

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 09:42:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068094.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_SRR6068094 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068094.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 09:42:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068094.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,826,840
Mapped reads	1,397,802 / 76.51%
Unmapped reads	429,038 / 23.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,160 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	247,744 / 13.56%
Duplication rate	12.97%
Clipped reads	818,266 / 44.79%

2.2. ACGT Content

Number/percentage of A's	24,065,181 / 27.14%
Number/percentage of C's	15,958,765 / 18%
Number/percentage of T's	28,640,844 / 32.3%
Number/percentage of G's	20,013,453 / 22.57%
Number/percentage of N's	1,759 / 0%
GC Percentage	40.56%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.3937
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2.4. Mapping Quality

Mean Mapping Quality	45.51
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2.5. Mismatches and indels

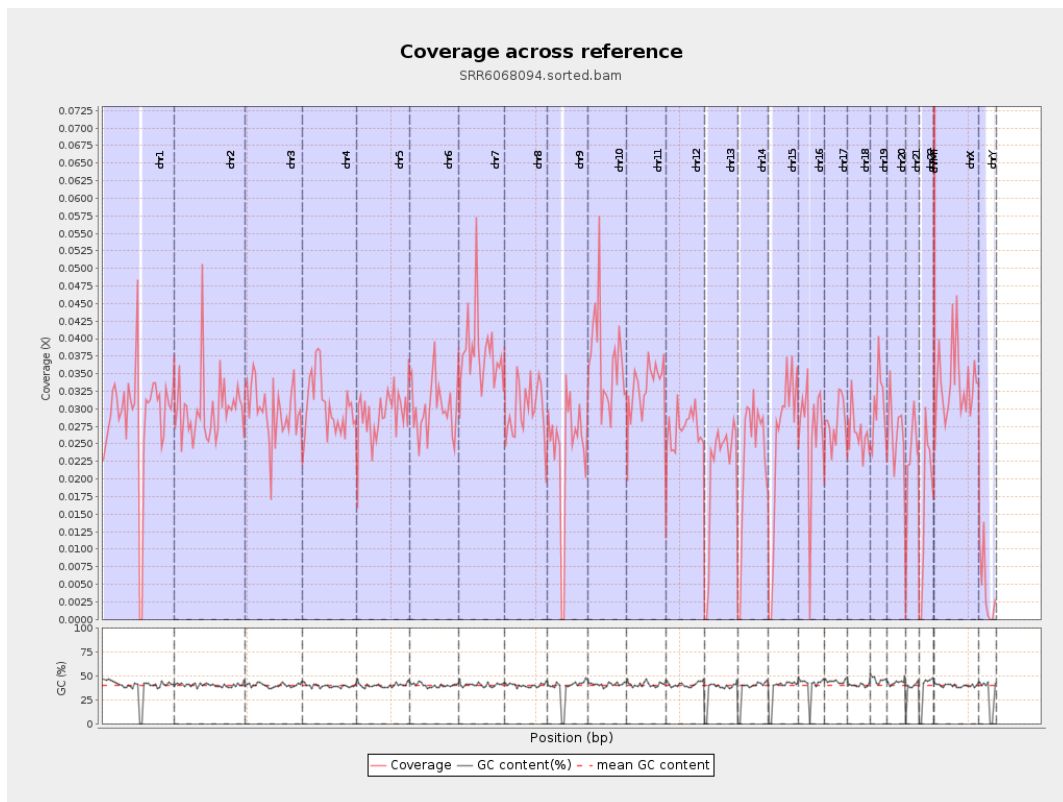
General error rate	0.79%
Mismatches	683,821
Insertions	7,056
Mapped reads with at least one insertion	0.5%
Deletions	21,661
Mapped reads with at least one deletion	1.53%
Homopolymer indels	46.39%

2.6. Chromosome stats

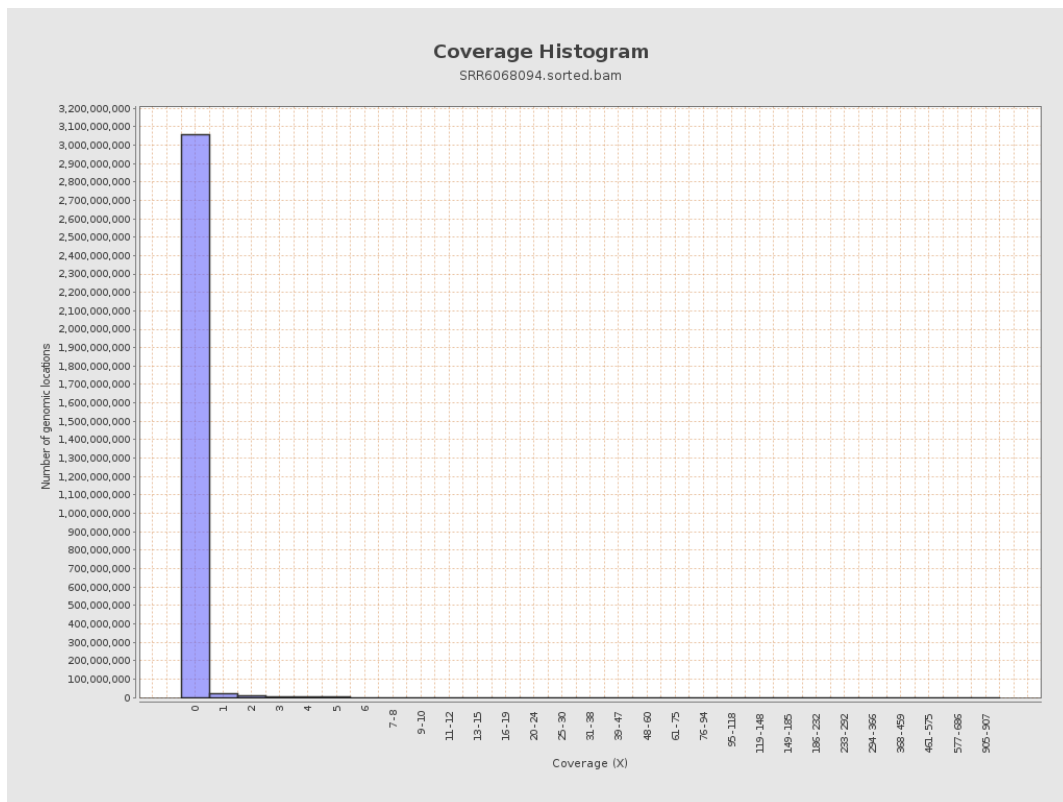
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7182626	0.0288	0.6008
chr2	243199373	7281506	0.0299	0.5194
chr3	198022430	5900722	0.0298	0.3247
chr4	191154276	5780802	0.0302	0.3554
chr5	180915260	5330615	0.0295	0.3209
chr6	171115067	5157082	0.0301	0.3419
chr7	159138663	6036129	0.0379	0.455

chr8	146364022	4351300	0.0297	0.4303
chr9	141213431	3409866	0.0241	0.3288
chr10	135534747	4989614	0.0368	0.4123
chr11	135006516	4479928	0.0332	0.365
chr12	133851895	3647592	0.0273	0.3088
chr13	115169878	2419185	0.021	0.2808
chr14	107349540	2444261	0.0228	0.2971
chr15	102531392	2586099	0.0252	0.3333
chr16	90354753	2395772	0.0265	0.3227
chr17	81195210	2277917	0.0281	0.3116
chr18	78077248	2068256	0.0265	0.4712
chr19	59128983	1793313	0.0303	0.4619
chr20	63025520	1673458	0.0266	0.3089
chr21	48129895	1095748	0.0228	0.2795
chr22	51304566	862681	0.0168	0.2312
chrMT	16571	69161	4.1736	4.1022
chrX	155270560	5232294	0.0337	0.3577
chrY	59373566	248782	0.0042	0.1457

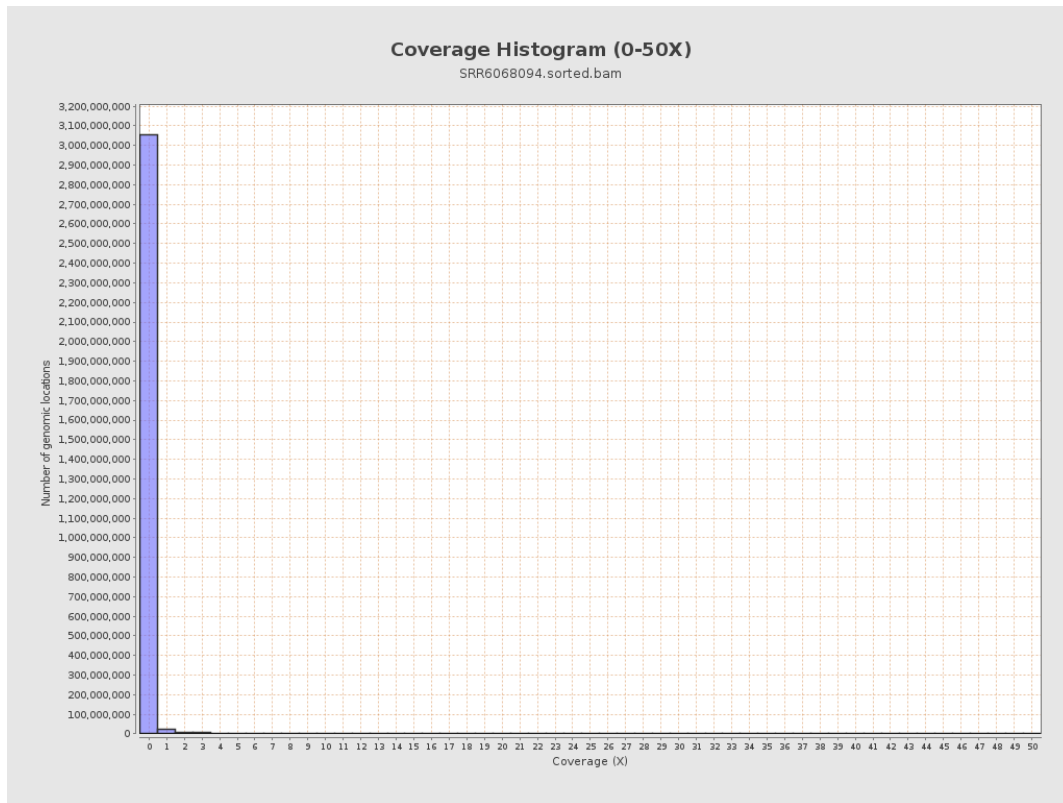
3. Results : Coverage across reference



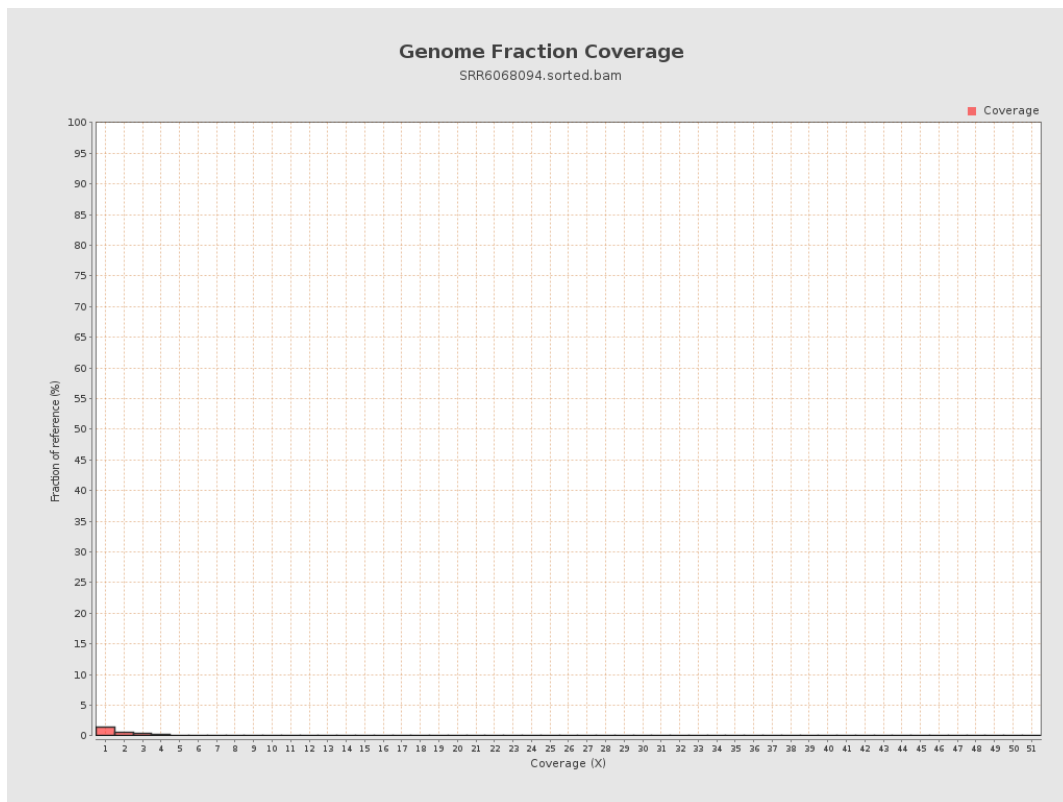
4. Results : Coverage Histogram



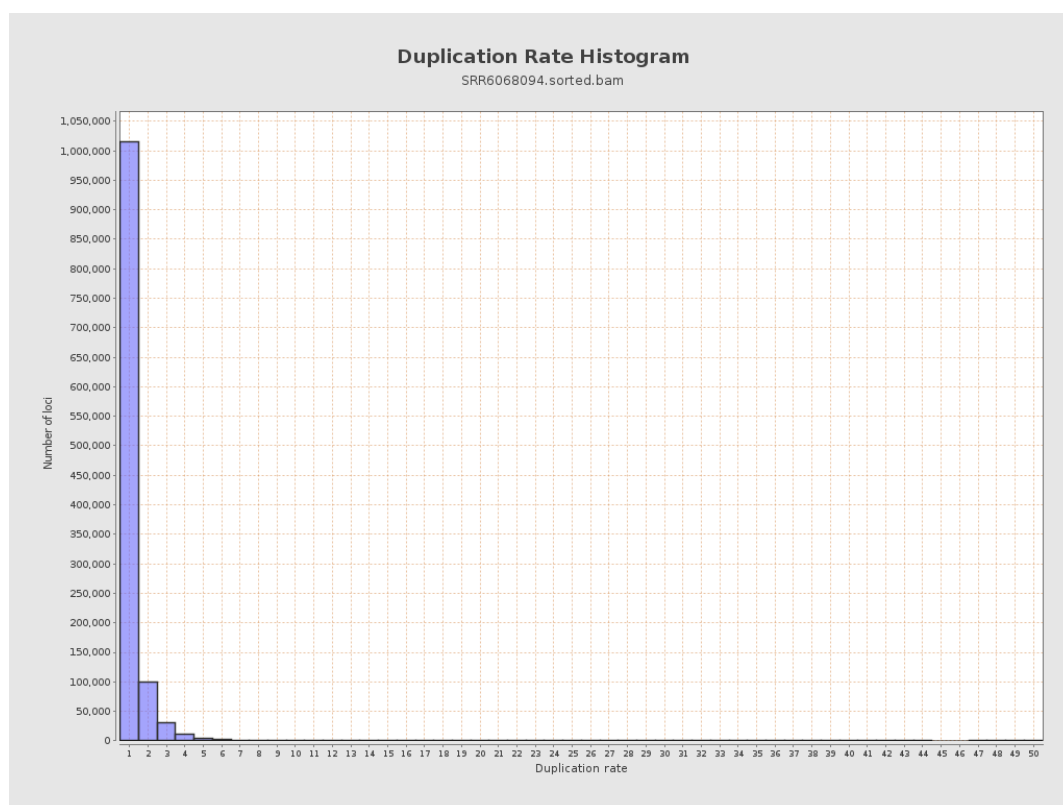
5. Results : Coverage Histogram (0-50X)



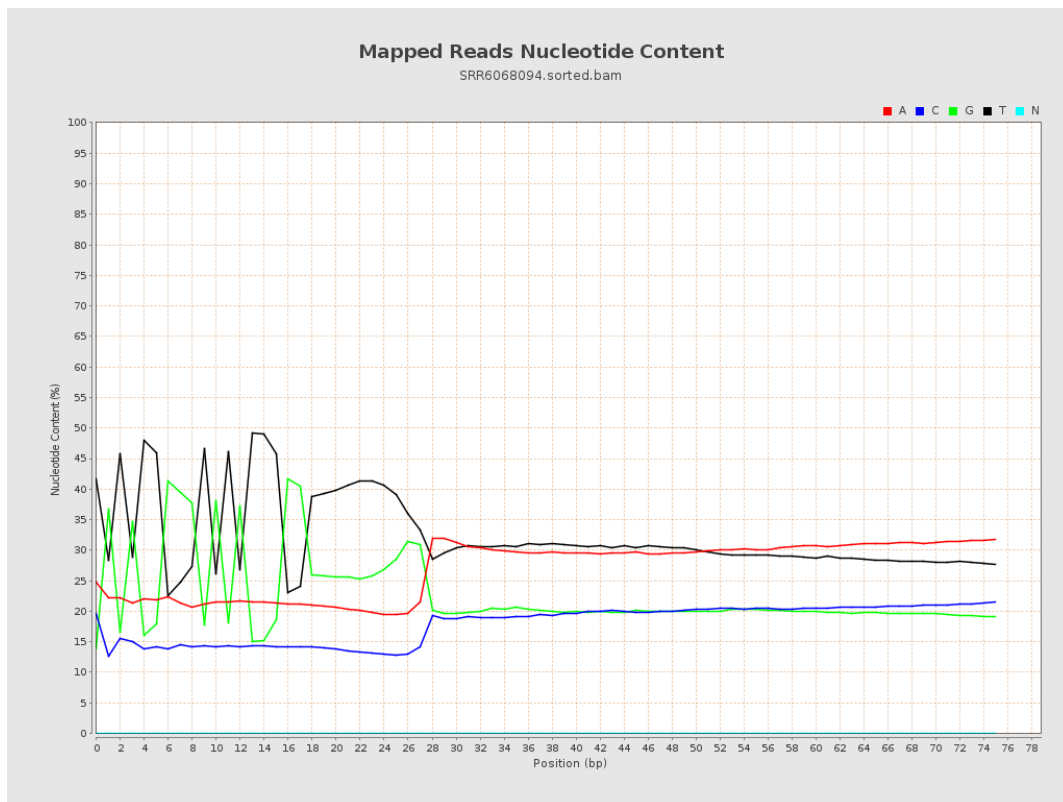
6. Results : Genome Fraction Coverage



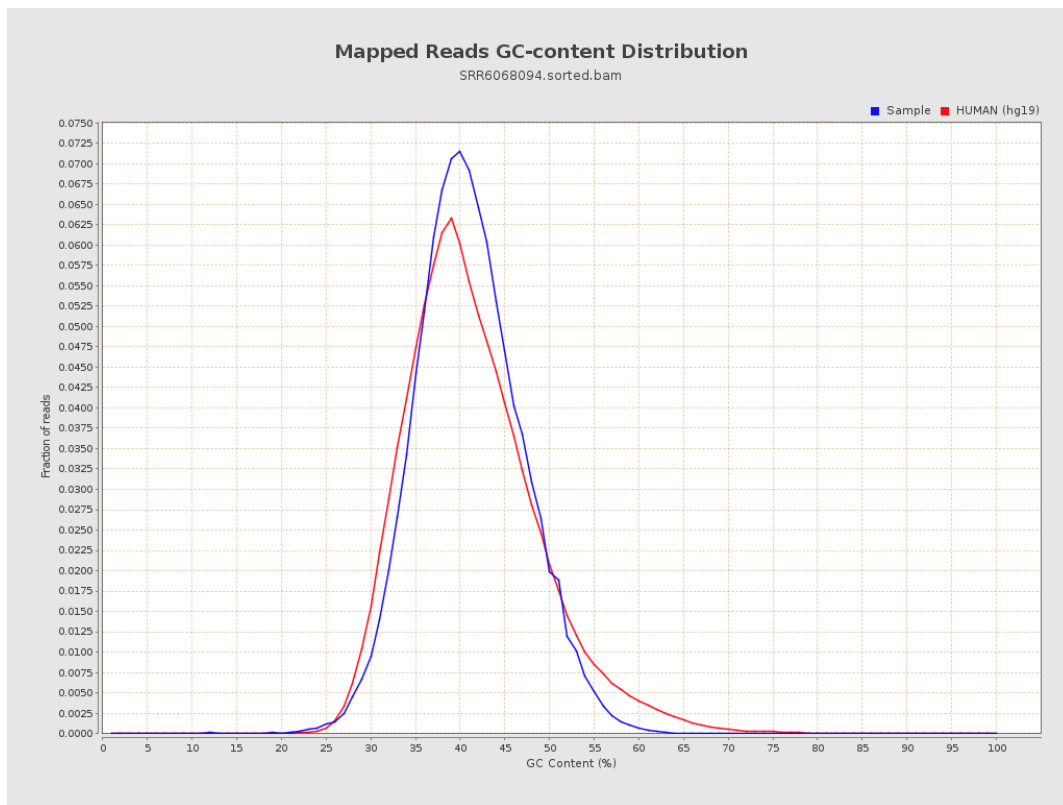
7. Results : Duplication Rate Histogram



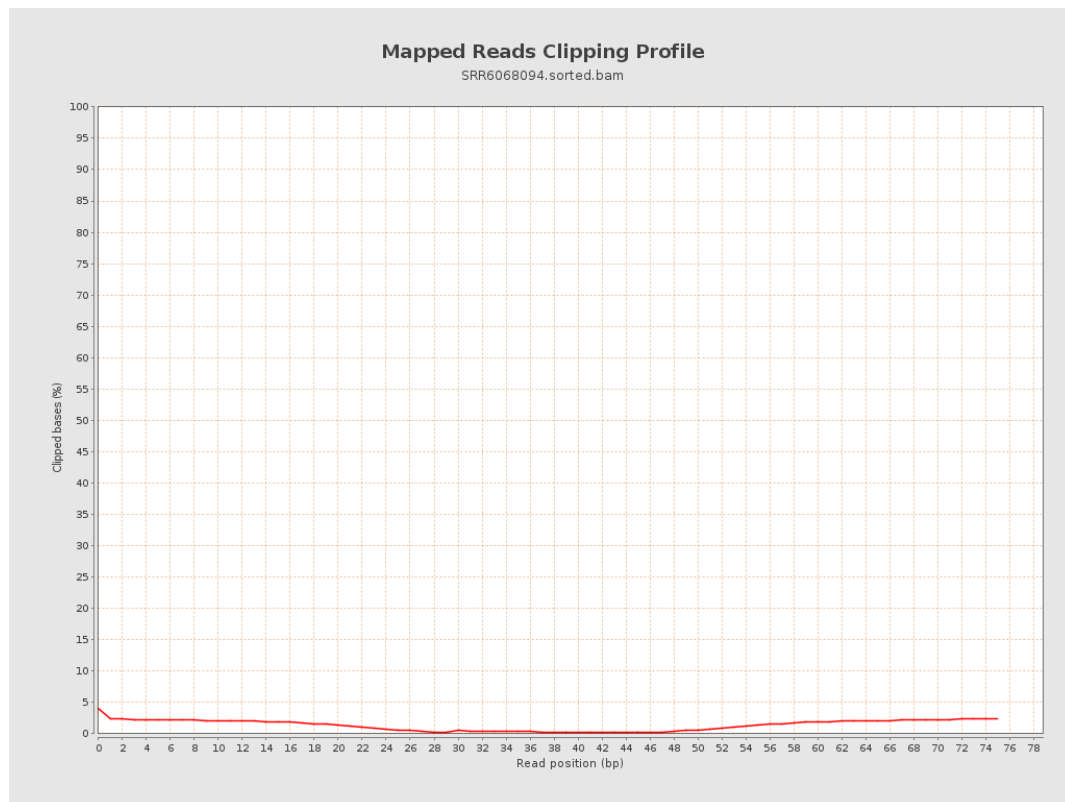
8. Results : Mapped Reads Nucleotide Content



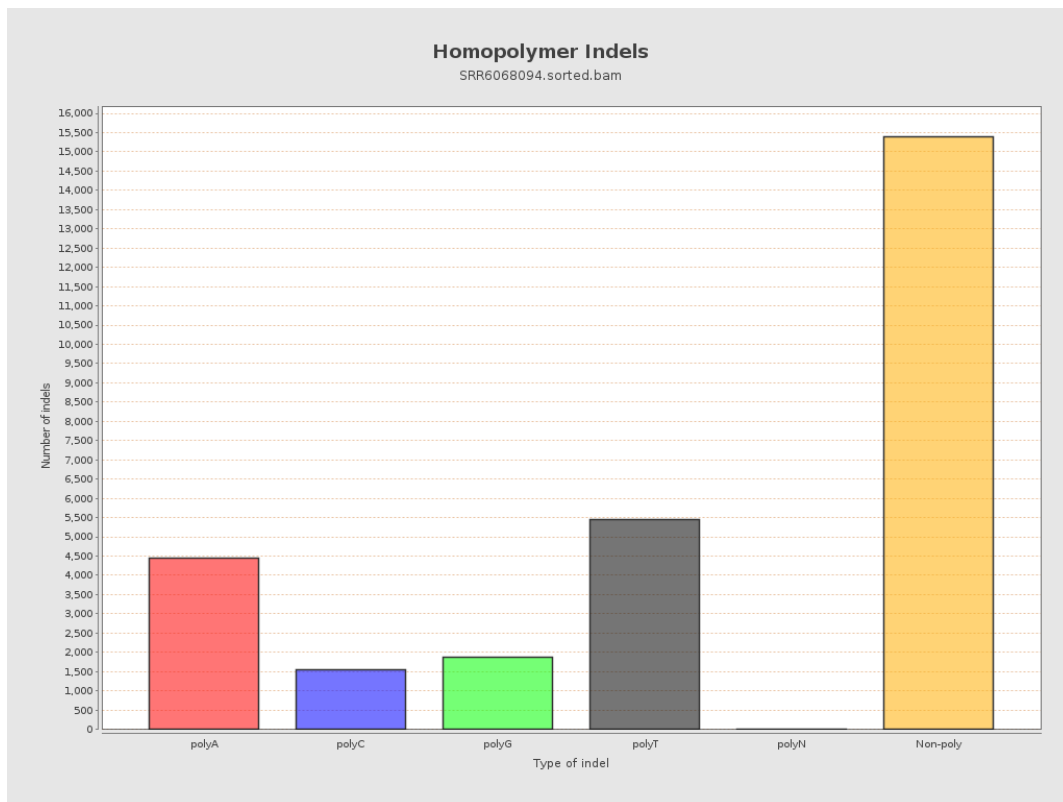
9. Results : Mapped Reads GC-content Distribution



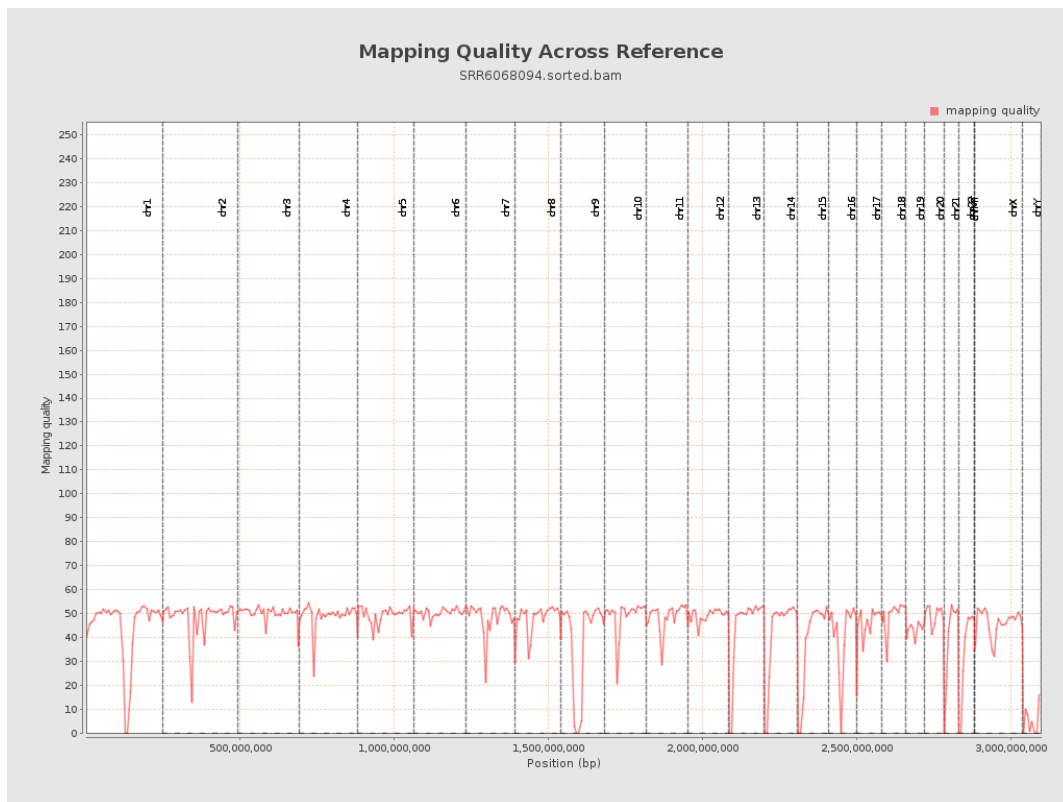
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

