

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:48:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234058.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_SRR6234058 /home/luna/Desktop/database/homo_hsa.fa SRR6234058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:48:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,970,193
Mapped reads	2,698,566 / 90.85%
Unmapped reads	271,627 / 9.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,889 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	196,892 / 6.63%
Duplication rate	5.59%
Clipped reads	1,323,904 / 44.57%

2.2. ACGT Content

Number/percentage of A's	46,622,392 / 26.25%
Number/percentage of C's	33,122,174 / 18.65%
Number/percentage of T's	56,157,677 / 31.62%
Number/percentage of G's	41,665,352 / 23.46%
Number/percentage of N's	16,431 / 0.01%
GC Percentage	42.11%

2.3. Coverage

Mean	0.0574

Standard Deviation	0.6379
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2.4. Mapping Quality

Mean Mapping Quality	38.36
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2.5. Mismatches and indels

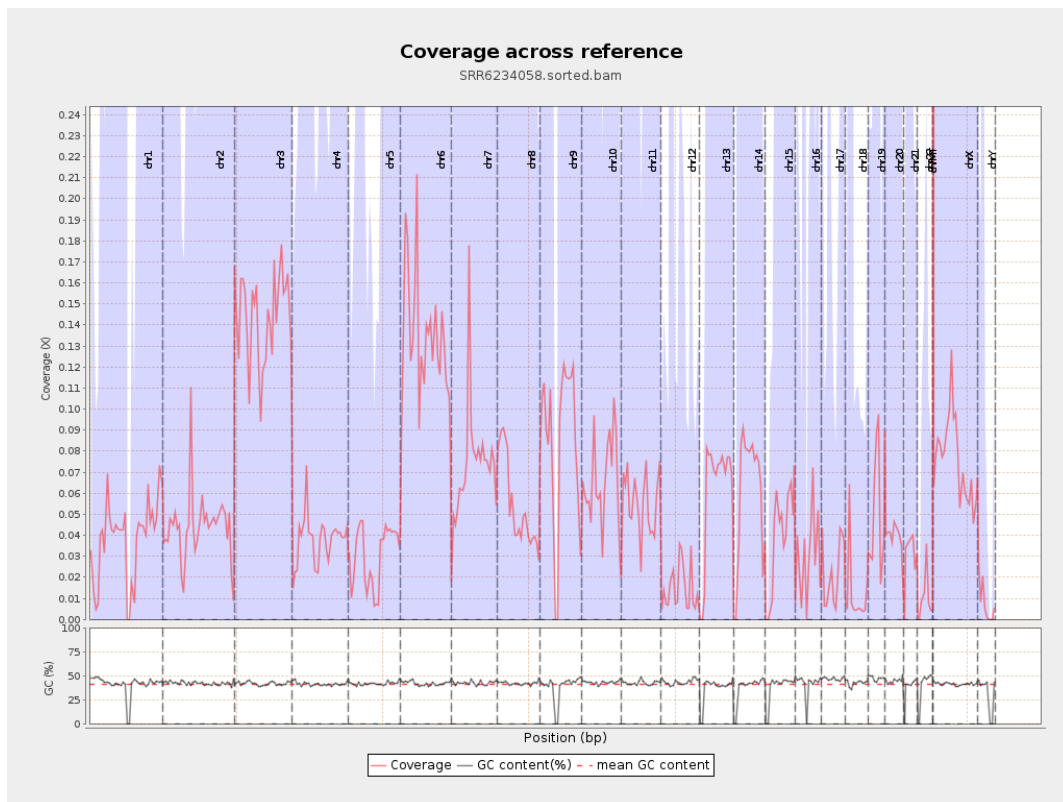
General error rate	0.68%
Mismatches	1,182,136
Insertions	14,596
Mapped reads with at least one insertion	0.54%
Deletions	45,544
Mapped reads with at least one deletion	1.67%
Homopolymer indels	44.32%

2.6. Chromosome stats

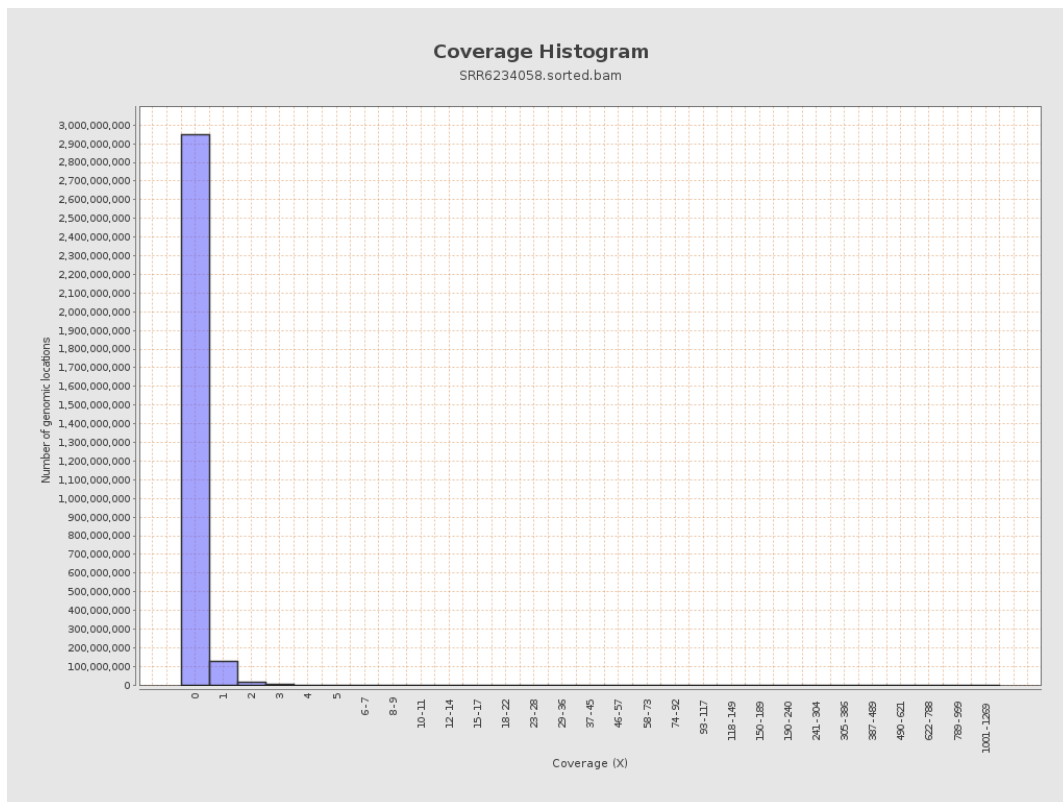
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9618634	0.0386	0.758
chr2	243199373	10747468	0.0442	0.7669
chr3	198022430	28475428	0.1438	0.4462
chr4	191154276	7311286	0.0382	0.2653
chr5	180915260	5498533	0.0304	0.2333
chr6	171115067	23126798	0.1352	0.8103
chr7	159138663	11747866	0.0738	1.4585

chr8	146364022	7891557	0.0539	0.392
chr9	141213431	12064659	0.0854	0.7086
chr10	135534747	8922353	0.0658	0.5621
chr11	135006516	7349142	0.0544	0.4832
chr12	133851895	1962847	0.0147	0.2384
chr13	115169878	7139570	0.062	0.2997
chr14	107349540	6613267	0.0616	0.4883
chr15	102531392	3823231	0.0373	0.2583
chr16	90354753	2680930	0.0297	0.4177
chr17	81195210	1780556	0.0219	0.2129
chr18	78077248	926793	0.0119	1.4082
chr19	59128983	3102444	0.0525	0.5423
chr20	63025520	2497253	0.0396	0.3158
chr21	48129895	1487726	0.0309	0.3223
chr22	51304566	544400	0.0106	0.1191
chrMT	16571	47989	2.896	2.5158
chrX	155270560	11834511	0.0762	0.4547
chrY	59373566	466696	0.0079	0.1765

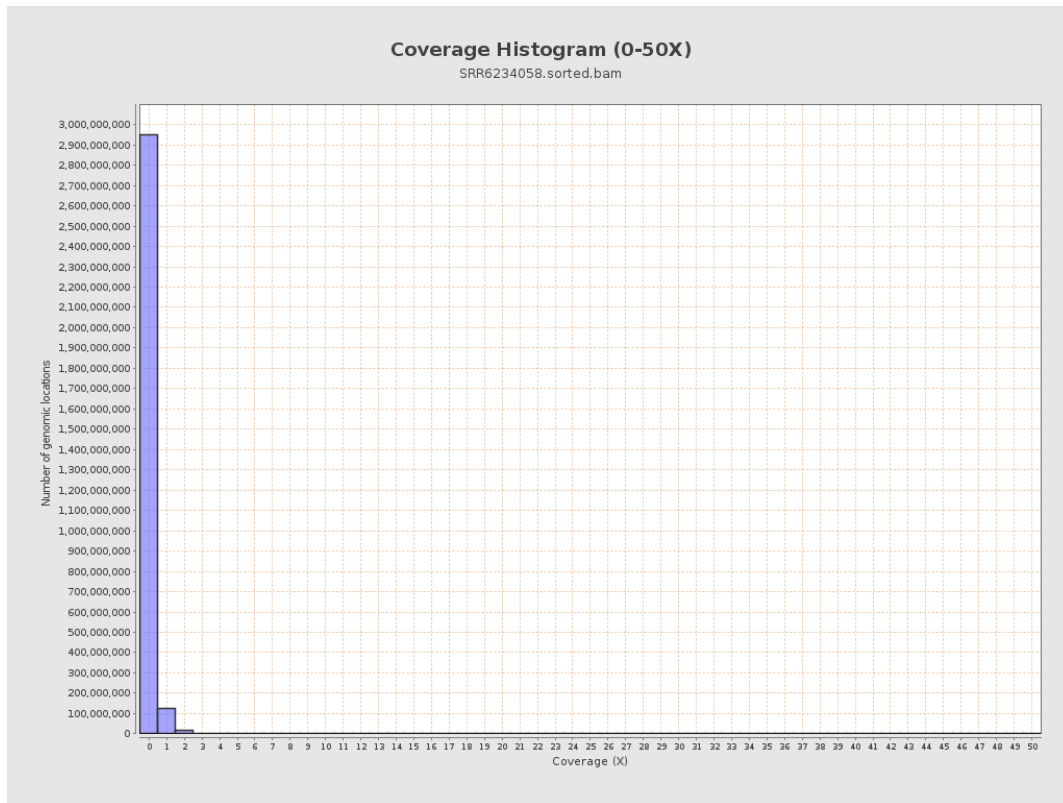
3. Results : Coverage across reference



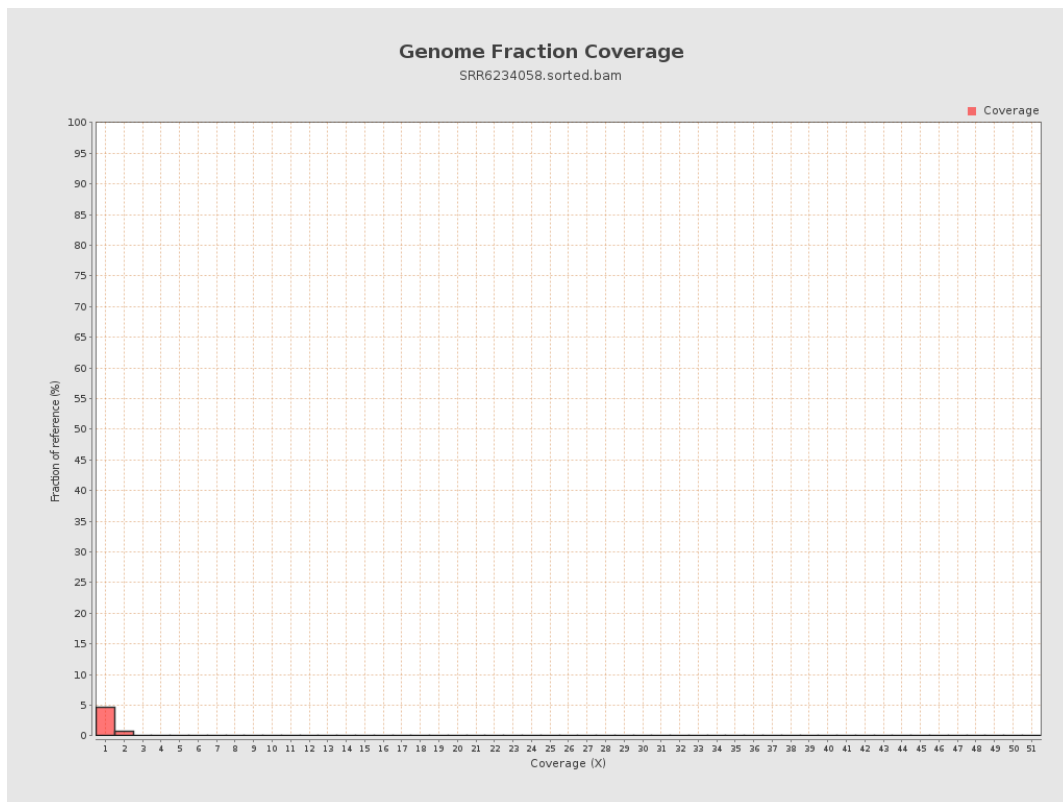
4. Results : Coverage Histogram



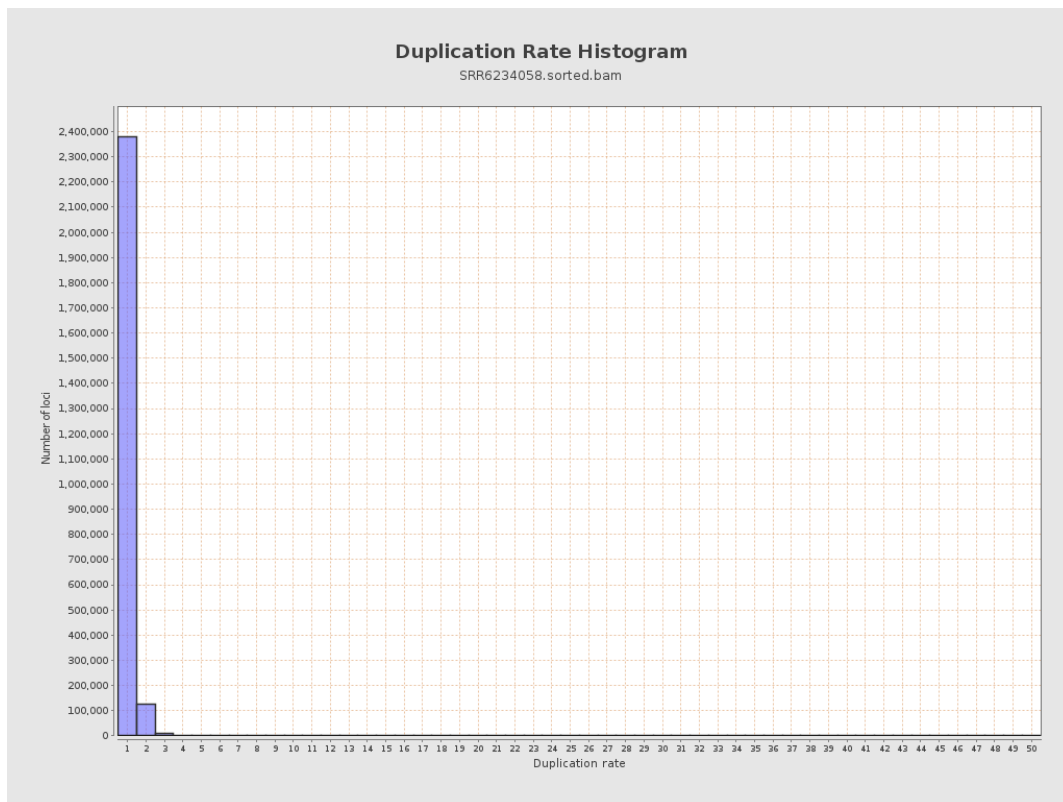
5. Results : Coverage Histogram (0-50X)



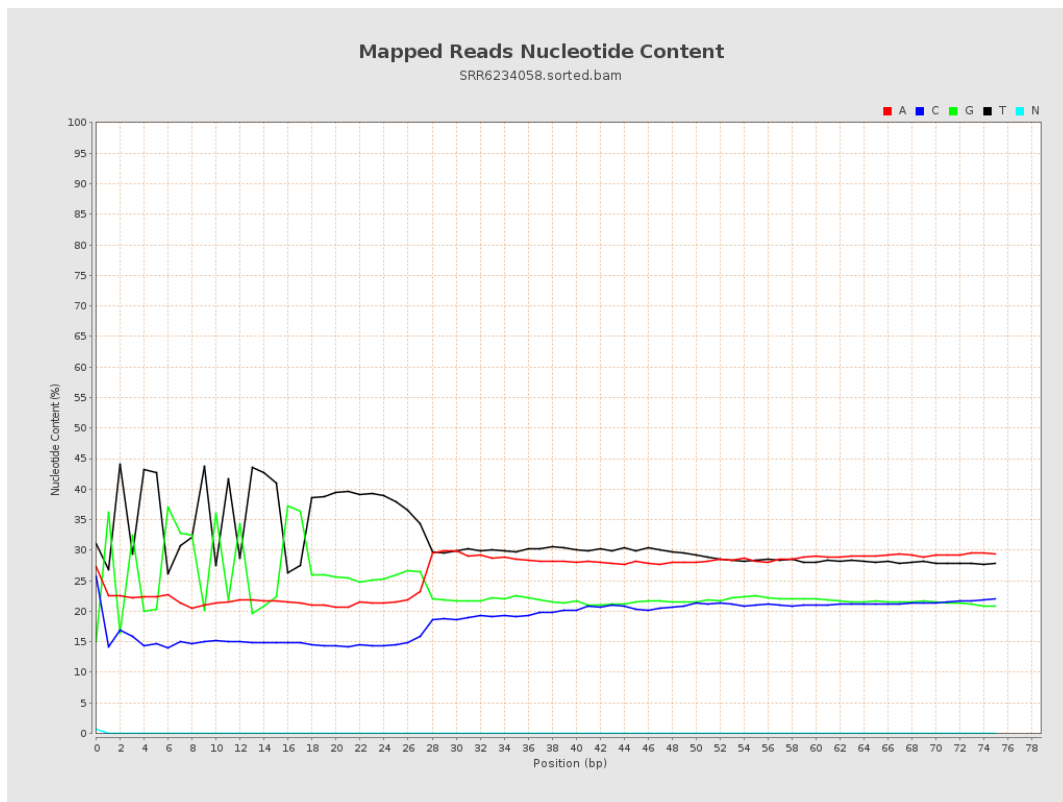
6. Results : Genome Fraction Coverage



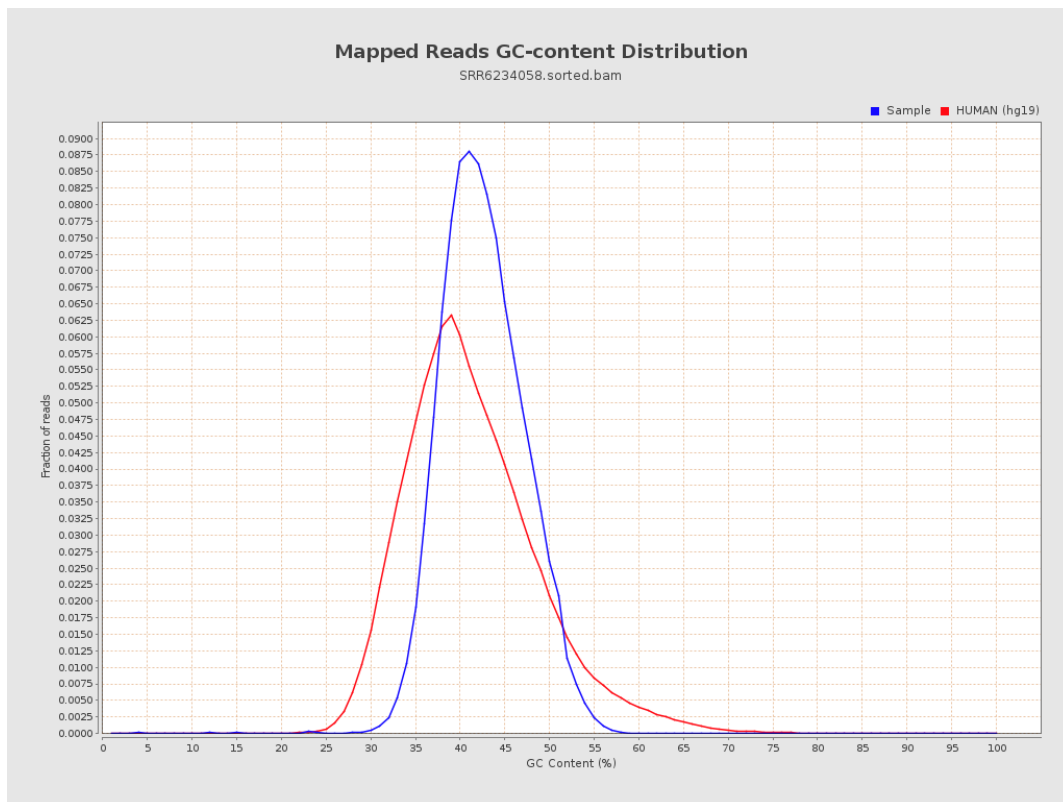
7. Results : Duplication Rate Histogram



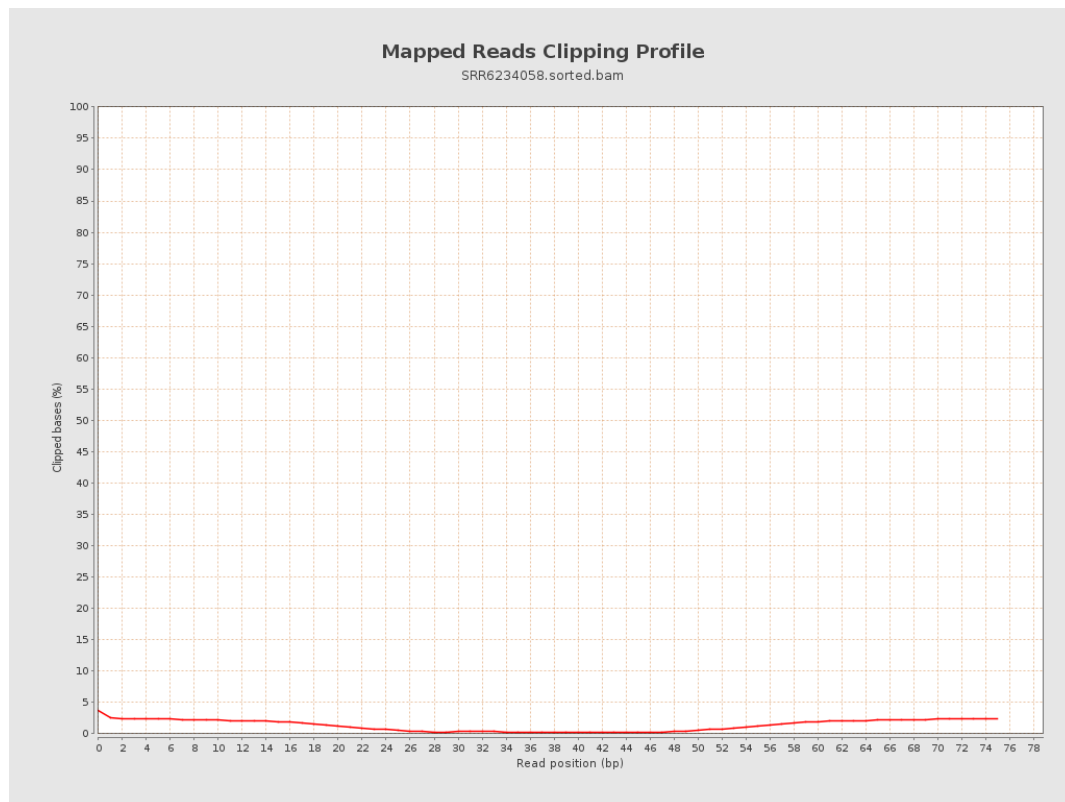
8. Results : Mapped Reads Nucleotide Content



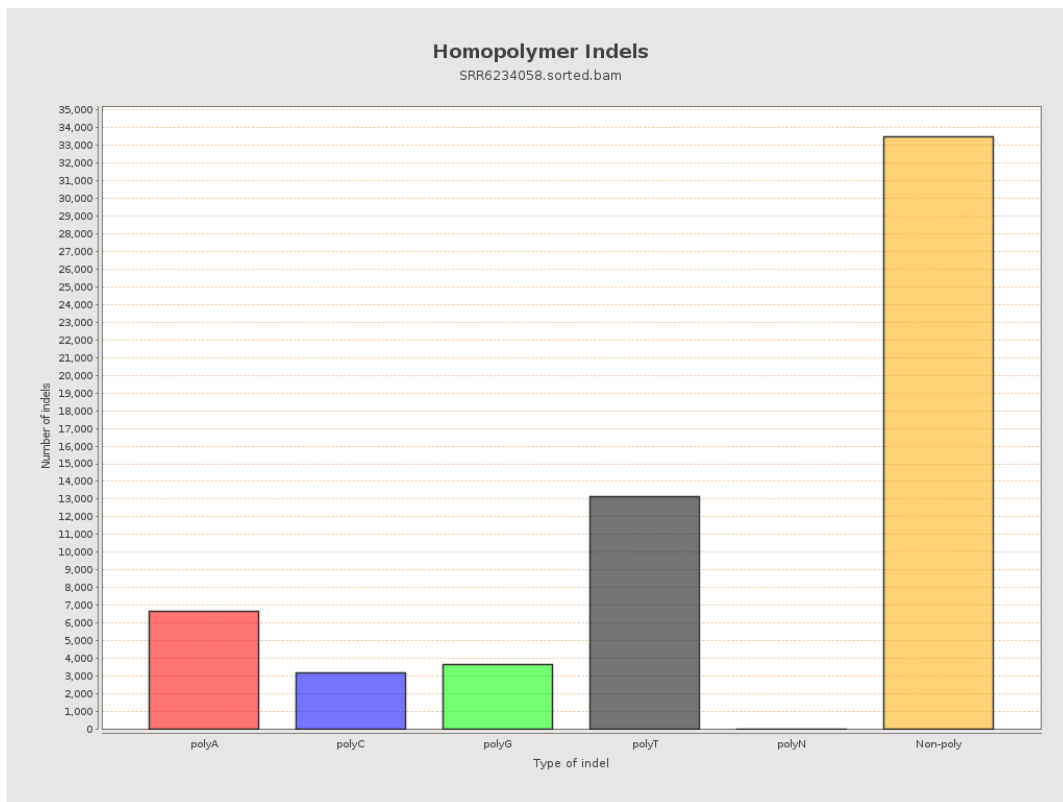
9. Results : Mapped Reads GC-content Distribution



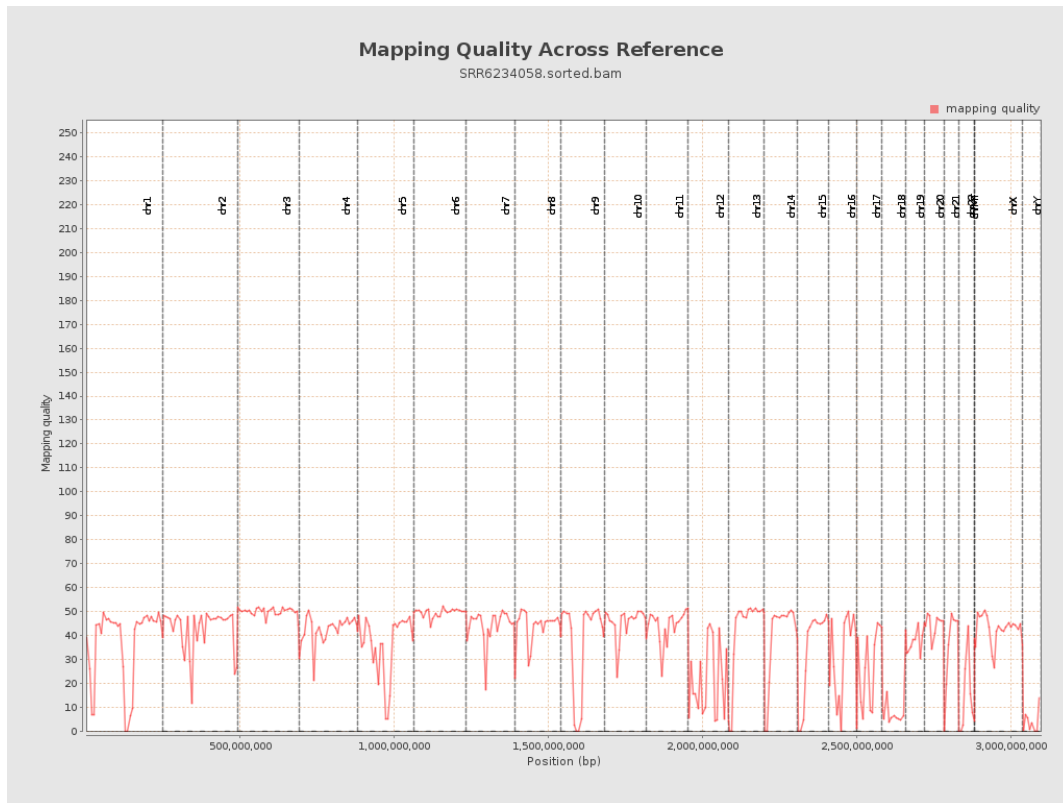
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

