Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:43:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549033.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_SRR1549033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549033.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:43:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,275,295
Mapped reads	8,408,039 / 81.83%
Unmapped reads	1,867,256 / 18.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	466,128 / 4.54%
Duplication rate	4.93%
Clipped reads	567,992 / 5.53%

2.2. ACGT Content

Number/percentage of A's	94,447,387 / 28.36%
Number/percentage of C's	70,421,566 / 21.14%
Number/percentage of T's	96,650,911 / 29.02%
Number/percentage of G's	71,533,173 / 21.48%
Number/percentage of N's	339 / 0%
GC Percentage	42.62%

2.3. Coverage

Mean	0.1076
Standard Deviation	0.5792

2.4. Mapping Quality

Mean Mapping Quality	41.96

2.5. Mismatches and indels

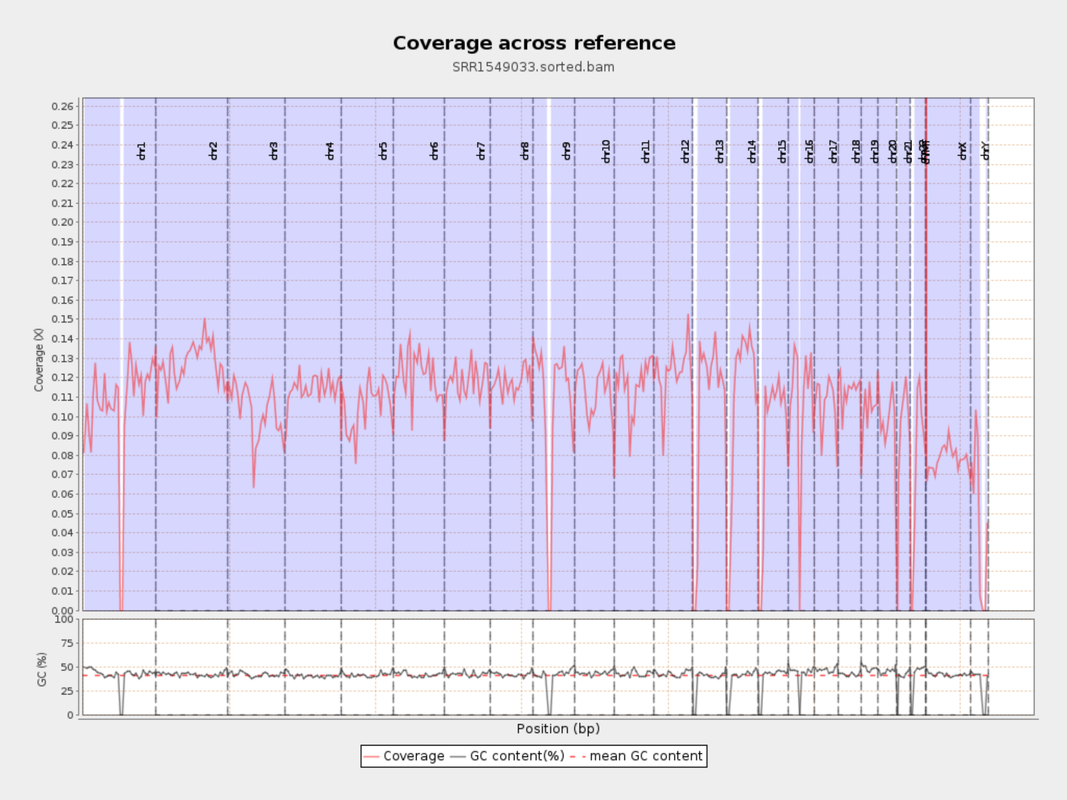
General error rate	0.24%
Mismatches	803,802
Insertions	8,969
Mapped reads with at least one insertion	0.11%
Deletions	23,080
Mapped reads with at least one deletion	0.27%
Homopolymer indels	42.47%

2.6. Chromosome stats

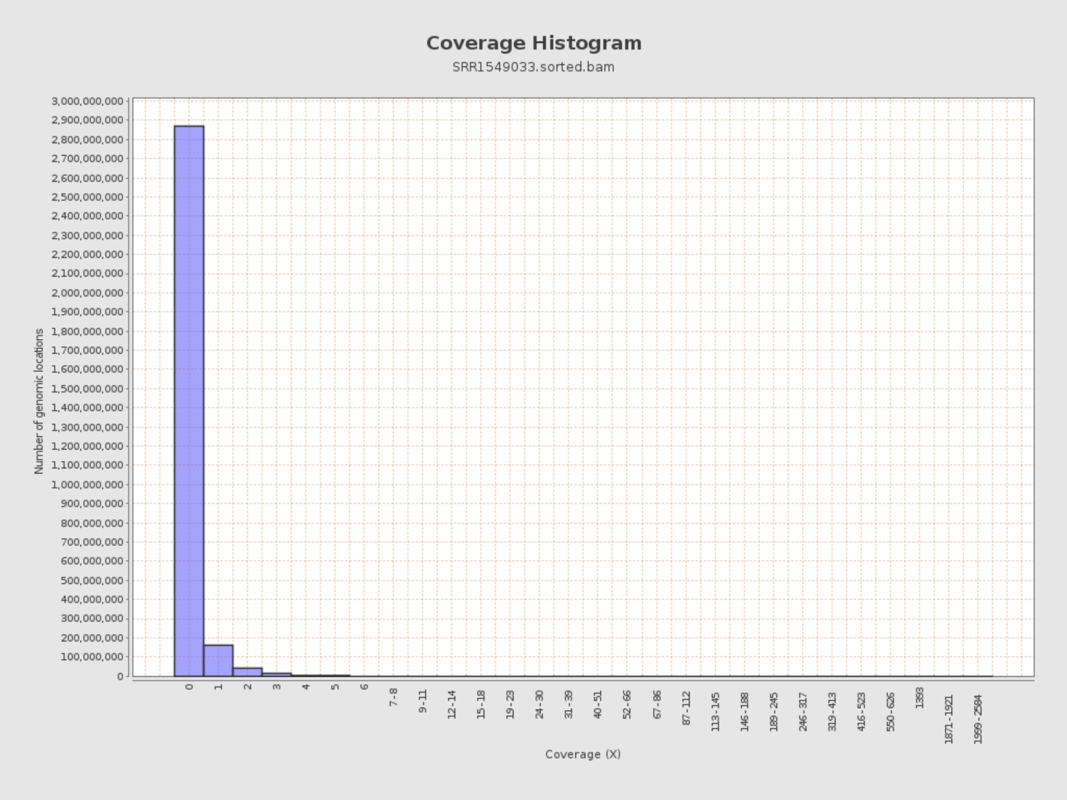
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26211741	0.1052	0.6214
chr2	243199373	31030125	0.1276	0.5583
chr3	198022430	20349723	0.1028	0.4539
chr4	191154276	21957086	0.1149	0.4866
chr5	180915260	19084315	0.1055	0.4517
chr6	171115067	20827130	0.1217	0.5011
chr7	159138663	18796100	0.1181	0.6029
chr8	146364022	17148054	0.1172	1.3495

chr9	141213431	14931062	0.1057	0.4991
chr10	135534747	15387626	0.1135	0.5215
chr11	135006516	15683315	0.1162	0.5111
chr12	133851895	16592356	0.124	0.5056
chr13	115169878	12050469	0.1046	0.4672
chr14	107349540	11700936	0.109	0.497
chr15	102531392	9037385	0.0881	0.4211
chr16	90354753	9371964	0.1037	0.4706
chr17	81195210	8743973	0.1077	0.4621
chr18	78077248	8874675	0.1137	0.6654
chr19	59128983	6169615	0.1043	0.6112
chr20	63025520	6182238	0.0981	0.4522
chr21	48129895	4322243	0.0898	0.4695
chr22	51304566	3751234	0.0731	0.5271
chrMT	16571	19876	1.1994	1.6624
chrX	155270560	12101134	0.0779	0.4004
chrY	59373566	2759452	0.0465	0.3511

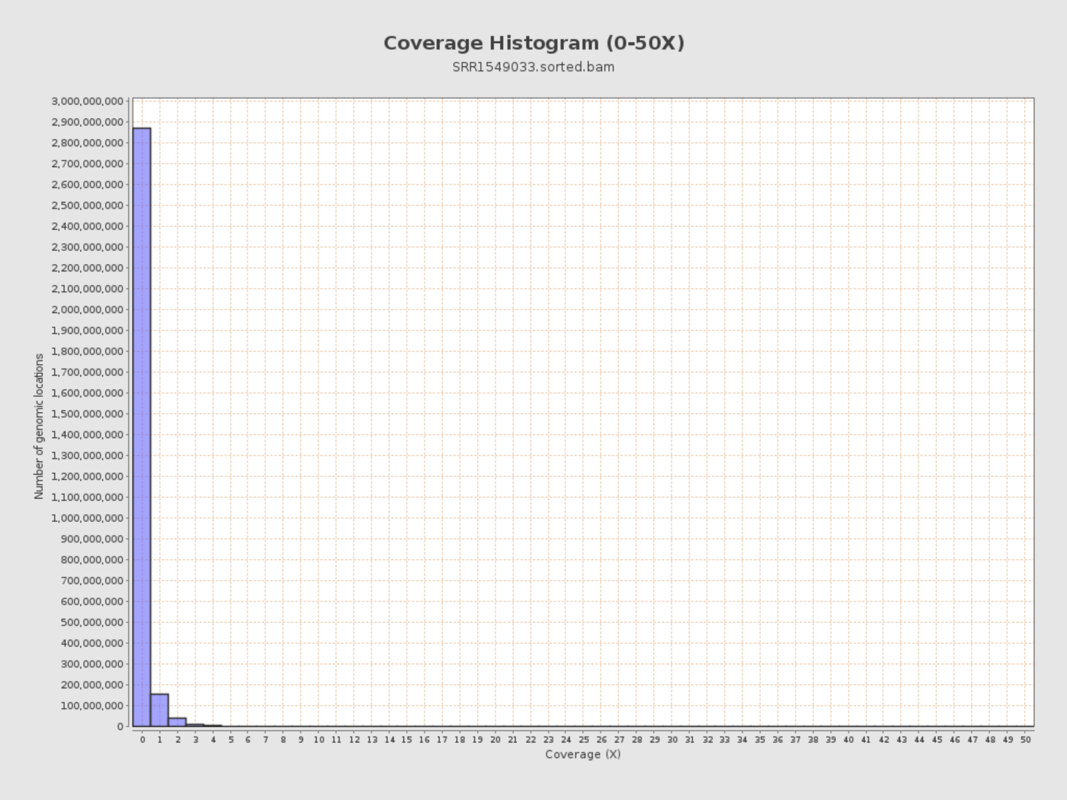
3. Results : Coverage across reference



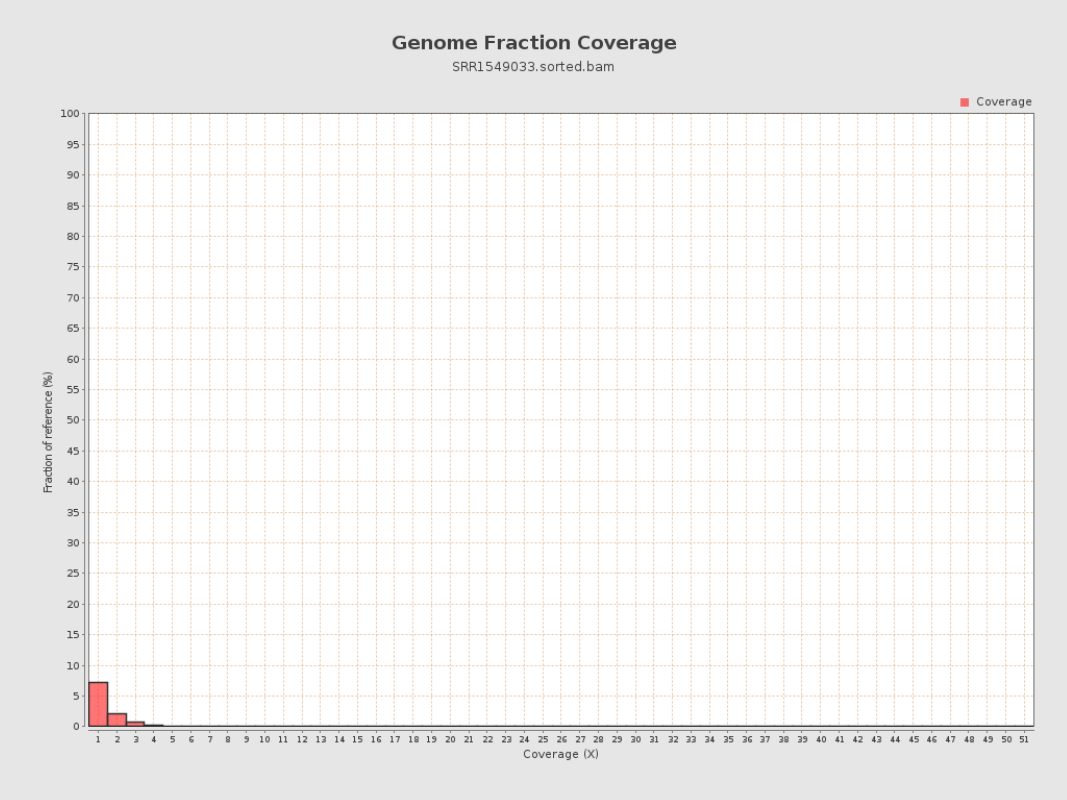
4. Results : Coverage Histogram



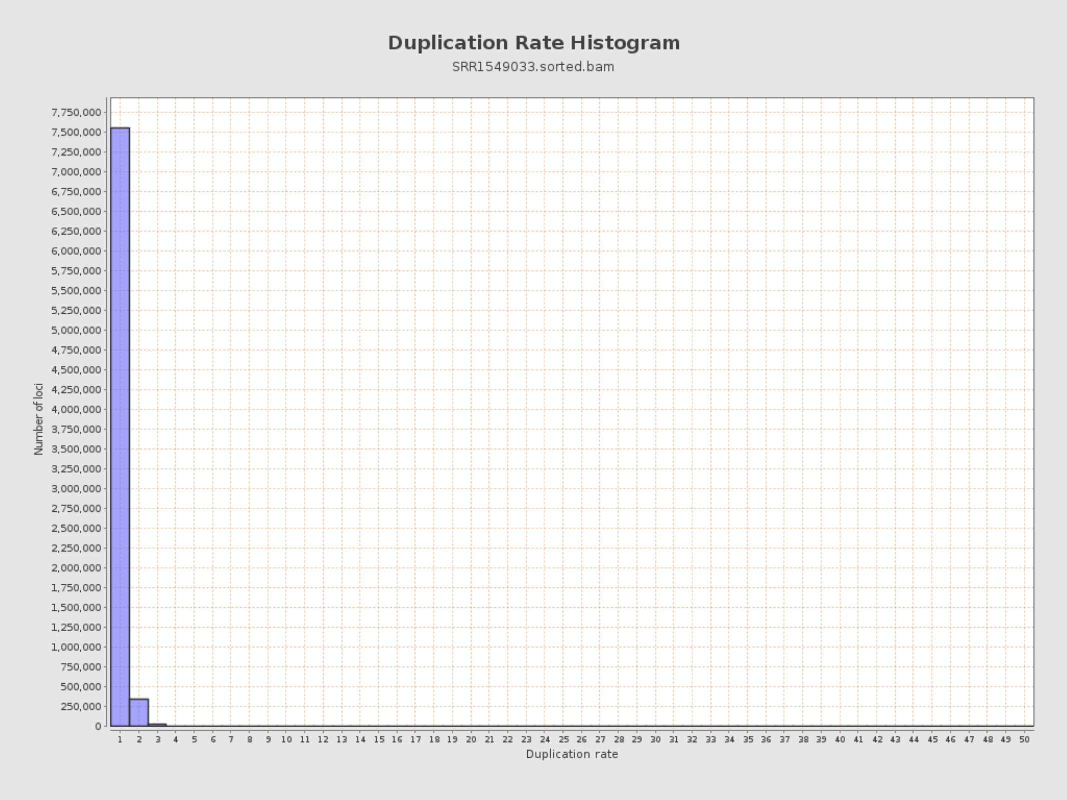
5. Results : Coverage Histogram (0-50X)



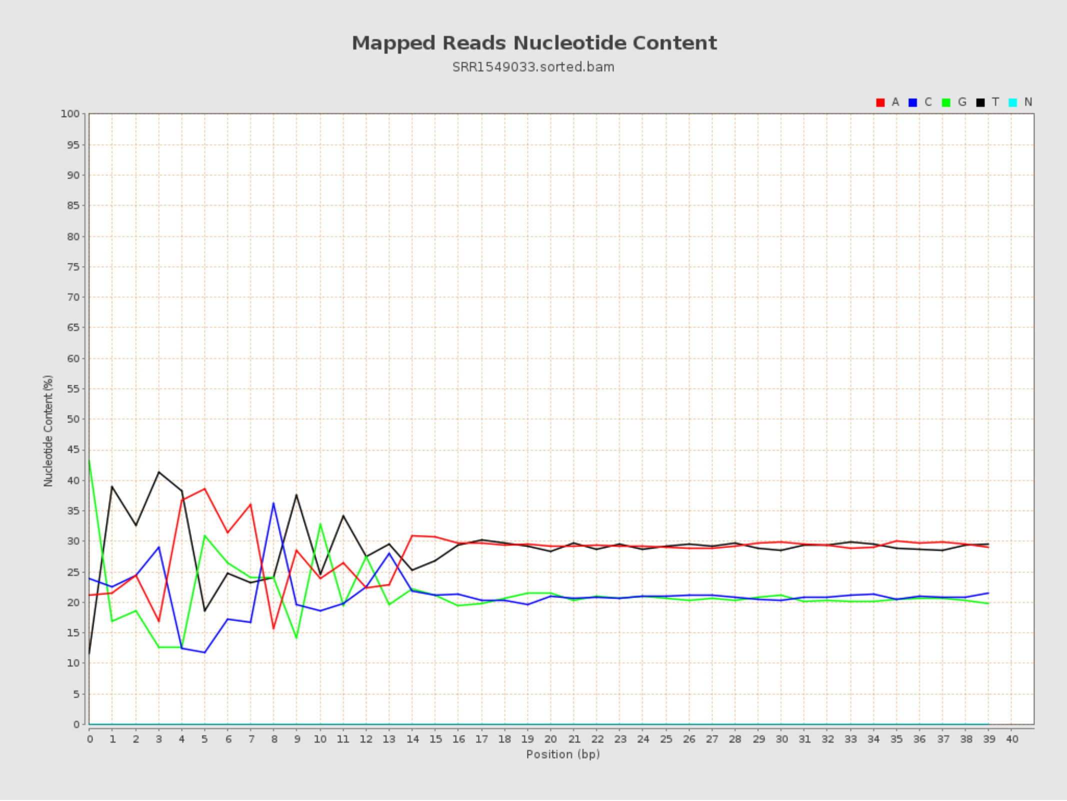
6. Results : Genome Fraction Coverage



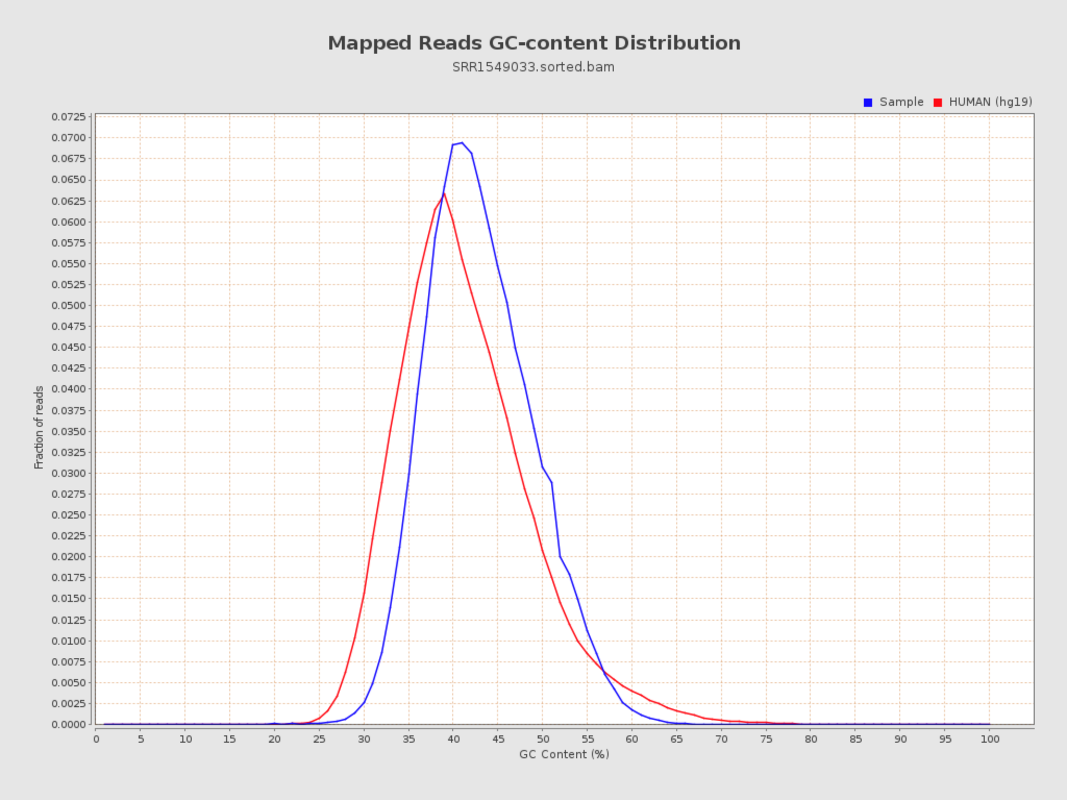
7. Results : Duplication Rate Histogram



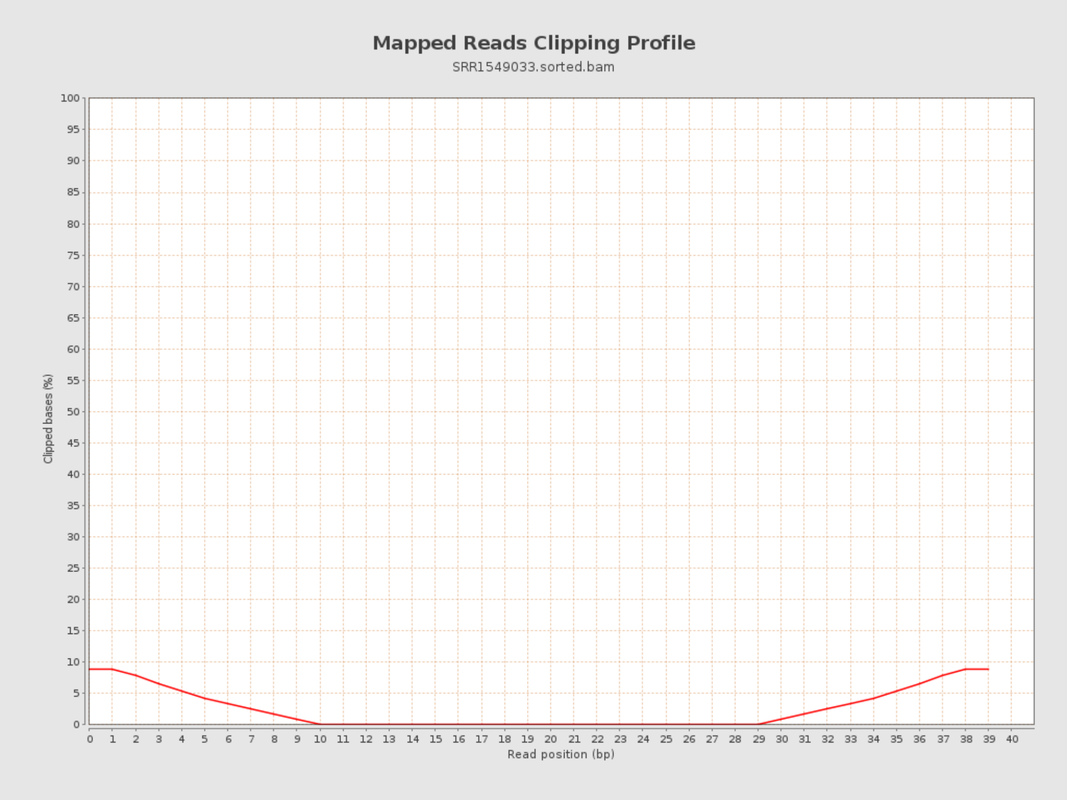
8. Results : Mapped Reads Nucleotide Content



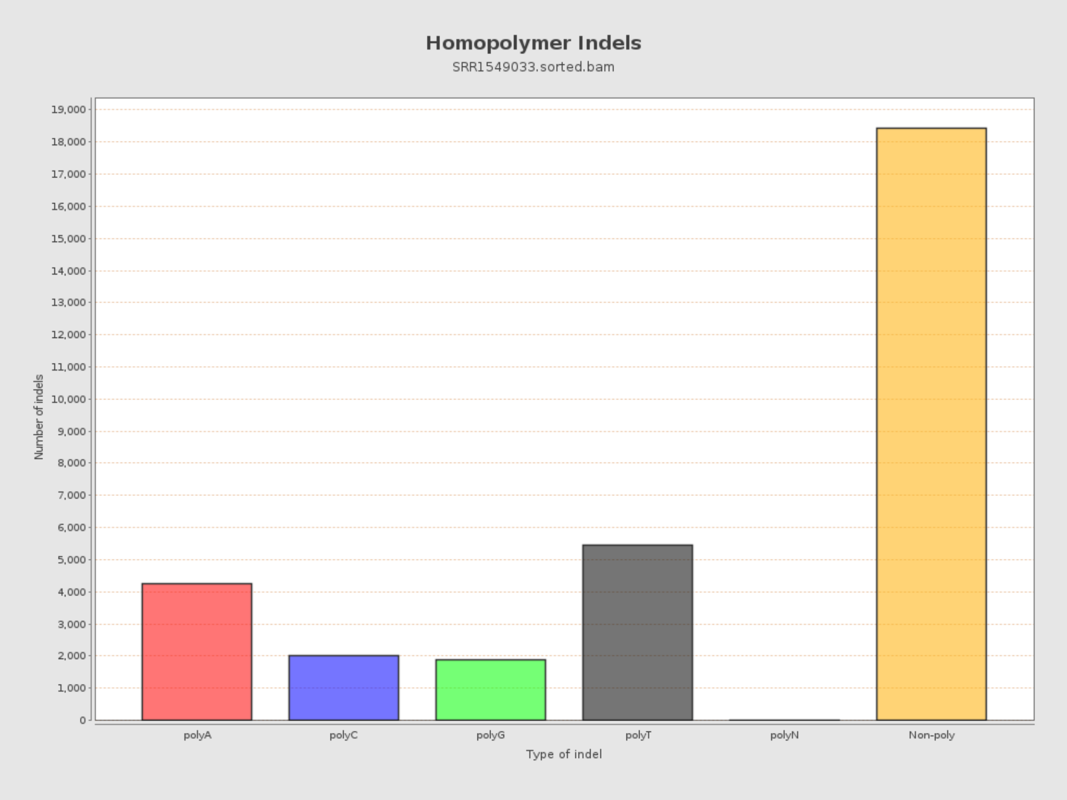
9. Results : Mapped Reads GC-content Distribution



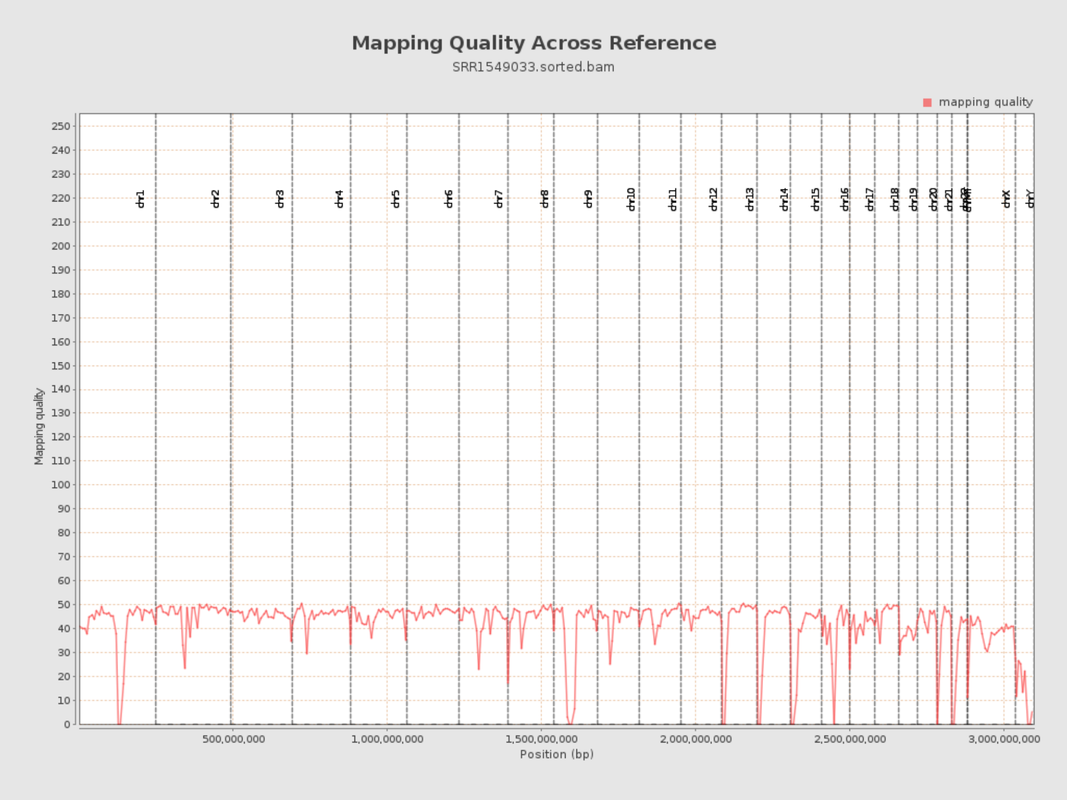
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram