

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:45:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549012.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_SRR1549012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549012.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:45:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,042,107
Mapped reads	5,185,698 / 85.83%
Unmapped reads	856,409 / 14.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	423,563 / 7.01%
Duplication rate	7.04%
Clipped reads	495,086 / 8.19%

2.2. ACGT Content

Number/percentage of A's	62,001,836 / 30.28%
Number/percentage of C's	40,093,830 / 19.58%
Number/percentage of T's	62,527,623 / 30.53%
Number/percentage of G's	40,150,237 / 19.61%
Number/percentage of N's	7,455 / 0%
GC Percentage	39.19%

2.3. Coverage

Mean	0.0662
Standard Deviation	1.0748

2.4. Mapping Quality

Mean Mapping Quality	43.48
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2.5. Mismatches and indels

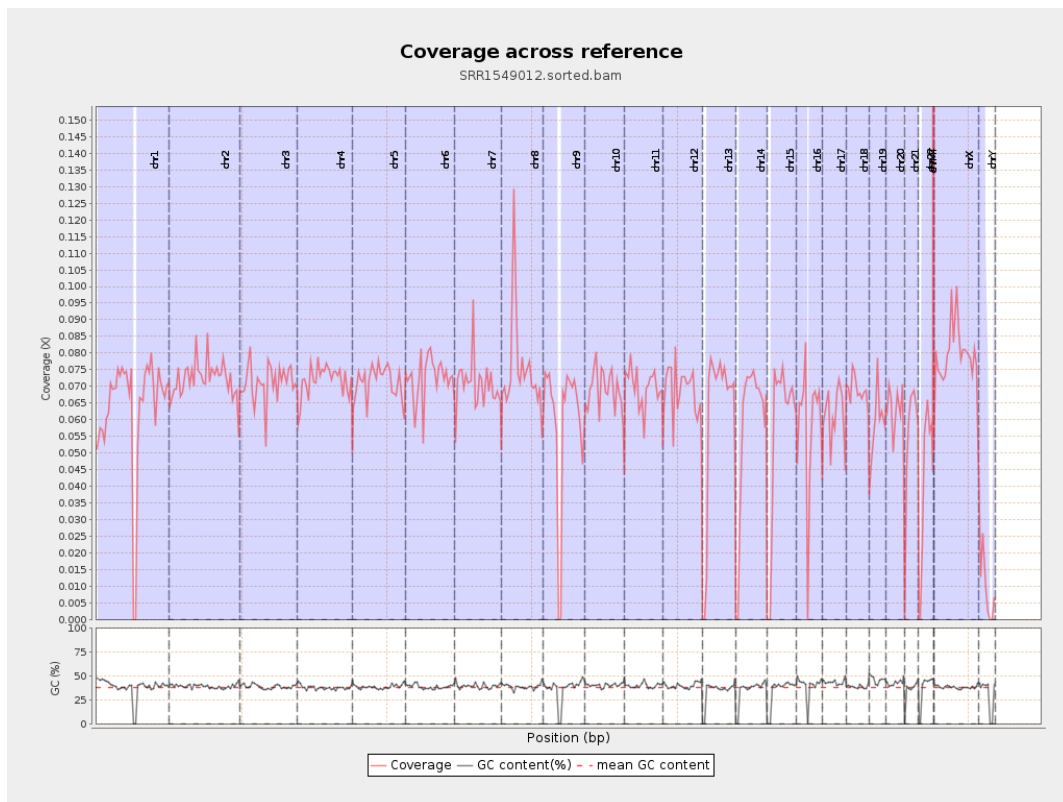
General error rate	0.27%
Mismatches	543,147
Insertions	8,198
Mapped reads with at least one insertion	0.16%
Deletions	18,746
Mapped reads with at least one deletion	0.36%
Homopolymer indels	44.01%

2.6. Chromosome stats

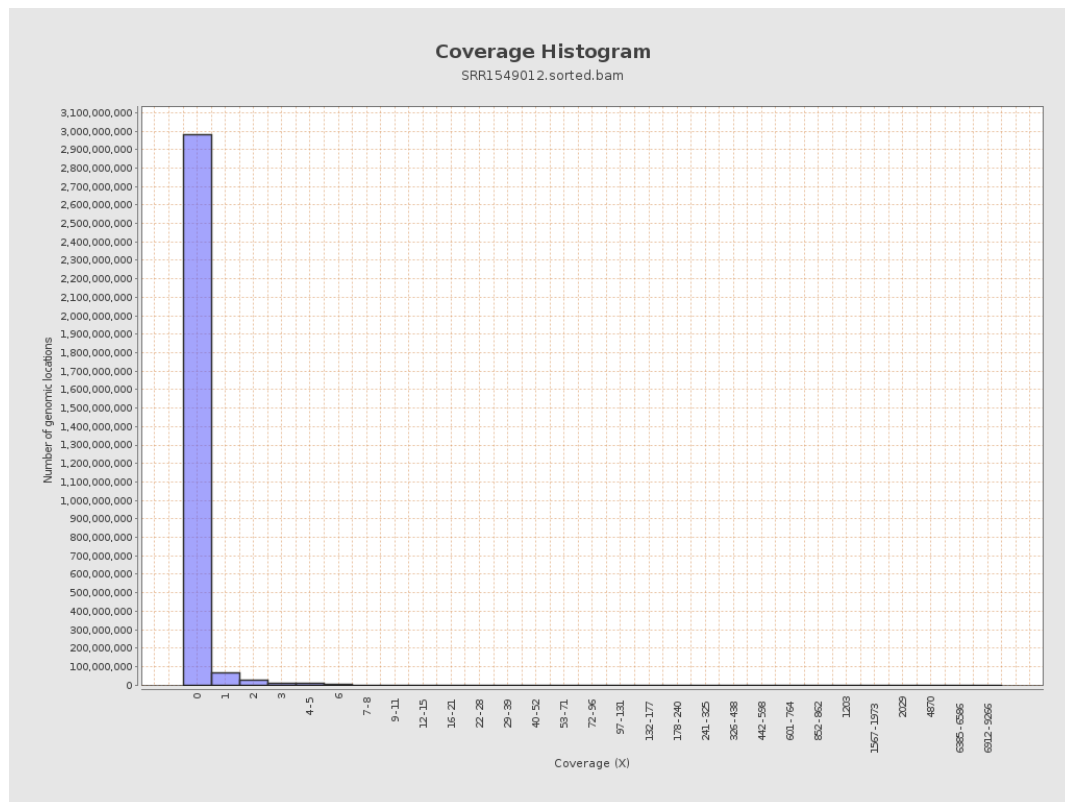
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15887297	0.0637	0.6268
chr2	243199373	17567007	0.0722	0.4894
chr3	198022430	14101635	0.0712	0.4345
chr4	191154276	13730480	0.0718	0.4458
chr5	180915260	12876182	0.0712	0.436
chr6	171115067	12403171	0.0725	0.4437
chr7	159138663	11279649	0.0709	0.5627
chr8	146364022	10939954	0.0747	4.4601

chr9	141213431	8358505	0.0592	0.4362
chr10	135534747	9387134	0.0693	0.4653
chr11	135006516	9364836	0.0694	0.5328
chr12	133851895	9189536	0.0687	0.4293
chr13	115169878	6985071	0.0607	0.4058
chr14	107349540	6182176	0.0576	0.4131
chr15	102531392	5826226	0.0568	0.3812
chr16	90354753	5274303	0.0584	0.3875
chr17	81195210	4937985	0.0608	0.4033
chr18	78077248	5377706	0.0689	0.6434
chr19	59128983	3504481	0.0593	0.559
chr20	63025520	3962878	0.0629	0.4068
chr21	48129895	2651868	0.0551	0.3912
chr22	51304566	2096799	0.0409	0.4005
chrMT	16571	15968	0.9636	1.7126
chrX	155270560	12312986	0.0793	0.493
chrY	59373566	591335	0.01	0.1662

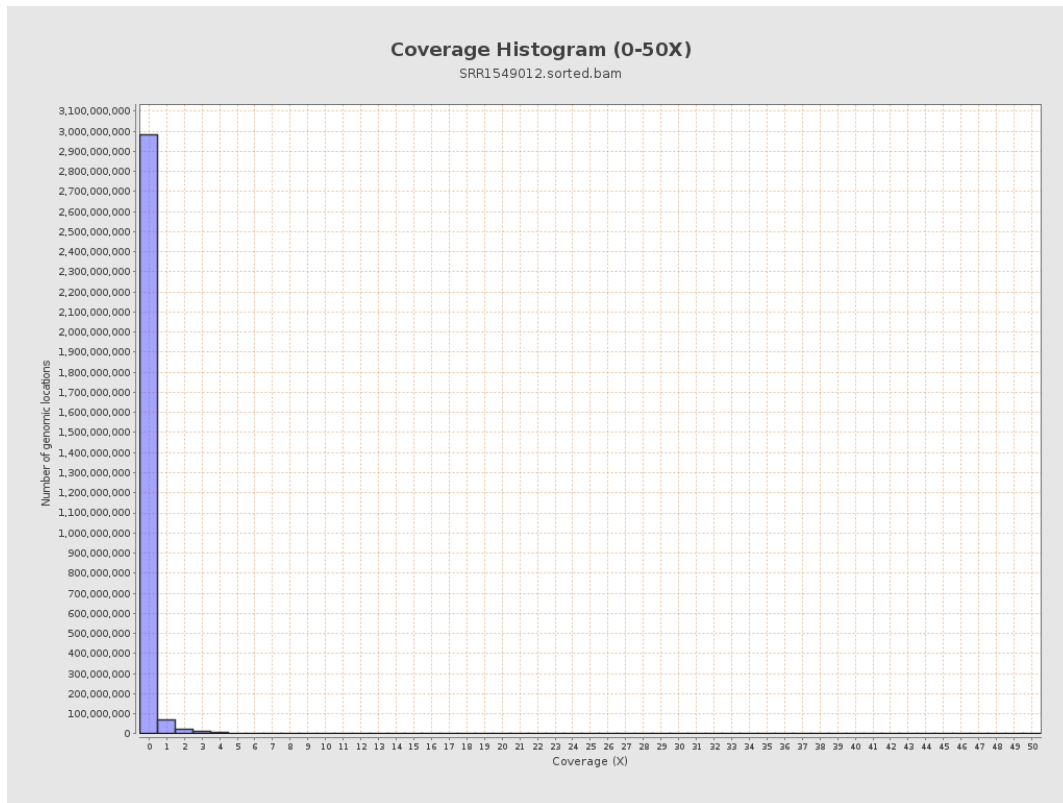
3. Results : Coverage across reference



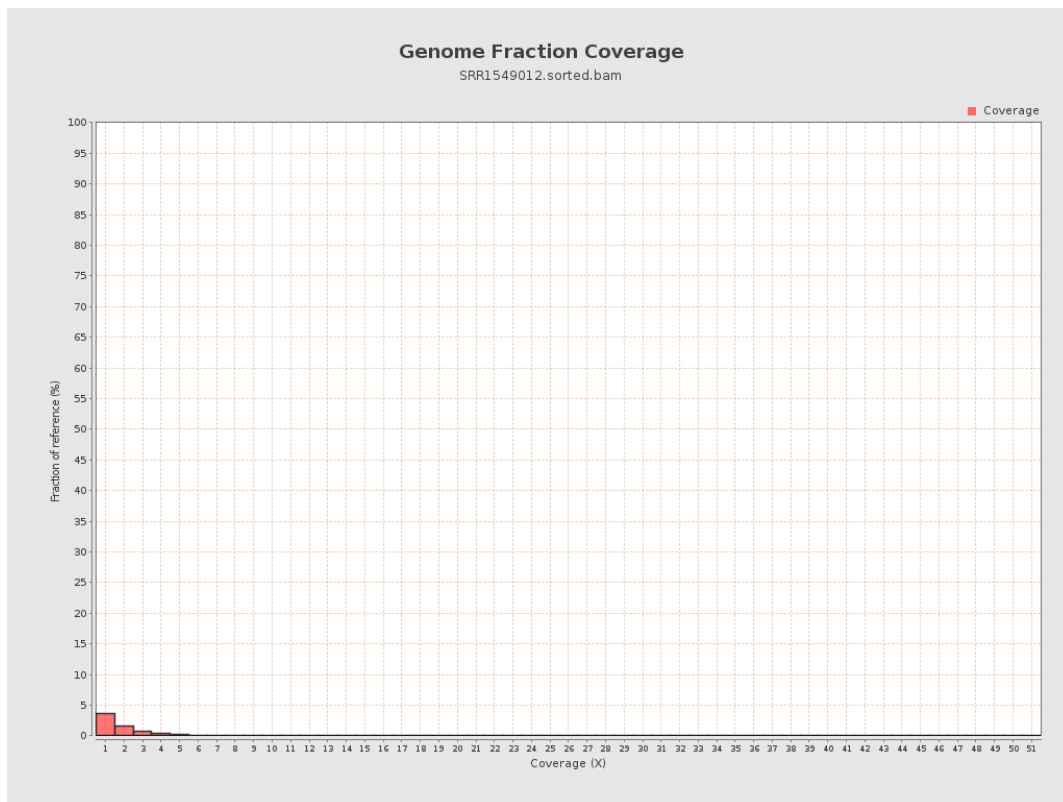
4. Results : Coverage Histogram



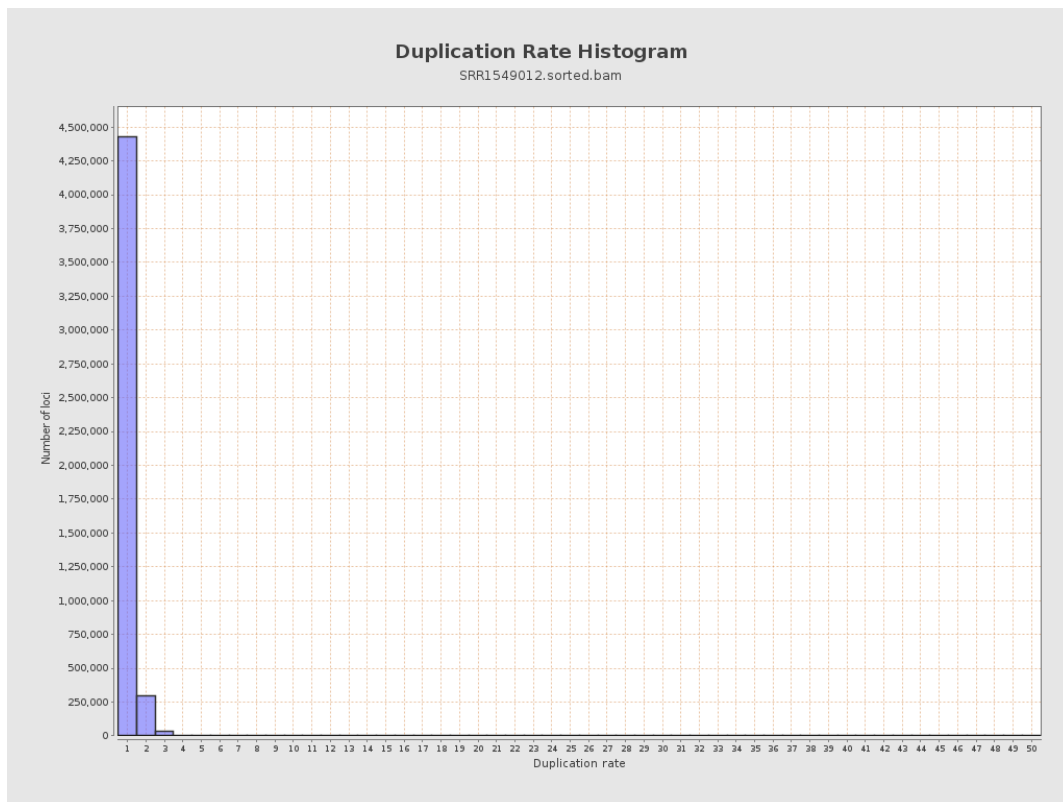
5. Results : Coverage Histogram (0-50X)



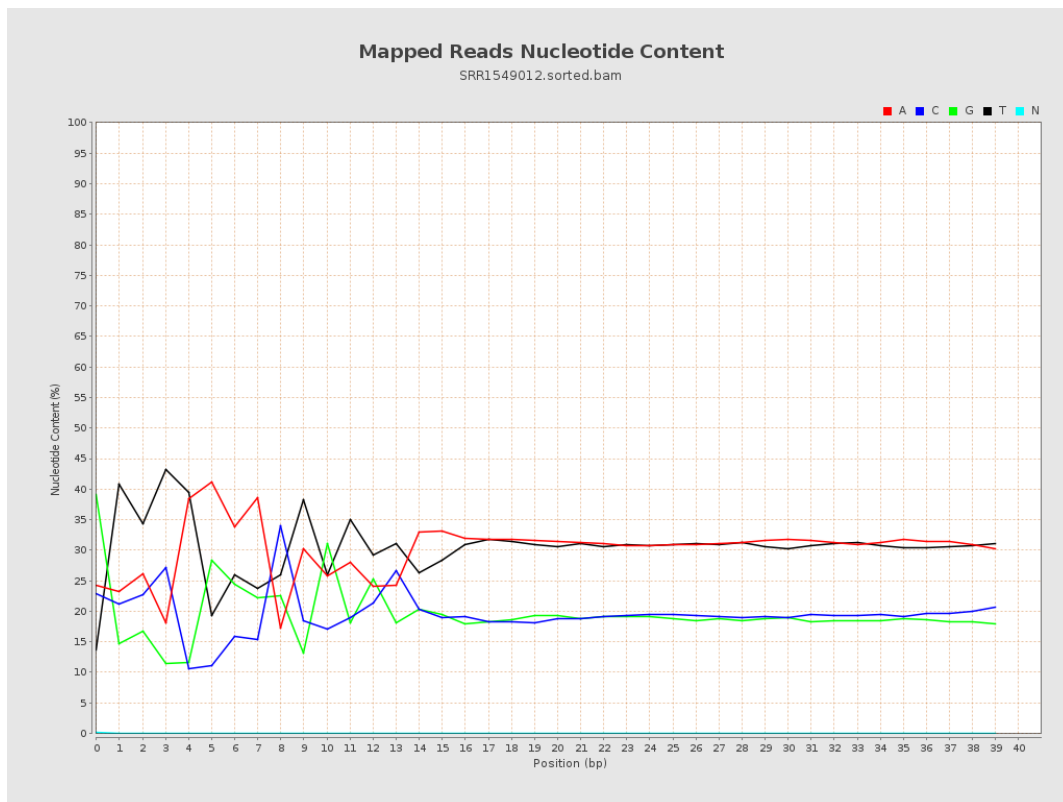
6. Results : Genome Fraction Coverage



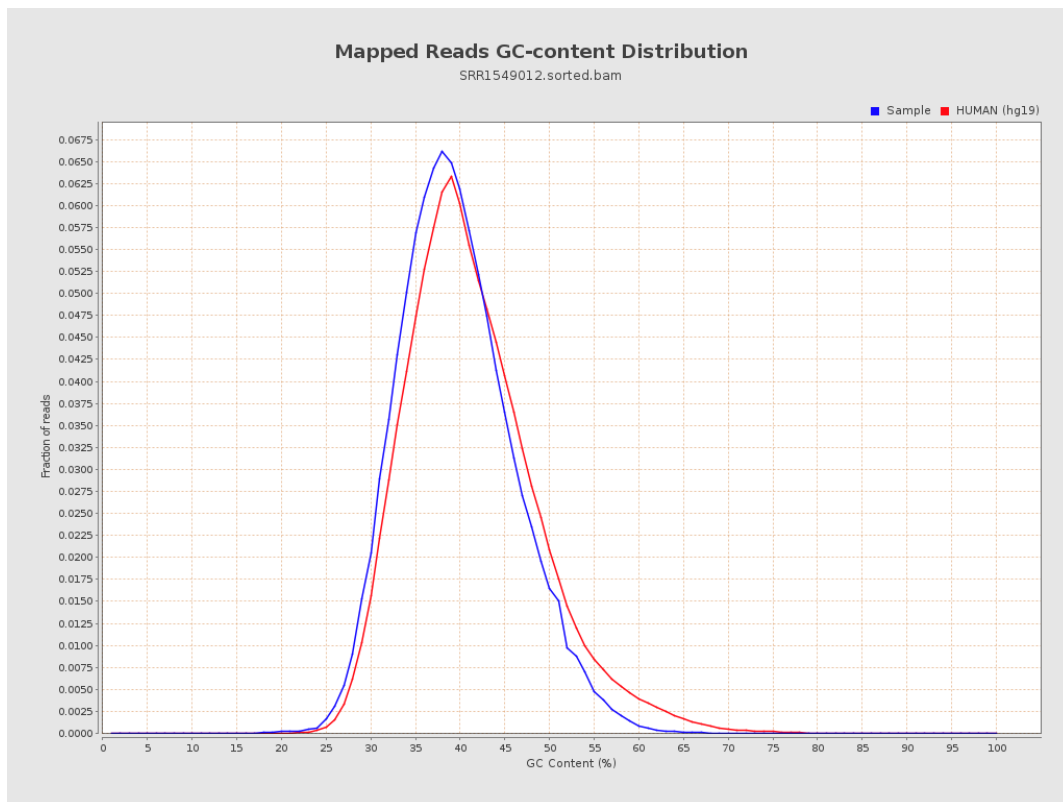
7. Results : Duplication Rate Histogram



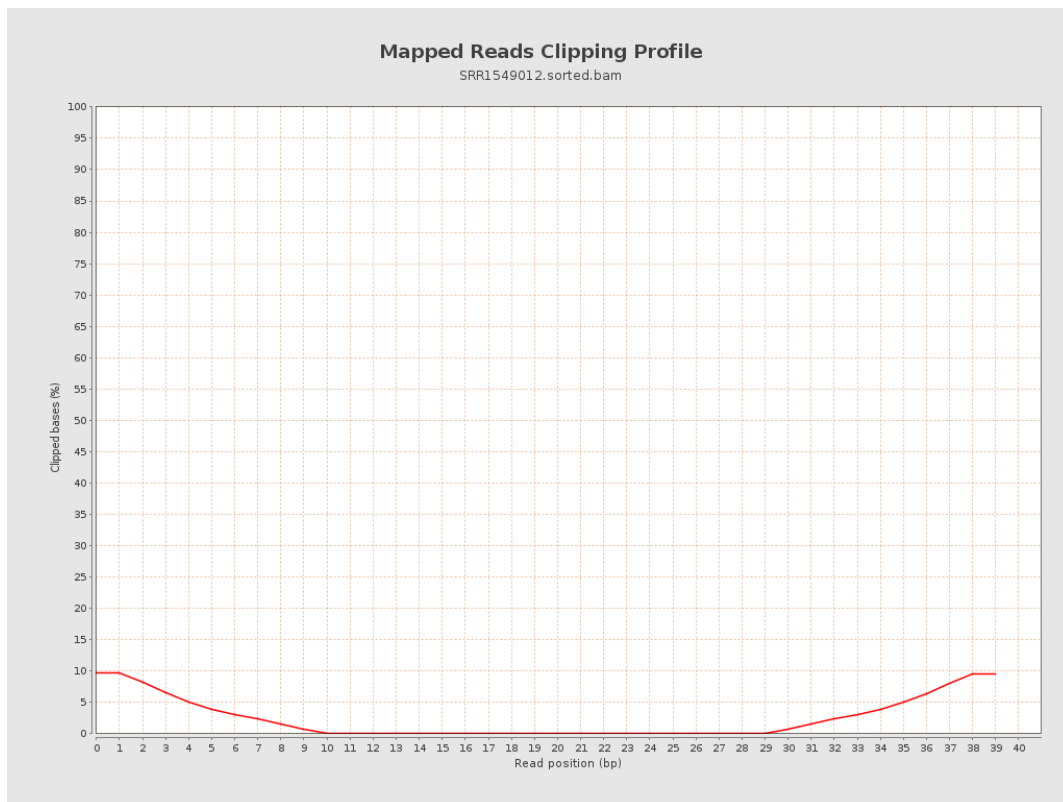
8. Results : Mapped Reads Nucleotide Content



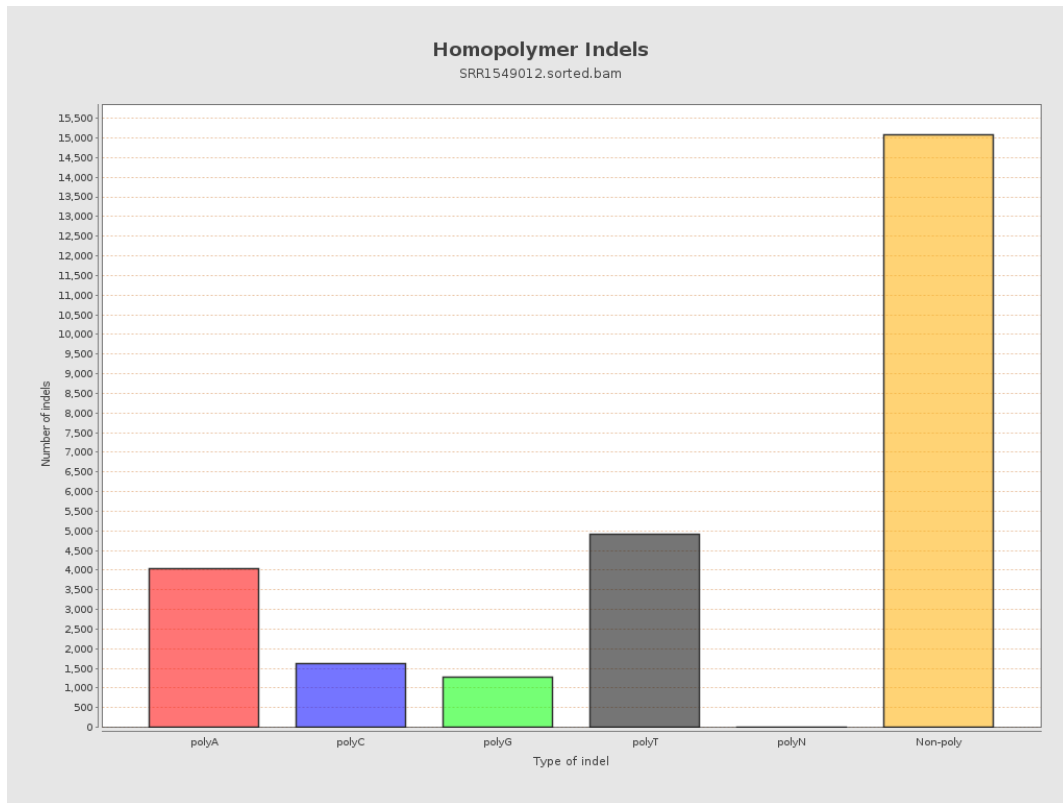
9. Results : Mapped Reads GC-content Distribution



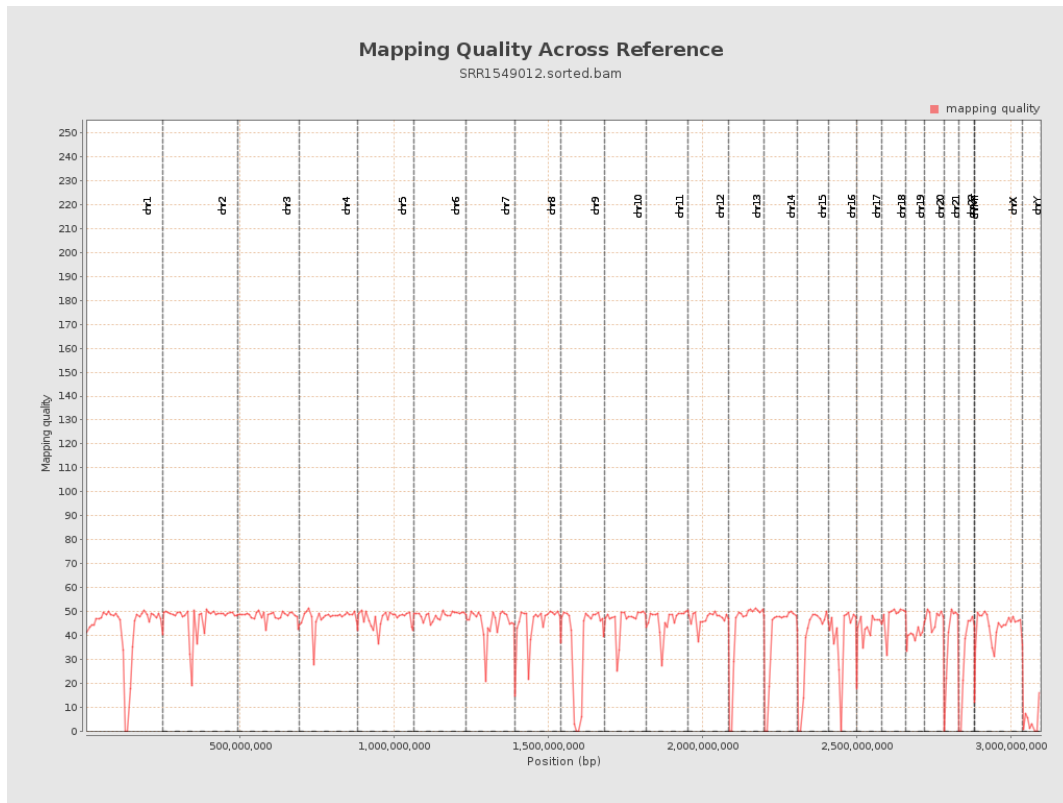
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

