

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:34:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004083.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_SRR6004083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004083.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:34:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,004,468
Mapped reads	2,774,175 / 92.33%
Unmapped reads	230,293 / 7.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,836 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	131,725 / 4.38%
Duplication rate	3.76%
Clipped reads	1,143,465 / 38.06%

2.2. ACGT Content

Number/percentage of A's	52,072,338 / 27.92%
Number/percentage of C's	34,205,552 / 18.34%
Number/percentage of T's	59,027,631 / 31.65%
Number/percentage of G's	41,123,668 / 22.05%
Number/percentage of N's	83,407 / 0.04%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0603

Standard Deviation	0.4625
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2.4. Mapping Quality

Mean Mapping Quality	46.3
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2.5. Mismatches and indels

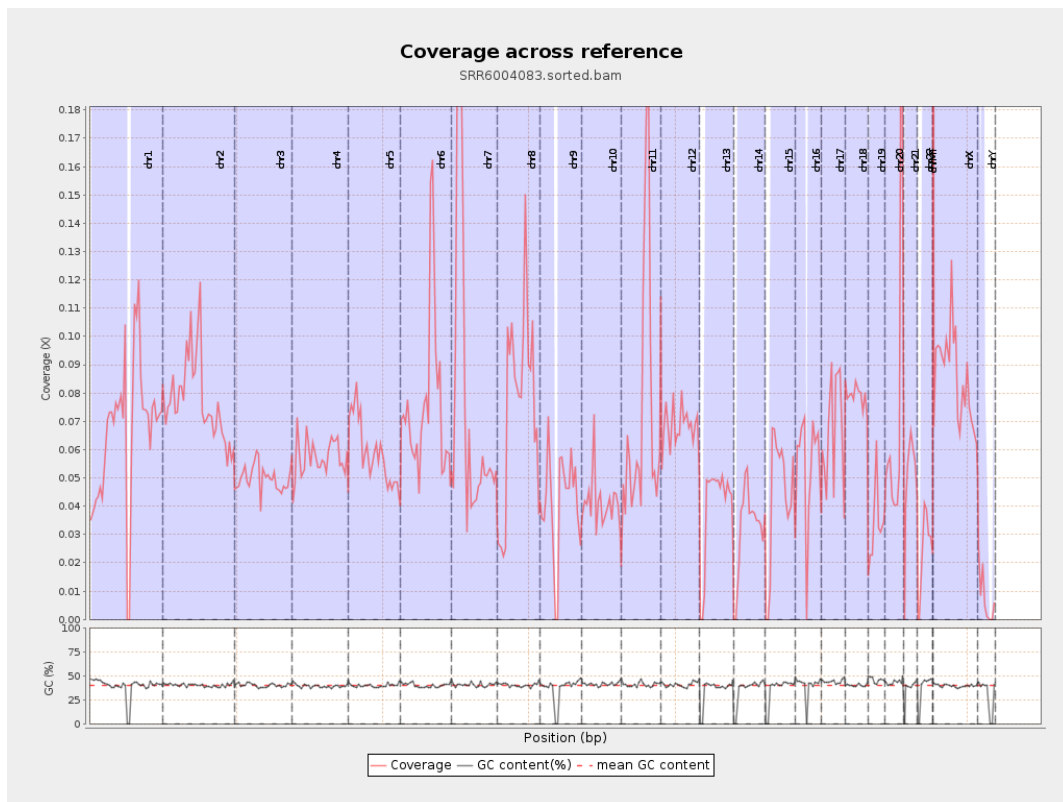
General error rate	0.75%
Mismatches	1,379,361
Insertions	12,906
Mapped reads with at least one insertion	0.46%
Deletions	45,575
Mapped reads with at least one deletion	1.63%
Homopolymer indels	47.41%

2.6. Chromosome stats

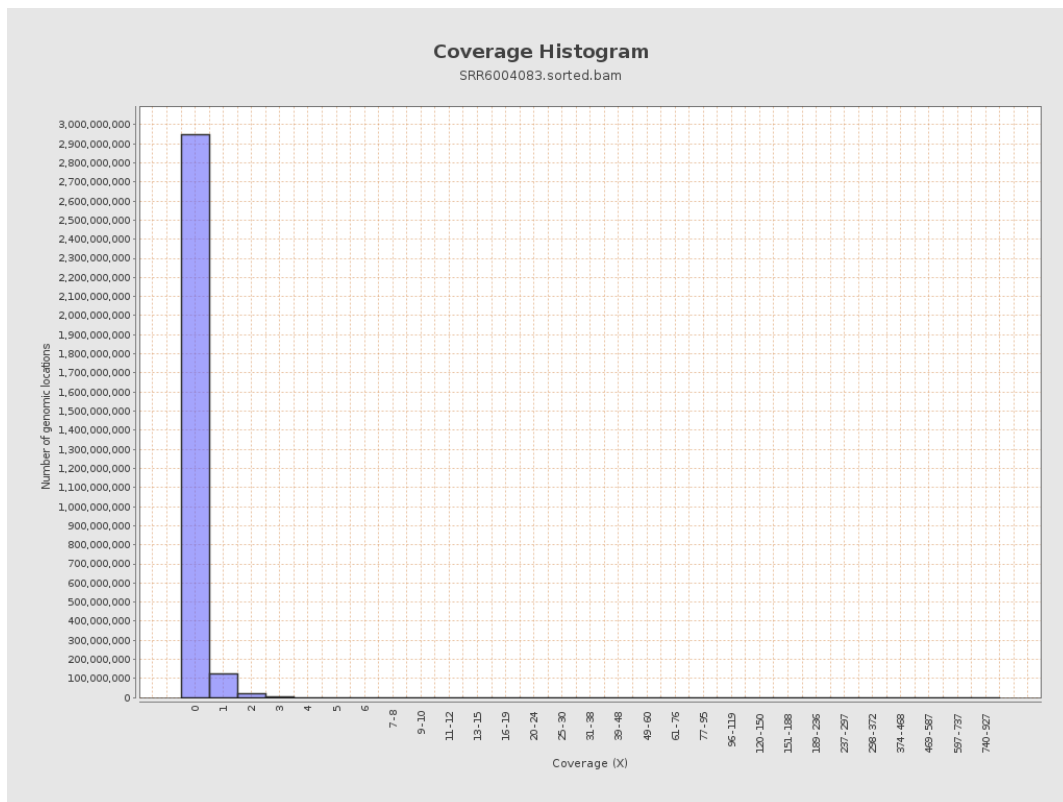
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16579918	0.0665	0.8451
chr2	243199373	18753747	0.0771	0.6008
chr3	198022430	9884029	0.0499	0.2614
chr4	191154276	11009971	0.0576	0.3035
chr5	180915260	10609888	0.0586	0.2879
chr6	171115067	12935122	0.0756	0.3815
chr7	159138663	11889214	0.0747	0.5194

chr8	146364022	11031495	0.0754	0.6258
chr9	141213431	5916239	0.0419	0.4033
chr10	135534747	5597794	0.0413	0.3855
chr11	135006516	9736946	0.0721	0.4787
chr12	133851895	9105224	0.068	0.3148
chr13	115169878	4566262	0.0396	0.2346
chr14	107349540	3506901	0.0327	0.2303
chr15	102531392	4422746	0.0431	0.2556
chr16	90354753	4779333	0.0529	0.287
chr17	81195210	5449150	0.0671	0.3415
chr18	78077248	6171064	0.079	0.7209
chr19	59128983	2044759	0.0346	0.5898
chr20	63025520	5235847	0.0831	0.3738
chr21	48129895	2364524	0.0491	0.2853
chr22	51304566	1245409	0.0243	0.1783
chrMT	16571	24429	1.4742	1.6637
chrX	155270560	13291285	0.0856	0.3959
chrY	59373566	440438	0.0074	0.1534

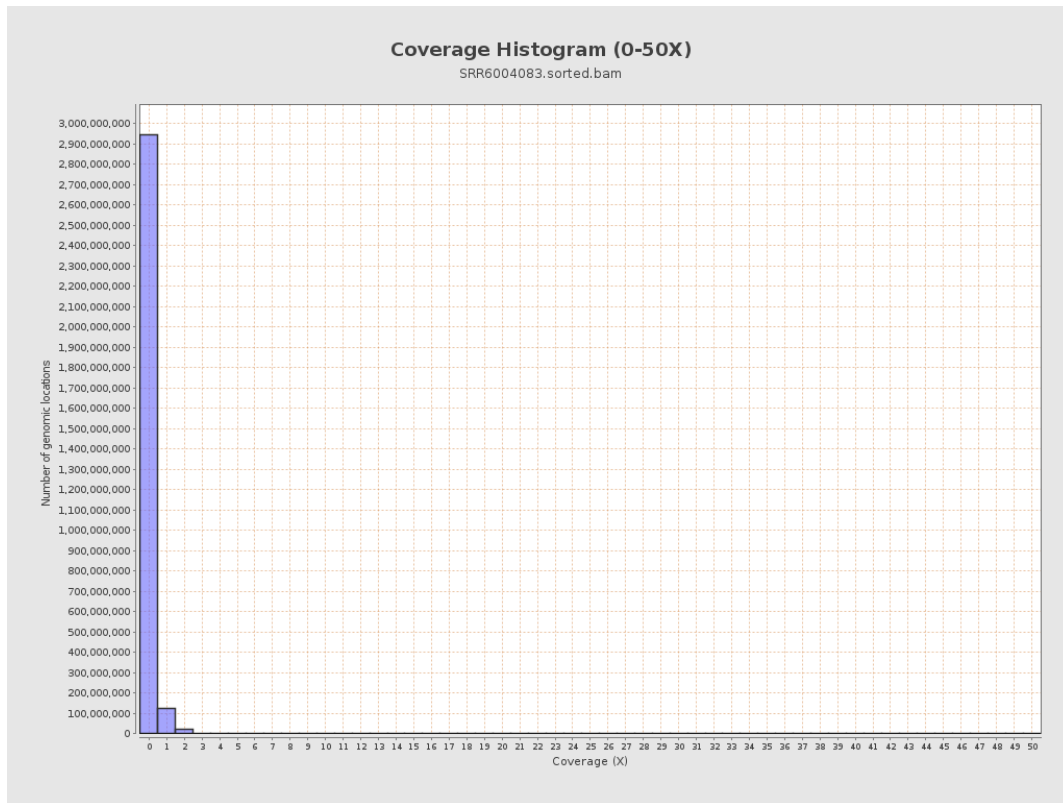
3. Results : Coverage across reference



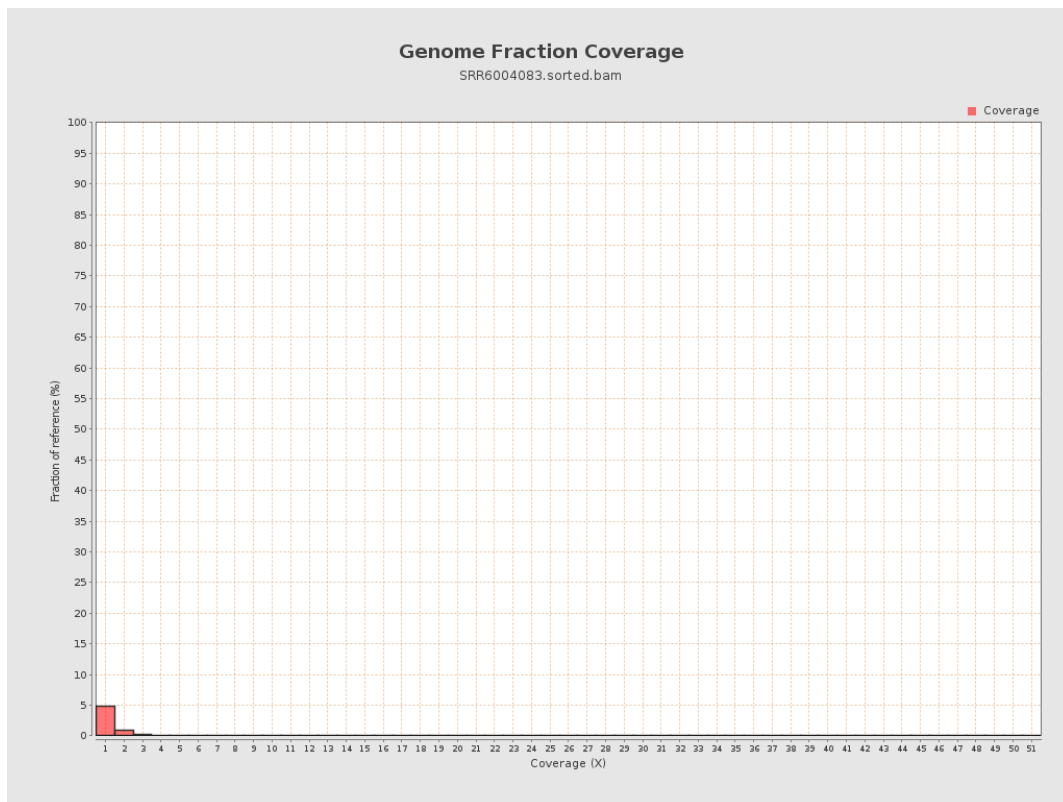
4. Results : Coverage Histogram



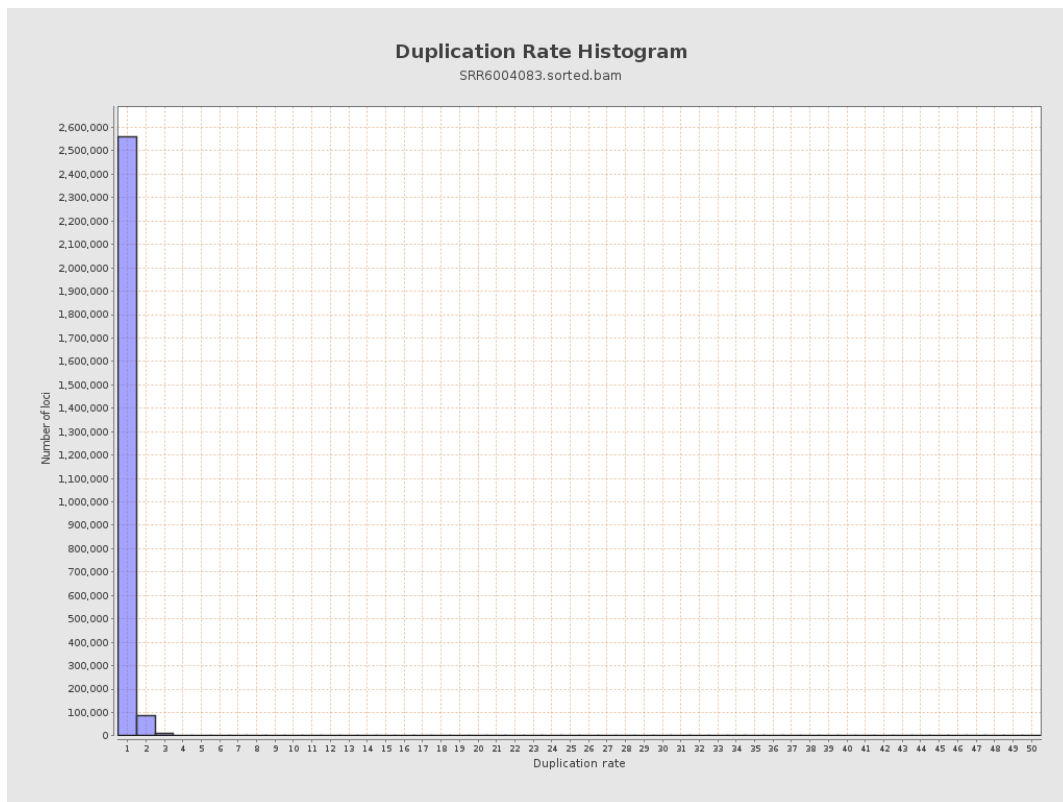
5. Results : Coverage Histogram (0-50X)



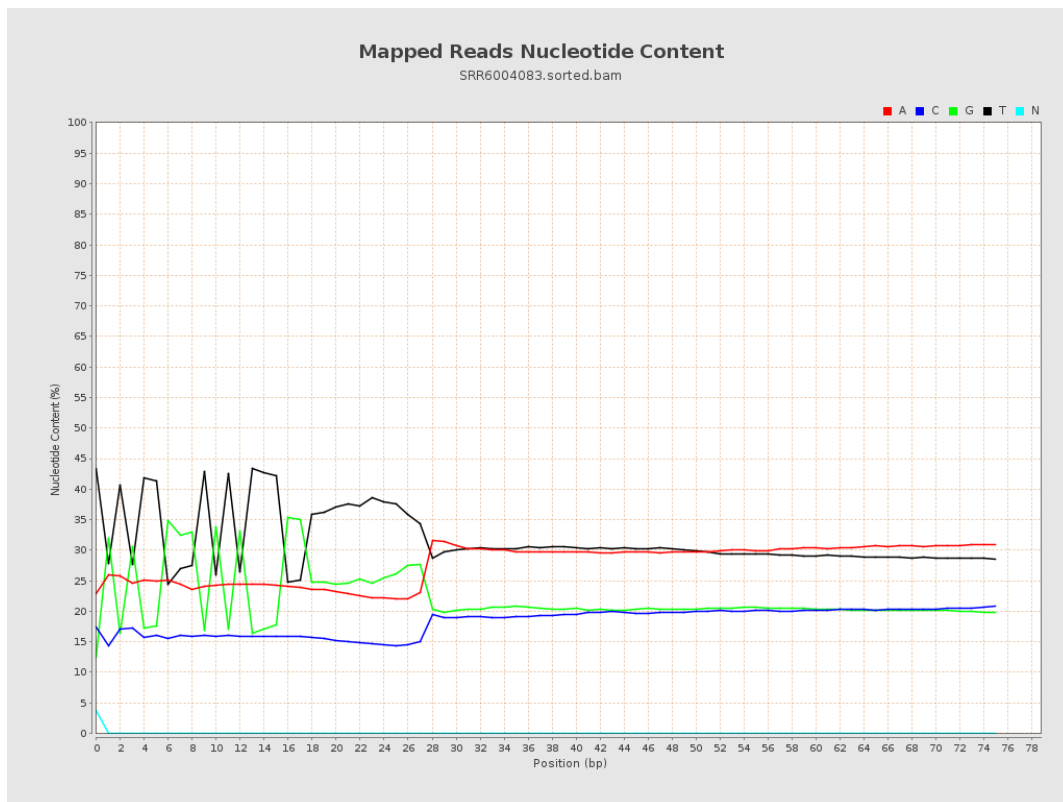
6. Results : Genome Fraction Coverage



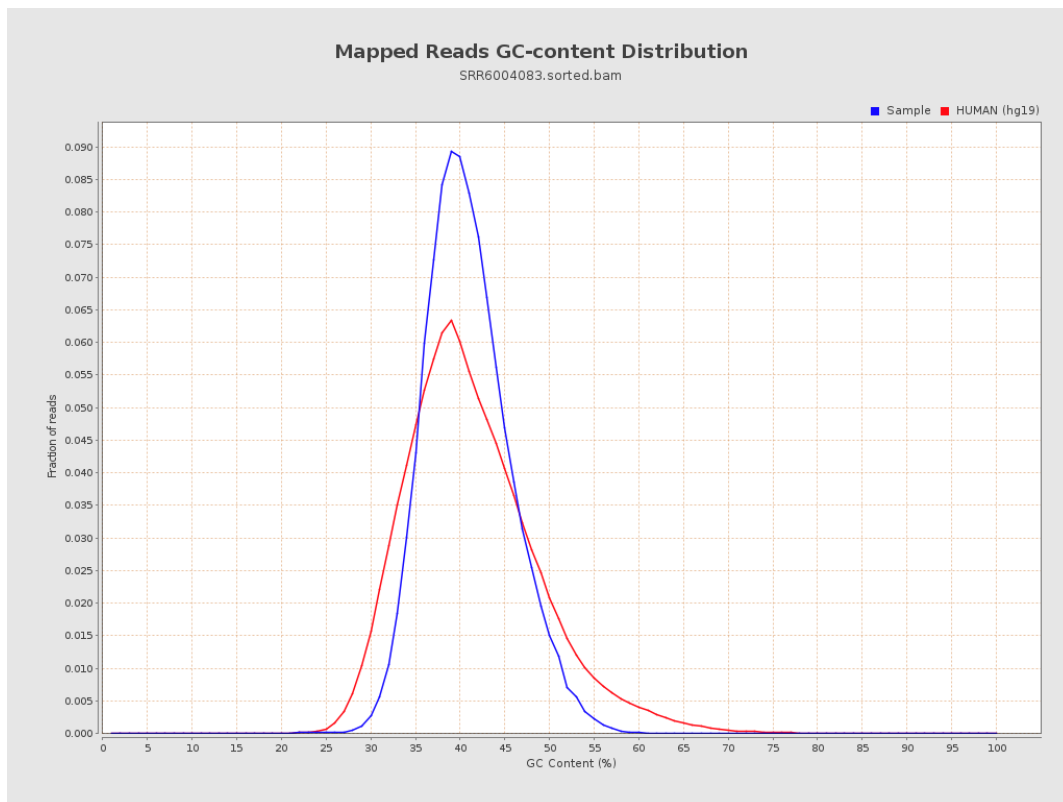
7. Results : Duplication Rate Histogram



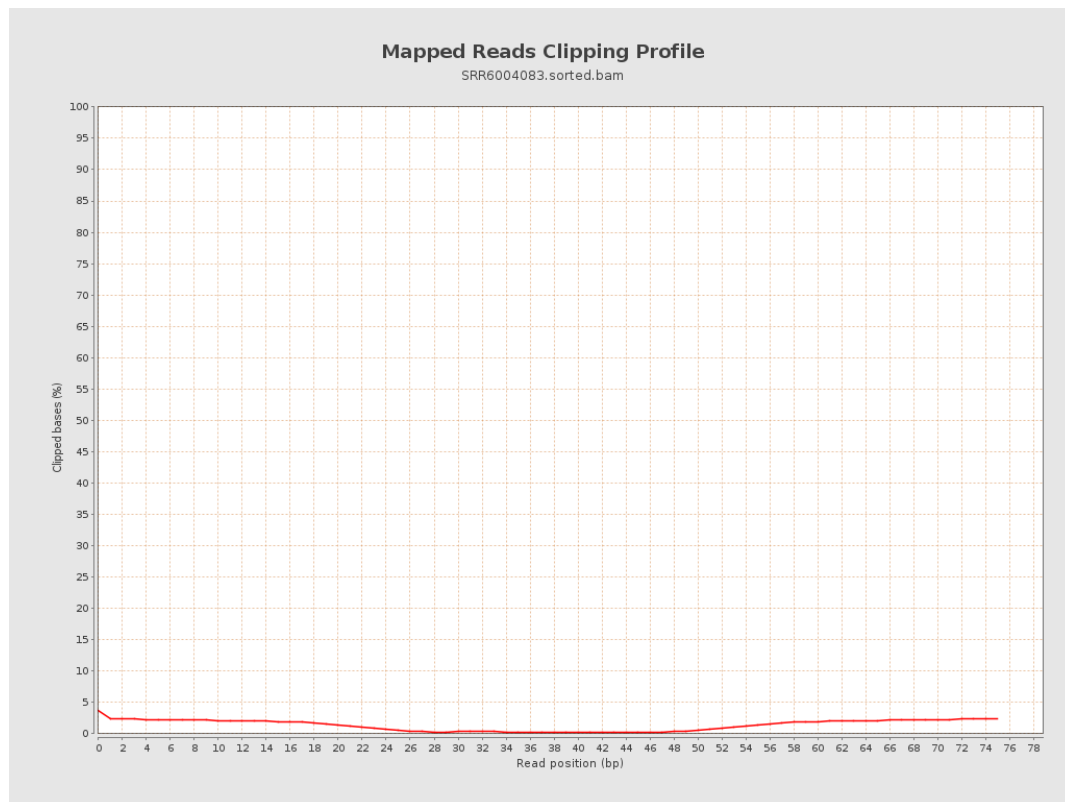
8. Results : Mapped Reads Nucleotide Content



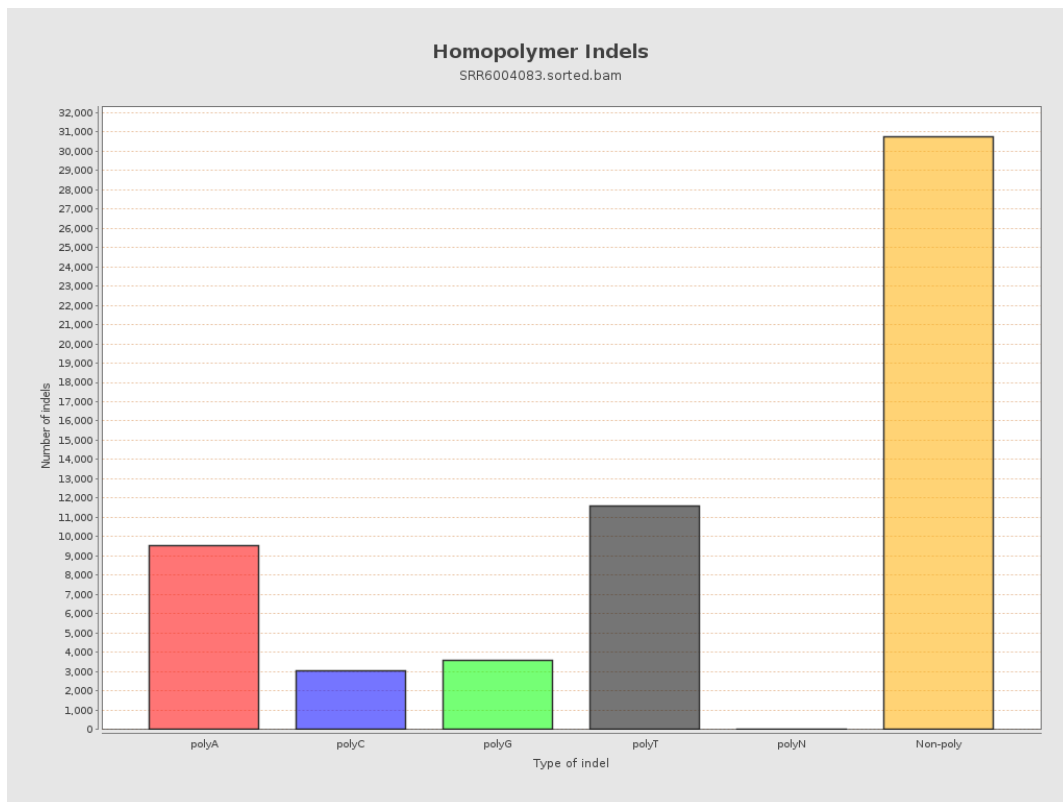
9. Results : Mapped Reads GC-content Distribution



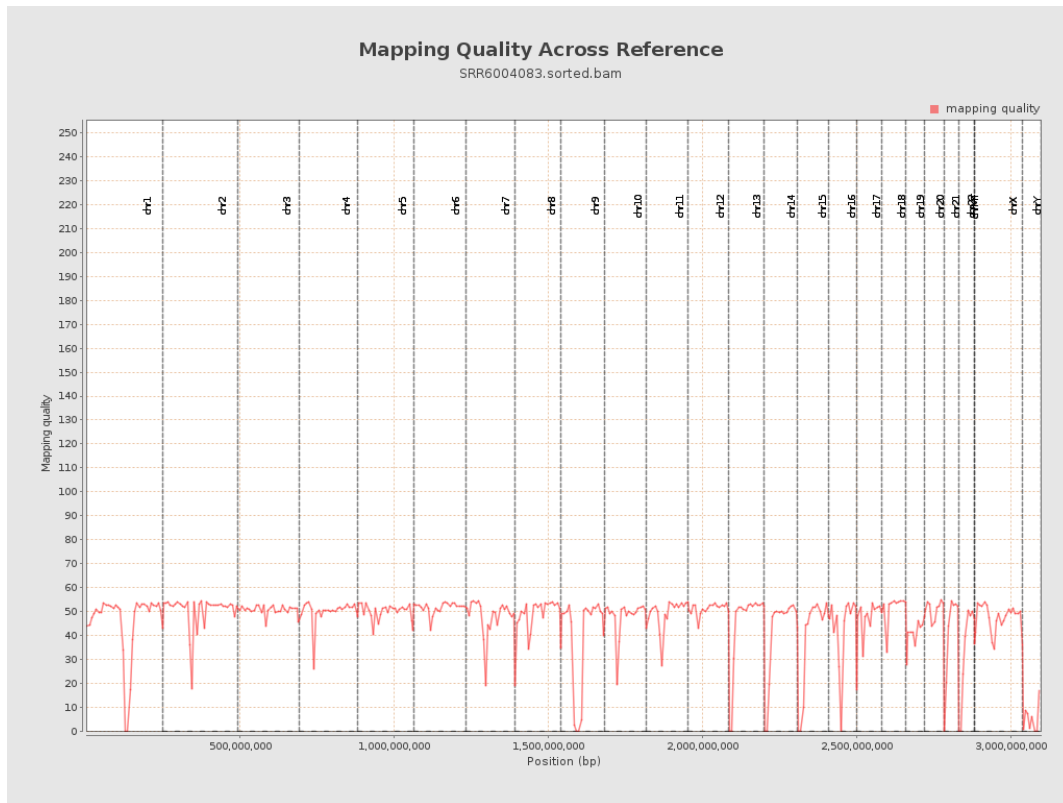
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

