

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 16:17:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013212.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_SRR6013212 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013212.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 16:17:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	826,746
Mapped reads	653,792 / 79.08%
Unmapped reads	172,954 / 20.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,582 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	9,077 / 1.1%
Duplication rate	1.2%
Clipped reads	298,277 / 36.08%

2.2. ACGT Content

Number/percentage of A's	13,275,215 / 30.47%
Number/percentage of C's	7,527,678 / 17.28%
Number/percentage of T's	13,419,741 / 30.8%
Number/percentage of G's	9,347,431 / 21.45%
Number/percentage of N's	531 / 0%
GC Percentage	38.73%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.1361
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2.4. Mapping Quality

Mean Mapping Quality	48.53
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2.5. Mismatches and indels

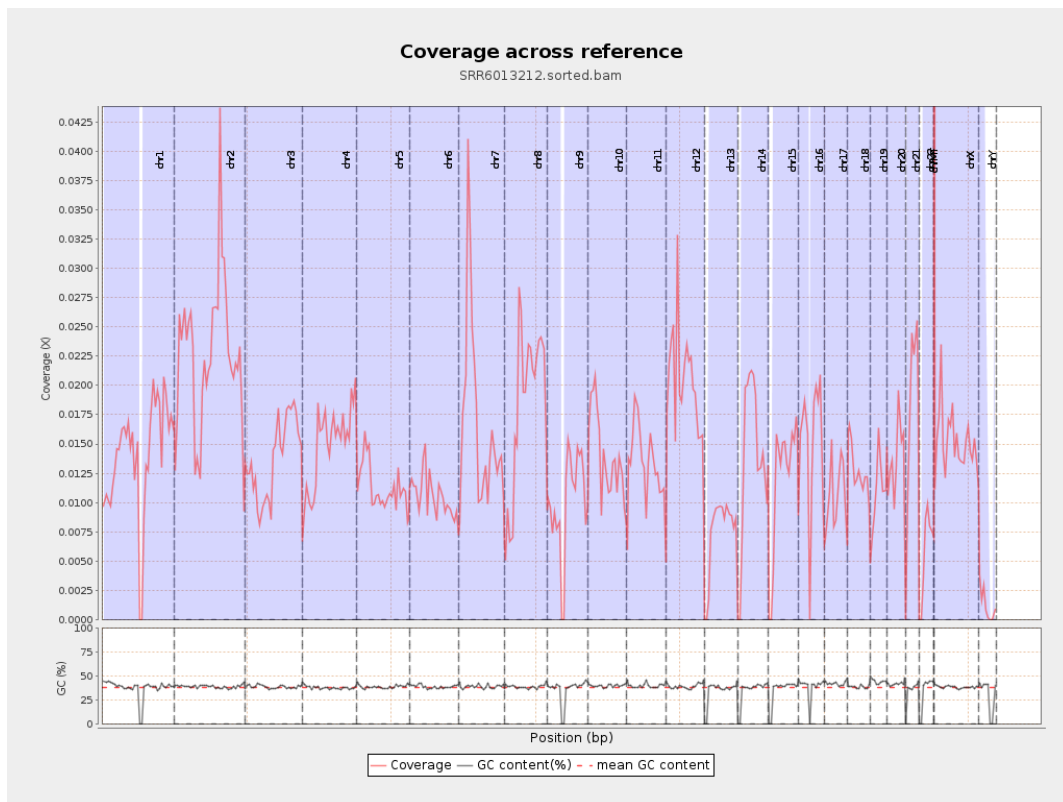
General error rate	0.86%
Mismatches	371,003
Insertions	2,881
Mapped reads with at least one insertion	0.44%
Deletions	12,643
Mapped reads with at least one deletion	1.92%
Homopolymer indels	50.05%

2.6. Chromosome stats

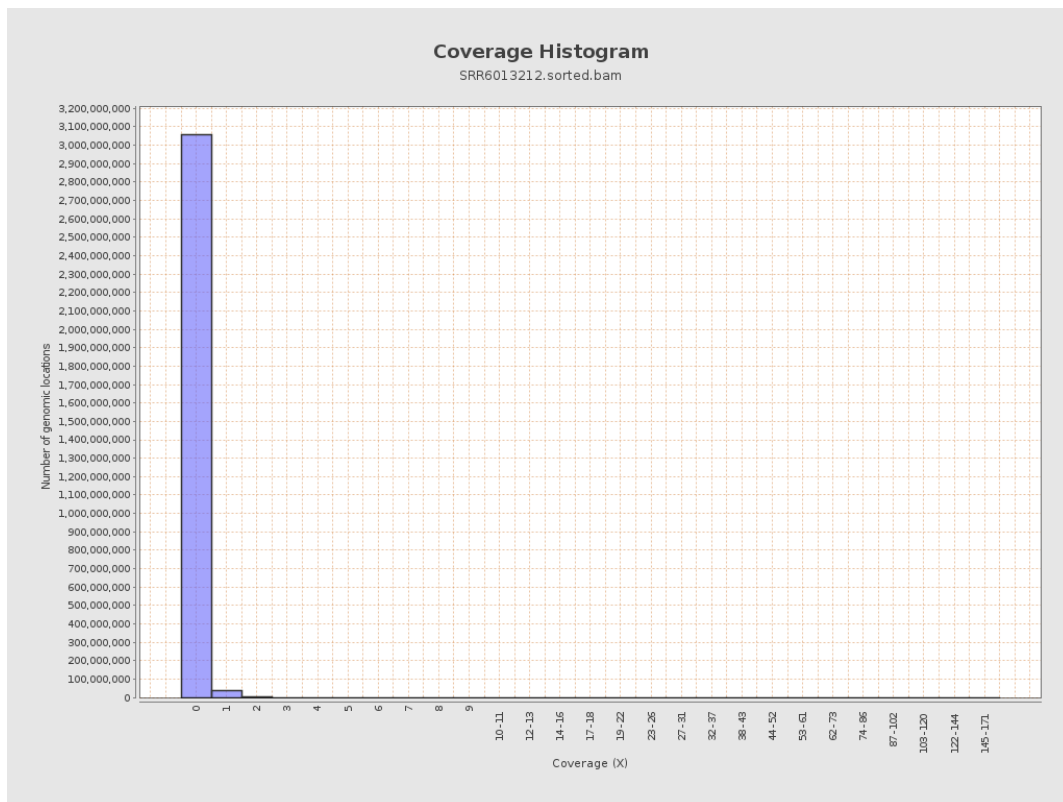
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3497484	0.014	0.1725
chr2	243199373	5527754	0.0227	0.1668
chr3	198022430	2712782	0.0137	0.1223
chr4	191154276	2842291	0.0149	0.1282
chr5	180915260	2044246	0.0113	0.1111
chr6	171115067	1809646	0.0106	0.111
chr7	159138663	2675554	0.0168	0.1716

chr8	146364022	2699234	0.0184	0.1655
chr9	141213431	1420378	0.0101	0.1124
chr10	135534747	1899058	0.014	0.1356
chr11	135006516	1815882	0.0135	0.13
chr12	133851895	2733358	0.0204	0.1496
chr13	115169878	855955	0.0074	0.0893
chr14	107349540	1493791	0.0139	0.1242
chr15	102531392	1227651	0.012	0.1154
chr16	90354753	1338173	0.0148	0.1281
chr17	81195210	862475	0.0106	0.1118
chr18	78077248	998387	0.0128	0.1568
chr19	59128983	660308	0.0112	0.1291
chr20	63025520	856142	0.0136	0.122
chr21	48129895	873016	0.0181	0.1434
chr22	51304566	303662	0.0059	0.08
chrMT	16571	5128	0.3095	0.63
chrX	155270560	2370728	0.0153	0.1317
chrY	59373566	69232	0.0012	0.0371

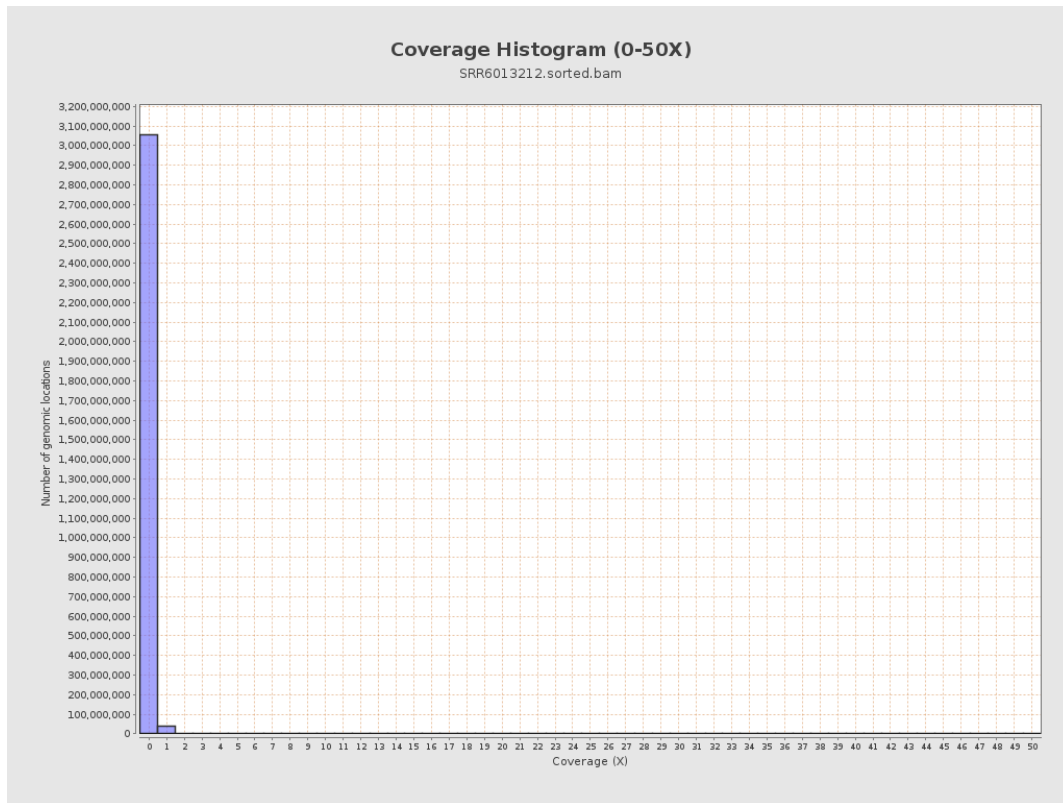
3. Results : Coverage across reference



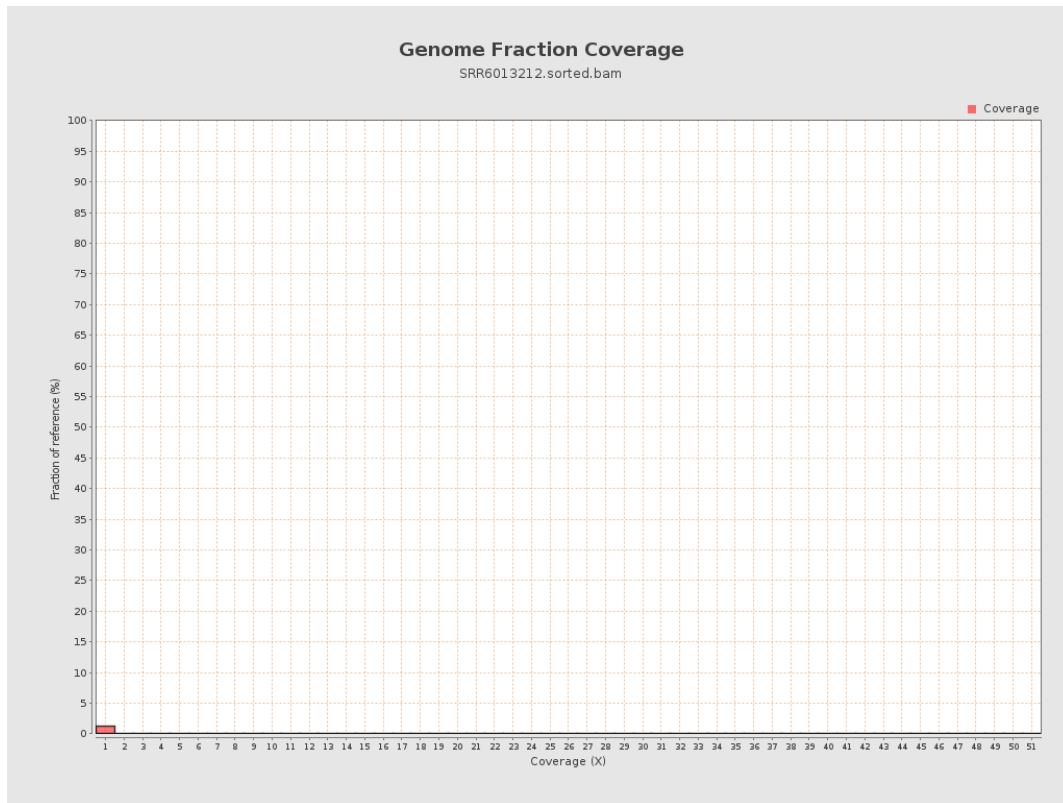
4. Results : Coverage Histogram



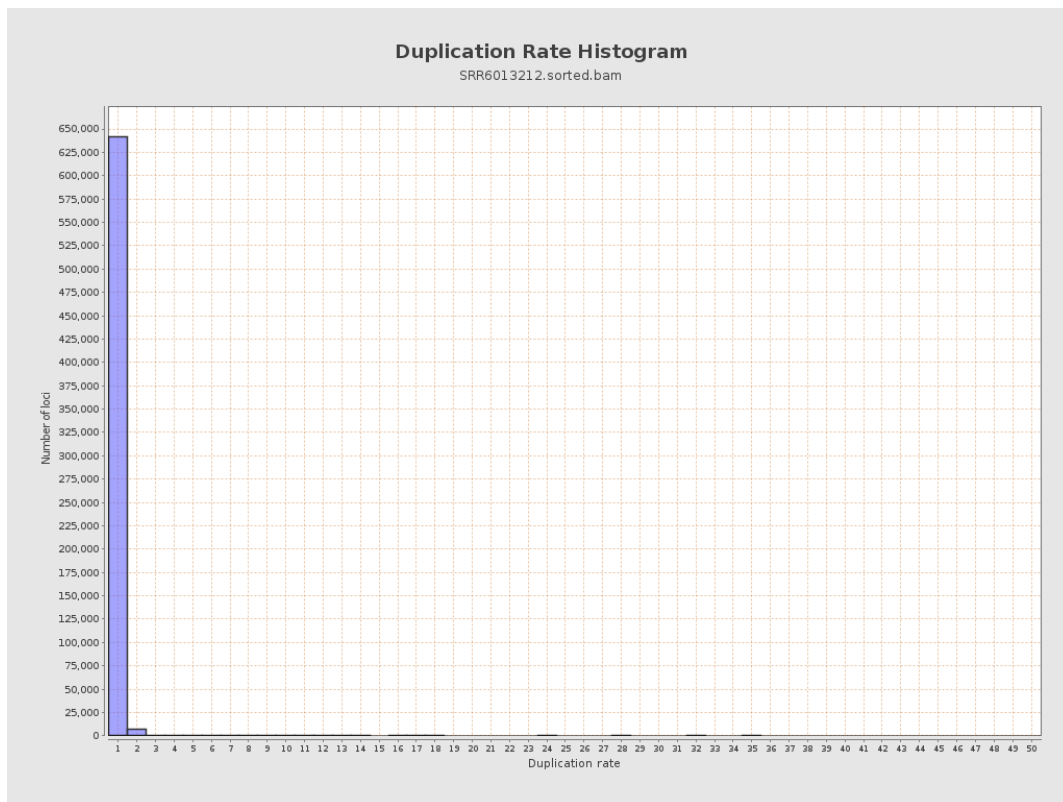
5. Results : Coverage Histogram (0-50X)



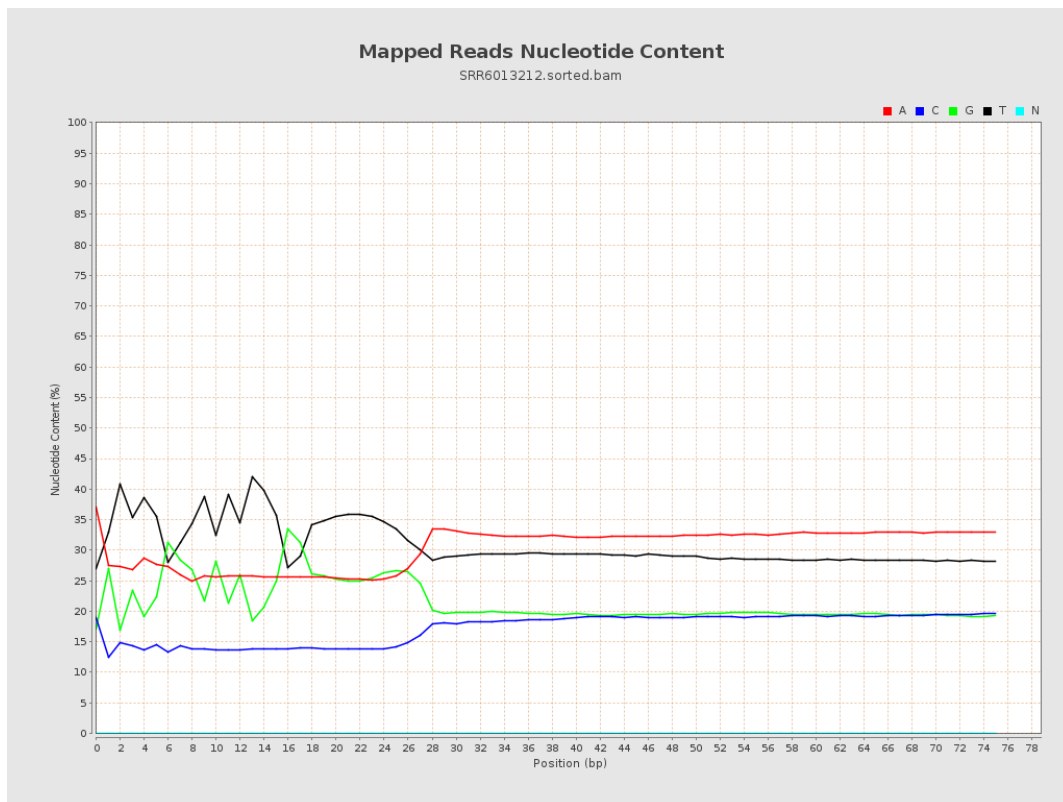
6. Results : Genome Fraction Coverage



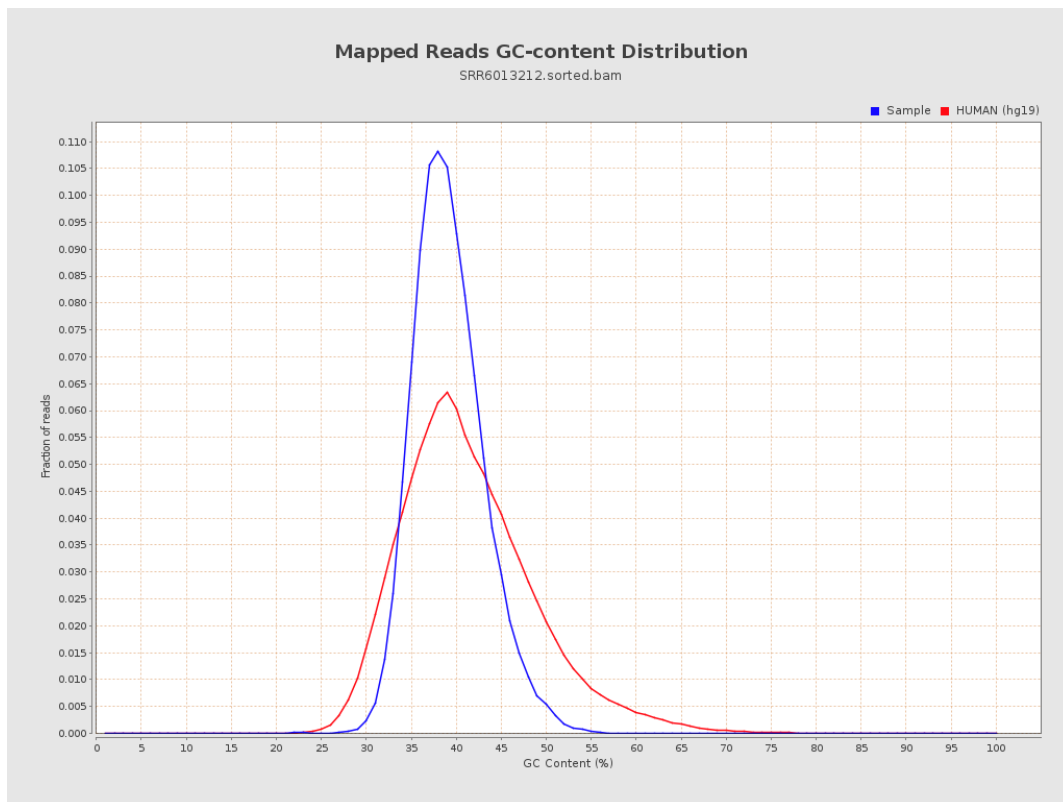
