

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:06:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237815.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_SRR6237815 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237815.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:06:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237815.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,563,347
Mapped reads	1,458,558 / 93.3%
Unmapped reads	104,789 / 6.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,159 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	76,357 / 4.88%
Duplication rate	4.26%
Clipped reads	608,590 / 38.93%

2.2. ACGT Content

Number/percentage of A's	31,003,252 / 30.6%
Number/percentage of C's	19,783,910 / 19.52%
Number/percentage of T's	30,011,093 / 29.62%
Number/percentage of G's	20,368,302 / 20.1%
Number/percentage of N's	161,927 / 0.16%
GC Percentage	39.63%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.4511
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2.4. Mapping Quality

Mean Mapping Quality	47.52
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2.5. Mismatches and indels

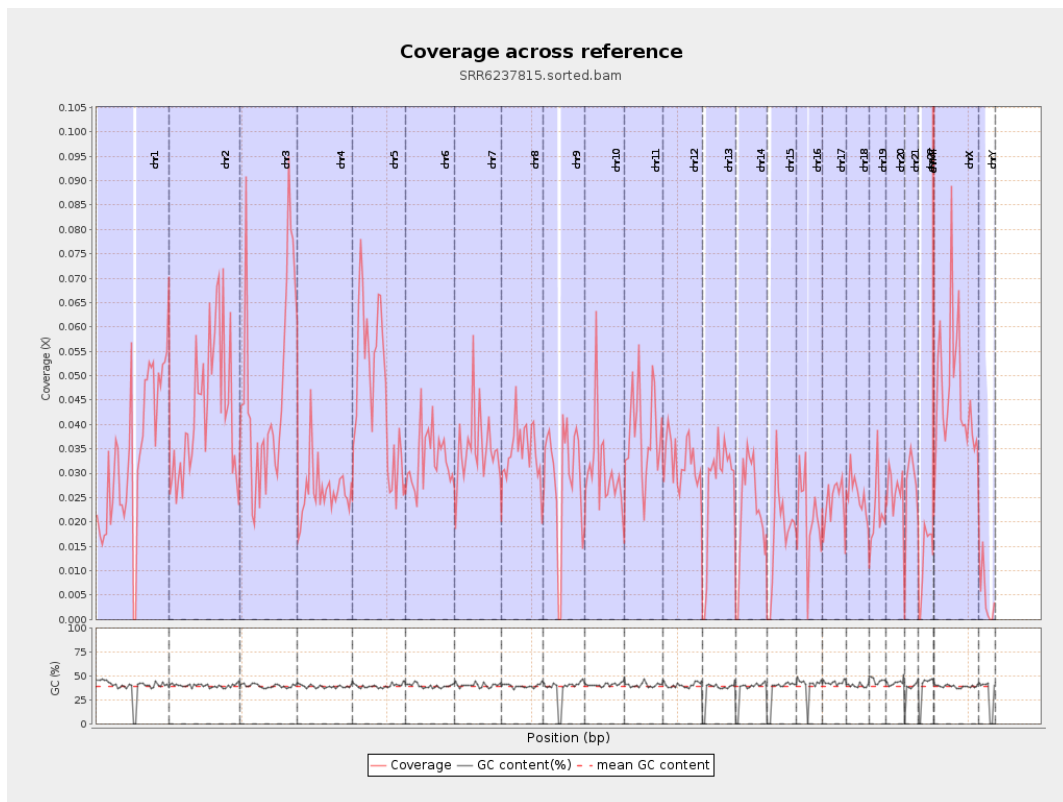
General error rate	0.91%
Mismatches	903,982
Insertions	7,371
Mapped reads with at least one insertion	0.5%
Deletions	26,984
Mapped reads with at least one deletion	1.83%
Homopolymer indels	44.56%

2.6. Chromosome stats

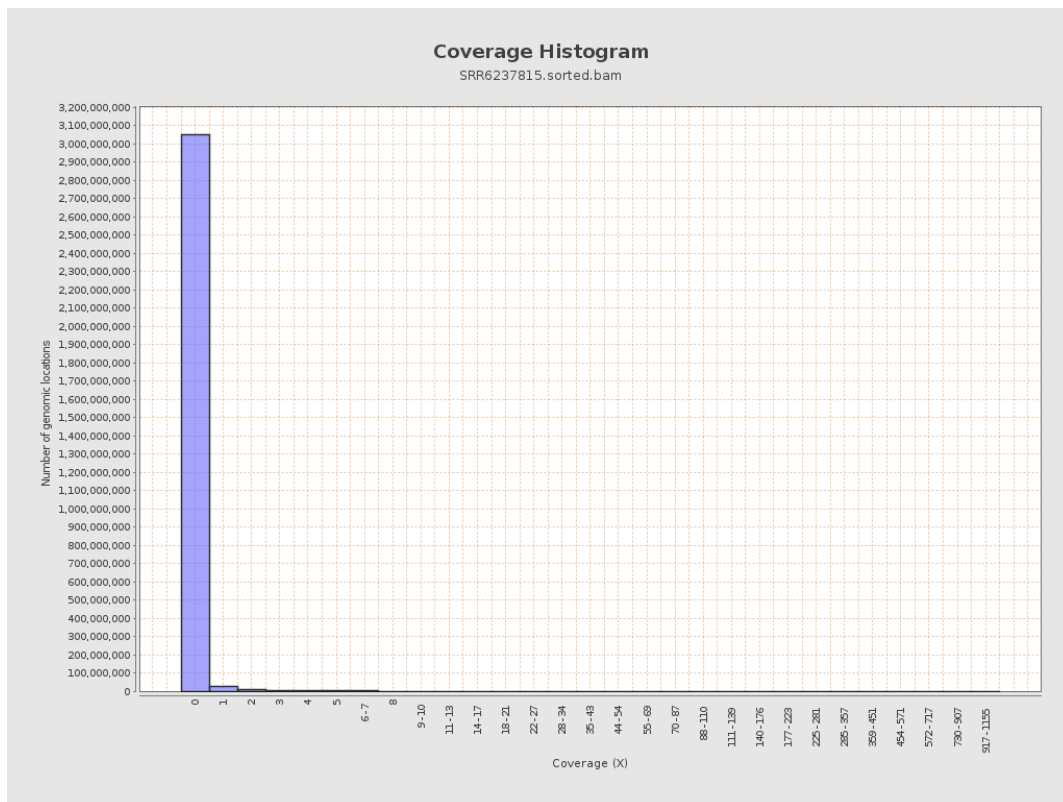
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8427268	0.0338	0.8141
chr2	243199373	10358664	0.0426	0.4558
chr3	198022430	9195802	0.0464	0.4233
chr4	191154276	5014673	0.0262	0.3243
chr5	180915260	8504956	0.047	0.4257
chr6	171115067	5610586	0.0328	0.3764
chr7	159138663	5639263	0.0354	0.4999

chr8	146364022	5040444	0.0344	0.4562
chr9	141213431	4170762	0.0295	0.3818
chr10	135534747	4154571	0.0307	0.4234
chr11	135006516	5118381	0.0379	0.5109
chr12	133851895	4313586	0.0322	0.3478
chr13	115169878	3097433	0.0269	0.3161
chr14	107349540	2401898	0.0224	0.2884
chr15	102531392	1845877	0.018	0.2552
chr16	90354753	1916012	0.0212	0.2948
chr17	81195210	1918362	0.0236	0.3347
chr18	78077248	2002611	0.0256	0.5572
chr19	59128983	1312801	0.0222	0.4279
chr20	63025520	1671649	0.0265	0.3183
chr21	48129895	1292321	0.0269	0.3254
chr22	51304566	639561	0.0125	0.2078
chrMT	16571	345303	20.8378	16.5119
chrX	155270560	7112010	0.0458	0.4308
chrY	59373566	271702	0.0046	0.1622

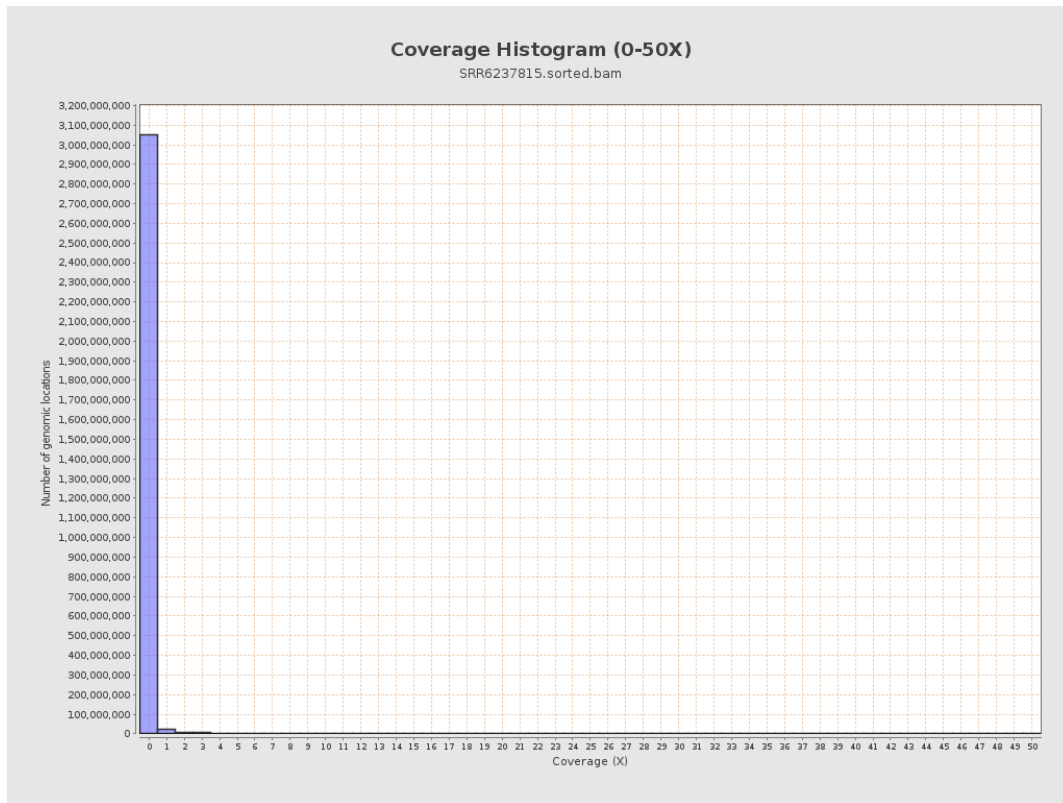
3. Results : Coverage across reference



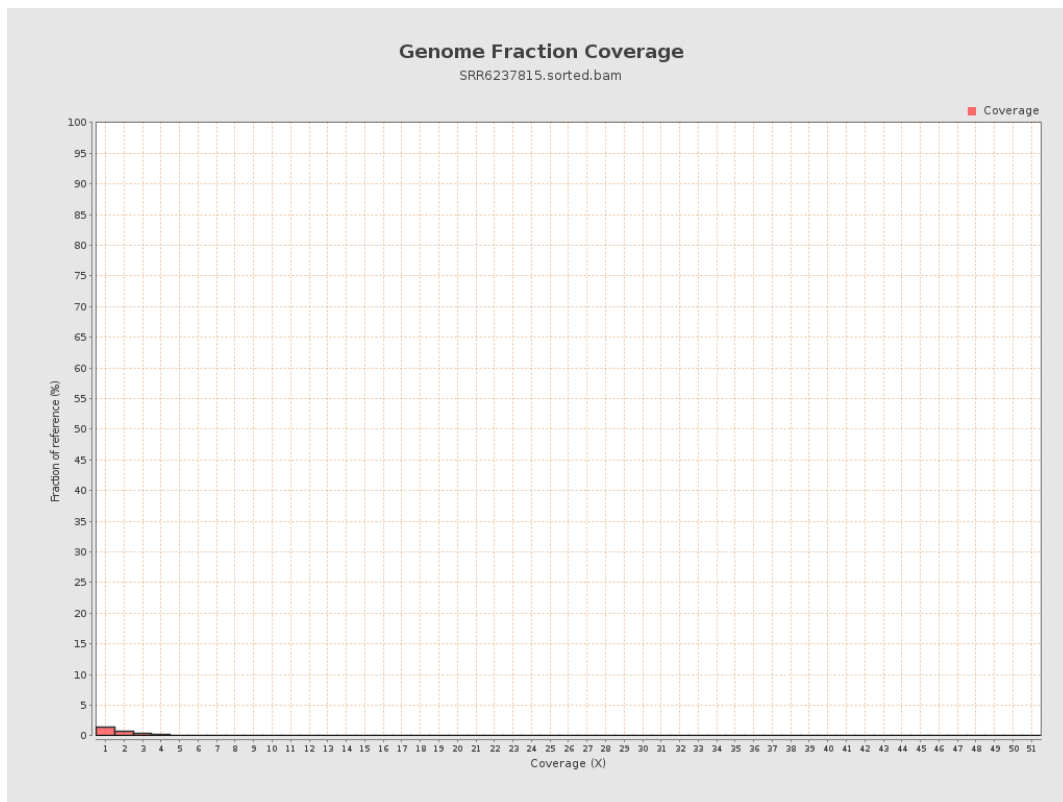
4. Results : Coverage Histogram



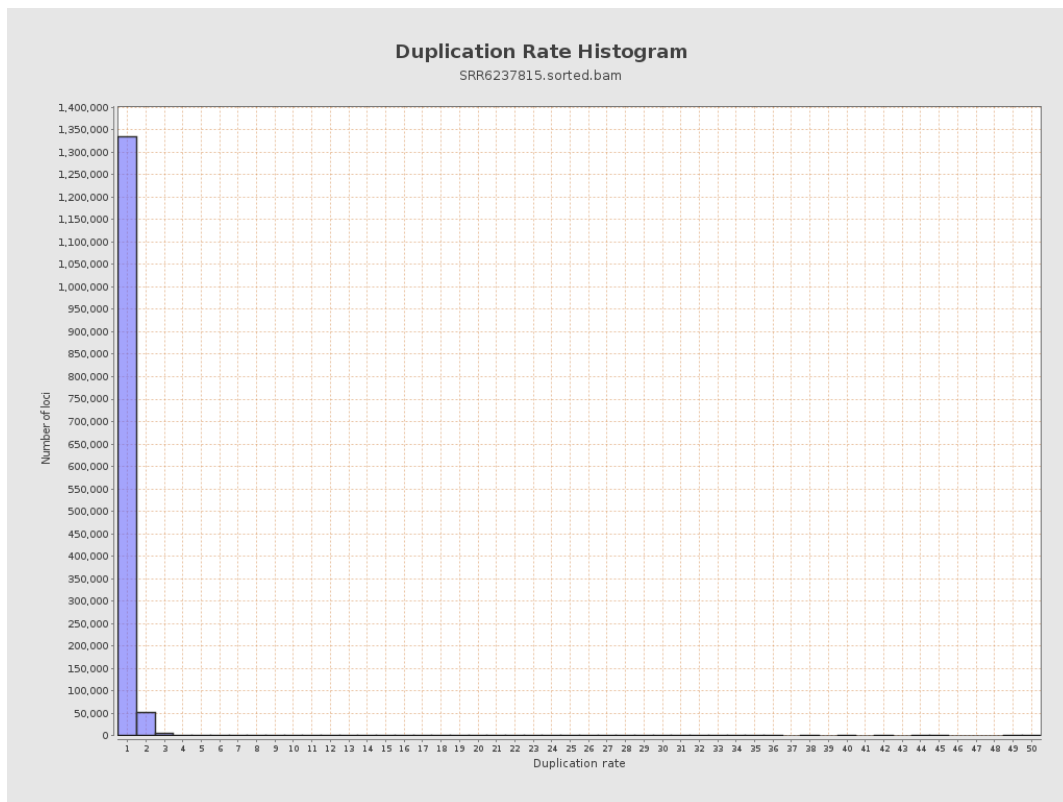
5. Results : Coverage Histogram (0-50X)



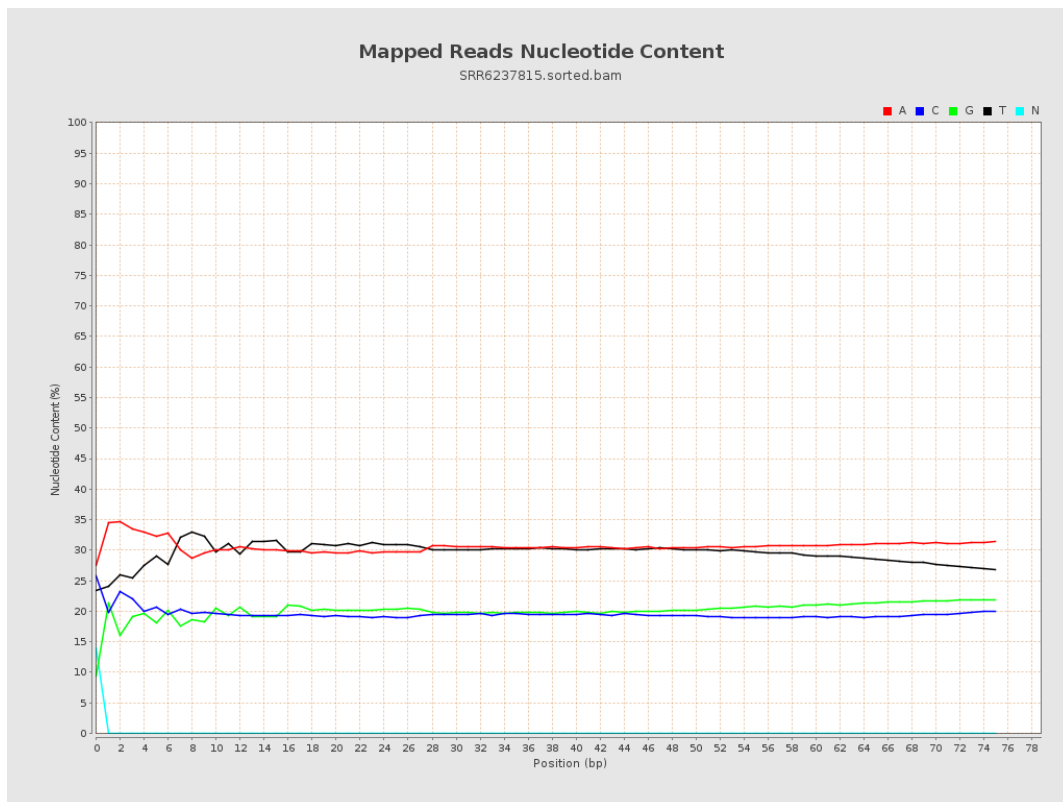
6. Results : Genome Fraction Coverage



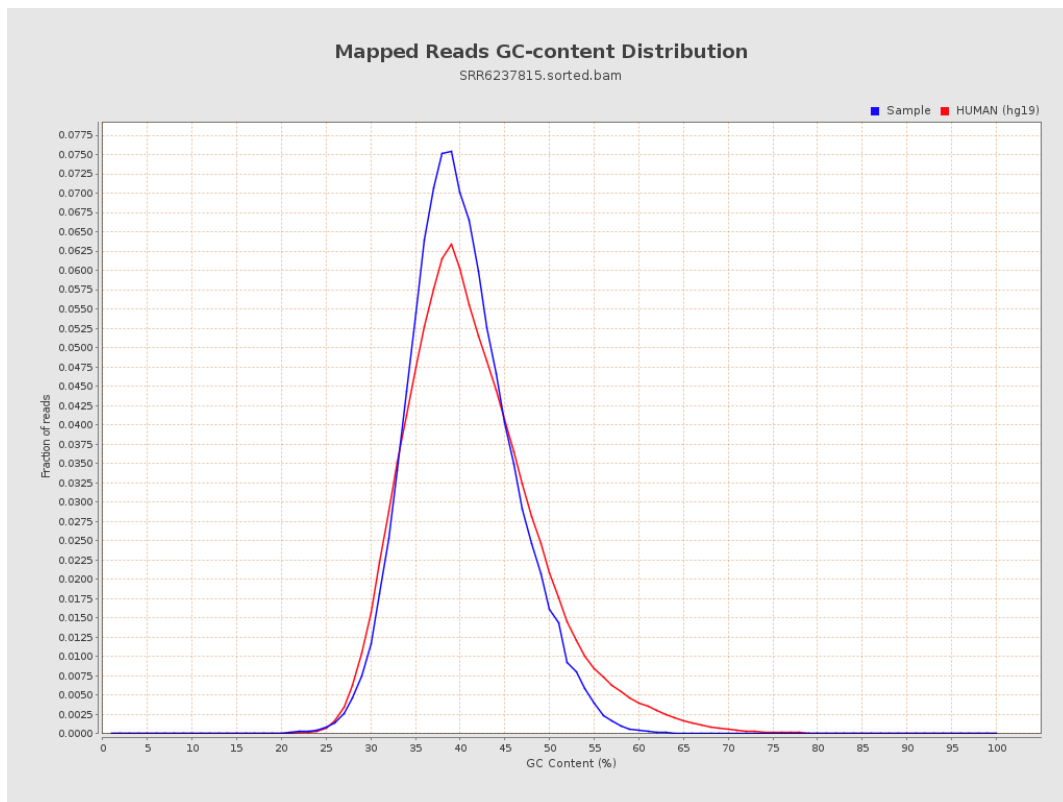
7. Results : Duplication Rate Histogram



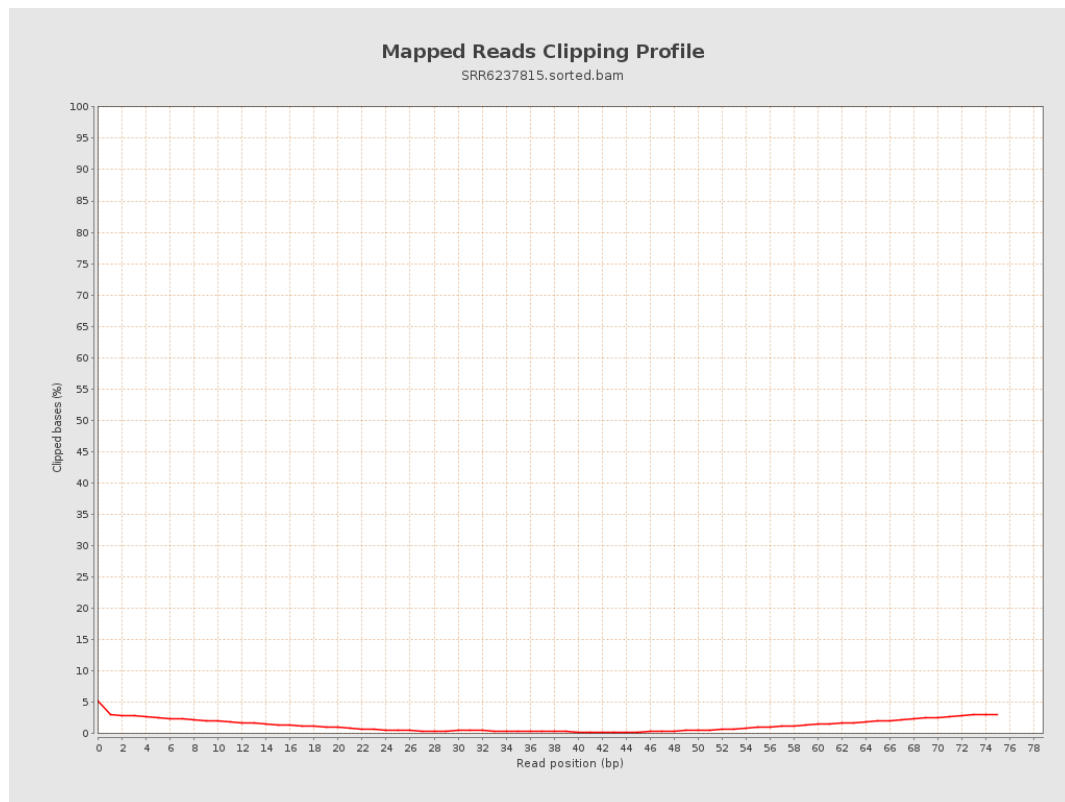
8. Results : Mapped Reads Nucleotide Content



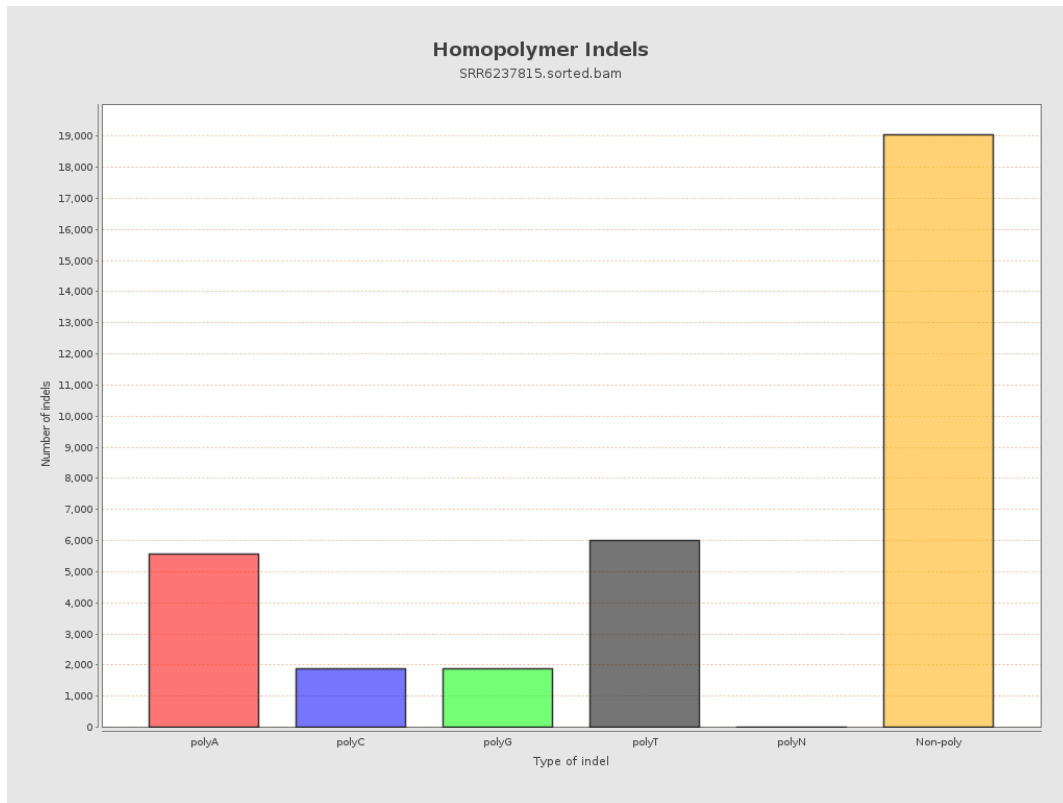
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

