

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:03:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549007.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_SRR1549007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549007.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:03:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,327,537
Mapped reads	8,078,059 / 86.6%
Unmapped reads	1,249,478 / 13.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	647,759 / 6.94%
Duplication rate	7.28%
Clipped reads	431,573 / 4.63%

2.2. ACGT Content

Number/percentage of A's	96,226,892 / 30.02%
Number/percentage of C's	63,506,446 / 19.81%
Number/percentage of T's	96,244,838 / 30.03%
Number/percentage of G's	64,565,485 / 20.14%
Number/percentage of N's	2,994 / 0%
GC Percentage	39.95%

2.3. Coverage

Mean	0.1036
Standard Deviation	0.787

2.4. Mapping Quality

Mean Mapping Quality	43.77
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2.5. Mismatches and indels

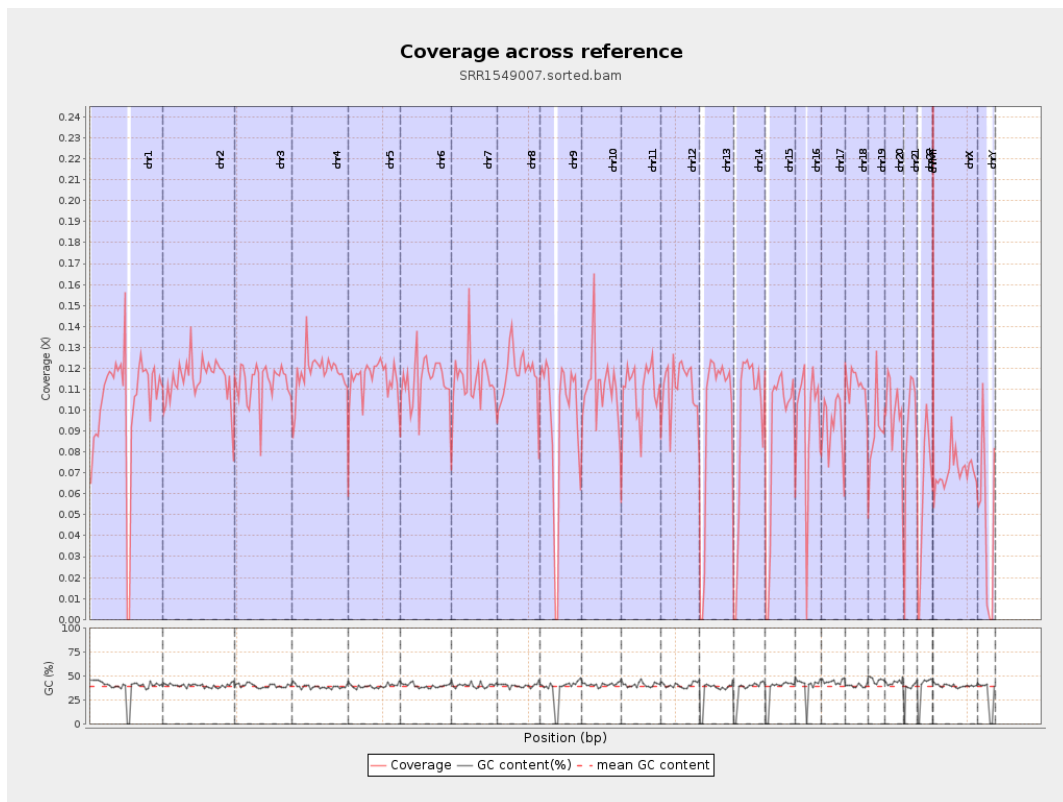
General error rate	0.31%
Mismatches	967,007
Insertions	9,911
Mapped reads with at least one insertion	0.12%
Deletions	28,459
Mapped reads with at least one deletion	0.35%
Homopolymer indels	43.21%

2.6. Chromosome stats

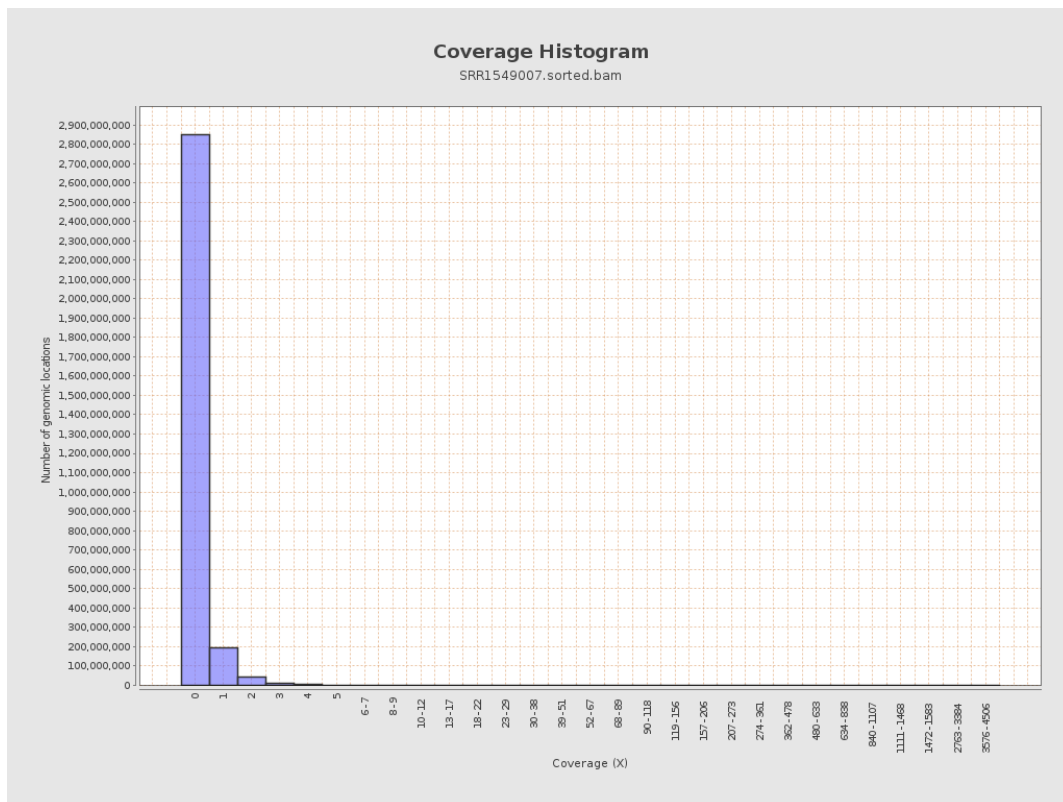
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	25840984	0.1037	1.2312
chr2	243199373	27911488	0.1148	0.5804
chr3	198022430	22422788	0.1132	0.4148
chr4	191154276	22555568	0.118	0.4673
chr5	180915260	20722316	0.1145	0.4253
chr6	171115067	19620459	0.1147	0.4951
chr7	159138663	18148478	0.114	0.8285
chr8	146364022	17099084	0.1168	2.2435

chr9	141213431	13503920	0.0956	0.5404
chr10	135534747	15068746	0.1112	0.6417
chr11	135006516	14823707	0.1098	0.5351
chr12	133851895	14912547	0.1114	0.4314
chr13	115169878	11099306	0.0964	0.3817
chr14	107349540	10199649	0.095	0.4777
chr15	102531392	8997736	0.0878	0.3636
chr16	90354753	8470933	0.0938	0.424
chr17	81195210	7590463	0.0935	0.4144
chr18	78077248	8759506	0.1122	1.09
chr19	59128983	5344311	0.0904	0.9647
chr20	63025520	6280607	0.0997	0.4157
chr21	48129895	4281549	0.089	0.4656
chr22	51304566	3101611	0.0605	0.3394
chrMT	16571	6165	0.372	0.7264
chrX	155270560	10989817	0.0708	0.4109
chrY	59373566	2831721	0.0477	0.4784

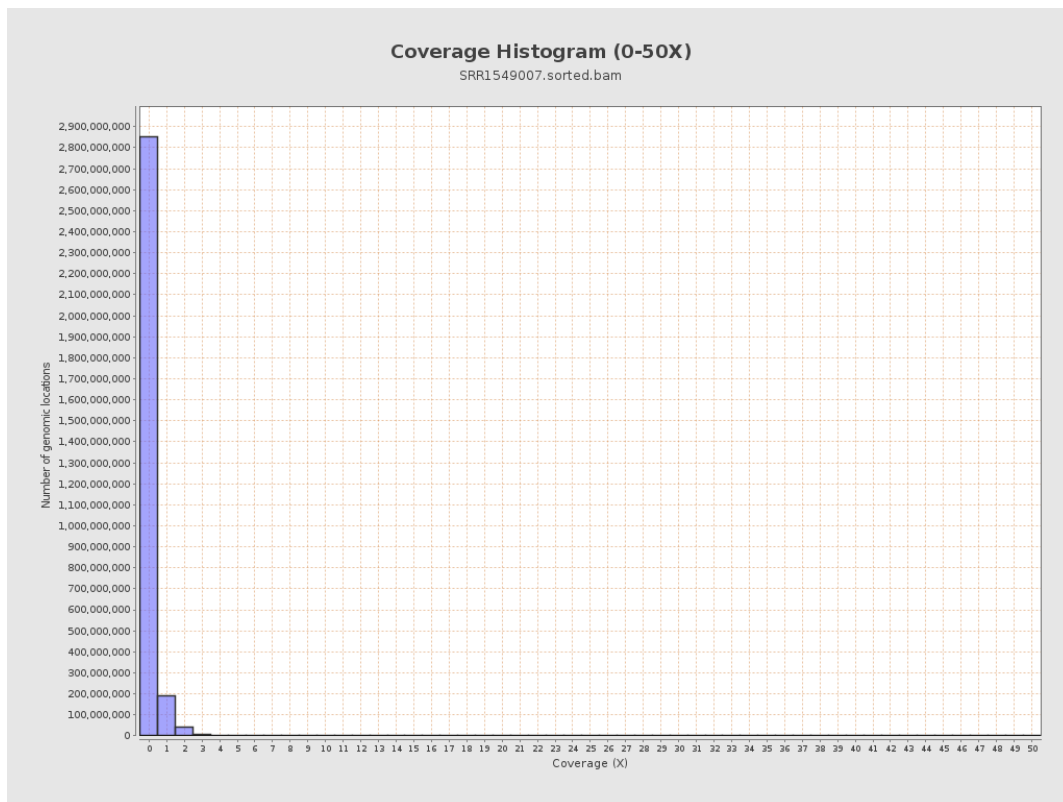
3. Results : Coverage across reference



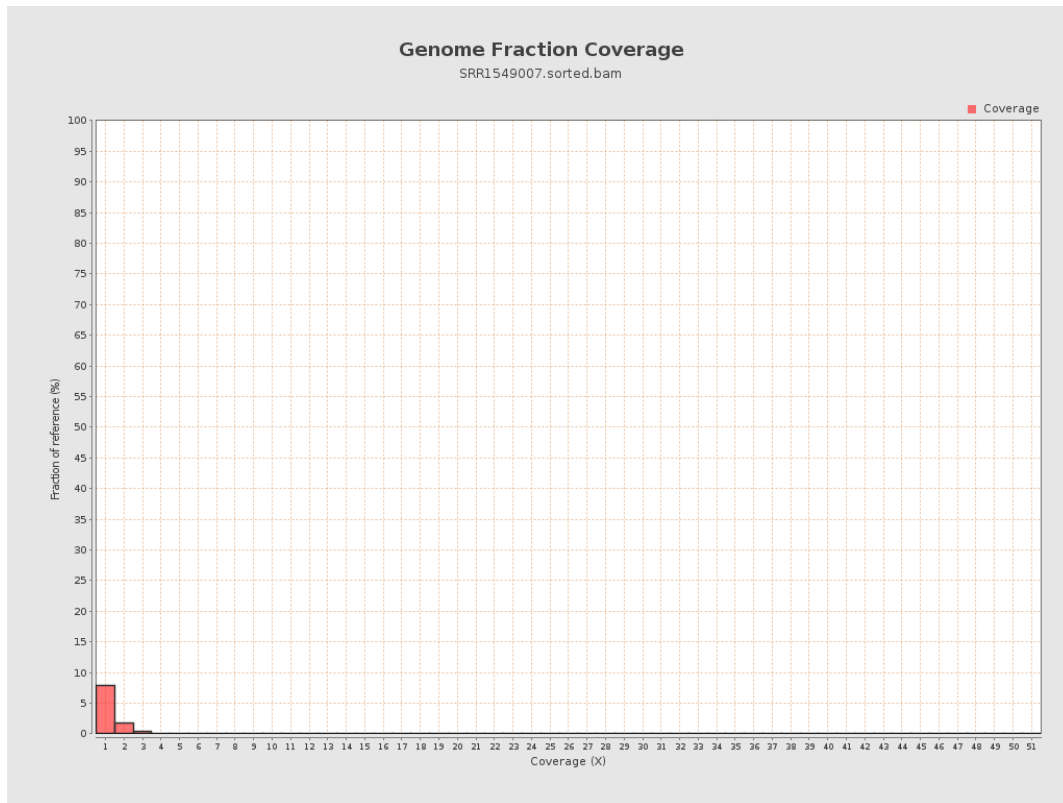
4. Results : Coverage Histogram



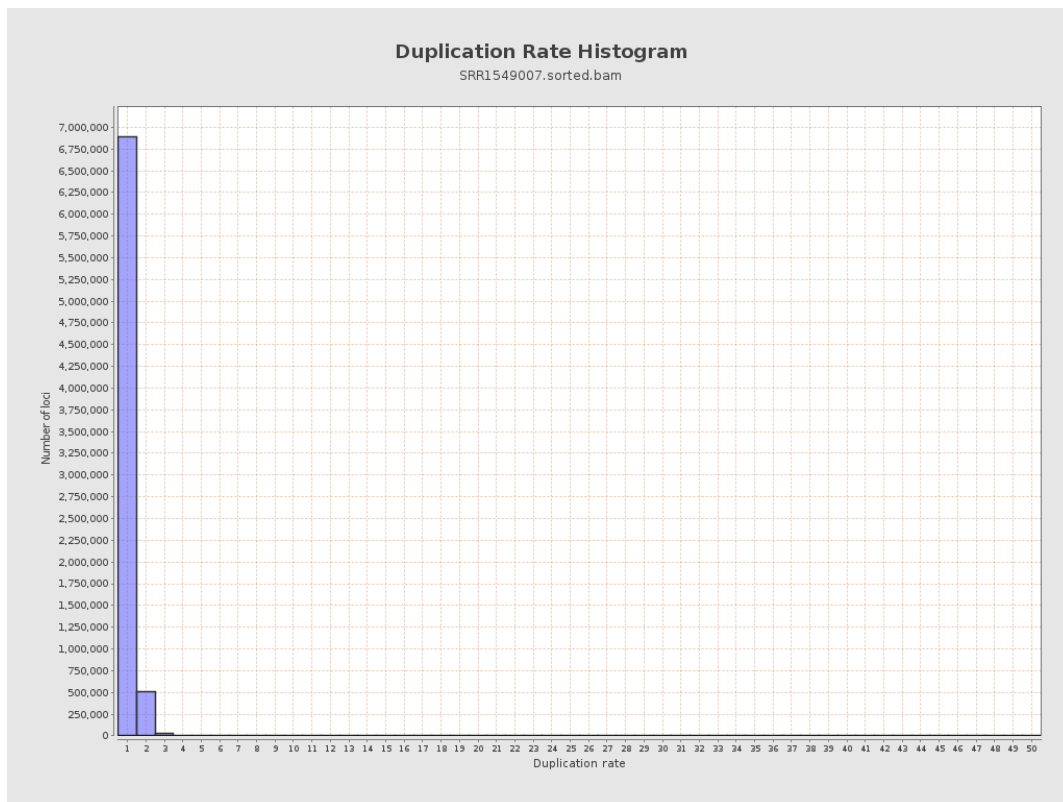
5. Results : Coverage Histogram (0-50X)



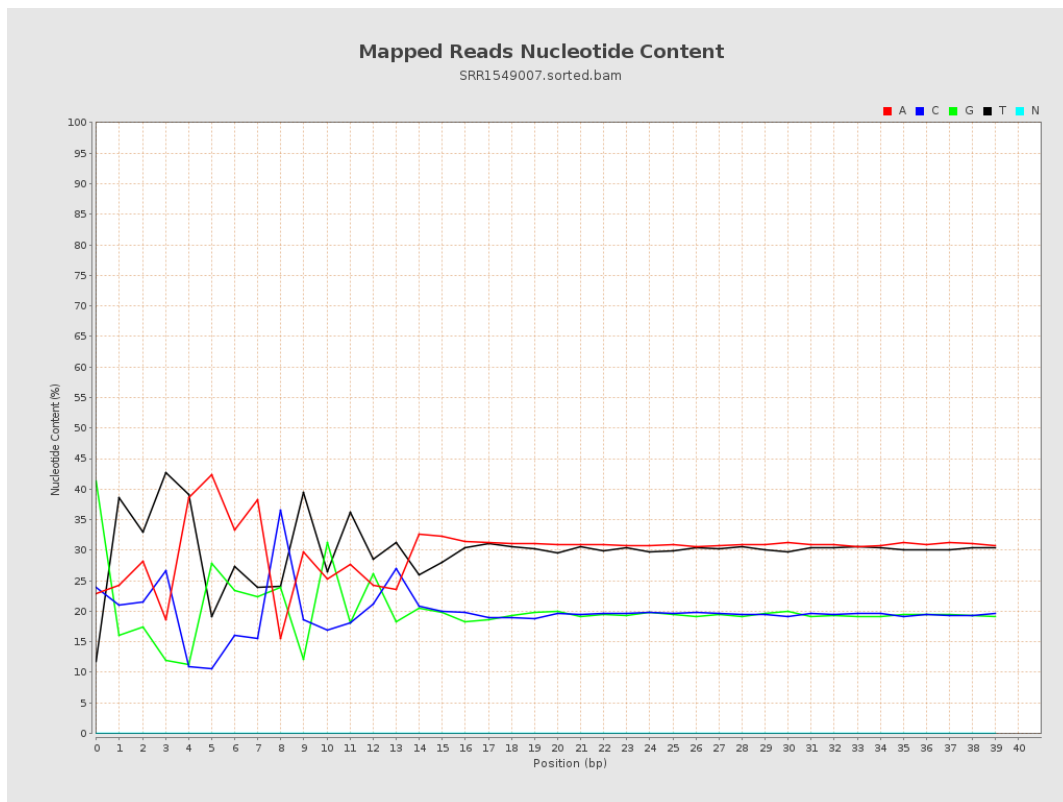
6. Results : Genome Fraction Coverage



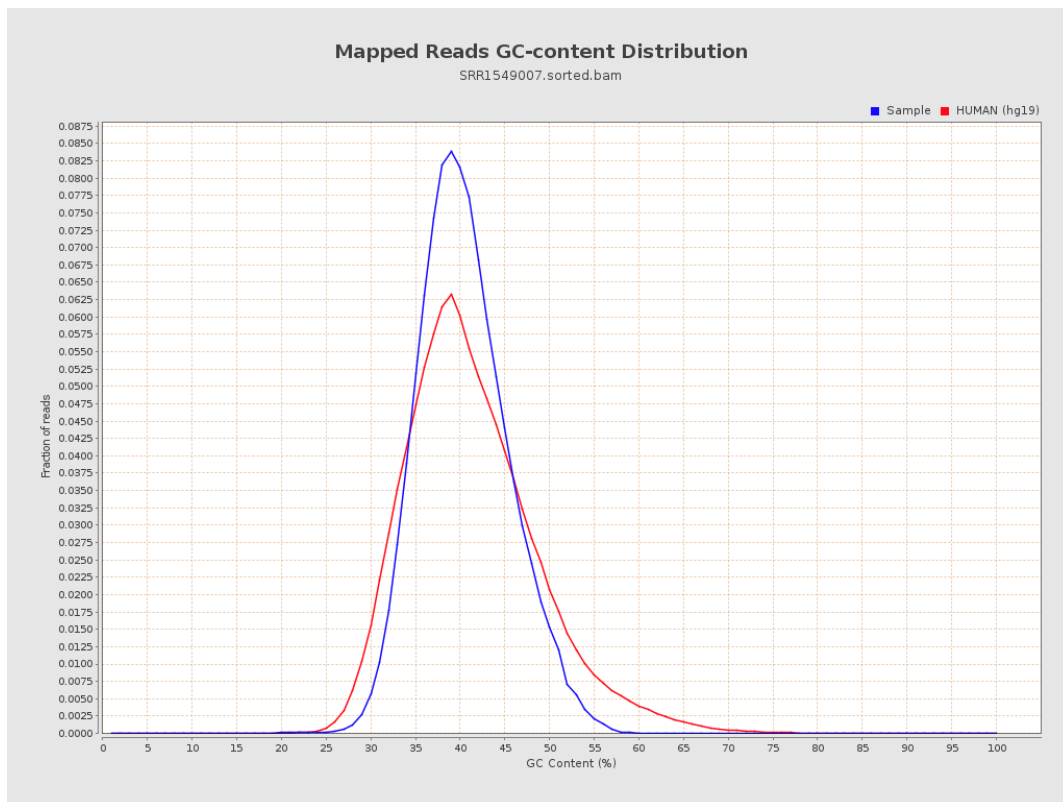
7. Results : Duplication Rate Histogram



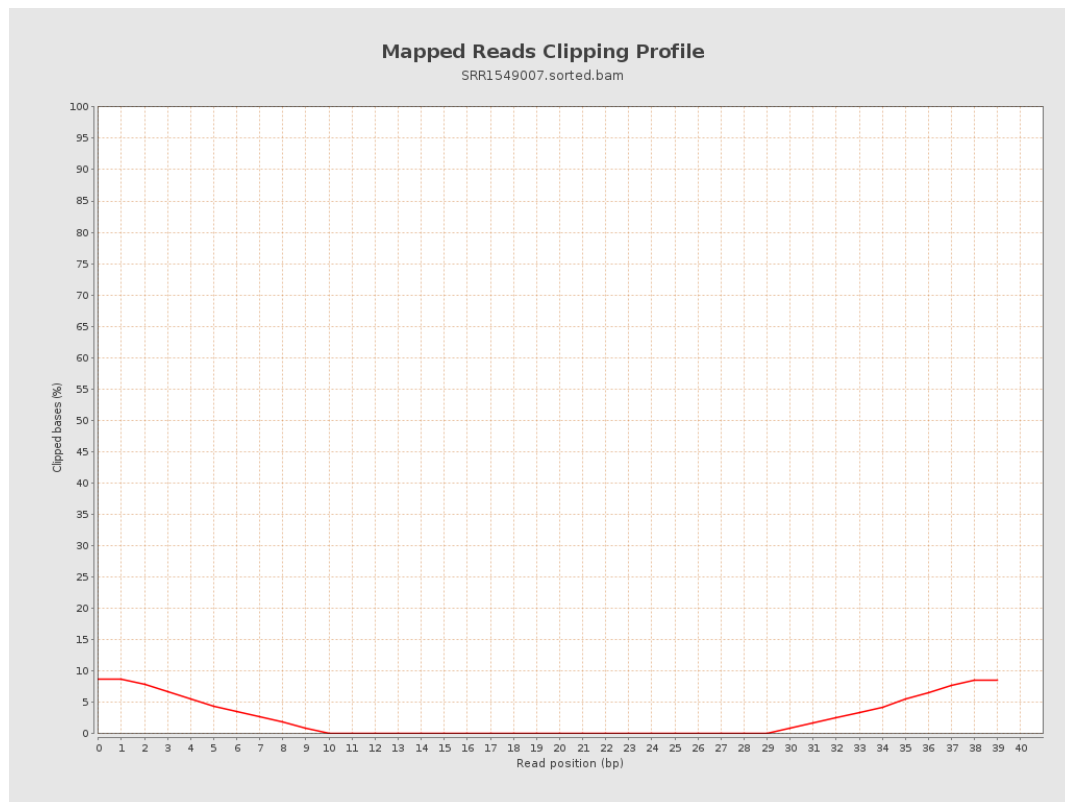
8. Results : Mapped Reads Nucleotide Content



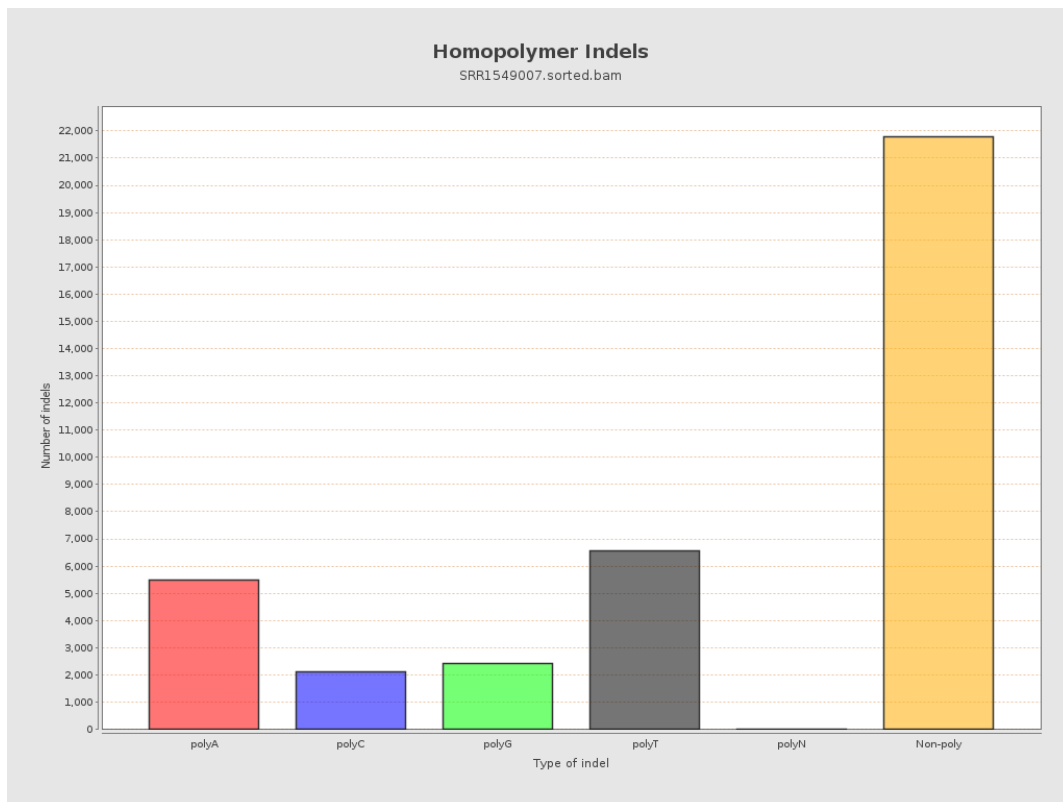
9. Results : Mapped Reads GC-content Distribution



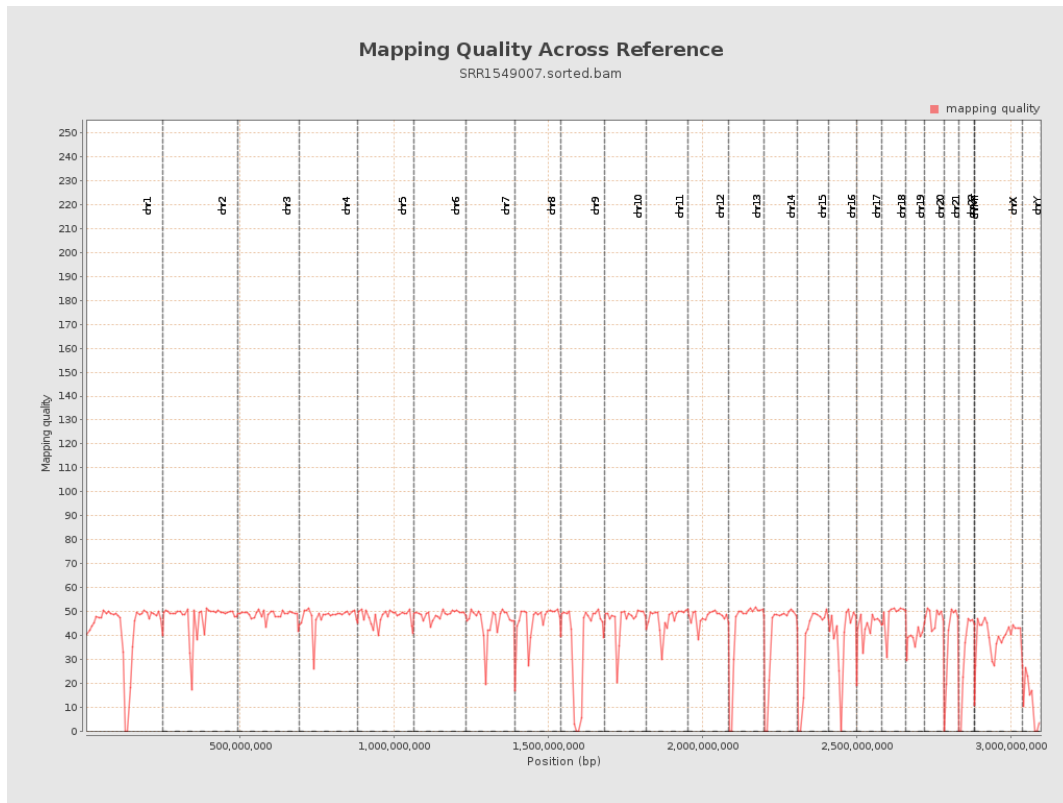
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