7. Results : Duplication Rate Histogram



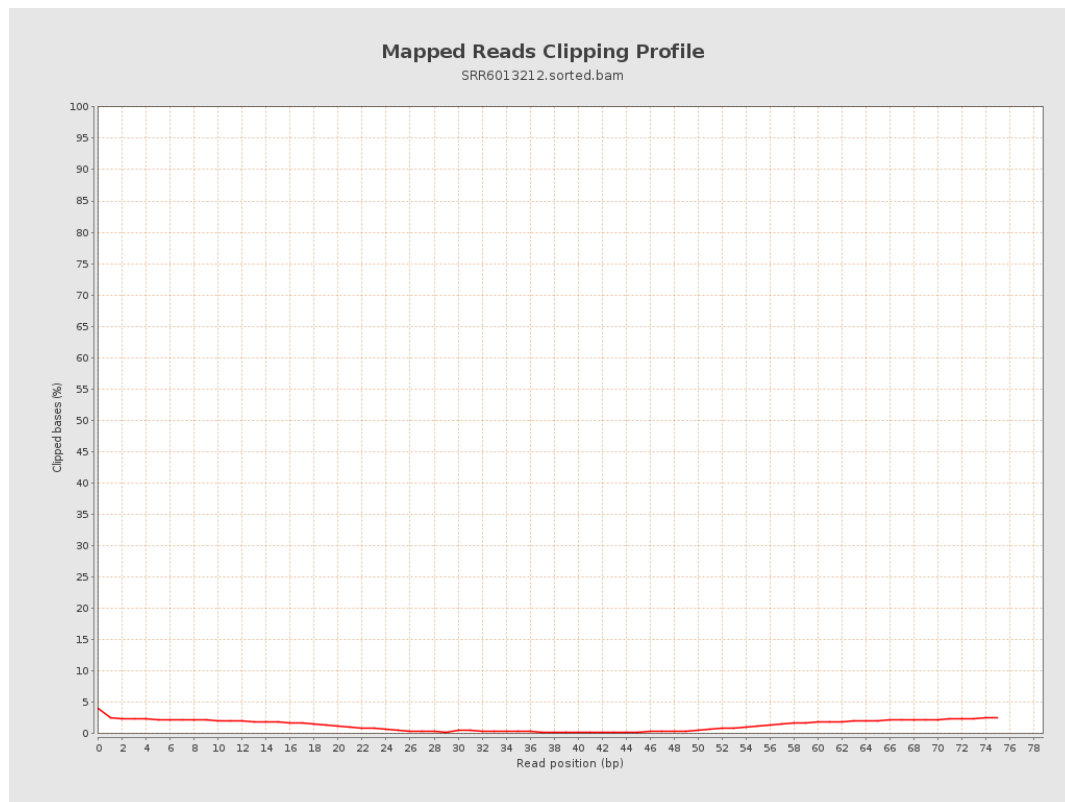
8. Results : Mapped Reads Nucleotide Content



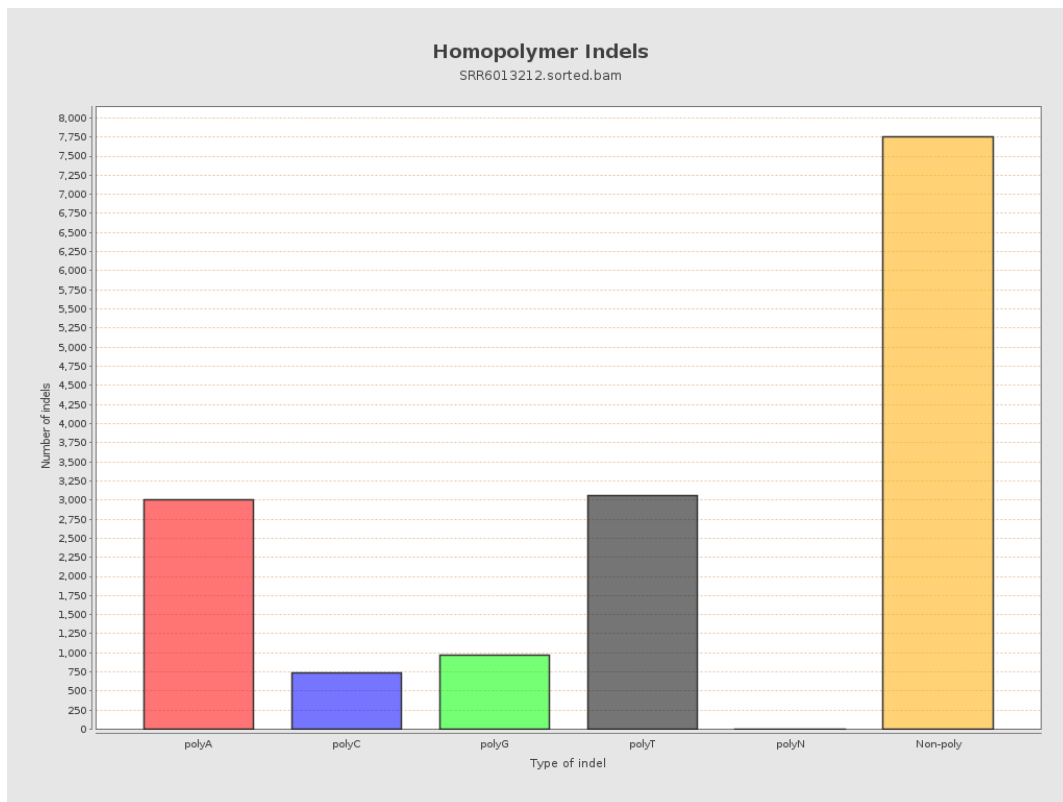
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

