

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:17:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063557.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_SRR6063557 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063557.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:17:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063557.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,506,940
Mapped reads	2,259,471 / 90.13%
Unmapped reads	247,469 / 9.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,571 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	99,901 / 3.98%
Duplication rate	3%
Clipped reads	1,129,521 / 45.06%

2.2. ACGT Content

Number/percentage of A's	40,248,650 / 27.18%
Number/percentage of C's	27,355,891 / 18.47%
Number/percentage of T's	46,425,273 / 31.35%
Number/percentage of G's	34,040,416 / 22.99%
Number/percentage of N's	2,952 / 0%
GC Percentage	41.46%

2.3. Coverage

Mean	0.0479

Standard Deviation	0.5705
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2.4. Mapping Quality

Mean Mapping Quality	43.75
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2.5. Mismatches and indels

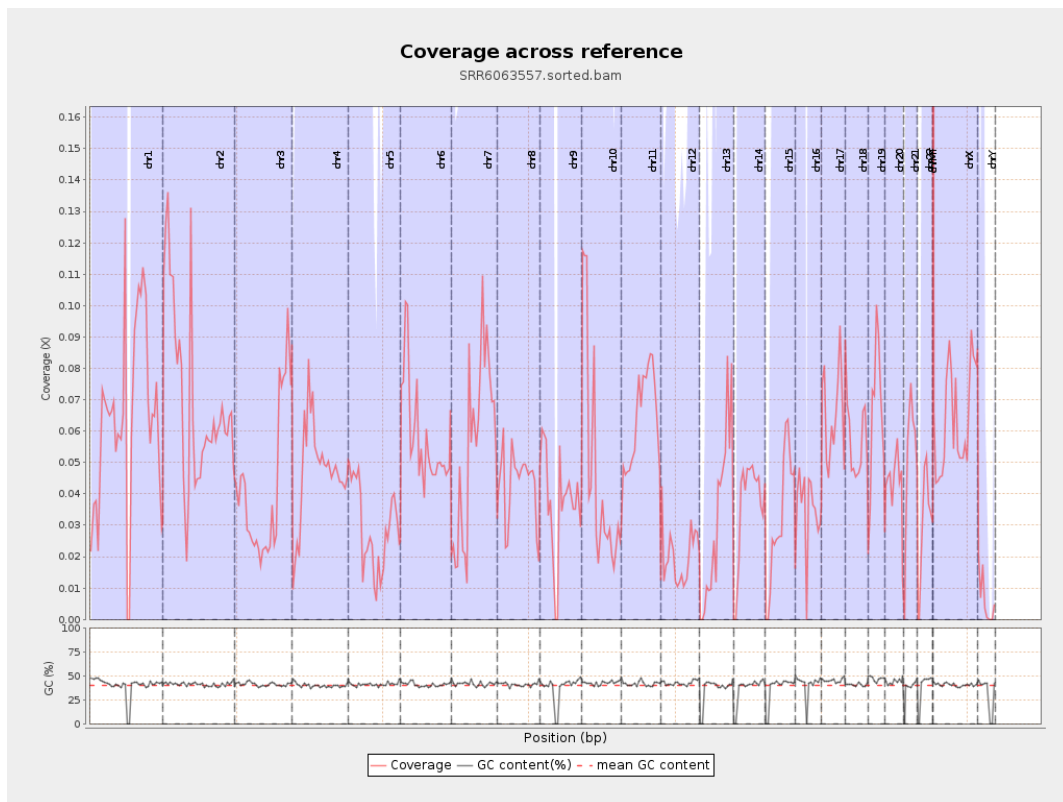
General error rate	0.82%
Mismatches	1,201,063
Insertions	11,150
Mapped reads with at least one insertion	0.49%
Deletions	41,762
Mapped reads with at least one deletion	1.83%
Homopolymer indels	45.28%

2.6. Chromosome stats

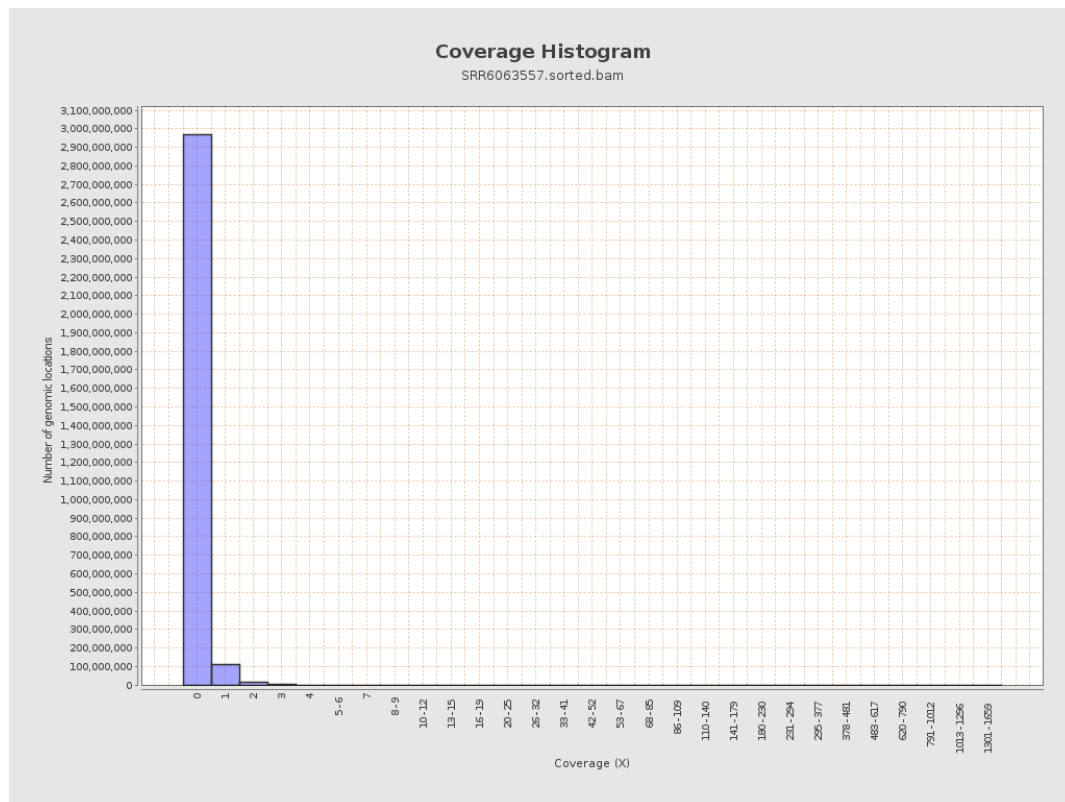
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15702612	0.063	1.3723
chr2	243199373	17128136	0.0704	0.6785
chr3	198022430	8380891	0.0423	0.2496
chr4	191154276	9028494	0.0472	0.2496
chr5	180915260	5224695	0.0289	0.1957
chr6	171115067	9961854	0.0582	0.3525
chr7	159138663	8787136	0.0552	0.6421

chr8	146364022	6247142	0.0427	0.5408
chr9	141213431	5254262	0.0372	0.4596
chr10	135534747	6199374	0.0457	0.5956
chr11	135006516	8607702	0.0638	0.4186
chr12	133851895	2702310	0.0202	0.1935
chr13	115169878	3764240	0.0327	0.2055
chr14	107349540	3911919	0.0364	0.2712
chr15	102531392	3291241	0.0321	0.2123
chr16	90354753	3113399	0.0345	0.2564
chr17	81195210	5400556	0.0665	0.3322
chr18	78077248	4460604	0.0571	0.7642
chr19	59128983	3952854	0.0669	0.9253
chr20	63025520	2797490	0.0444	0.2577
chr21	48129895	2410711	0.0501	0.2672
chr22	51304566	1552579	0.0303	0.1945
chrMT	16571	18204	1.0985	1.2911
chrX	155270560	9880306	0.0636	0.3444
chrY	59373566	362335	0.0061	0.1554

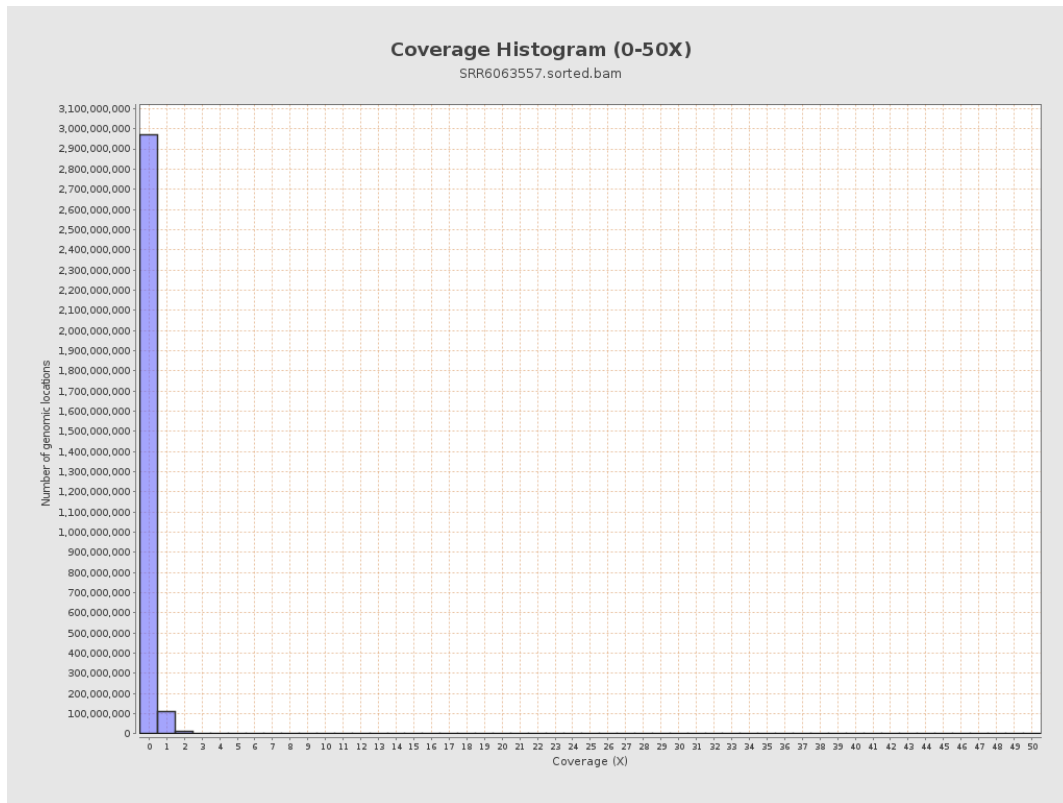
3. Results : Coverage across reference



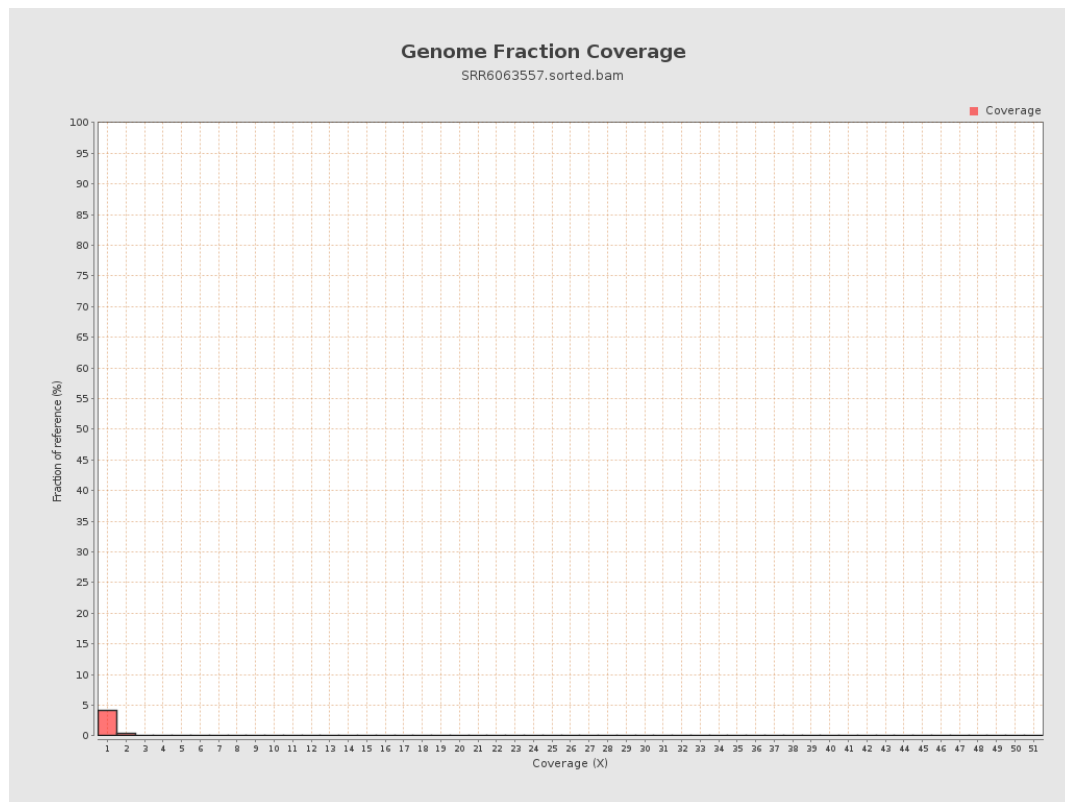
4. Results : Coverage Histogram



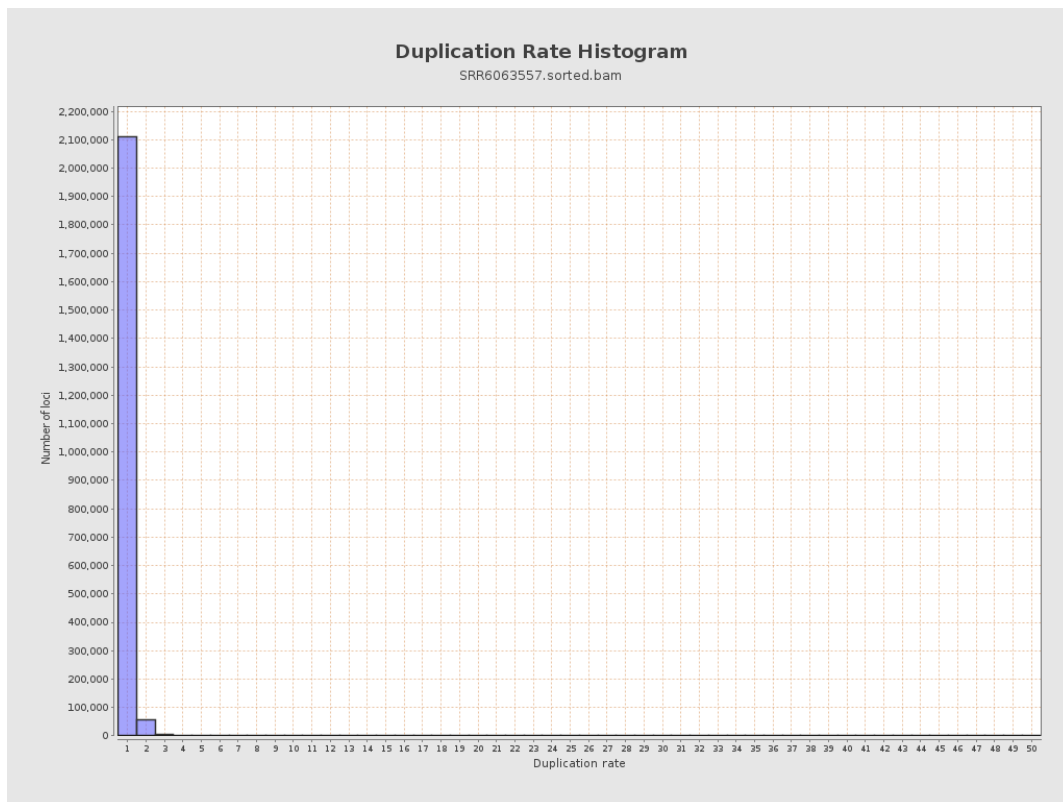
5. Results : Coverage Histogram (0-50X)



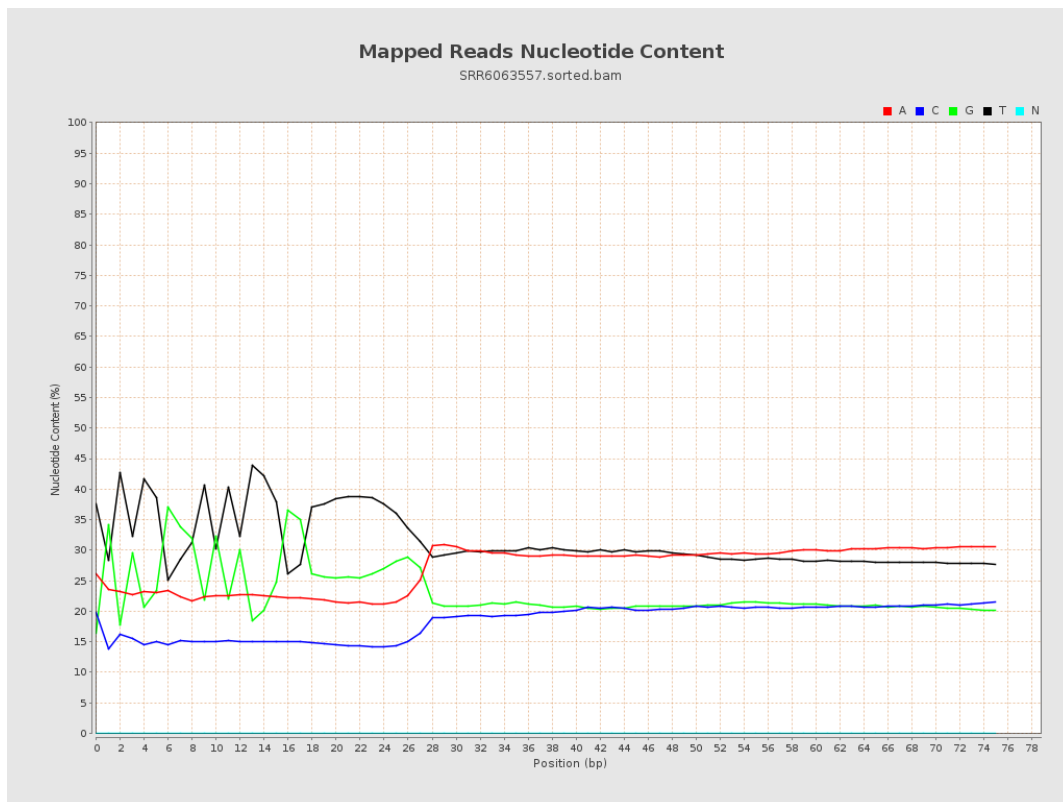
6. Results : Genome Fraction Coverage



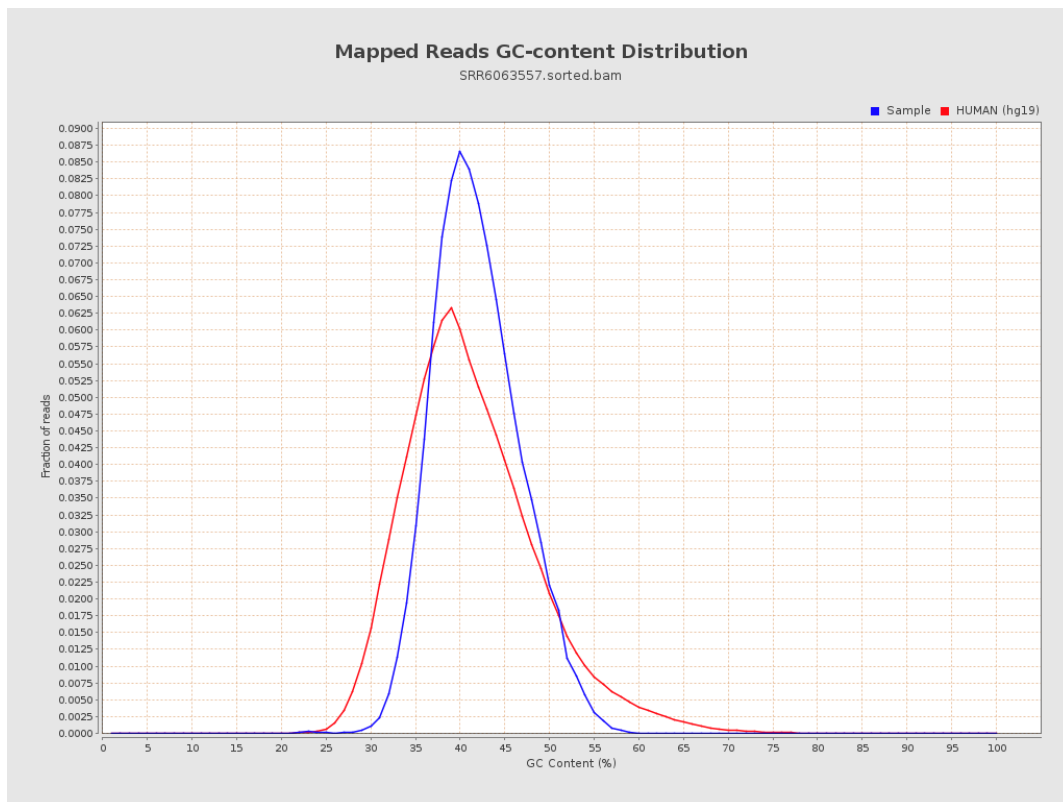
7. Results : Duplication Rate Histogram



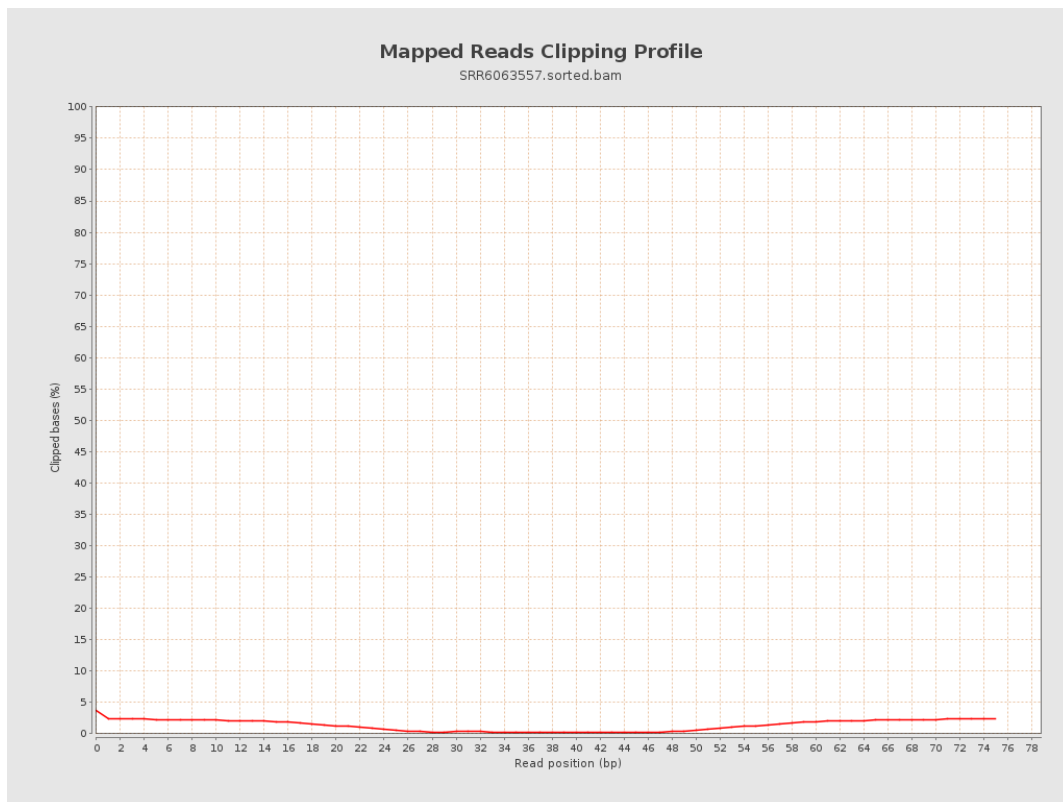
8. Results : Mapped Reads Nucleotide Content



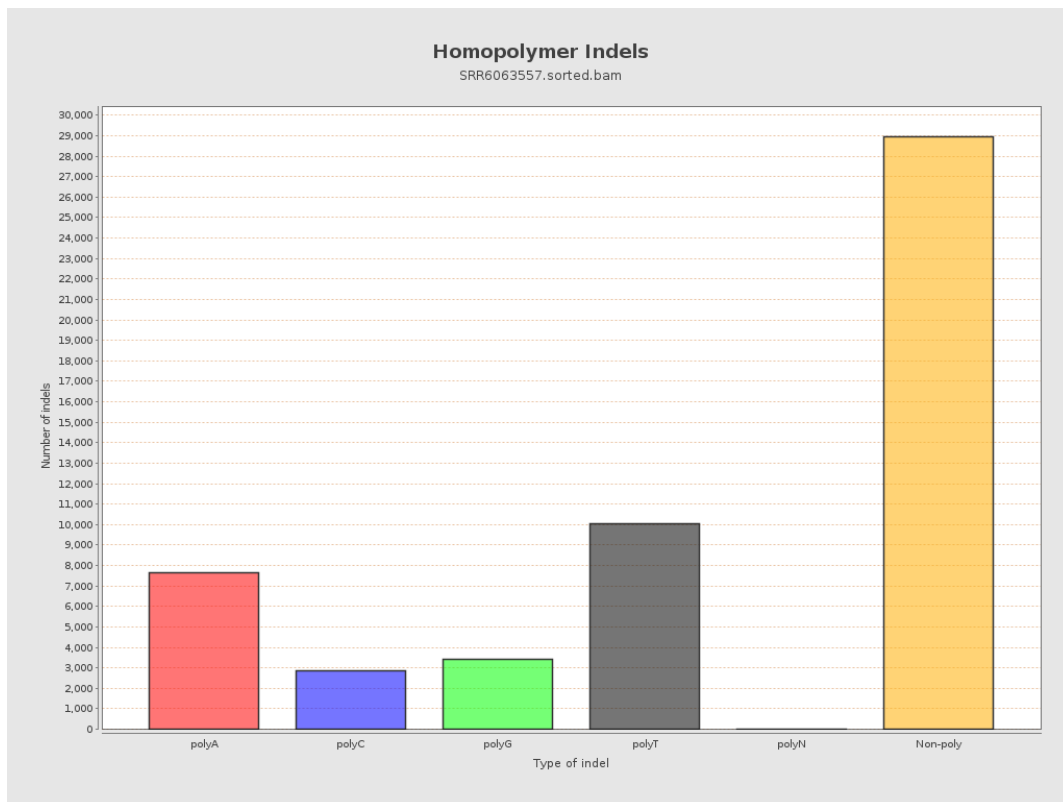
9. Results : Mapped Reads GC-content Distribution



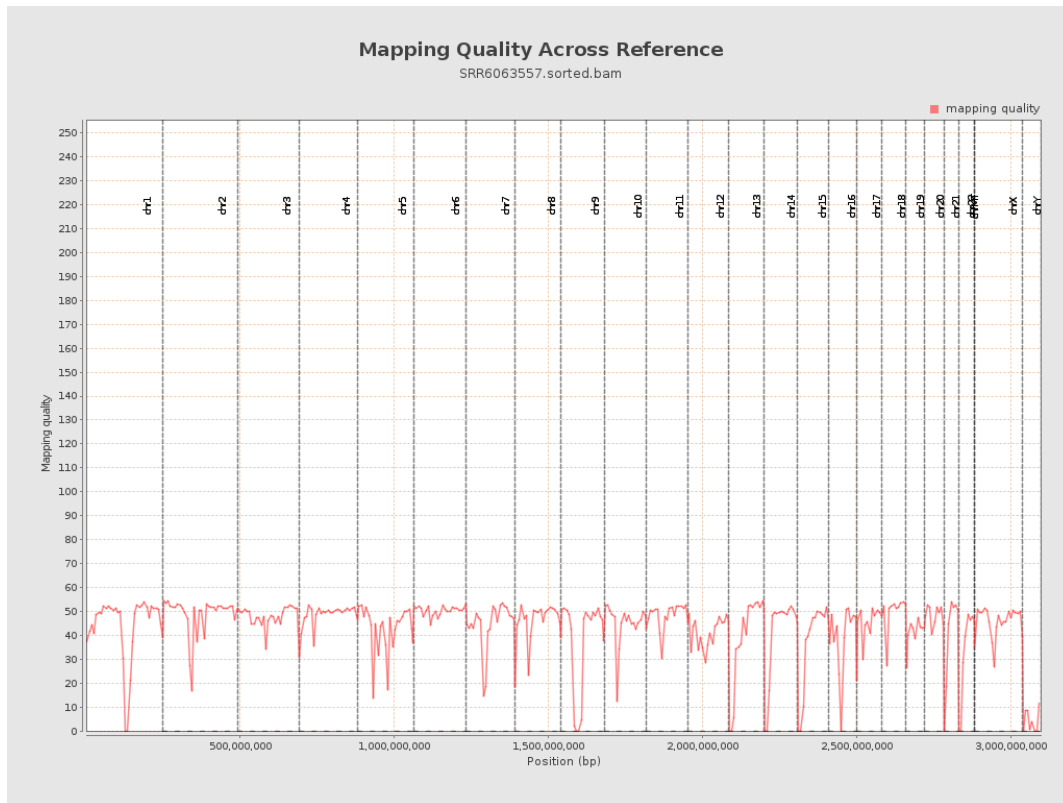
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

