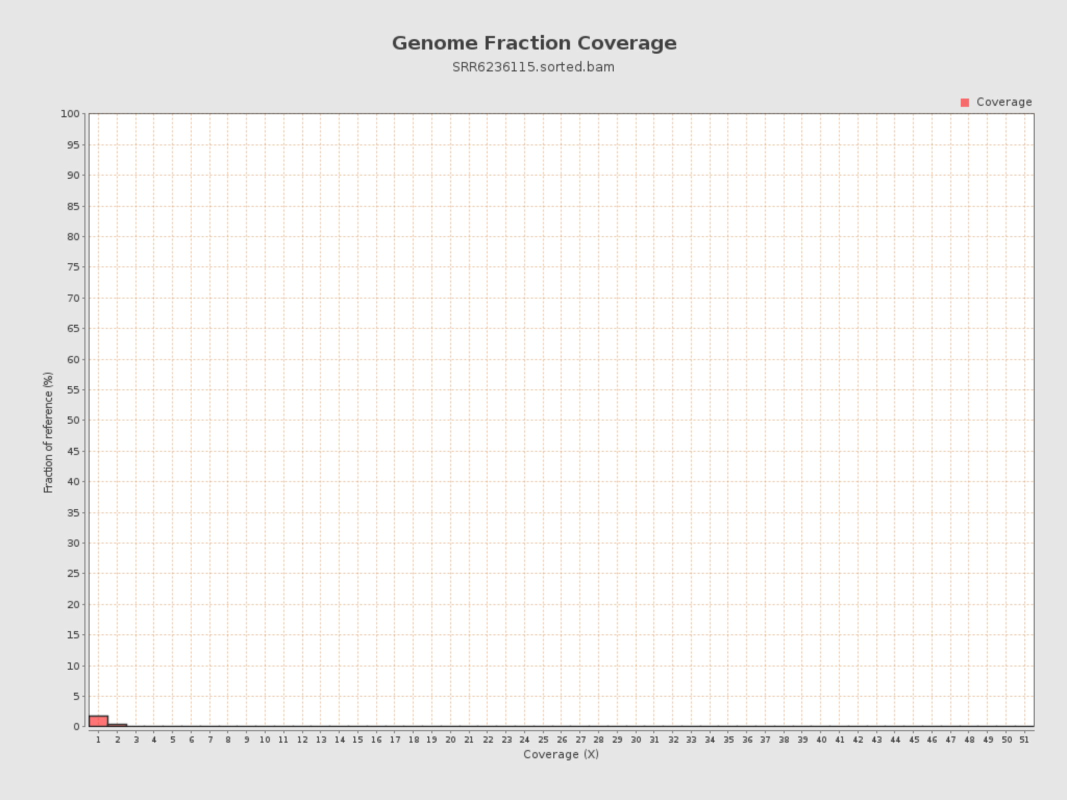
4. Results : Coverage Histogram



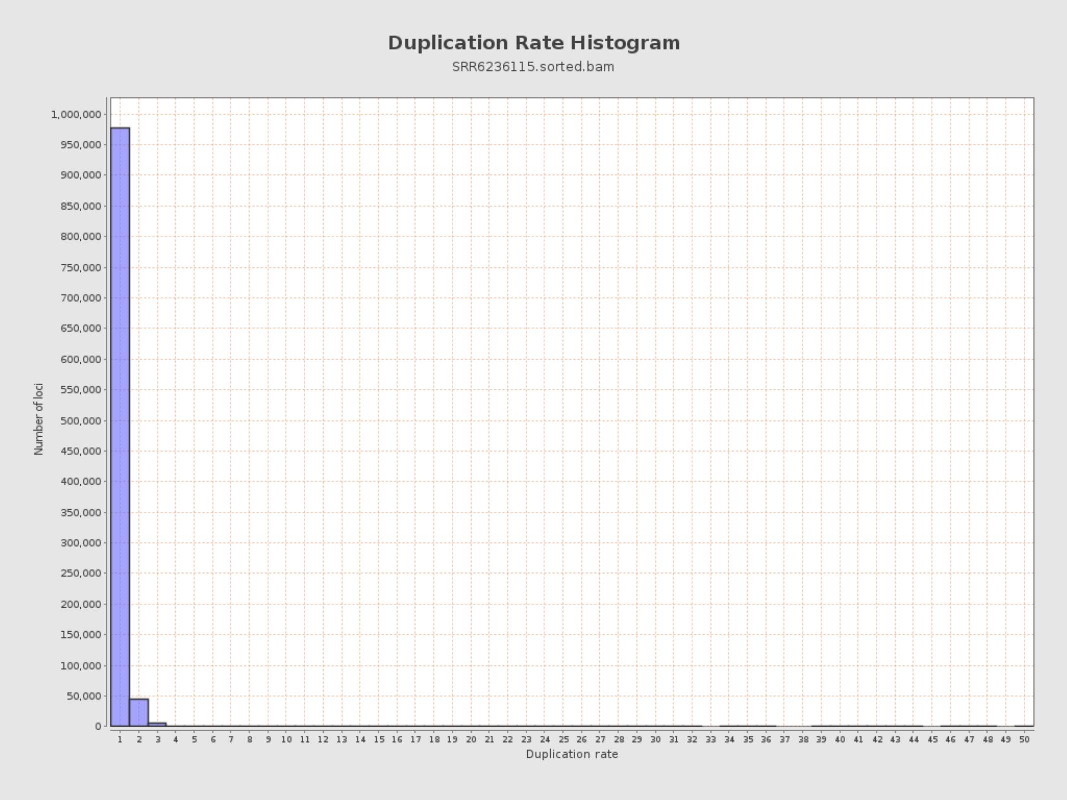
