

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:07:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549036.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_SRR1549036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549036.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:07:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,208,192
Mapped reads	7,079,038 / 86.24%
Unmapped reads	1,129,154 / 13.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	313,731 / 3.82%
Duplication rate	3.91%
Clipped reads	434,060 / 5.29%

2.2. ACGT Content

Number/percentage of A's	80,520,893 / 28.68%
Number/percentage of C's	59,687,241 / 21.26%
Number/percentage of T's	80,862,041 / 28.81%
Number/percentage of G's	59,640,928 / 21.25%
Number/percentage of N's	210 / 0%
GC Percentage	42.51%

2.3. Coverage

Mean	0.0907
Standard Deviation	0.5082

2.4. Mapping Quality

Mean Mapping Quality	42.29
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2.5. Mismatches and indels

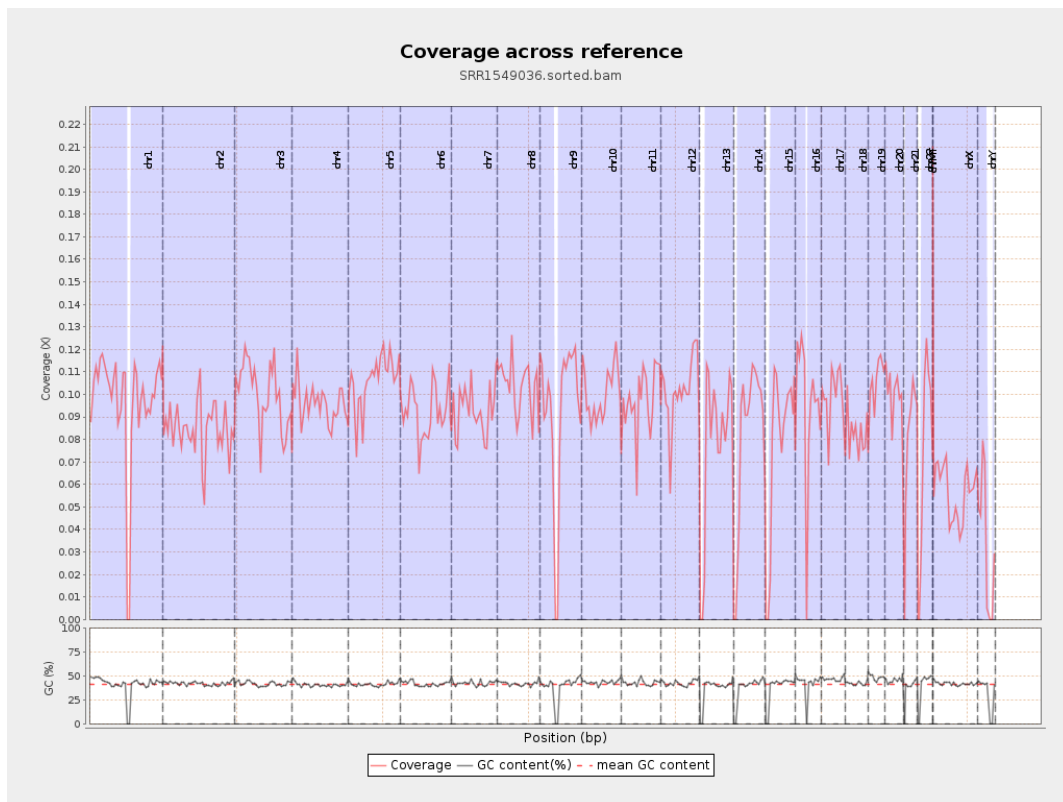
General error rate	0.24%
Mismatches	677,220
Insertions	7,496
Mapped reads with at least one insertion	0.11%
Deletions	19,516
Mapped reads with at least one deletion	0.28%
Homopolymer indels	42.91%

2.6. Chromosome stats

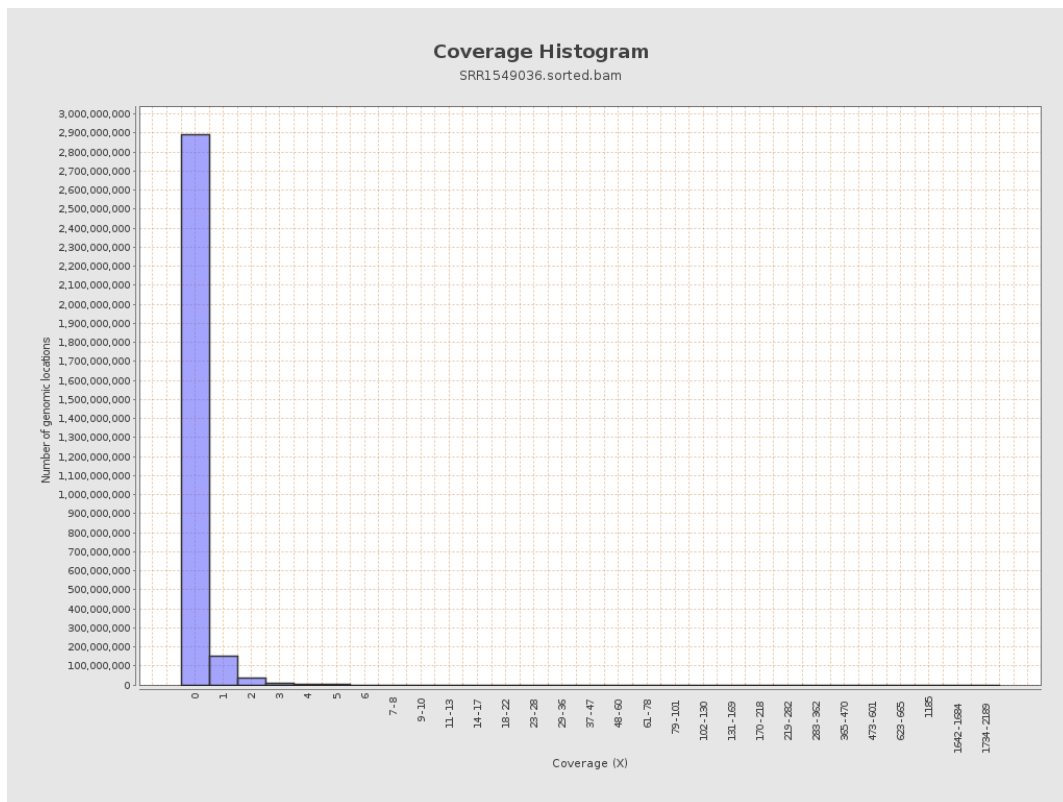
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	24106852	0.0967	0.6611
chr2	243199373	20445867	0.0841	0.4232
chr3	198022430	19760469	0.0998	0.4202
chr4	191154276	18411113	0.0963	0.4191
chr5	180915260	19244363	0.1064	0.4332
chr6	171115067	15763867	0.0921	0.4085
chr7	159138663	14745834	0.0927	0.4412
chr8	146364022	15035978	0.1027	1.1506

chr9	141213431	12997035	0.092	0.4431
chr10	135534747	13668224	0.1008	0.4662
chr11	135006516	13082364	0.0969	0.427
chr12	133851895	13723688	0.1025	0.431
chr13	115169878	8971153	0.0779	0.3749
chr14	107349540	8951069	0.0834	0.4122
chr15	102531392	7733811	0.0754	0.3649
chr16	90354753	8484568	0.0939	0.426
chr17	81195210	8099784	0.0998	0.423
chr18	78077248	6432842	0.0824	0.5555
chr19	59128983	6254597	0.1058	0.651
chr20	63025520	6278117	0.0996	0.4312
chr21	48129895	3839230	0.0798	0.4144
chr22	51304566	3832833	0.0747	0.5451
chrMT	16571	3486	0.2104	0.5964
chrX	155270560	8830734	0.0569	0.3219
chrY	59373566	2039385	0.0343	0.2693

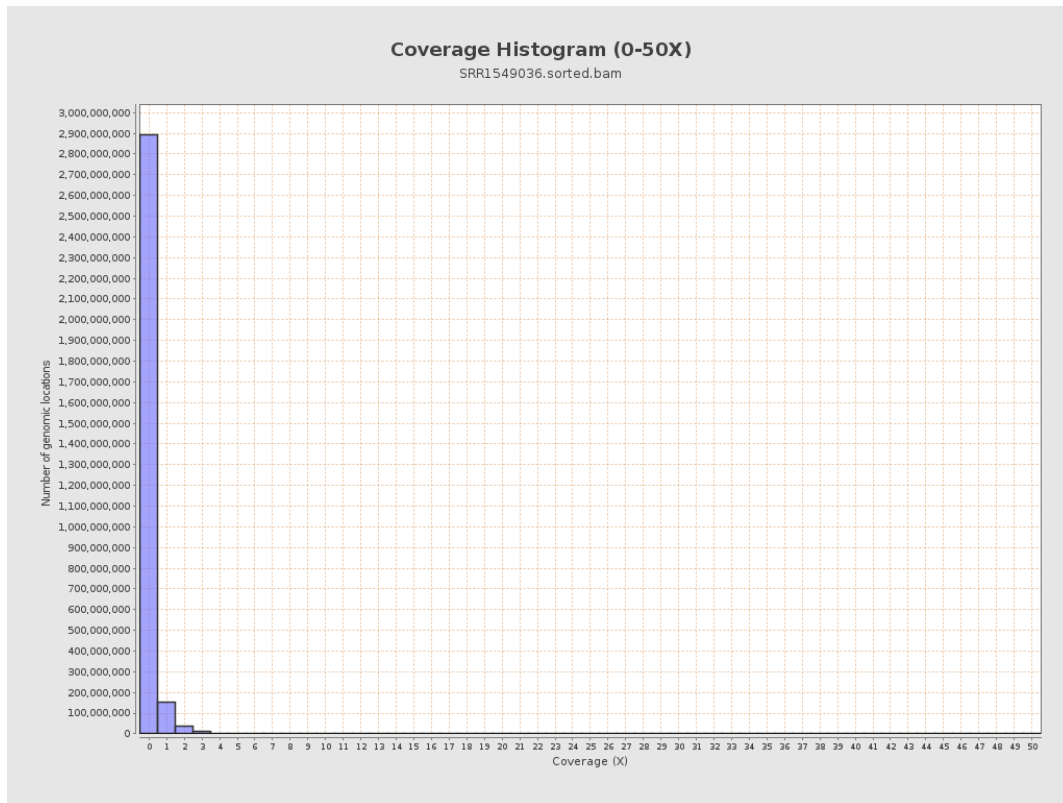
3. Results : Coverage across reference



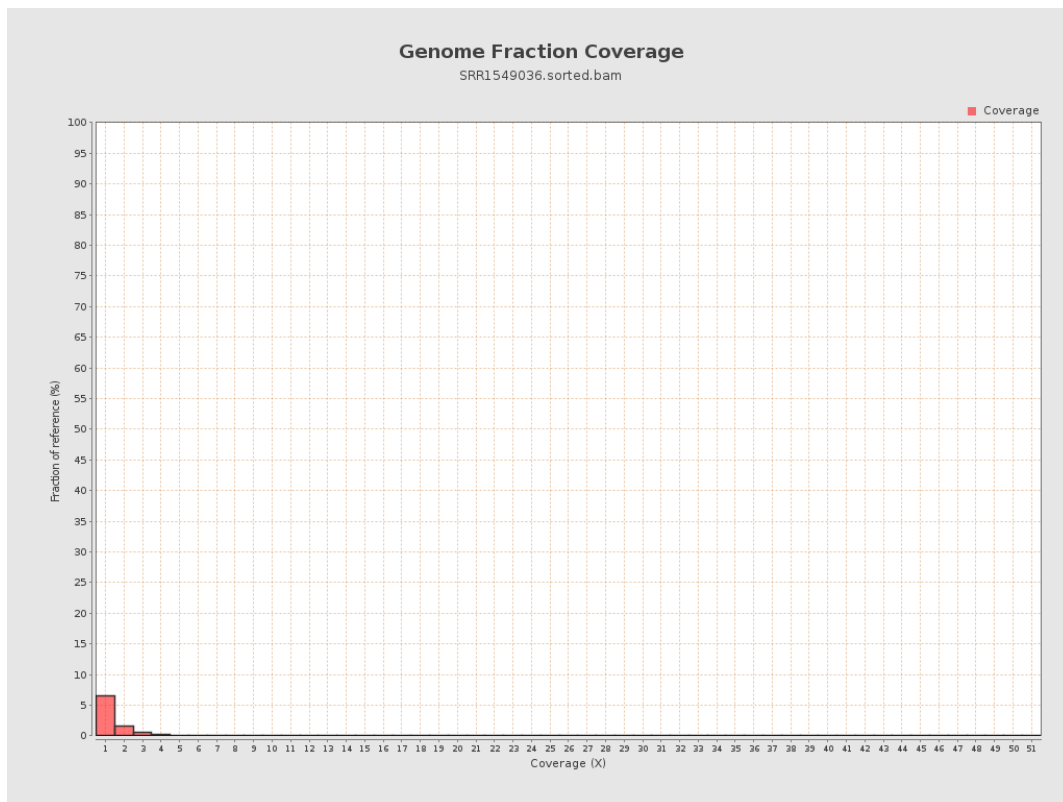
4. Results : Coverage Histogram



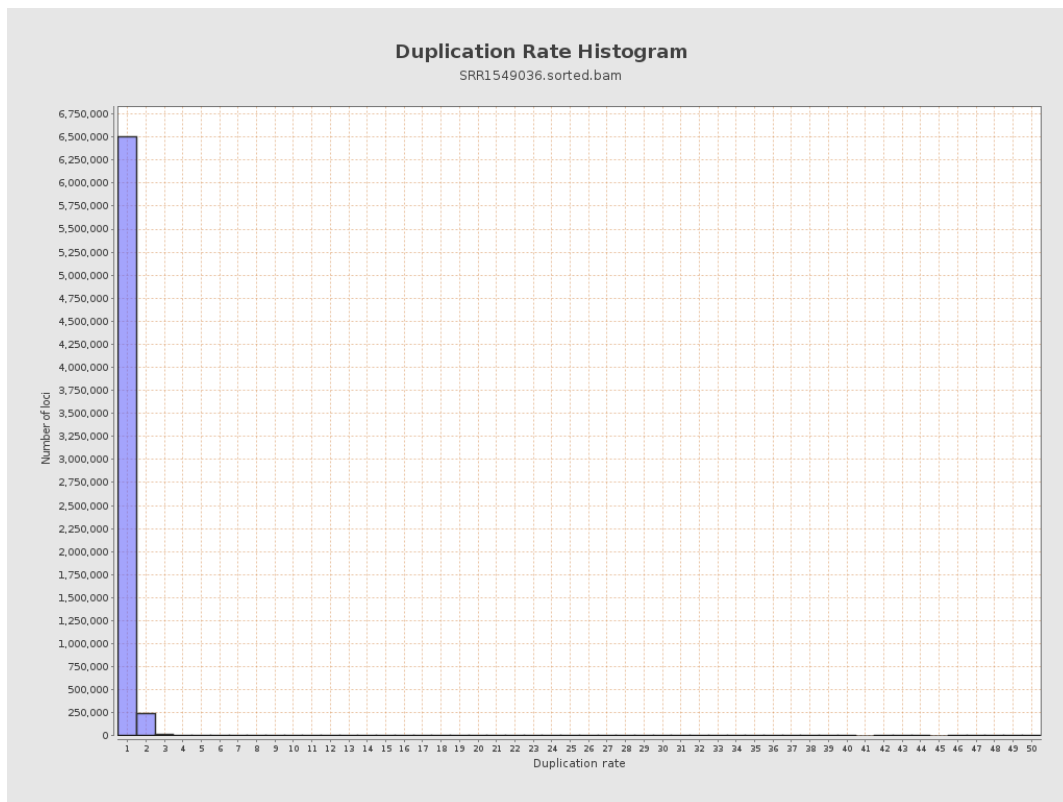
5. Results : Coverage Histogram (0-50X)



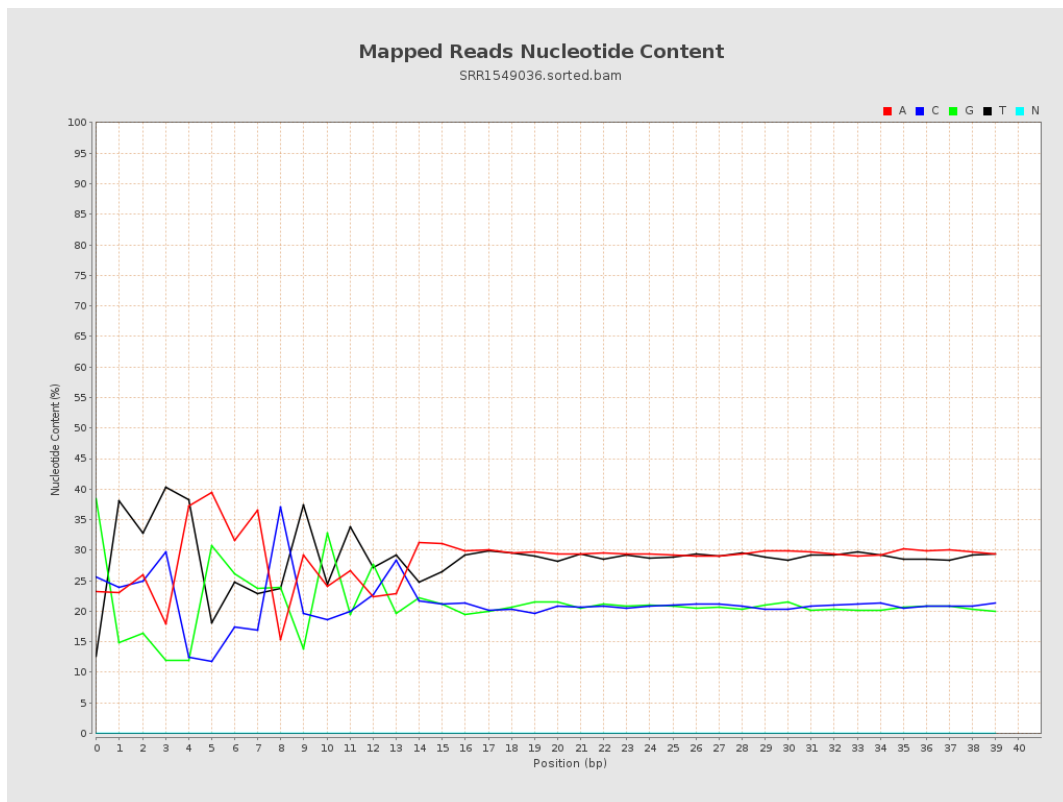
6. Results : Genome Fraction Coverage



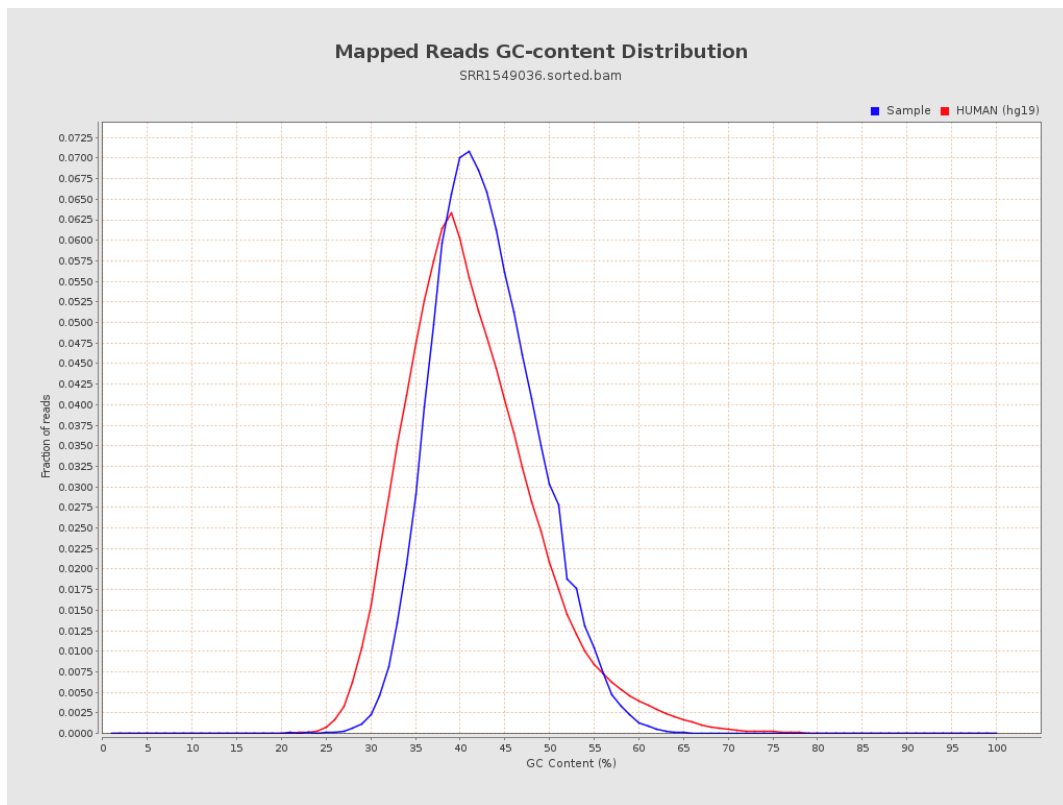
7. Results : Duplication Rate Histogram



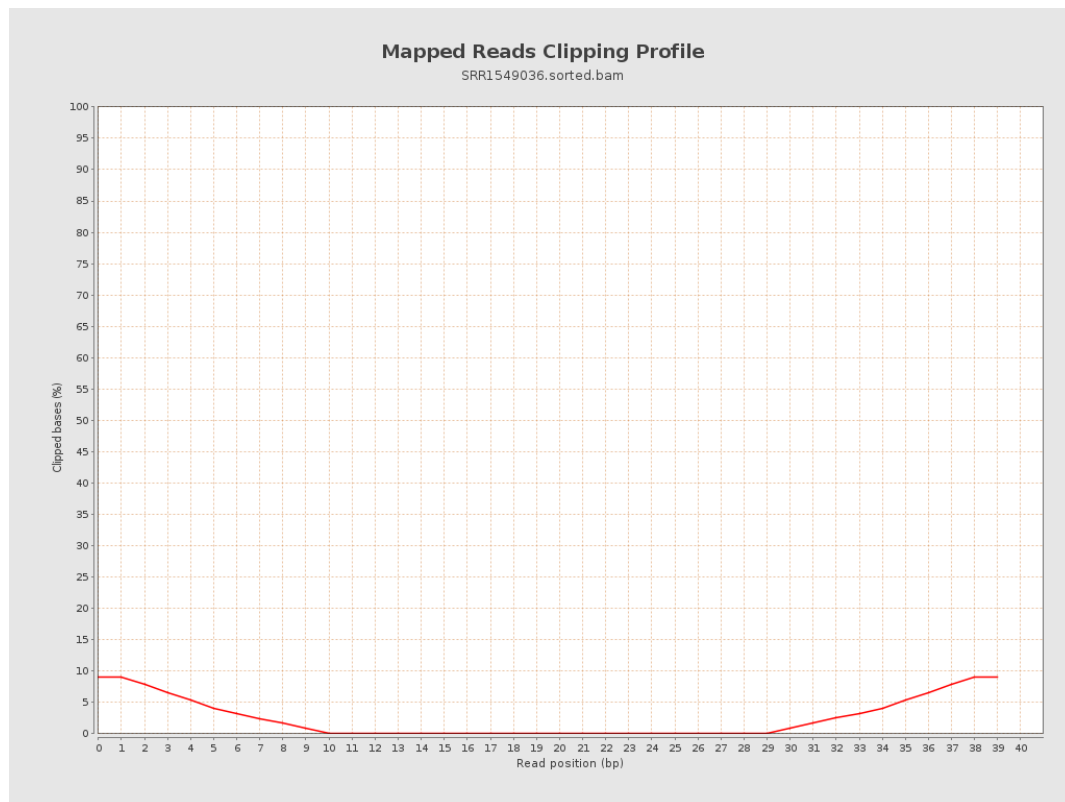
8. Results : Mapped Reads Nucleotide Content



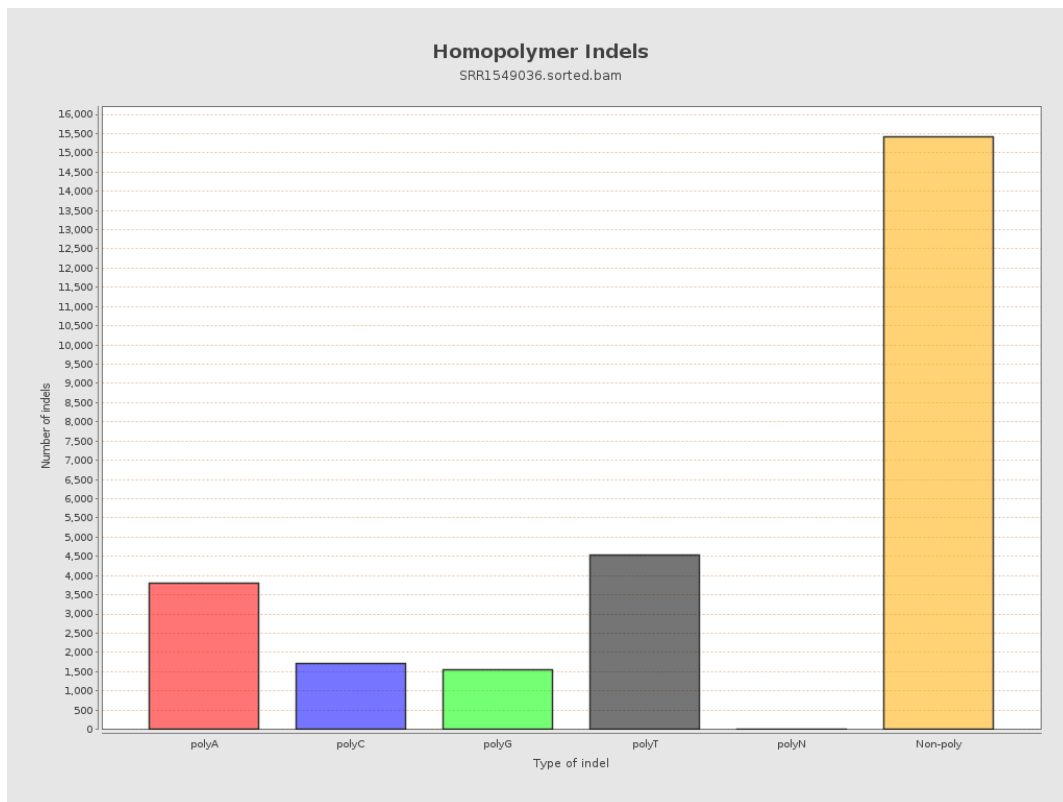
9. Results : Mapped Reads GC-content Distribution



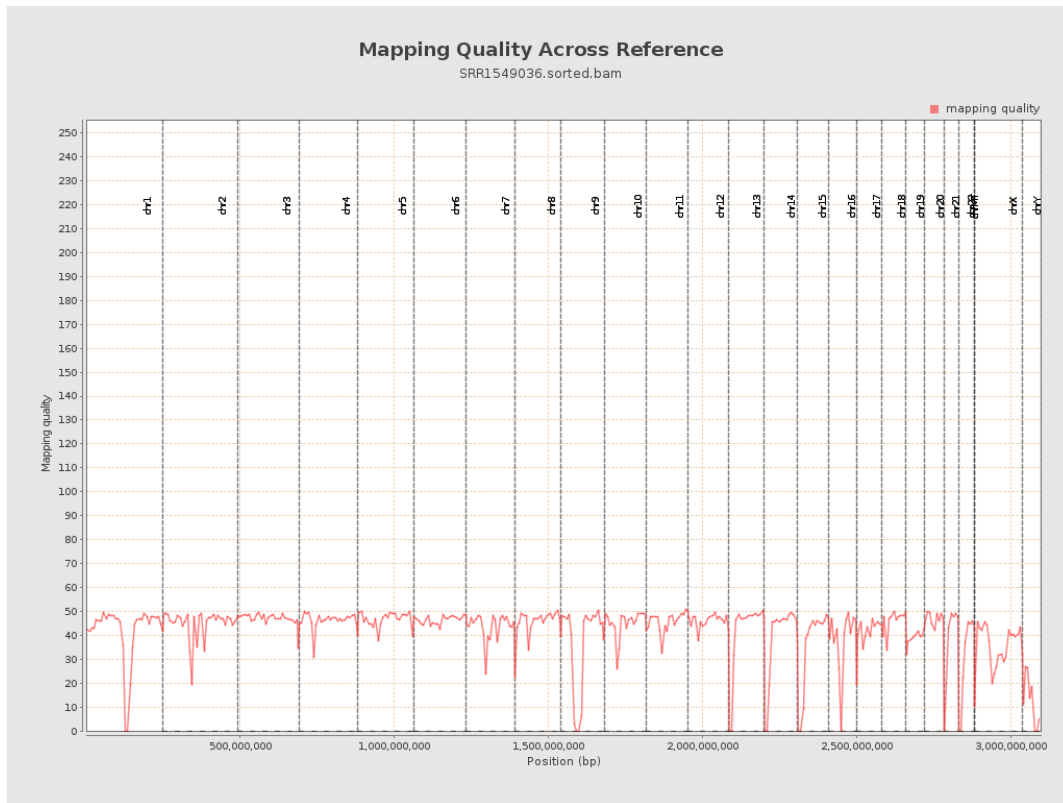
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

