

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:21:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237819.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_SRR6237819 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237819.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:21:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237819.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,112,196
Mapped reads	3,951,867 / 96.1%
Unmapped reads	160,329 / 3.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,816 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	262,402 / 6.38%
Duplication rate	4.62%
Clipped reads	685,203 / 16.66%

2.2. ACGT Content

Number/percentage of A's	88,903,144 / 30.64%
Number/percentage of C's	56,220,441 / 19.38%
Number/percentage of T's	88,507,916 / 30.5%
Number/percentage of G's	56,016,358 / 19.31%
Number/percentage of N's	511,520 / 0.18%
GC Percentage	38.68%

2.3. Coverage

Mean	0.0938

Standard Deviation	1.2424
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	47.21
----------------------	-------

2.5. Mismatches and indels

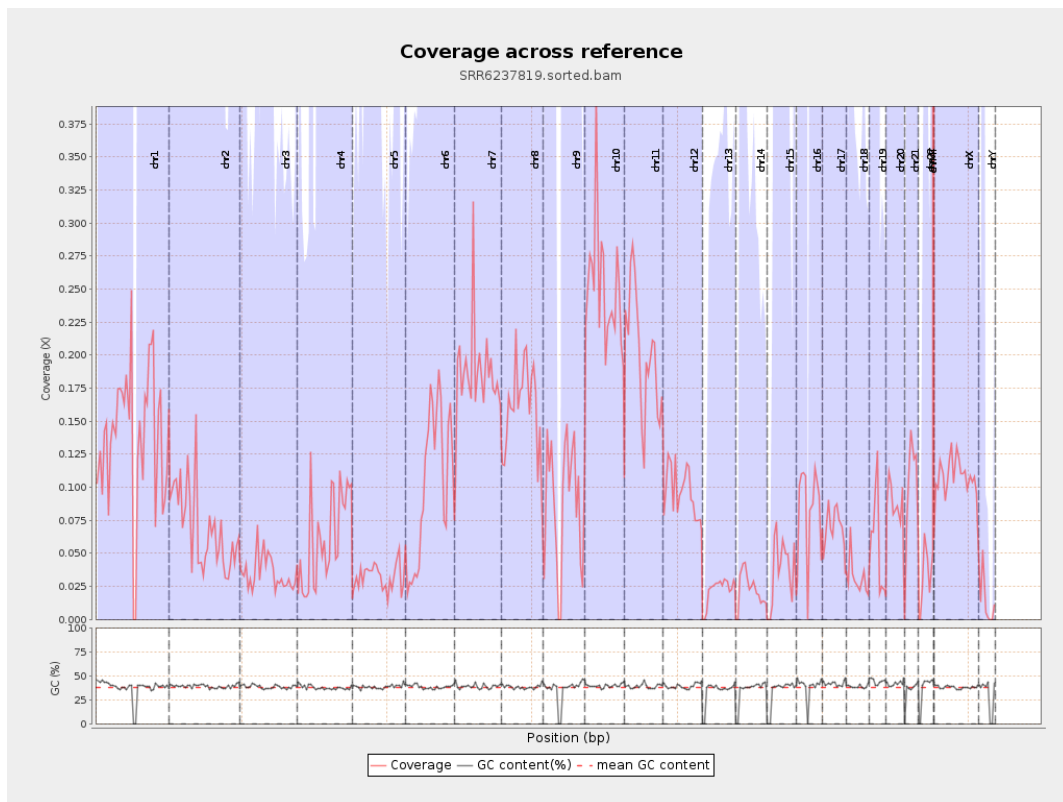
General error rate	0.9%
Mismatches	2,548,440
Insertions	23,229
Mapped reads with at least one insertion	0.58%
Deletions	89,769
Mapped reads with at least one deletion	2.24%
Homopolymer indels	45.35%

2.6. Chromosome stats

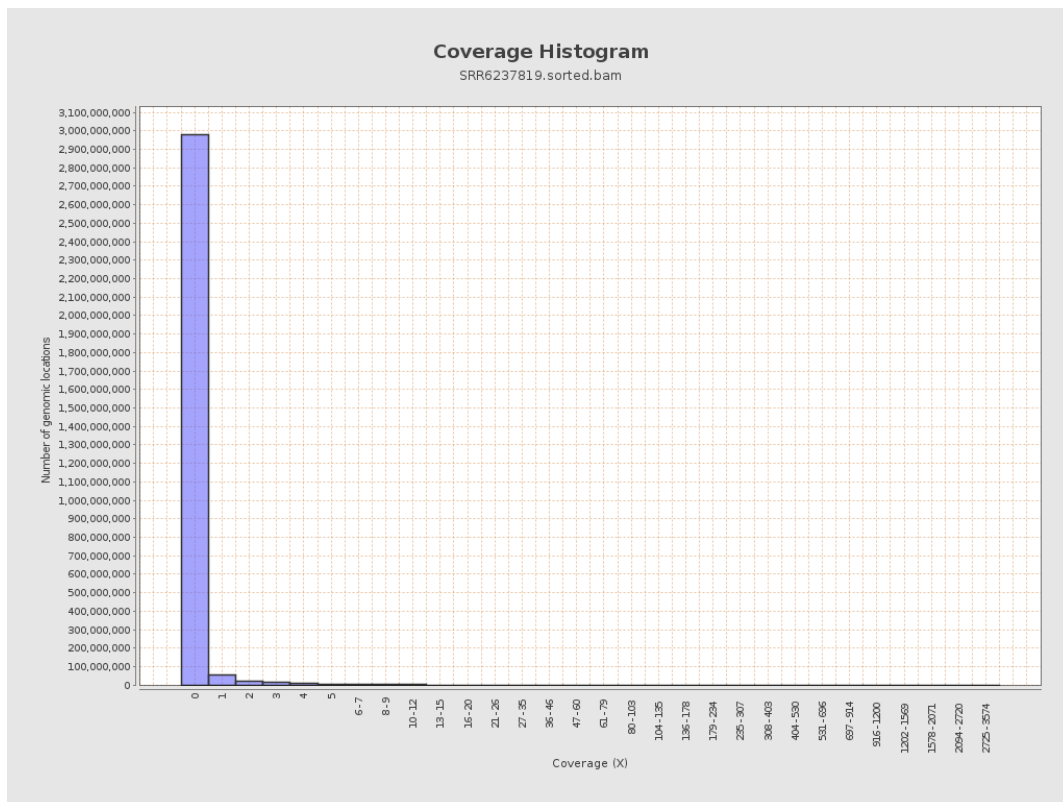
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	34418994	0.1381	2.6382
chr2	243199373	16931966	0.0696	0.8471
chr3	198022430	6891798	0.0348	0.4112
chr4	191154276	11714090	0.0613	0.6532
chr5	180915260	5804911	0.0321	0.3797
chr6	171115067	17387251	0.1016	0.7271
chr7	159138663	29866436	0.1877	2.4305

chr8	146364022	23428018	0.1601	1.2807
chr9	141213431	12529169	0.0887	0.8816
chr10	135534747	33929485	0.2503	1.7286
chr11	135006516	27035616	0.2003	1.4933
chr12	133851895	12896725	0.0964	0.6484
chr13	115169878	2521571	0.0219	0.295
chr14	107349540	2381742	0.0222	0.3671
chr15	102531392	3794465	0.037	0.3908
chr16	90354753	7587298	0.084	0.6965
chr17	81195210	5574326	0.0687	0.7243
chr18	78077248	2505107	0.0321	1.4126
chr19	59128983	3457099	0.0585	1.4222
chr20	63025520	5540771	0.0879	0.6325
chr21	48129895	4707971	0.0978	0.7461
chr22	51304566	1614518	0.0315	0.3438
chrMT	16571	342666	20.6787	15.2451
chrX	155270560	16655692	0.1073	0.7629
chrY	59373566	805018	0.0136	0.4524

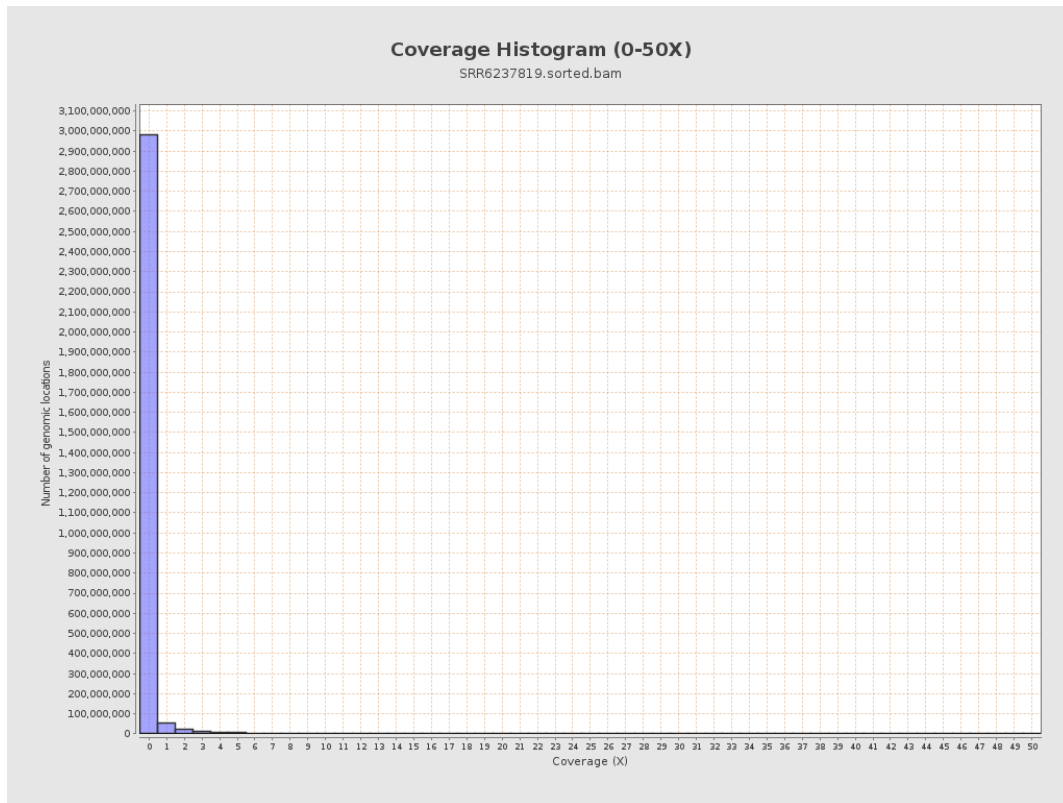
3. Results : Coverage across reference



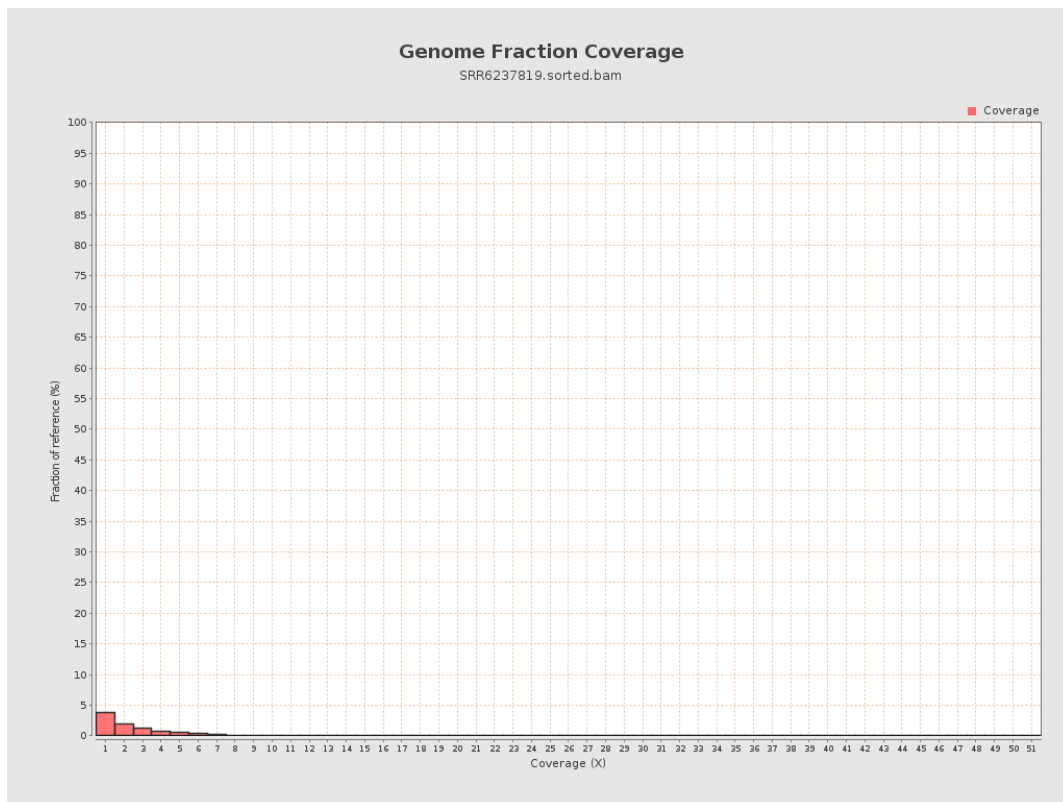
4. Results : Coverage Histogram



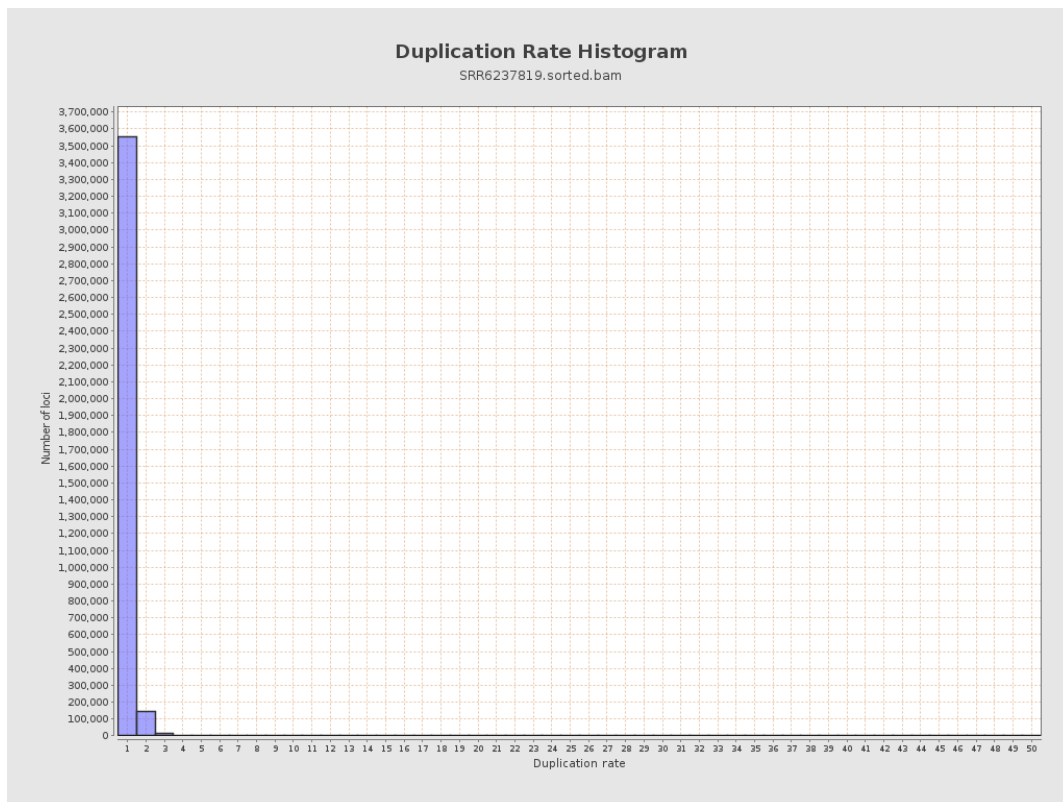
5. Results : Coverage Histogram (0-50X)



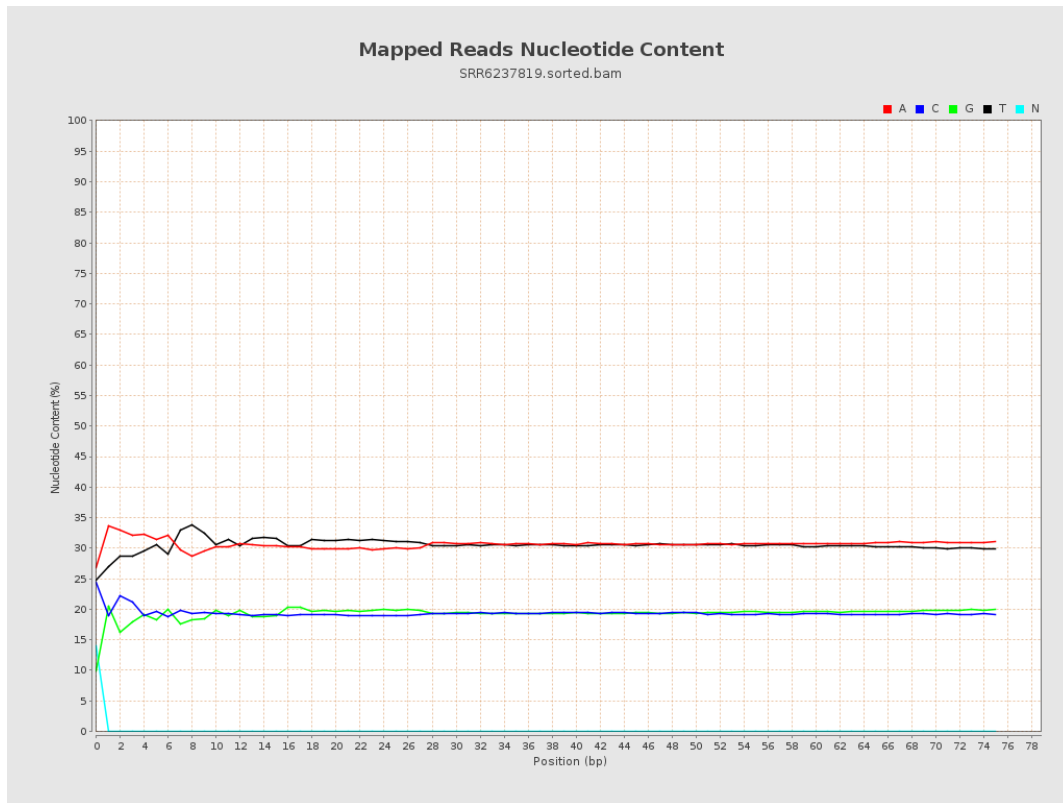
6. Results : Genome Fraction Coverage



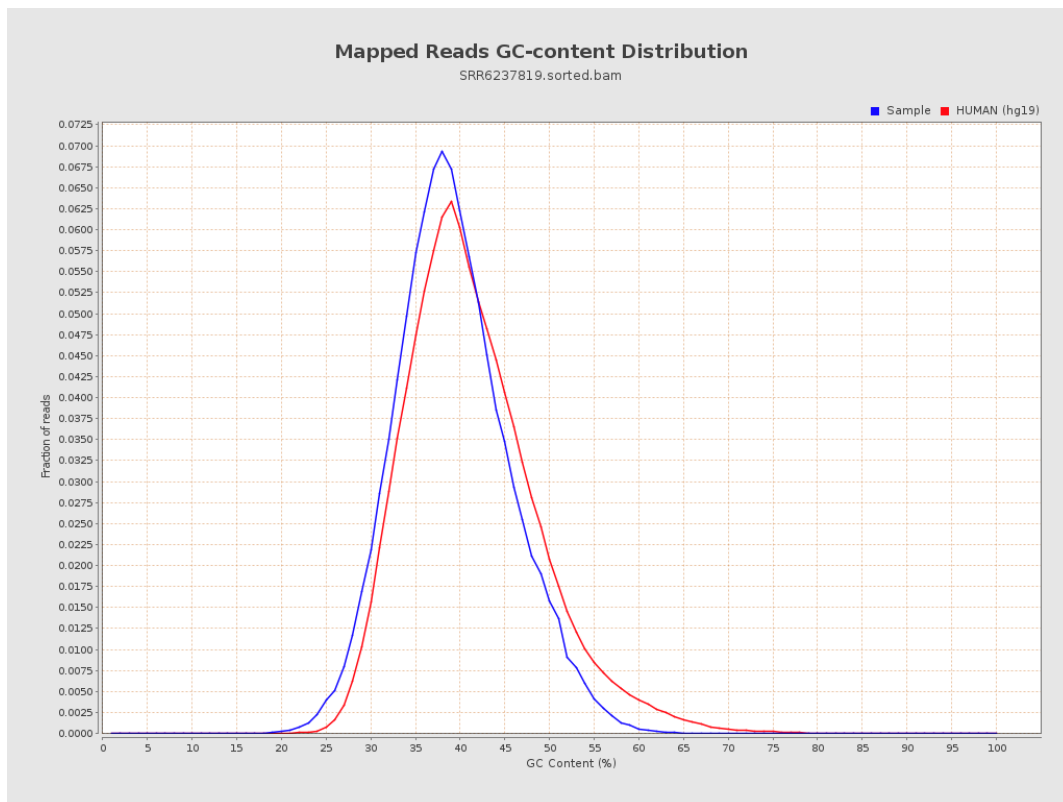
7. Results : Duplication Rate Histogram



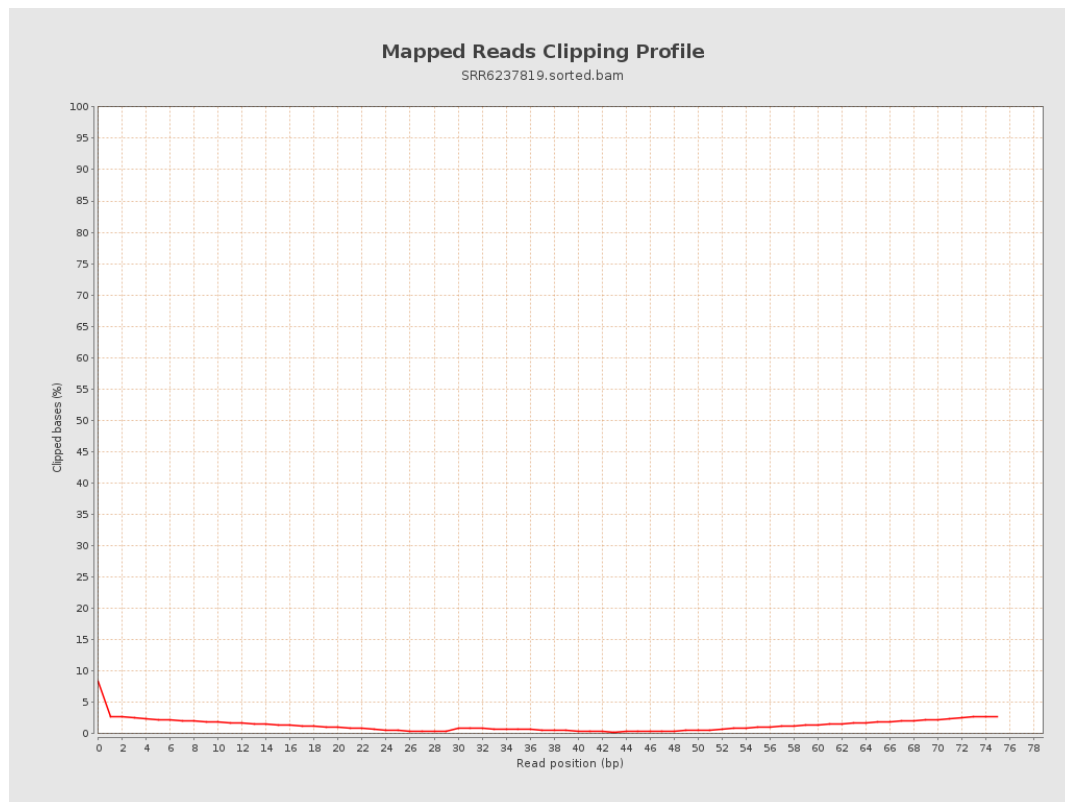
8. Results : Mapped Reads Nucleotide Content



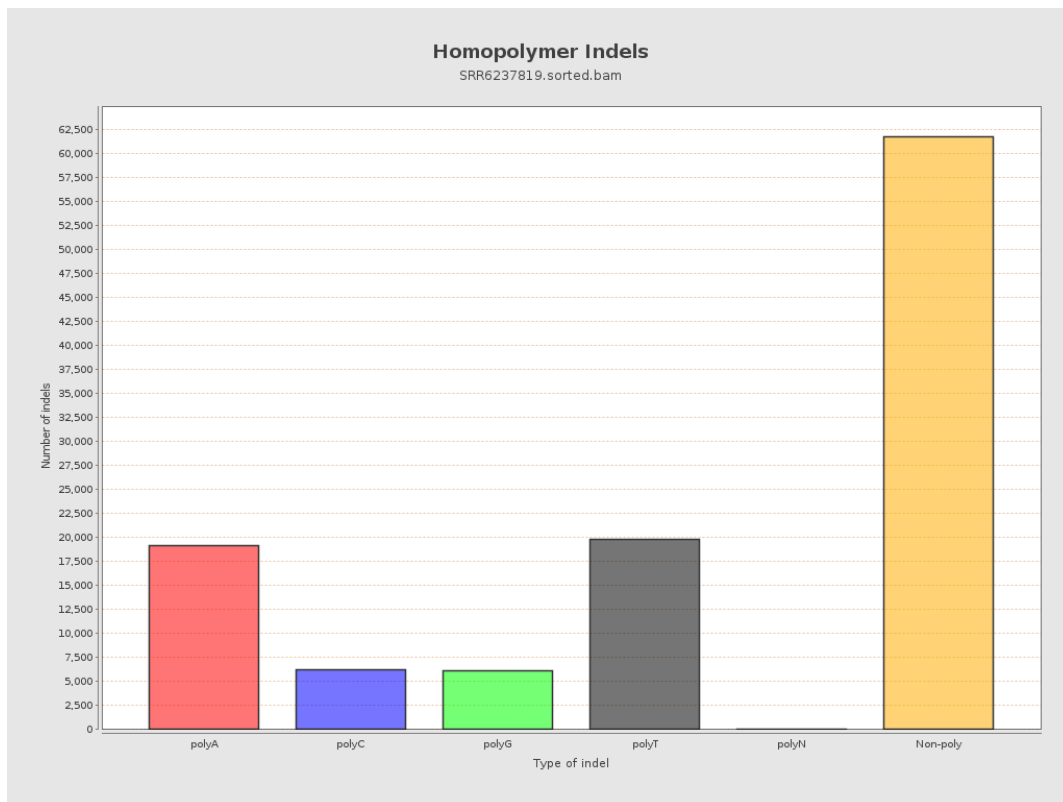
9. Results : Mapped Reads GC-content Distribution



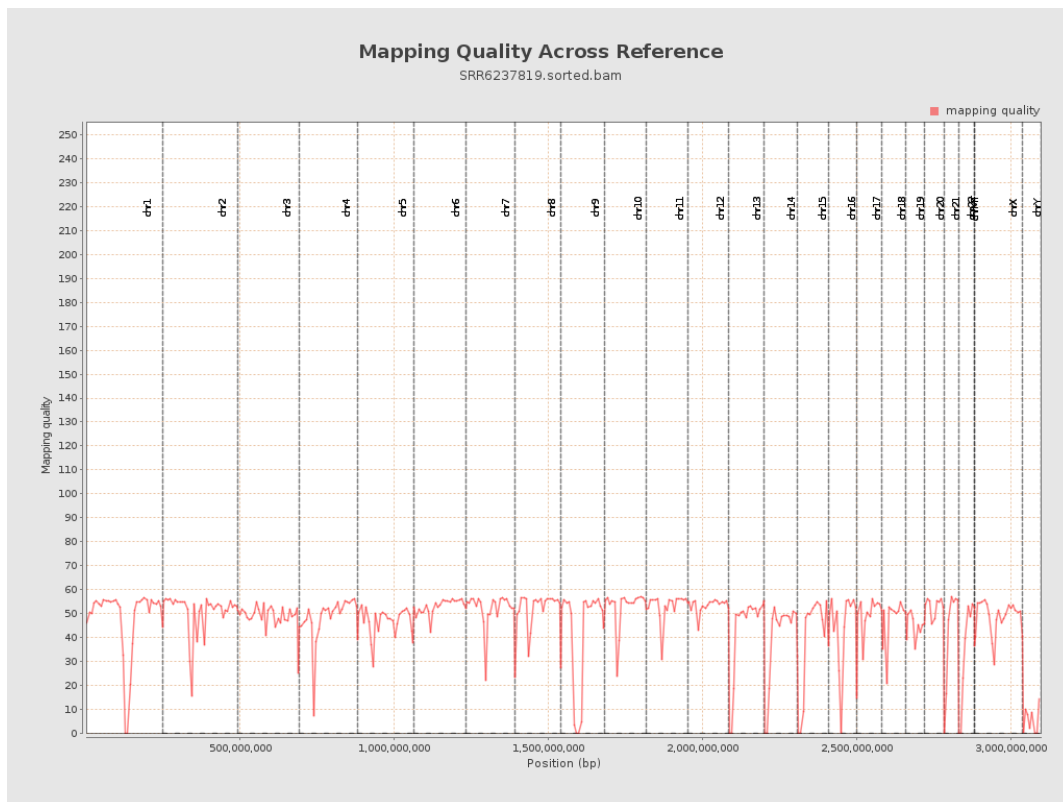
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