5. Results : Coverage Histogram (0-50X)



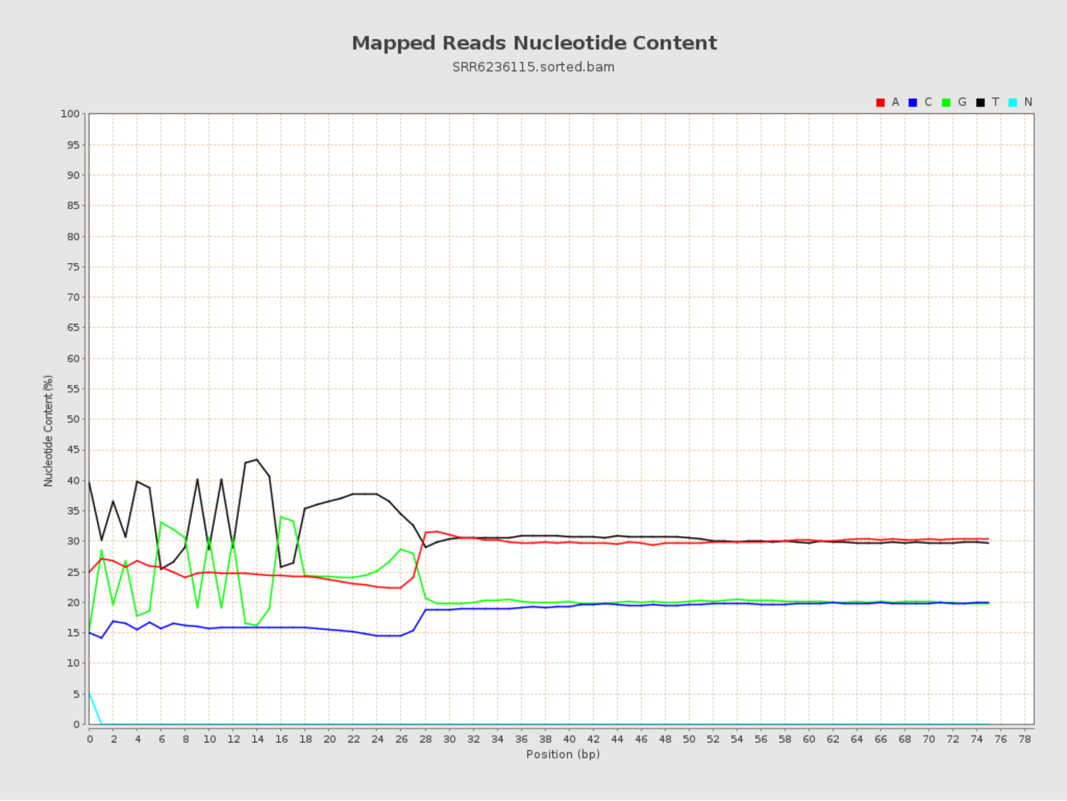
6. Results : Genome Fraction Coverage



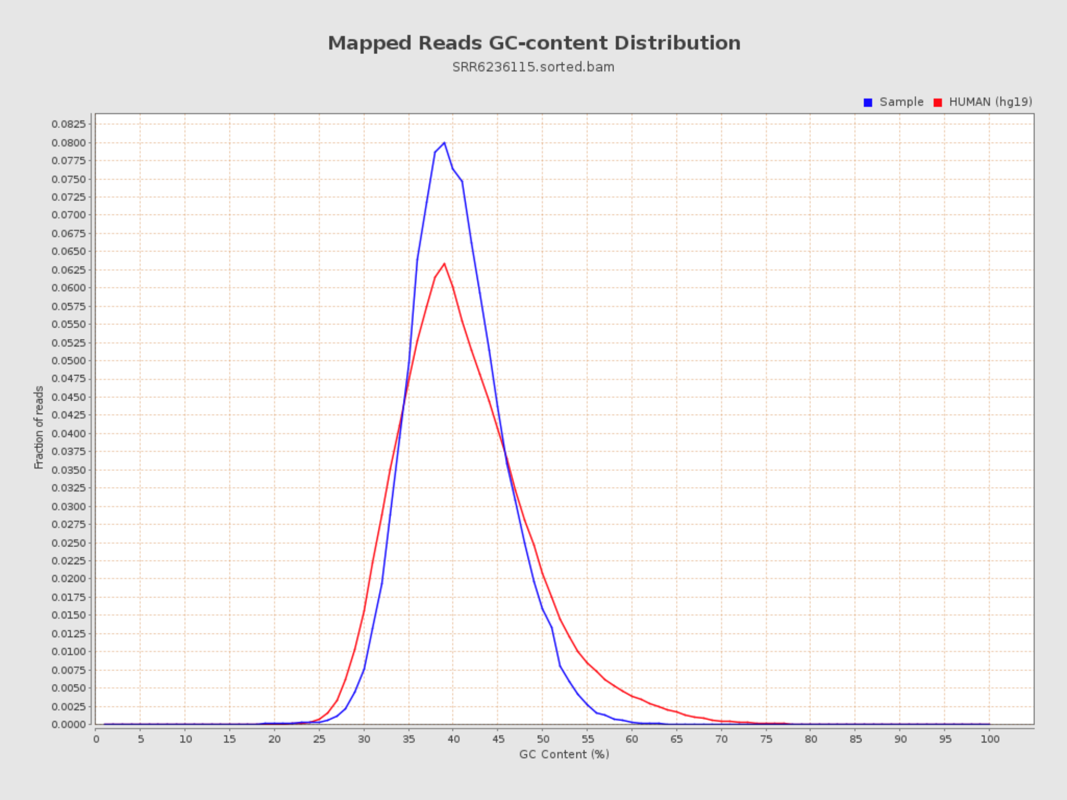
7. Results : Duplication Rate Histogram



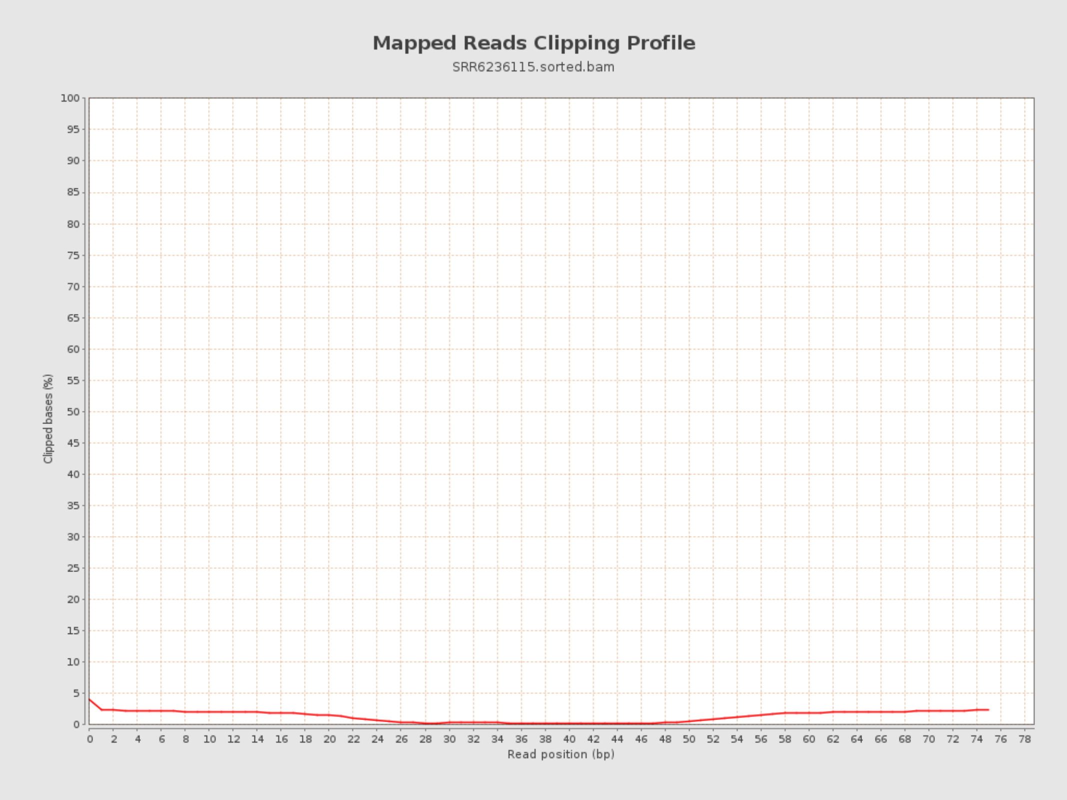
