

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 12:42:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068144.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_SRR6068144 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068144.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 12:42:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,883,973
Mapped reads	2,736,482 / 94.89%
Unmapped reads	147,491 / 5.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,780 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	384,440 / 13.33%
Duplication rate	11.54%
Clipped reads	1,196,433 / 41.49%

2.2. ACGT Content

Number/percentage of A's	49,697,536 / 27.37%
Number/percentage of C's	32,428,677 / 17.86%
Number/percentage of T's	59,413,180 / 32.72%
Number/percentage of G's	40,005,198 / 22.03%
Number/percentage of N's	21,566 / 0.01%
GC Percentage	39.89%

2.3. Coverage

Mean	0.0587

Standard Deviation	0.6484
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2.4. Mapping Quality

Mean Mapping Quality	46.55
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2.5. Mismatches and indels

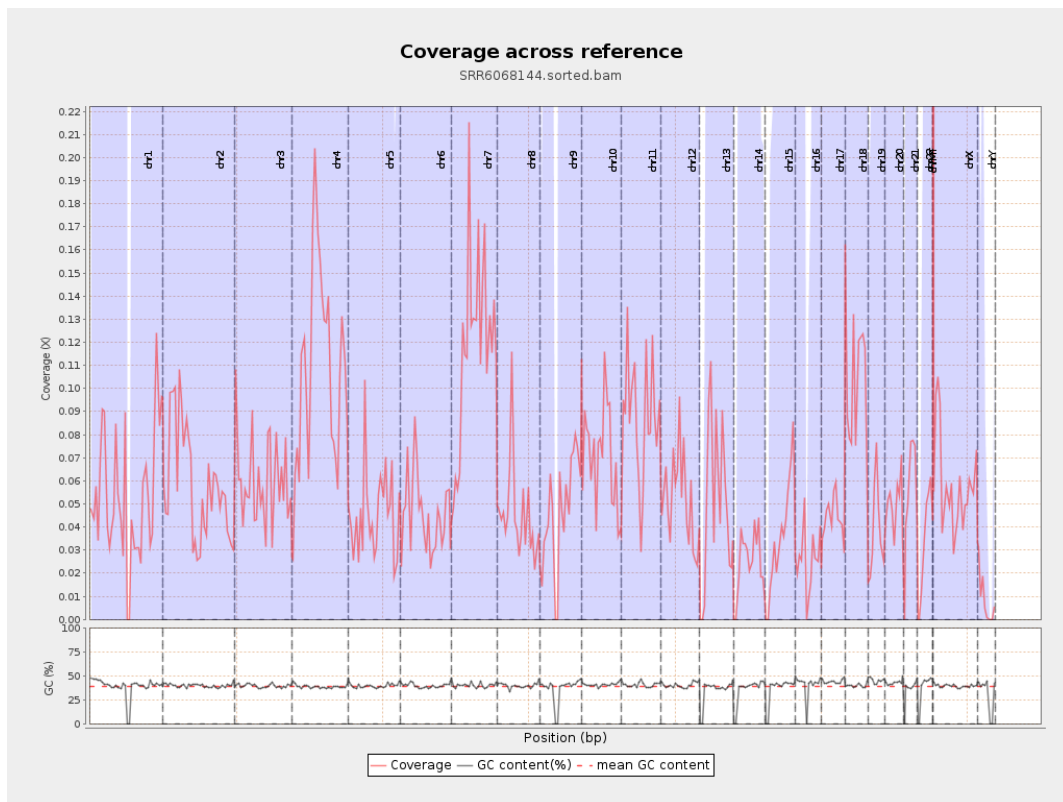
General error rate	0.53%
Mismatches	938,145
Insertions	11,894
Mapped reads with at least one insertion	0.43%
Deletions	39,217
Mapped reads with at least one deletion	1.42%
Homopolymer indels	46.67%

2.6. Chromosome stats

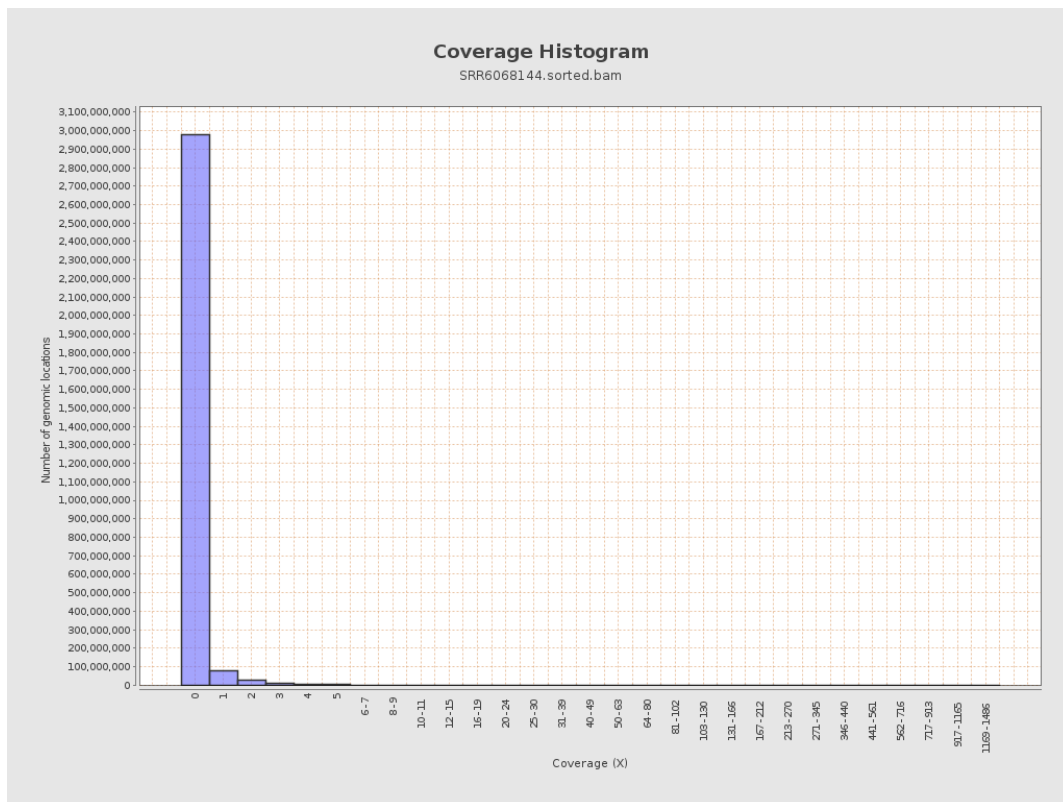
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13176625	0.0529	1.0644
chr2	243199373	14161233	0.0582	0.5544
chr3	198022430	11751561	0.0593	0.3478
chr4	191154276	20604672	0.1078	0.4825
chr5	180915260	8267658	0.0457	0.3042
chr6	171115067	7857443	0.0459	0.3908
chr7	159138663	18694729	0.1175	1.659

chr8	146364022	6550470	0.0448	0.942
chr9	141213431	6714995	0.0476	0.3748
chr10	135534747	9565420	0.0706	0.5164
chr11	135006516	11737473	0.0869	0.5294
chr12	133851895	6914564	0.0517	0.3294
chr13	115169878	5731059	0.0498	0.3302
chr14	107349540	2765963	0.0258	0.2351
chr15	102531392	3683136	0.0359	0.2798
chr16	90354753	2307981	0.0255	0.2475
chr17	81195210	3624086	0.0446	0.3404
chr18	78077248	8096101	0.1037	0.8287
chr19	59128983	2351231	0.0398	0.6147
chr20	63025520	3215765	0.051	0.3287
chr21	48129895	2675405	0.0556	0.3484
chr22	51304566	1745164	0.034	0.2587
chrMT	16571	40099	2.4198	2.4038
chrX	155270560	8932868	0.0575	0.3593
chrY	59373566	470302	0.0079	0.1399

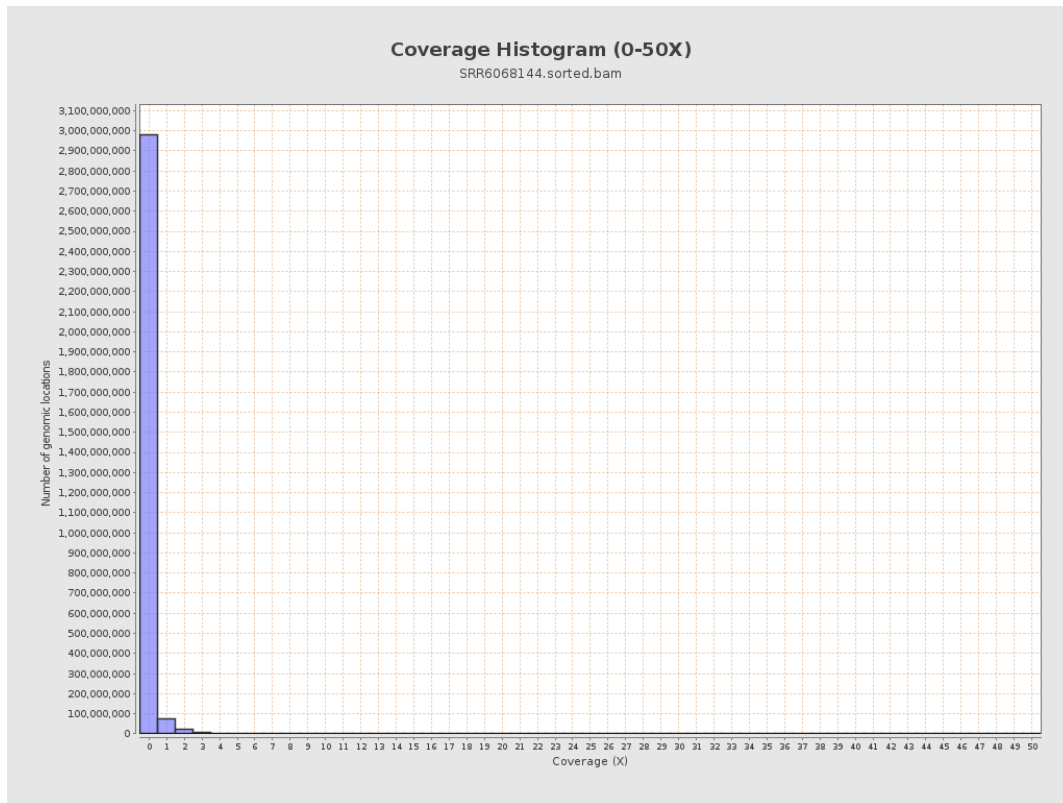
3. Results : Coverage across reference



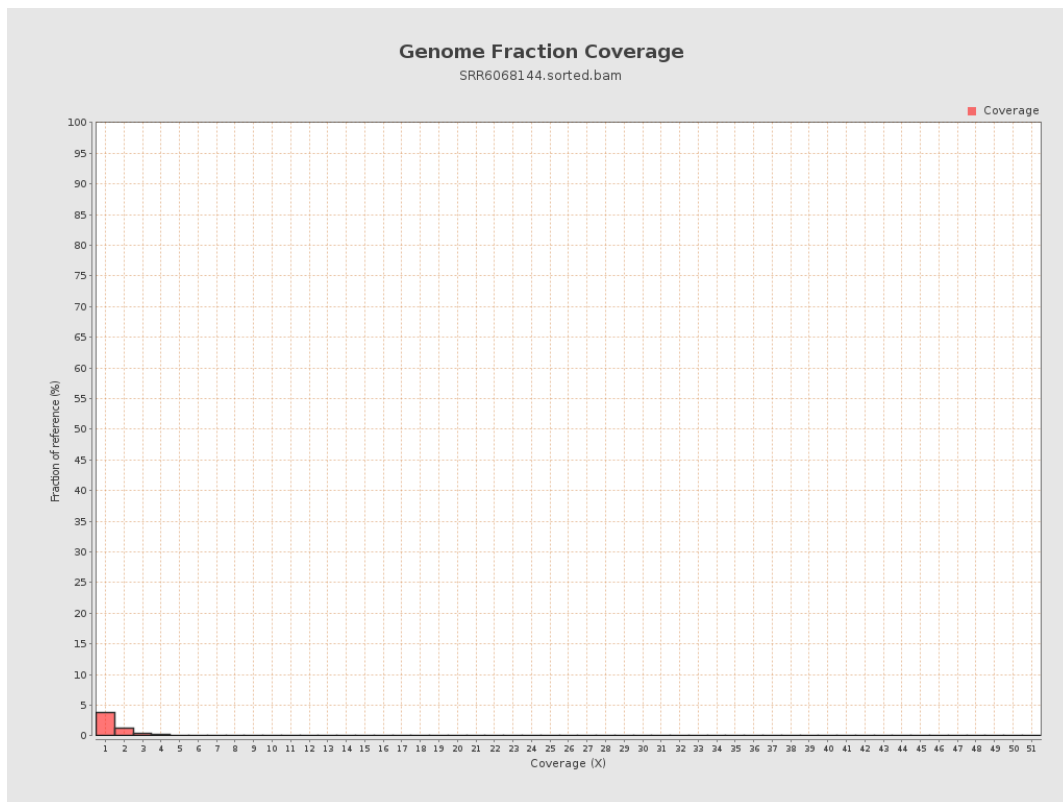
4. Results : Coverage Histogram



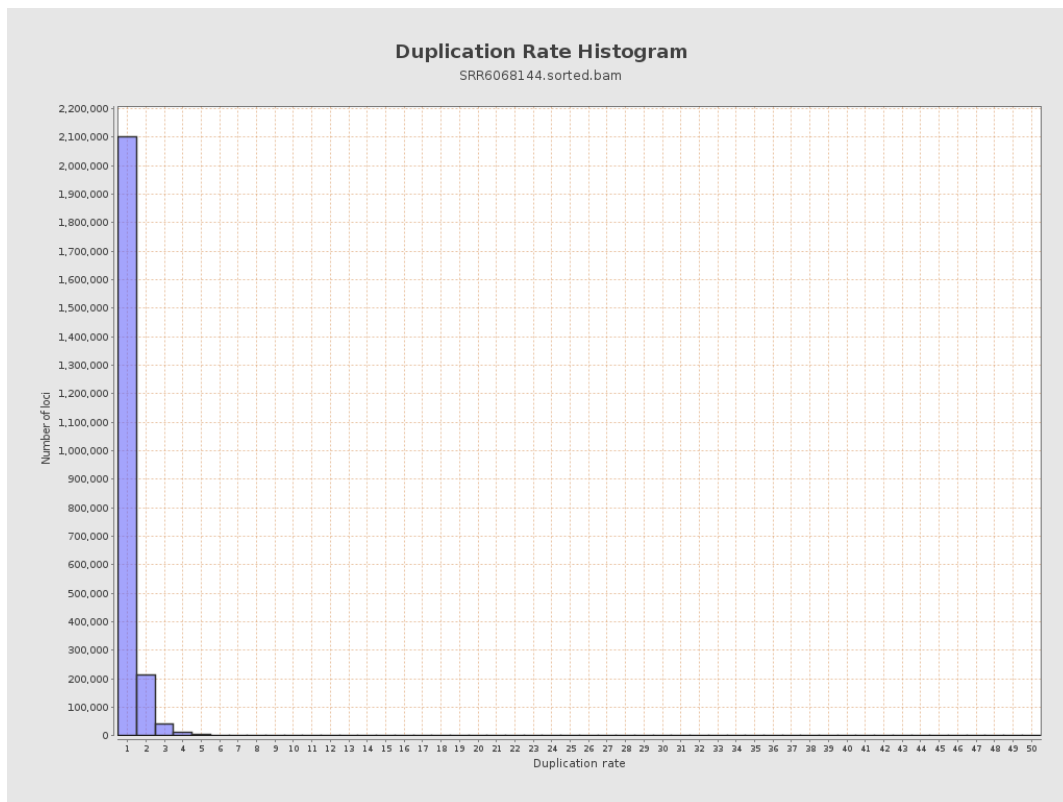
5. Results : Coverage Histogram (0-50X)



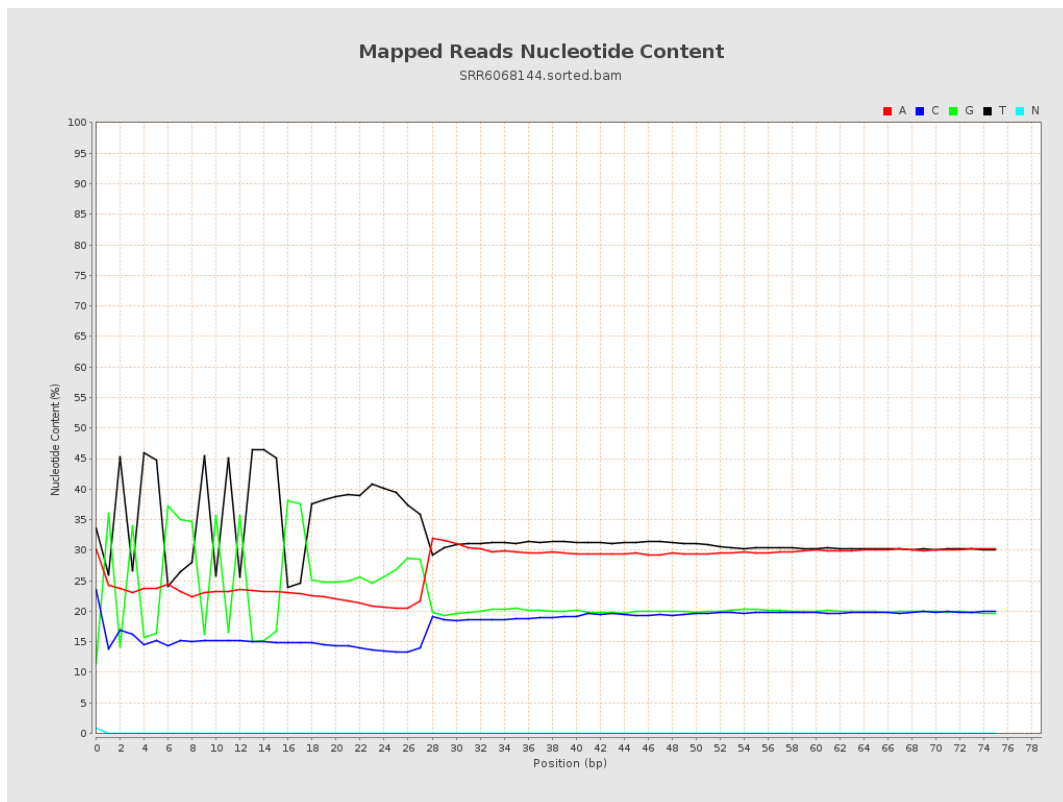
6. Results : Genome Fraction Coverage



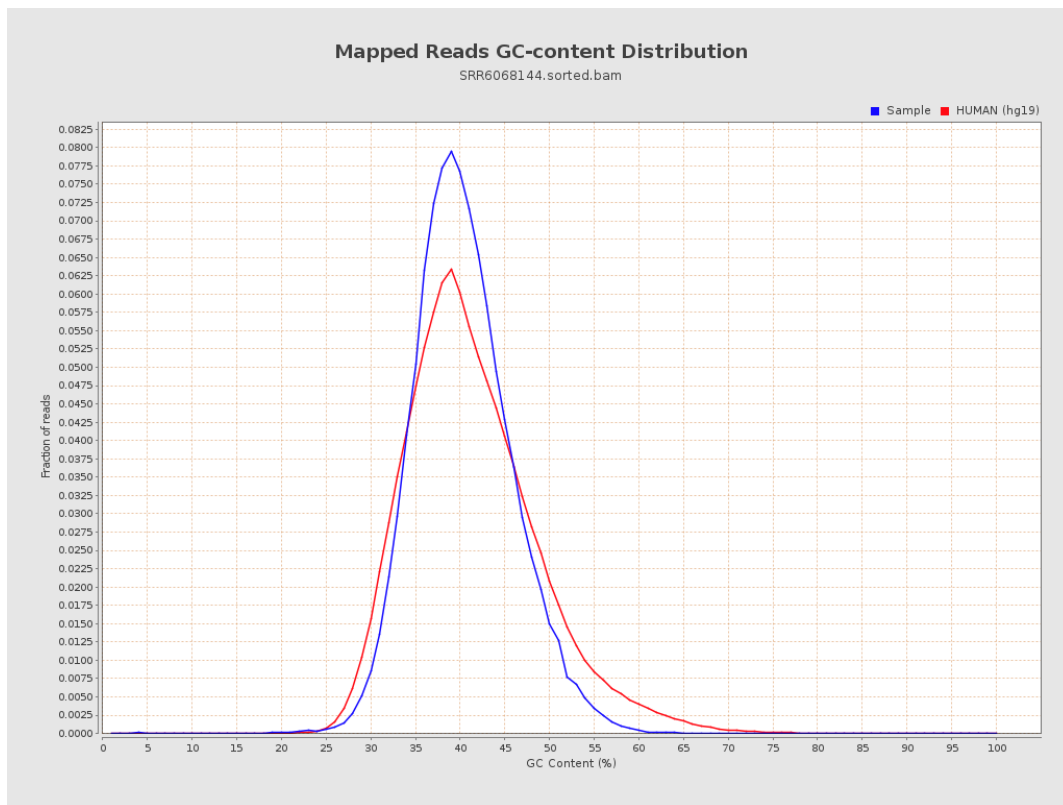
7. Results : Duplication Rate Histogram



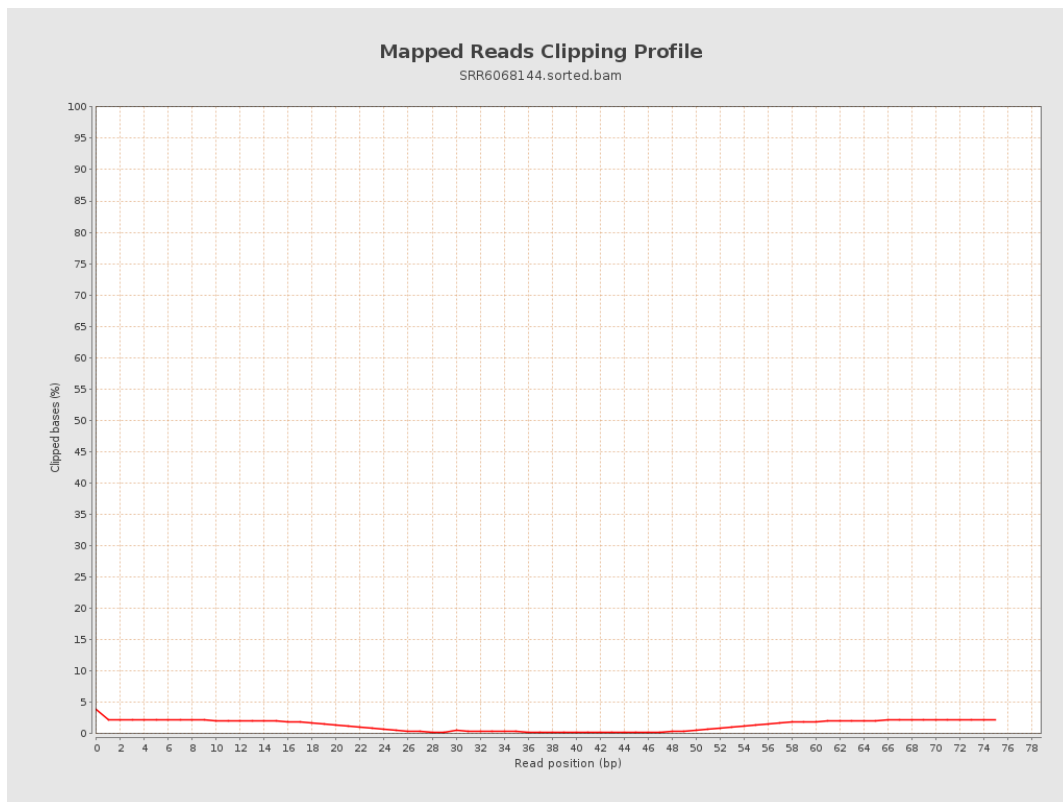
8. Results : Mapped Reads Nucleotide Content



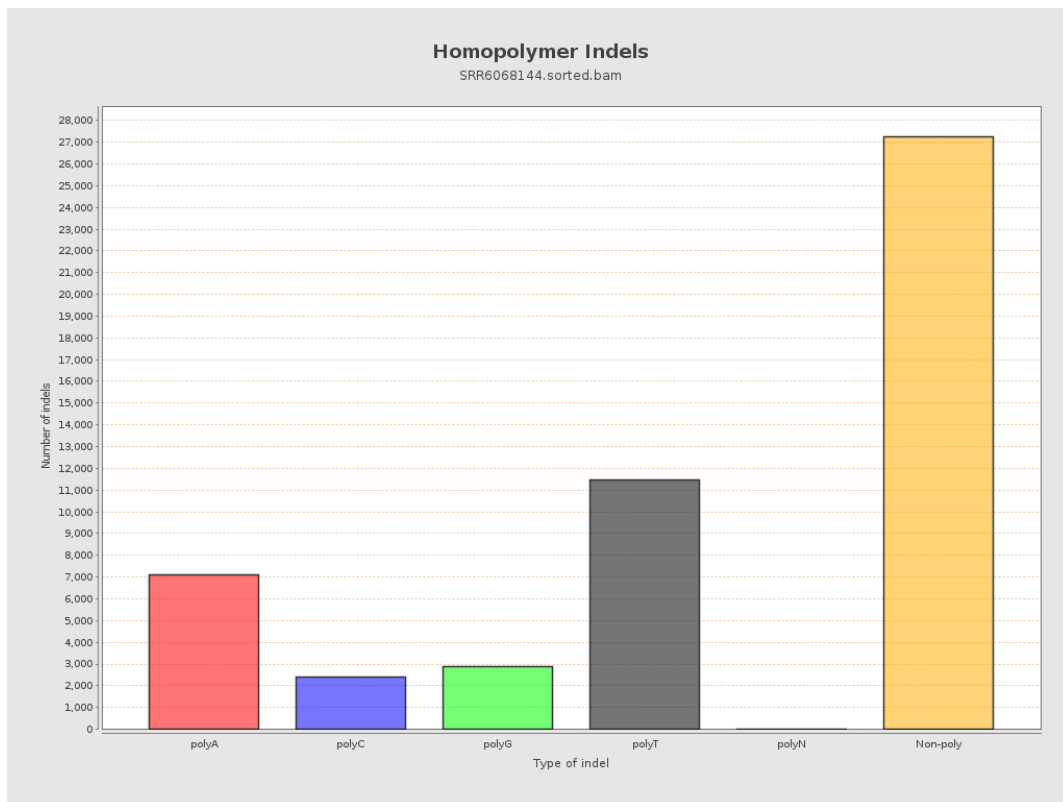
9. Results : Mapped Reads GC-content Distribution



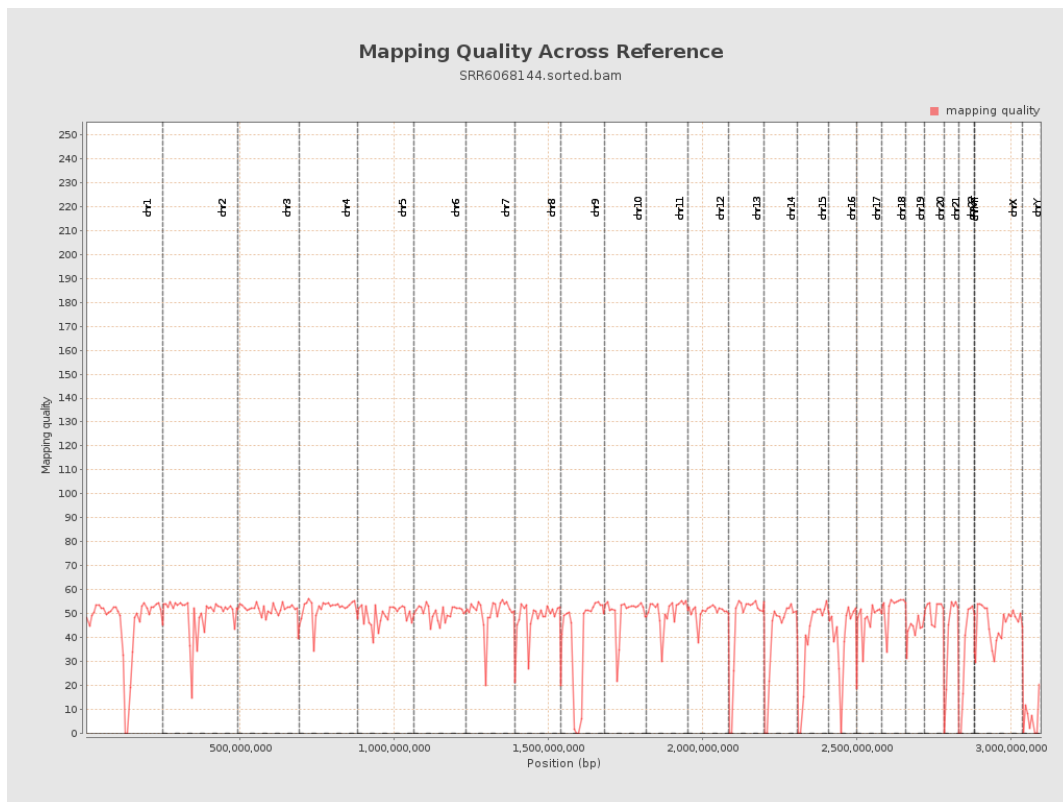
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

