

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:55:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008754.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_SRR6008754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:55:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,276,360
Mapped reads	1,634,103 / 19.74%
Unmapped reads	6,642,257 / 80.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,647 / 0.07%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	63,119 / 0.76%
Duplication rate	2.95%
Clipped reads	1,068,744 / 12.91%

2.2. ACGT Content

Number/percentage of A's	27,645,423 / 27.53%
Number/percentage of C's	18,475,579 / 18.4%
Number/percentage of T's	29,410,872 / 29.29%
Number/percentage of G's	24,844,730 / 24.74%
Number/percentage of N's	28,254 / 0.03%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.2548
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2.4. Mapping Quality

Mean Mapping Quality	44.41
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2.5. Mismatches and indels

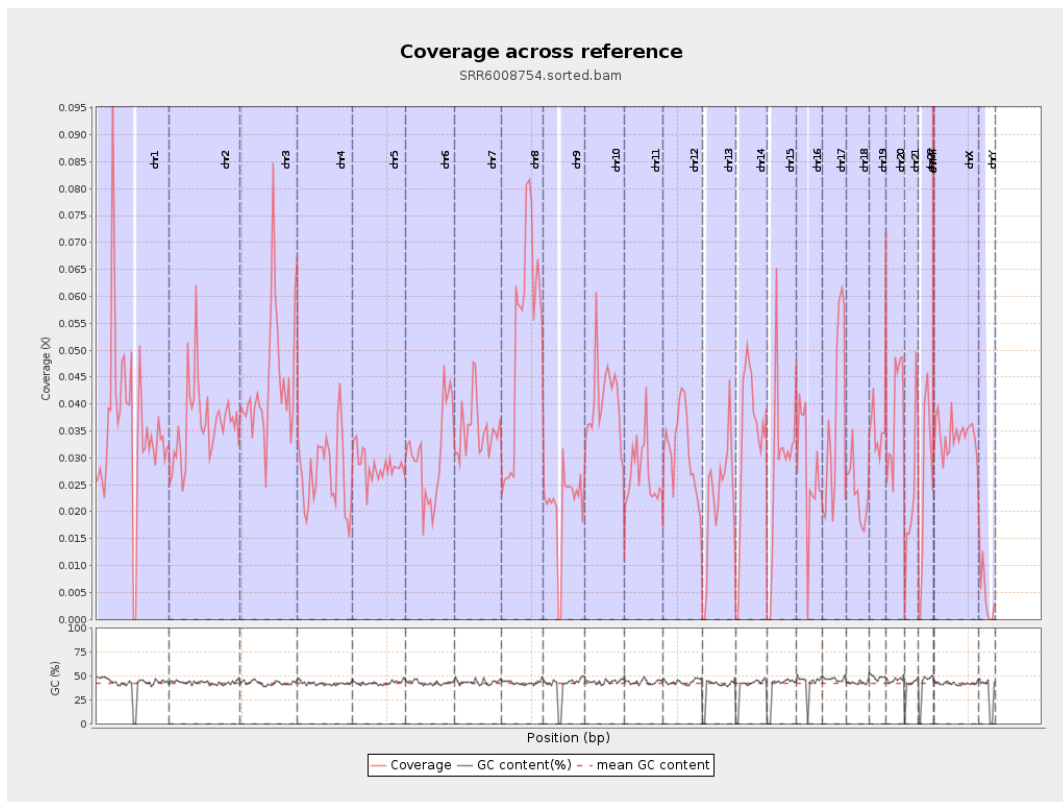
General error rate	1.03%
Mismatches	1,021,121
Insertions	7,331
Mapped reads with at least one insertion	0.44%
Deletions	31,718
Mapped reads with at least one deletion	1.92%
Homopolymer indels	46.51%

2.6. Chromosome stats

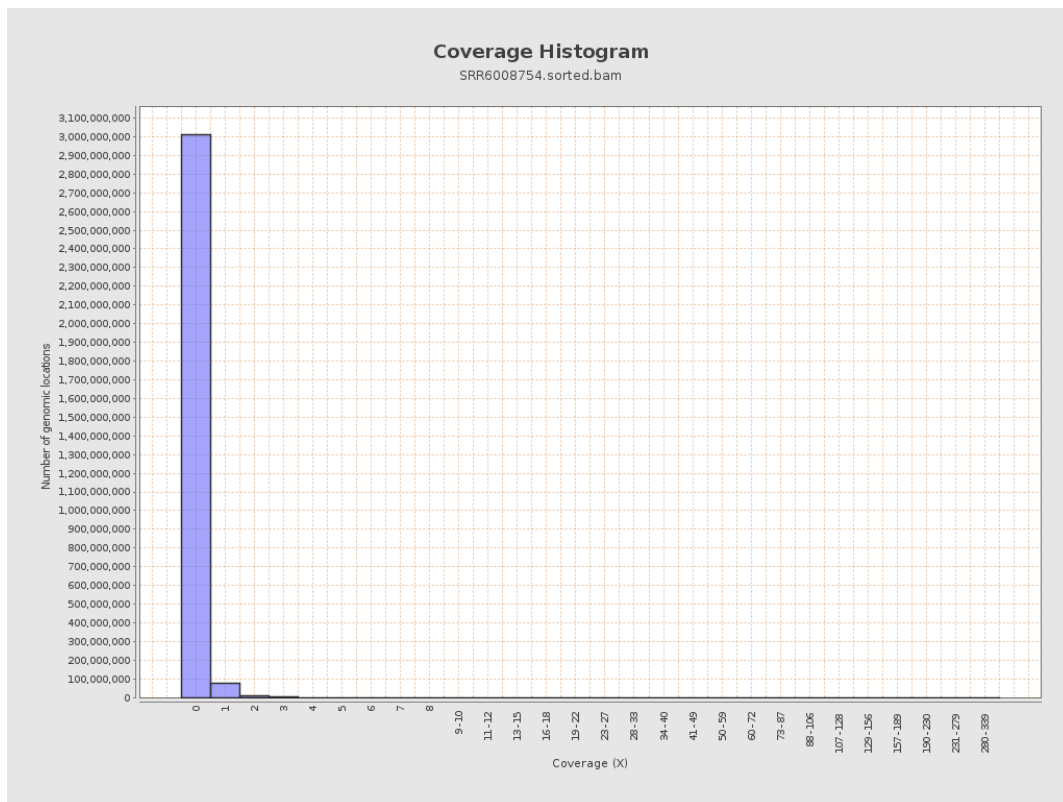
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8788266	0.0353	0.3662
chr2	243199373	8867223	0.0365	0.3115
chr3	198022430	8700286	0.0439	0.2435
chr4	191154276	5136387	0.0269	0.1928
chr5	180915260	5154157	0.0285	0.1931
chr6	171115067	5203230	0.0304	0.2164
chr7	159138663	5631645	0.0354	0.3104

chr8	146364022	7641958	0.0522	0.2995
chr9	141213431	2955600	0.0209	0.2119
chr10	135534747	5514467	0.0407	0.31
chr11	135006516	3648464	0.027	0.2286
chr12	133851895	4187624	0.0313	0.2041
chr13	115169878	2556804	0.0222	0.1747
chr14	107349540	3609251	0.0336	0.2113
chr15	102531392	2926590	0.0285	0.2035
chr16	90354753	2511594	0.0278	0.2155
chr17	81195210	3025753	0.0373	0.2442
chr18	78077248	1824087	0.0234	0.3264
chr19	59128983	2131340	0.036	0.2782
chr20	63025520	2398070	0.038	0.2261
chr21	48129895	1127804	0.0234	0.1862
chr22	51304566	1306437	0.0255	0.185
chrMT	16571	42051	2.5376	2.5634
chrX	155270560	5302536	0.0342	0.2246
chrY	59373566	262741	0.0044	0.0999

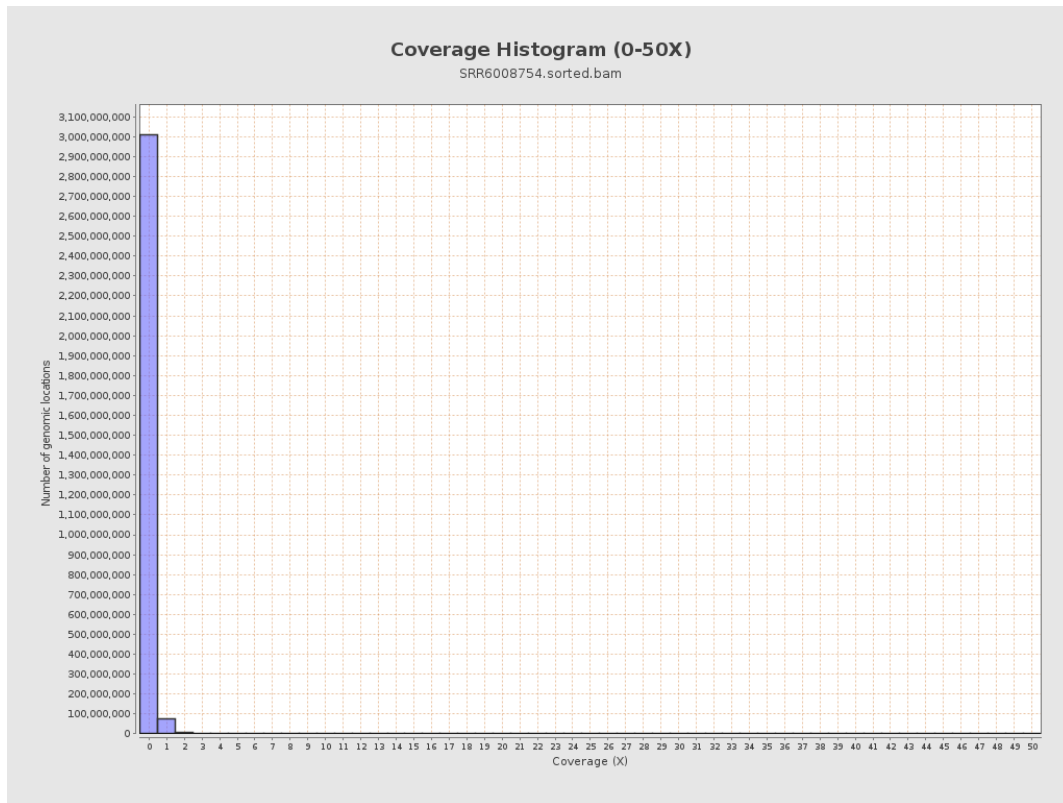
3. Results : Coverage across reference



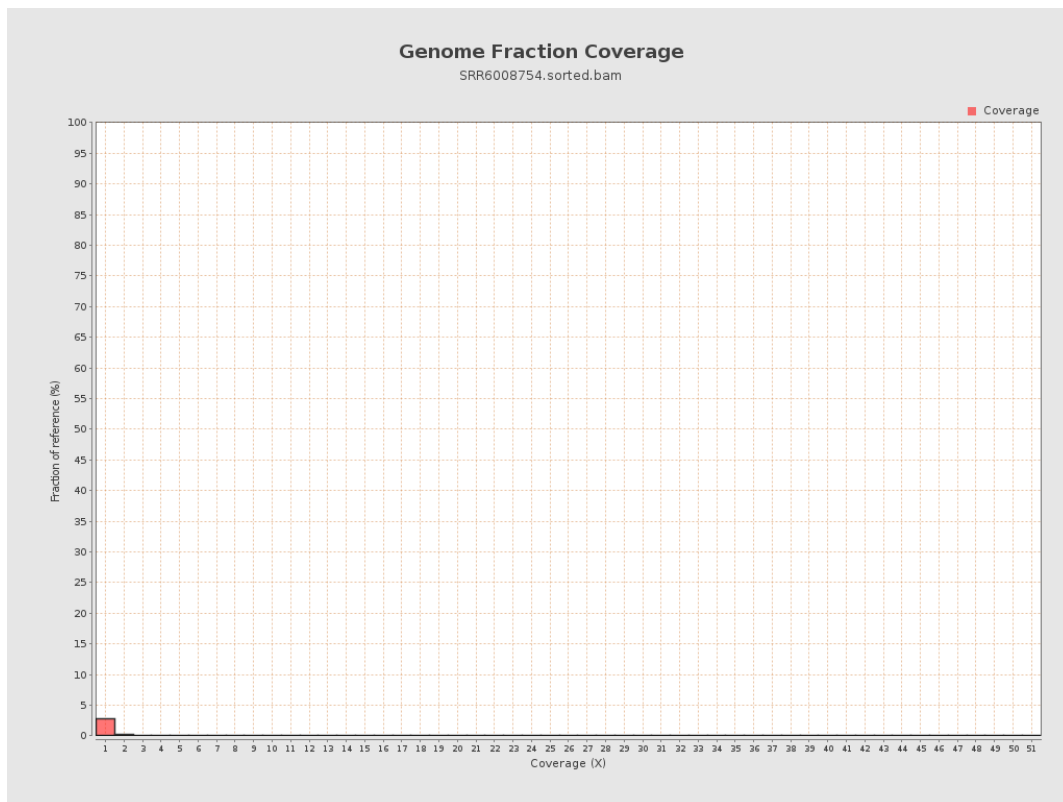
4. Results : Coverage Histogram



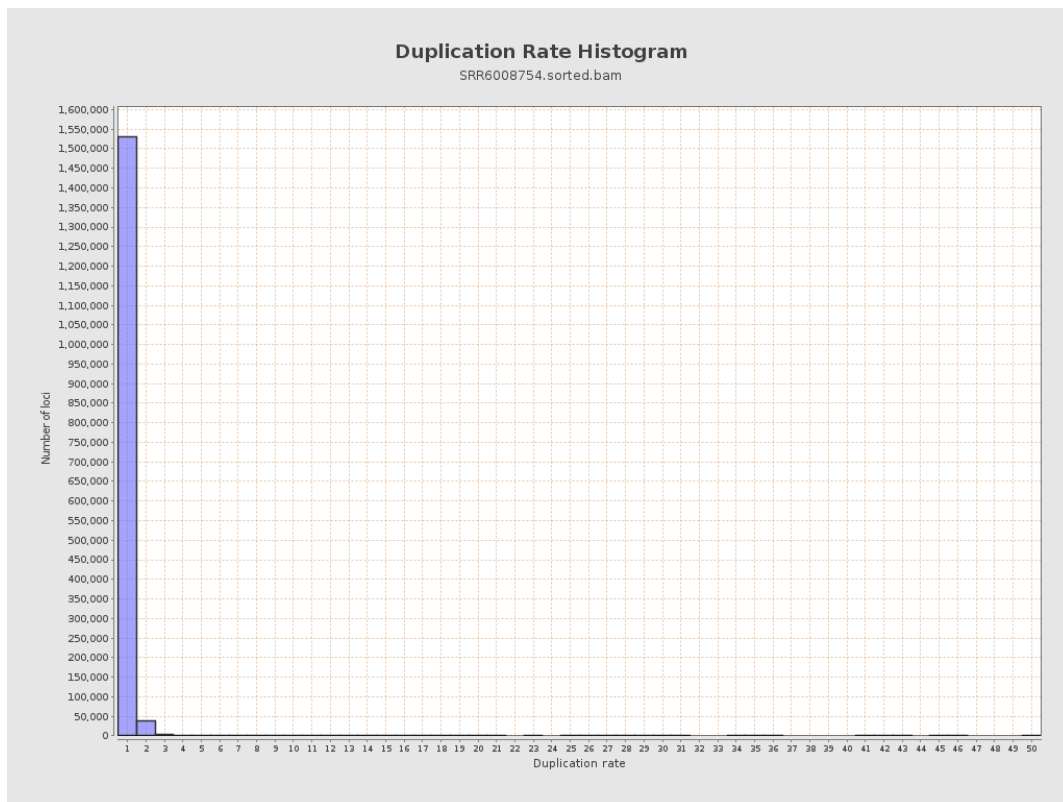
5. Results : Coverage Histogram (0-50X)



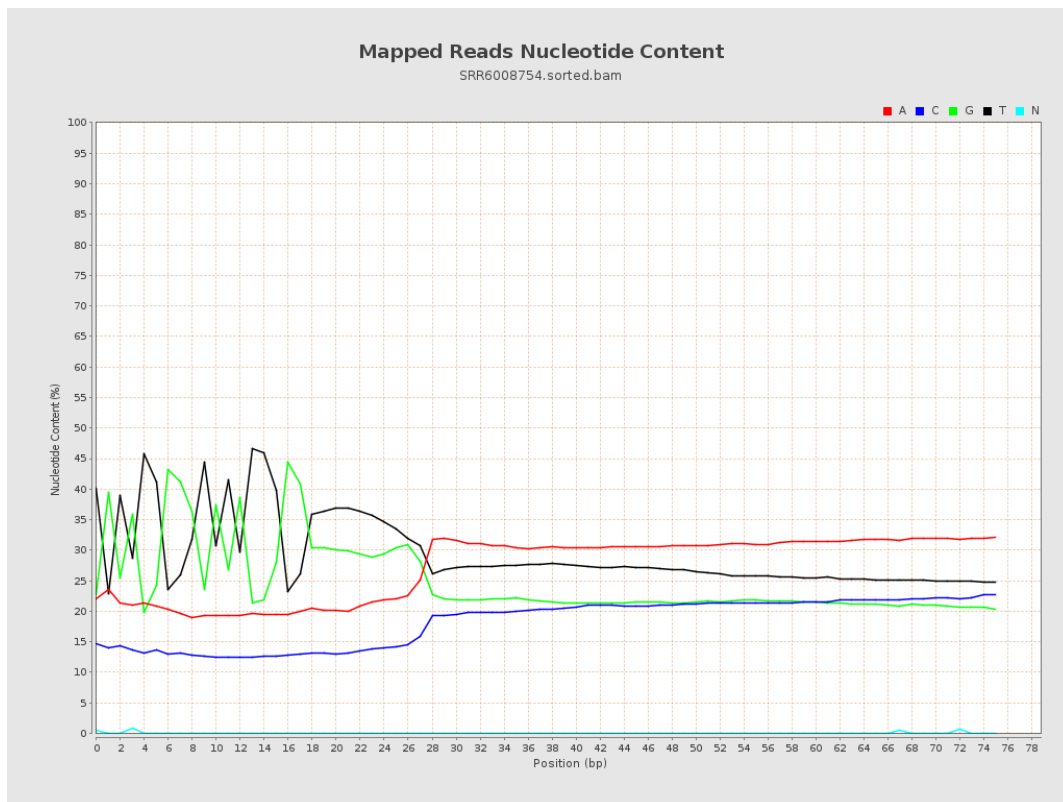
6. Results : Genome Fraction Coverage



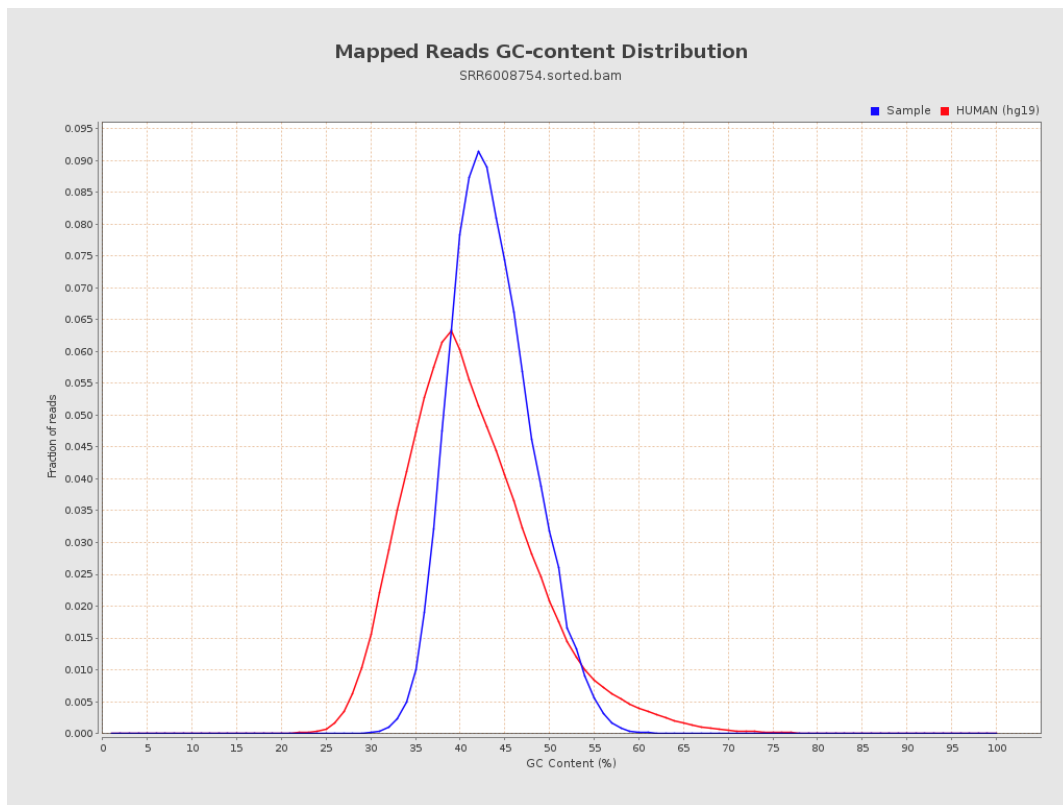
7. Results : Duplication Rate Histogram



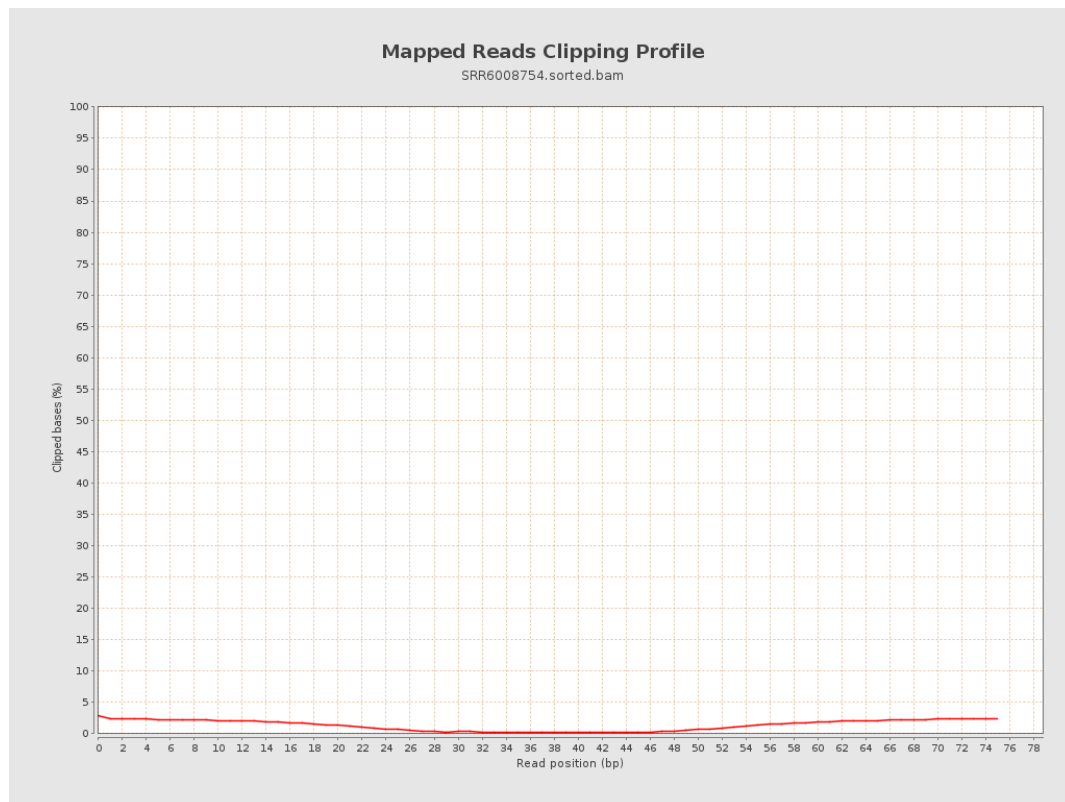
8. Results : Mapped Reads Nucleotide Content



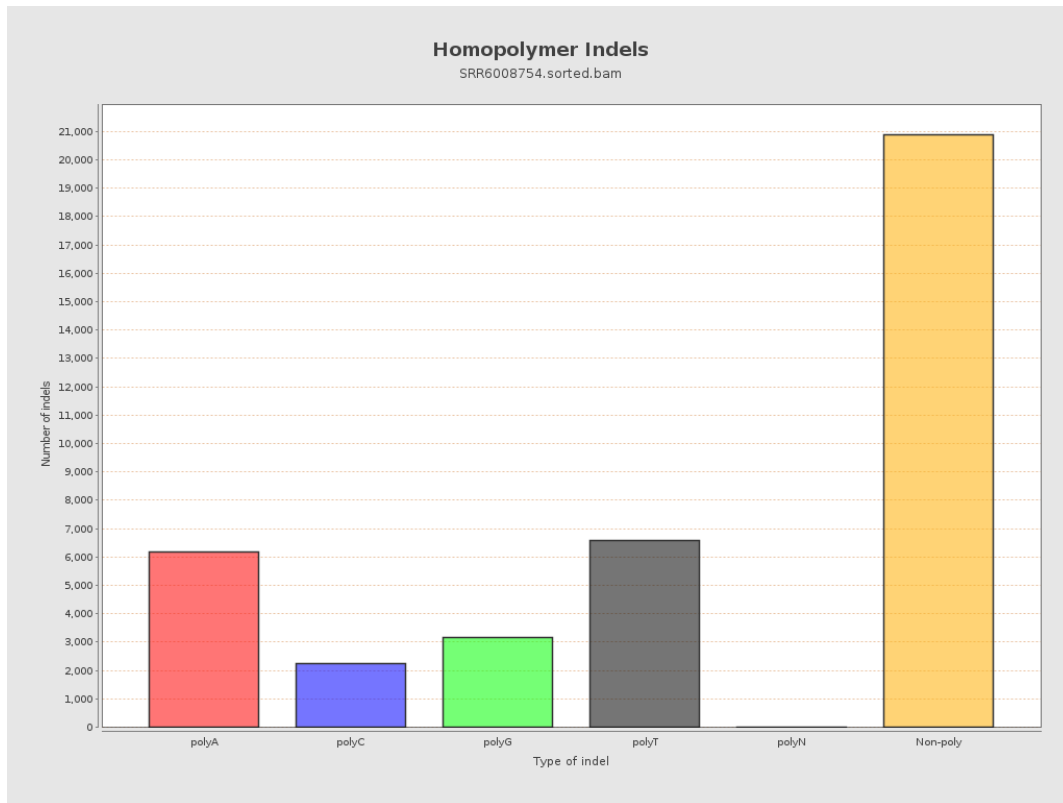
9. Results : Mapped Reads GC-content Distribution



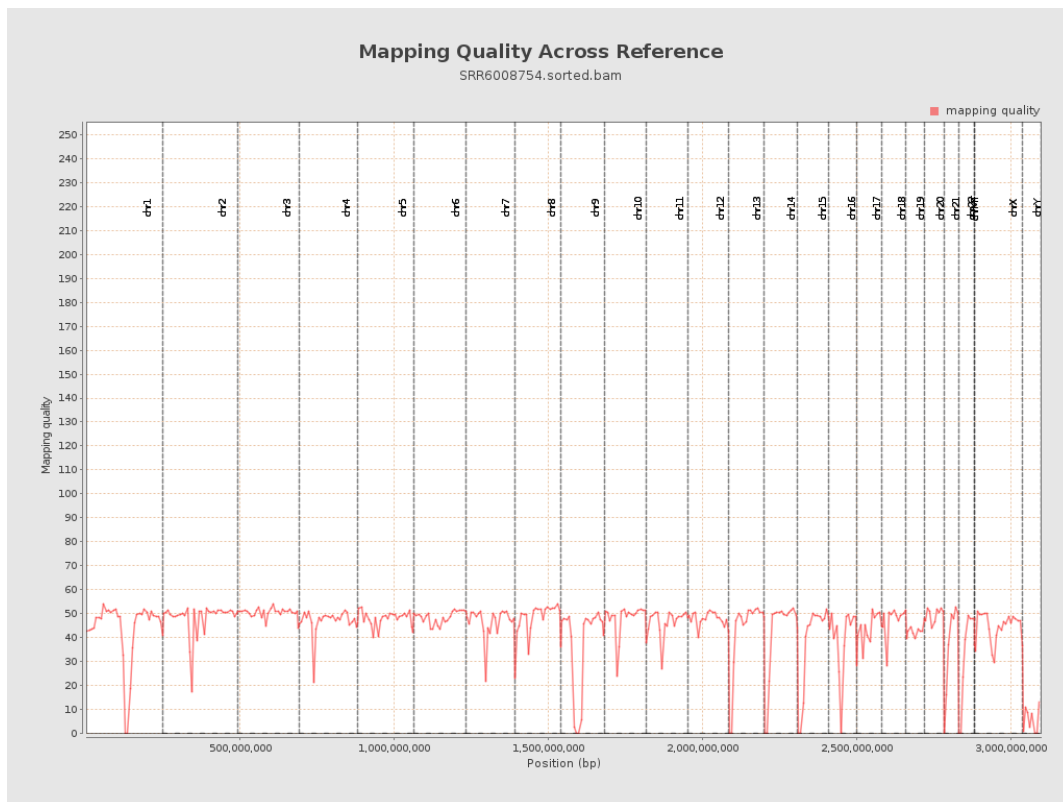
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