8. Results : Mapped Reads Nucleotide Content



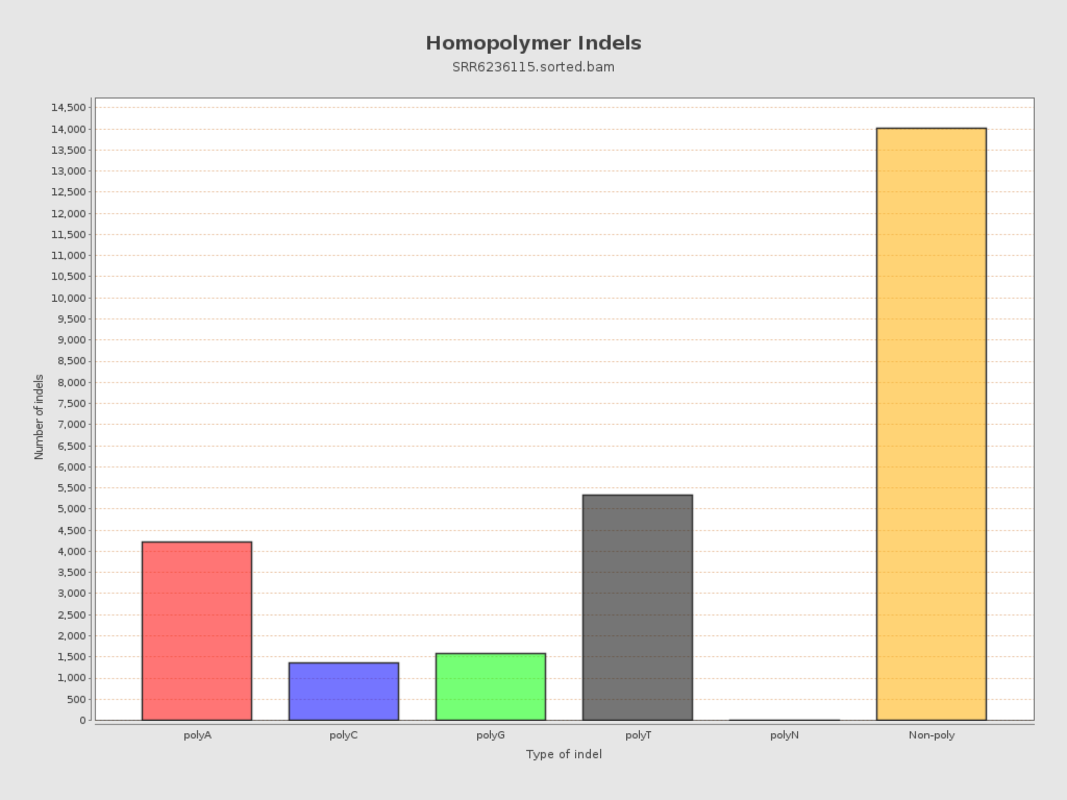
9. Results : Mapped Reads GC-content Distribution



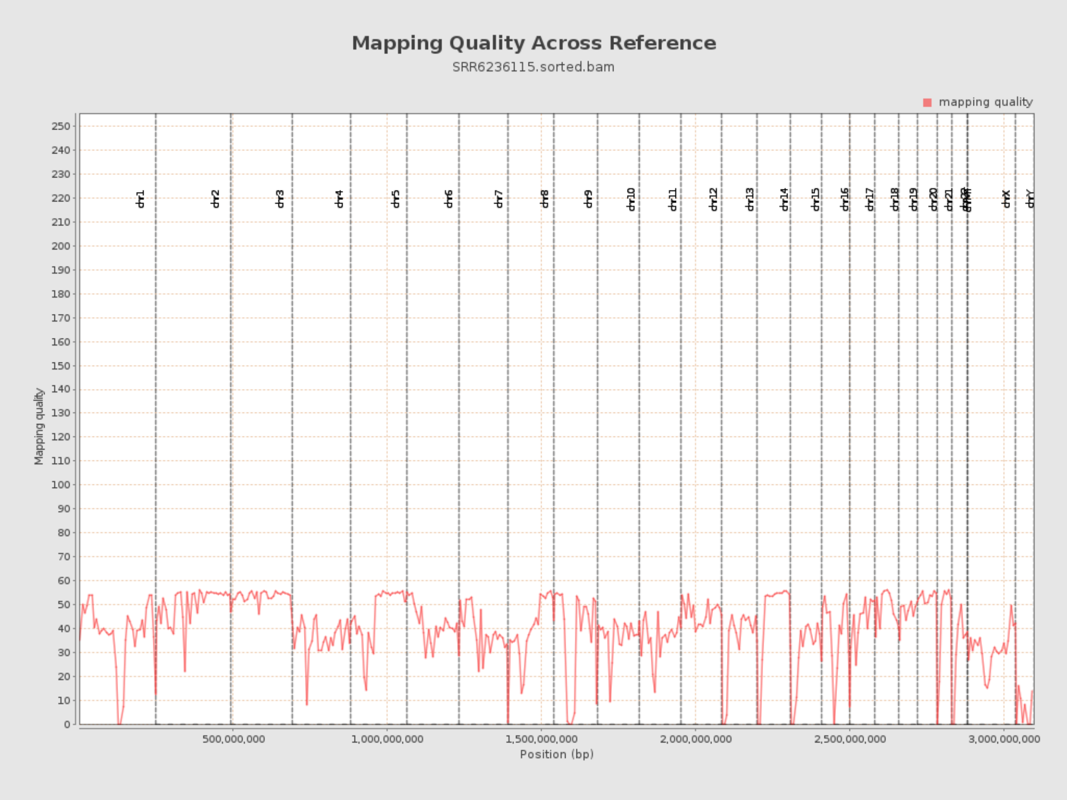
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram