Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:43:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549073.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_SRR1549073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:43:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,447,076
Mapped reads	8,175,440 / 86.54%
Unmapped reads	1,271,636 / 13.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	296,274 / 3.14%
Duplication rate	2.55%
Clipped reads	352,318 / 3.73%

2.2. ACGT Content

Number/percentage of A's	95,937,993 / 29.53%
Number/percentage of C's	66,476,250 / 20.46%
Number/percentage of T's	96,181,365 / 29.6%
Number/percentage of G's	66,316,327 / 20.41%
Number/percentage of N's	5,978 / 0%
GC Percentage	40.87%

2.3. Coverage

Mean	0.105
Standard Deviation	0.8989

2.4. Mapping Quality

Mean Mapping Quality	44.52

2.5. Mismatches and indels

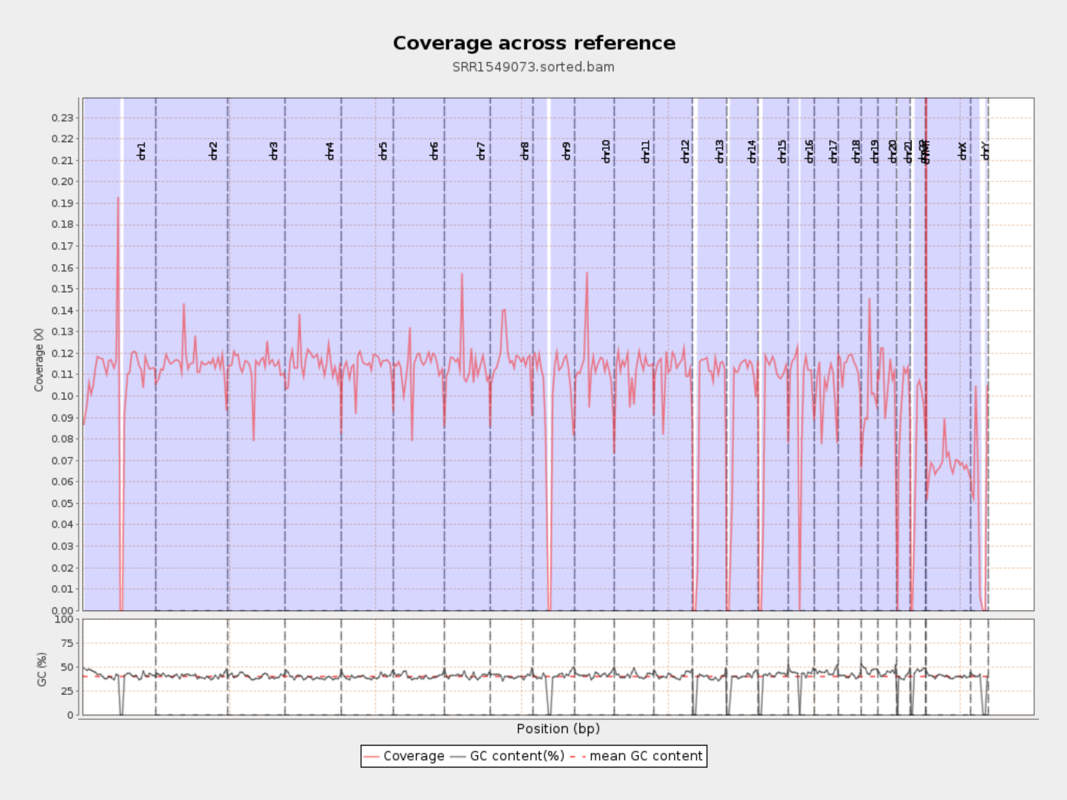
General error rate	0.3%
Mismatches	973,730
Insertions	7,745
Mapped reads with at least one insertion	0.09%
Deletions	25,326
Mapped reads with at least one deletion	0.31%
Homopolymer indels	44.93%

2.6. Chromosome stats

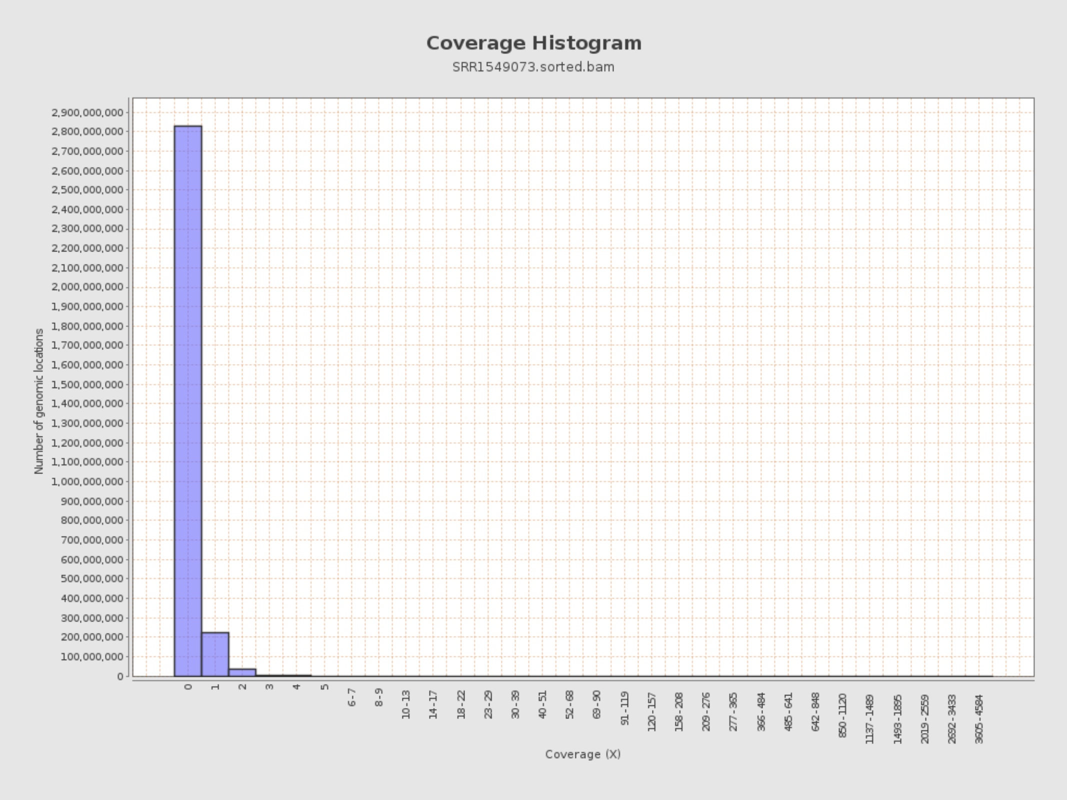
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26636023	0.1069	1.9396
chr2	243199373	28077014	0.1154	0.5653
chr3	198022430	22592046	0.1141	0.3972
chr4	191154276	22125607	0.1157	0.4319
chr5	180915260	20547468	0.1136	0.3997
chr6	171115067	19465476	0.1138	0.462
chr7	159138663	18207566	0.1144	0.8204
chr8	146364022	17170616	0.1173	2.2719

chr9	141213431	13797220	0.0977	0.5184
chr10	135534747	15469696	0.1141	0.6279
chr11	135006516	15114593	0.112	0.5596
chr12	133851895	15071661	0.1126	0.406
chr13	115169878	10920629	0.0948	0.3524
chr14	107349540	10072155	0.0938	0.4009
chr15	102531392	9426202	0.0919	0.3483
chr16	90354753	8905166	0.0986	0.4163
chr17	81195210	8377594	0.1032	0.4096
chr18	78077248	8912956	0.1142	1.058
chr19	59128983	5895901	0.0997	1.365
chr20	63025520	6804655	0.108	0.3985
chr21	48129895	4290074	0.0891	0.4152
chr22	51304566	3605098	0.0703	0.3405
chrMT	16571	10554	0.6369	1.0756
chrX	155270560	10545004	0.0679	0.3848
chrY	59373566	2909175	0.049	0.5261

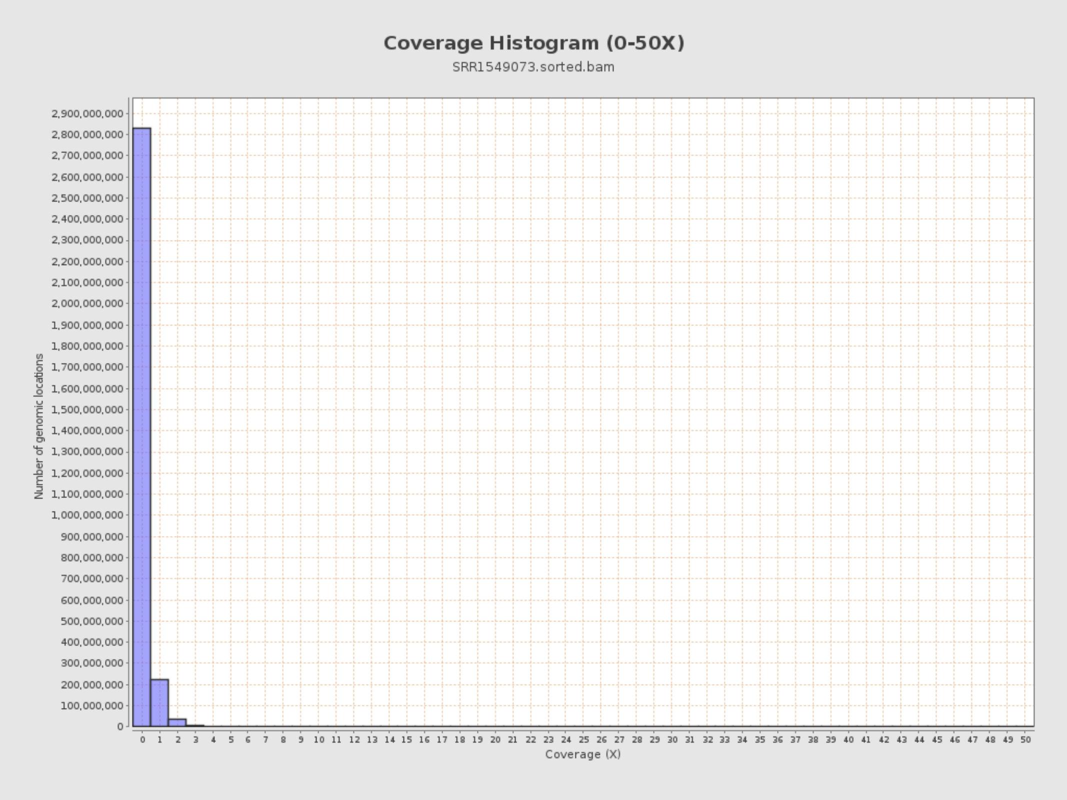
3. Results : Coverage across reference



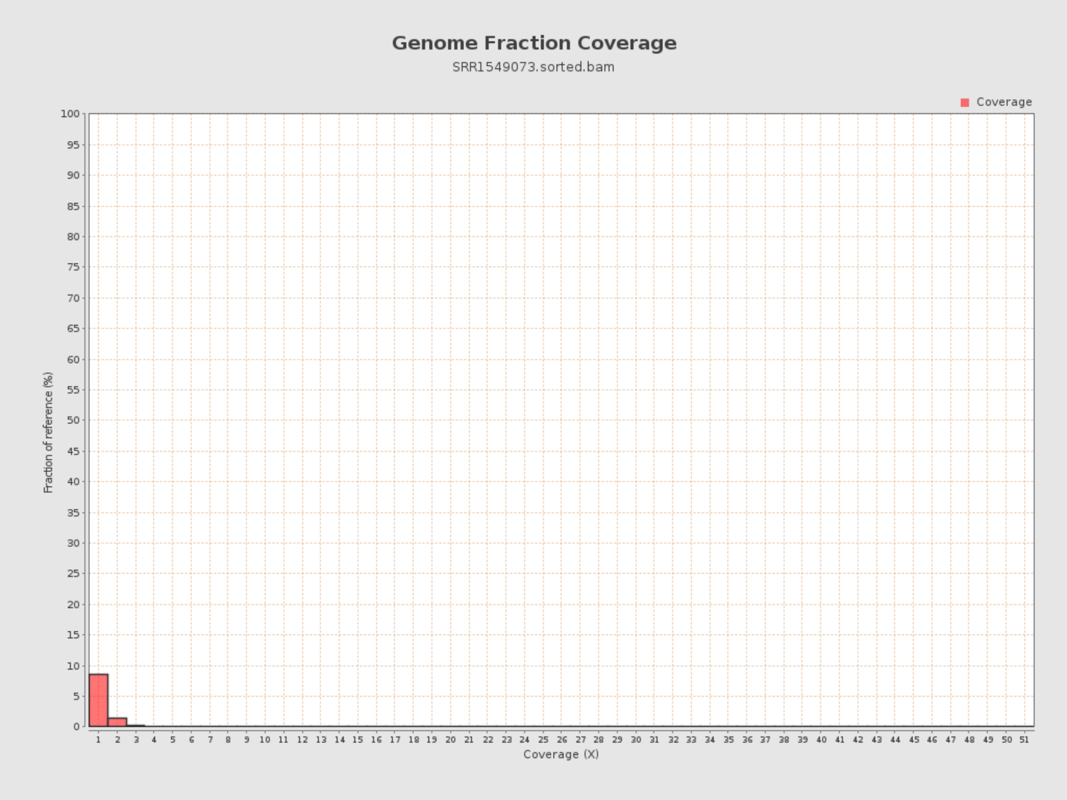
4. Results : Coverage Histogram



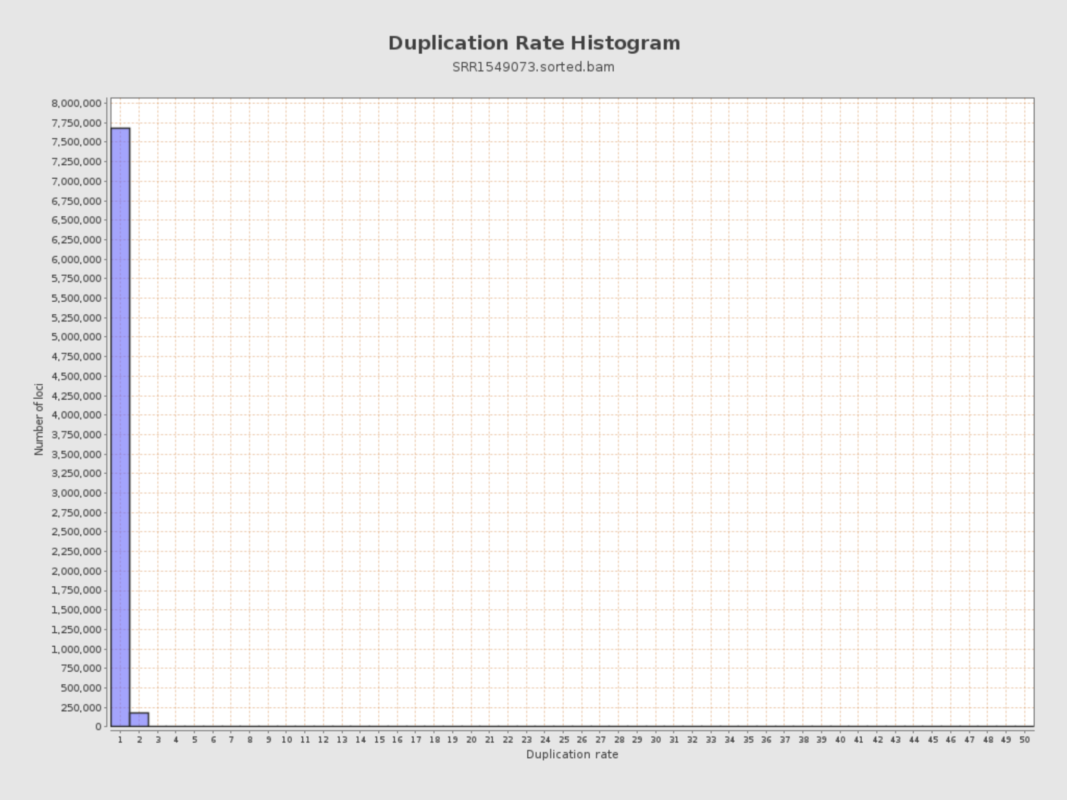
5. Results : Coverage Histogram (0-50X)



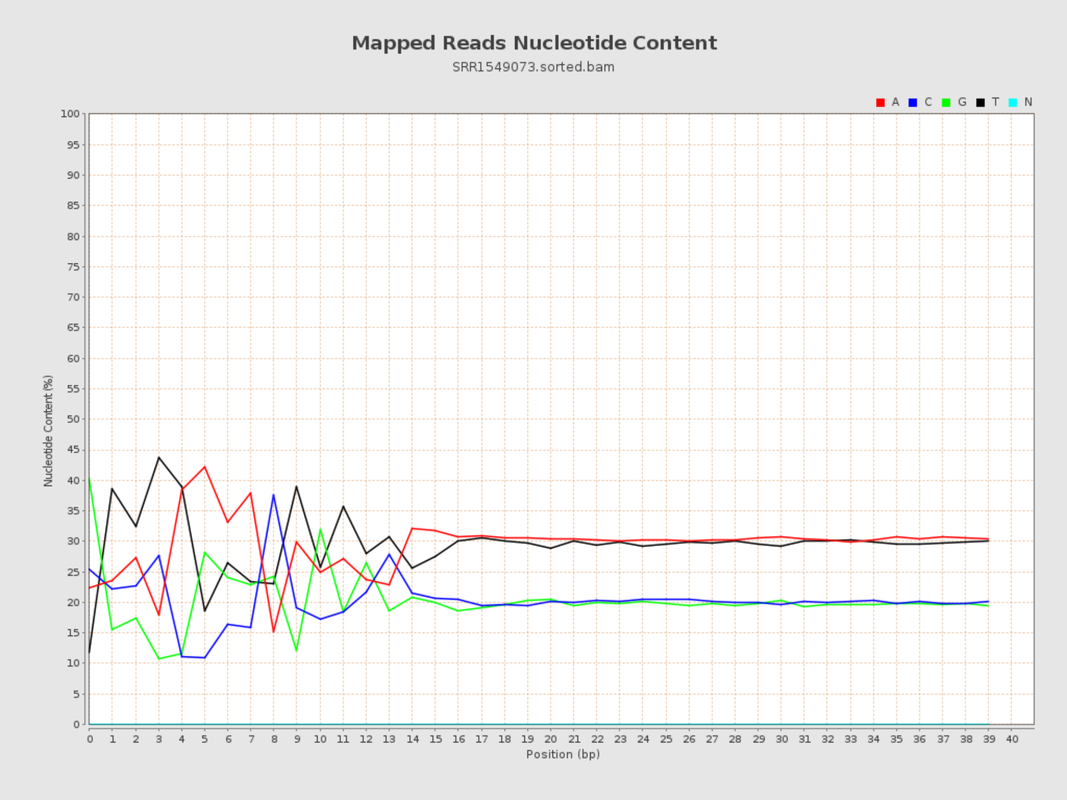
6. Results : Genome Fraction Coverage



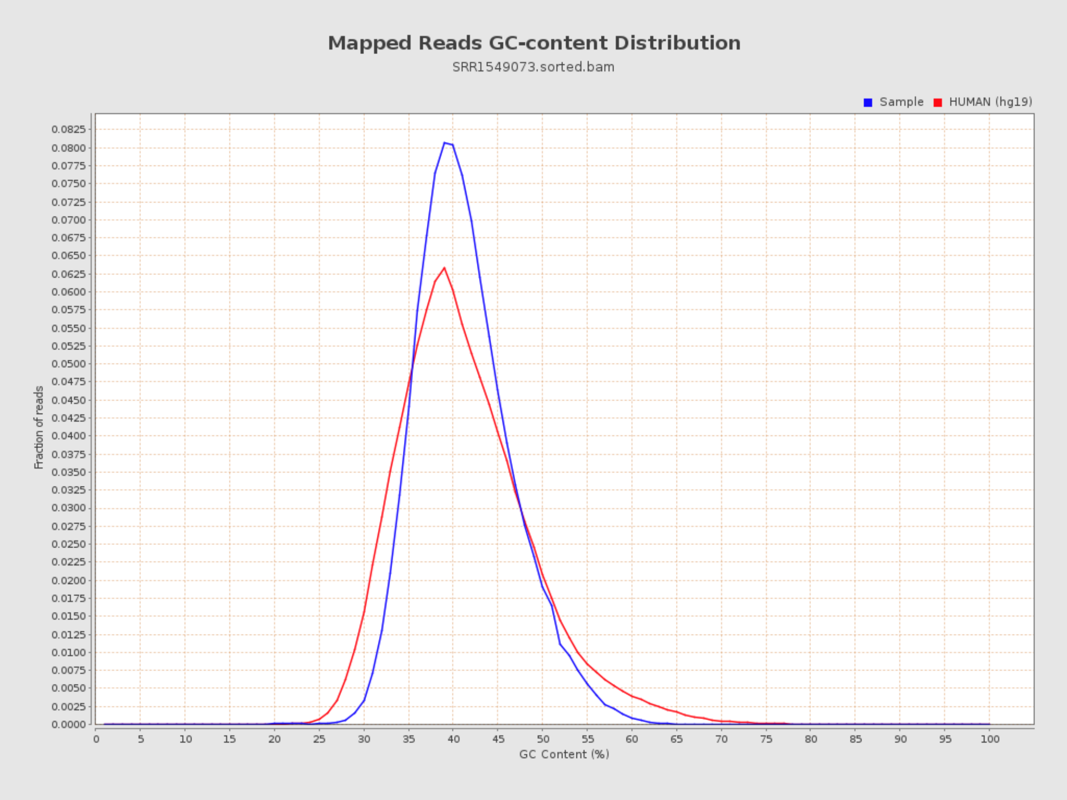
7. Results : Duplication Rate Histogram



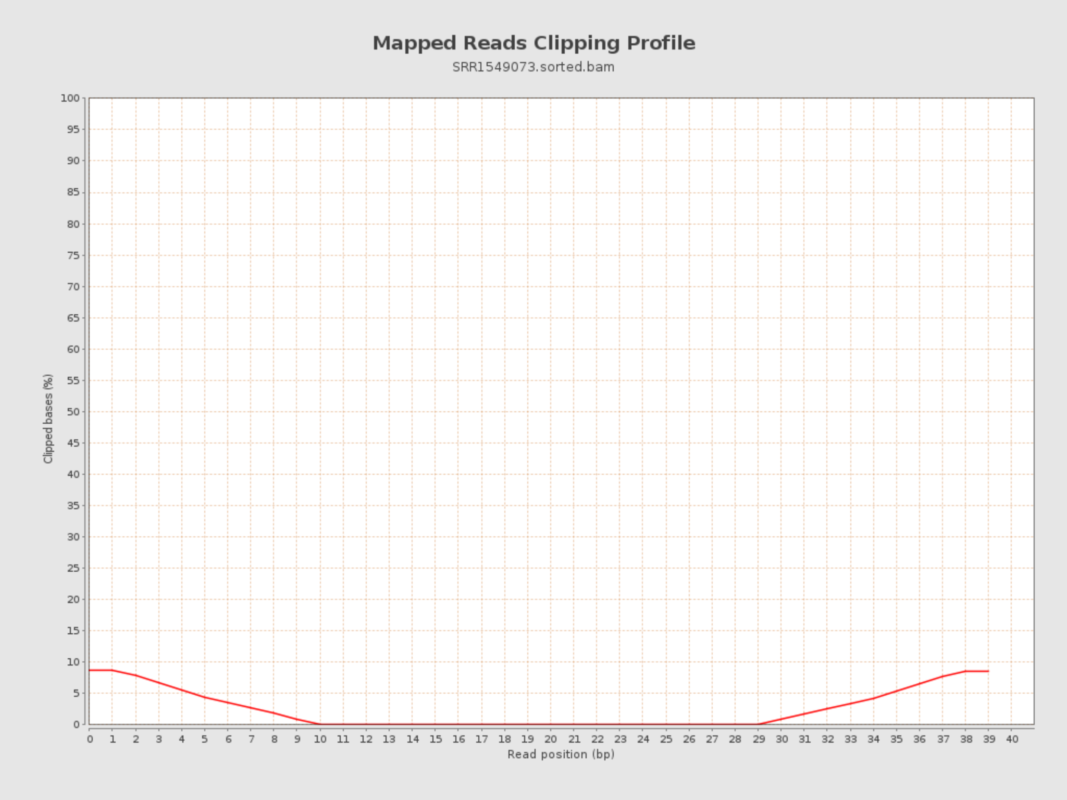
8. Results : Mapped Reads Nucleotide Content



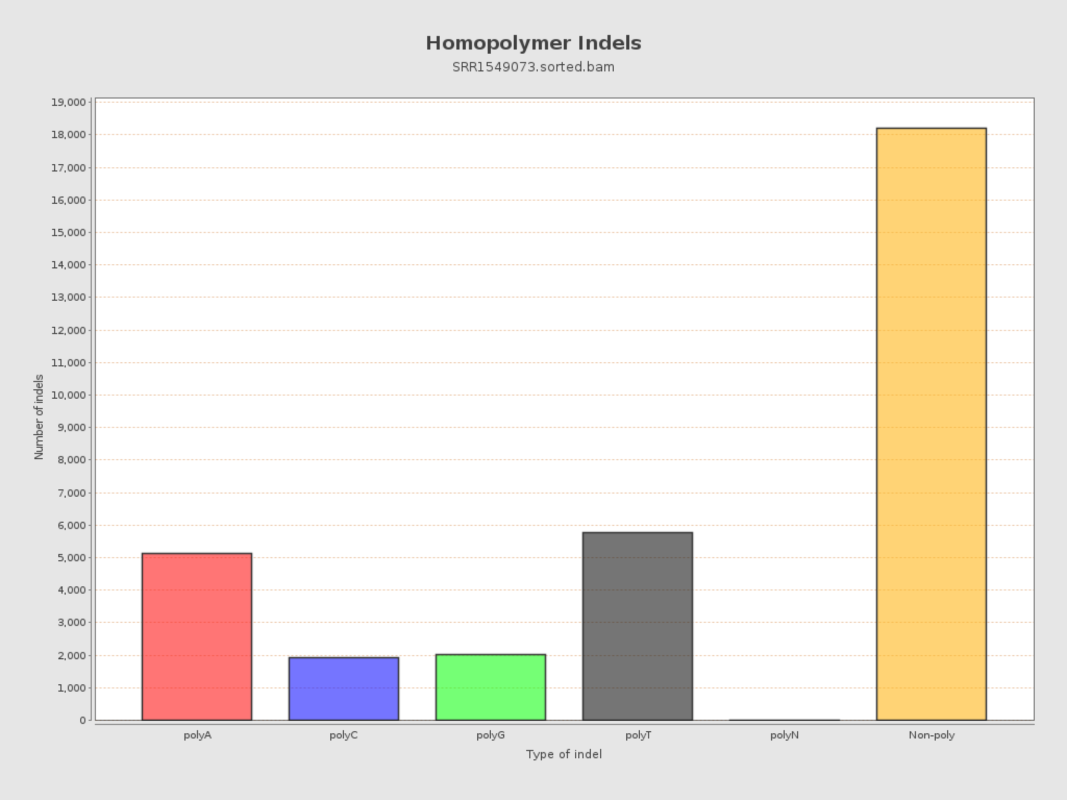
9. Results : Mapped Reads GC-content Distribution



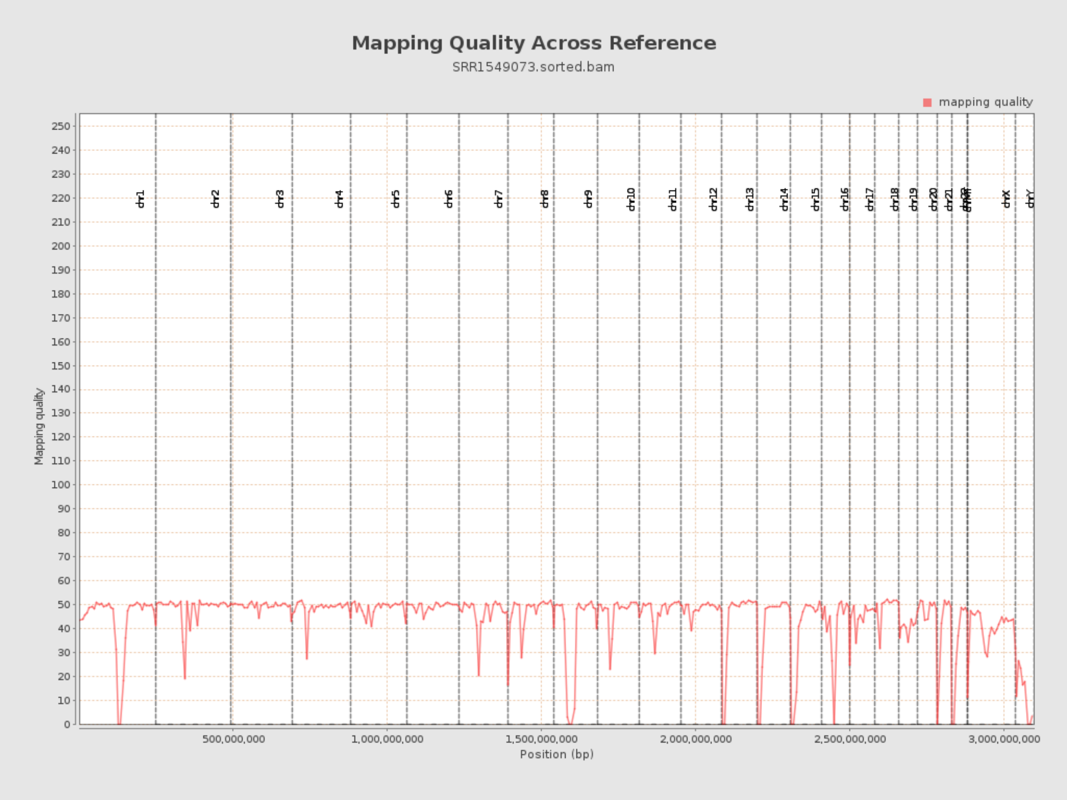
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram