Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:38:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549102.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_SRR1549102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549102.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:38:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,687,610
Mapped reads	9,111,926 / 85.26%
Unmapped reads	1,575,684 / 14.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	421,564 / 3.94%
Duplication rate	3.44%
Clipped reads	473,830 / 4.43%

2.2. ACGT Content

Number/percentage of A's	109,034,417 / 30.16%
Number/percentage of C's	71,175,503 / 19.69%
Number/percentage of T's	110,102,692 / 30.46%
Number/percentage of G's	71,202,307 / 19.7%
Number/percentage of N's	1,442 / 0%
GC Percentage	39.38%

2.3. Coverage

Mean	0.1168
Standard Deviation	0.8339

2.4. Mapping Quality

Mean Mapping Quality	44.14

2.5. Mismatches and indels

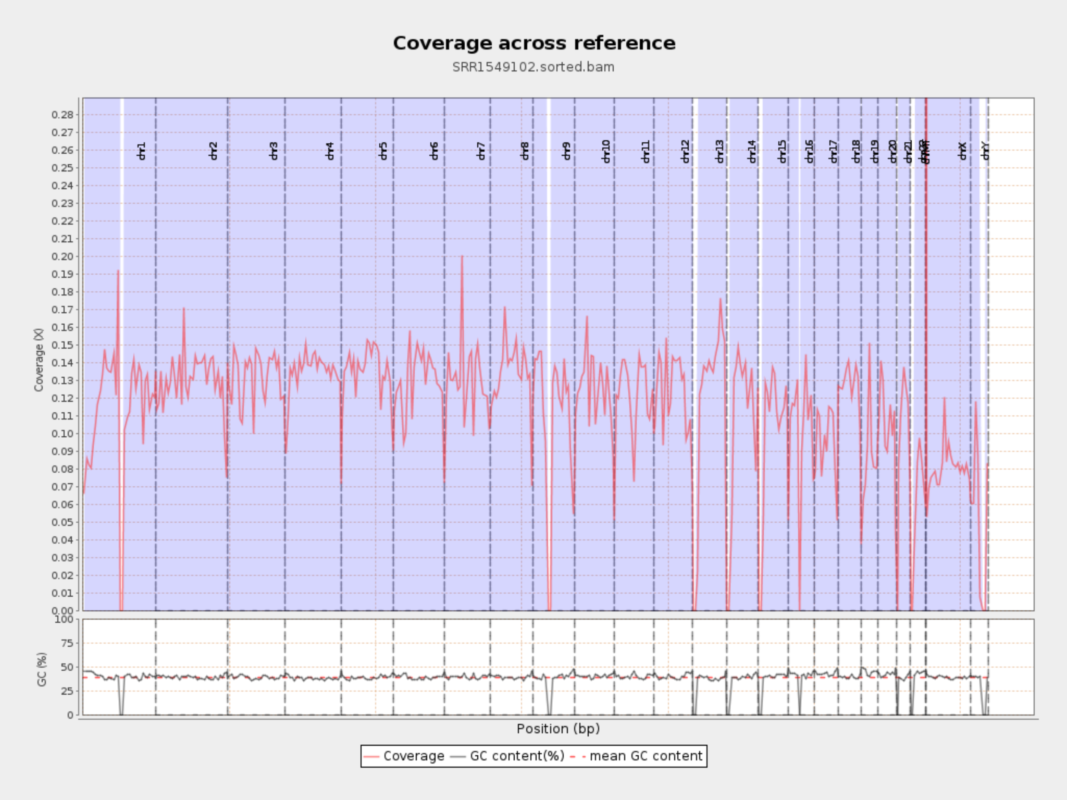
General error rate	0.3%
Mismatches	1,079,455
Insertions	9,113
Mapped reads with at least one insertion	0.1%
Deletions	26,615
Mapped reads with at least one deletion	0.29%
Homopolymer indels	45.33%

2.6. Chromosome stats

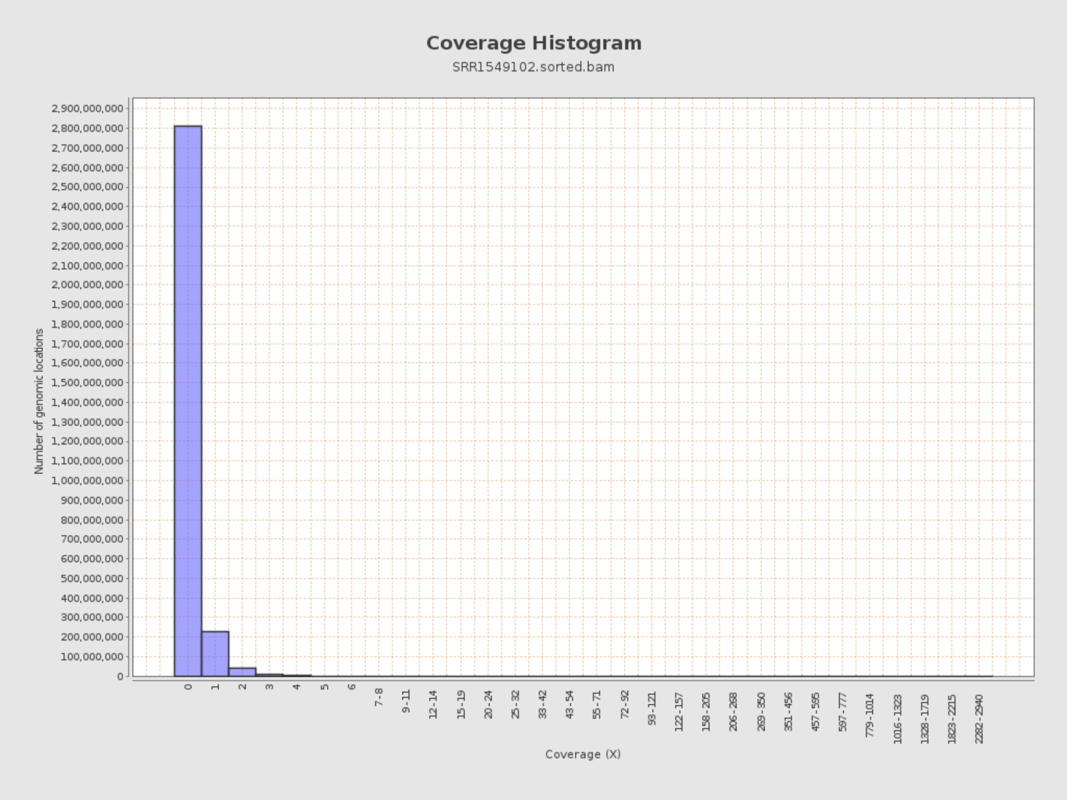
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28165794	0.113	1.6625
chr2	243199373	31668620	0.1302	0.6858
chr3	198022430	26184866	0.1322	0.4451
chr4	191154276	25817745	0.1351	0.4672
chr5	180915260	24395314	0.1348	0.4603
chr6	171115067	22359254	0.1307	0.5151
chr7	159138663	20628299	0.1296	1.1351
chr8	146364022	19663749	0.1343	1.5334

chr9	141213431	15335615	0.1086	0.6561
chr10	135534747	17039740	0.1257	0.6718
chr11	135006516	16432872	0.1217	0.6394
chr12	133851895	16617440	0.1241	0.4594
chr13	115169878	13620524	0.1183	0.4143
chr14	107349540	11294227	0.1052	0.5343
chr15	102531392	10000389	0.0975	0.3742
chr16	90354753	8970912	0.0993	0.4564
chr17	81195210	7827944	0.0964	0.4264
chr18	78077248	10078806	0.1291	1.4278
chr19	59128983	5171553	0.0875	1.2868
chr20	63025520	6794359	0.1078	0.4329
chr21	48129895	4800527	0.0997	0.4664
chr22	51304566	3020425	0.0589	0.3136
chrMT	16571	87692	5.2919	6.5018
chrX	155270560	12491664	0.0805	0.4639
chrY	59373566	3081338	0.0519	0.4467

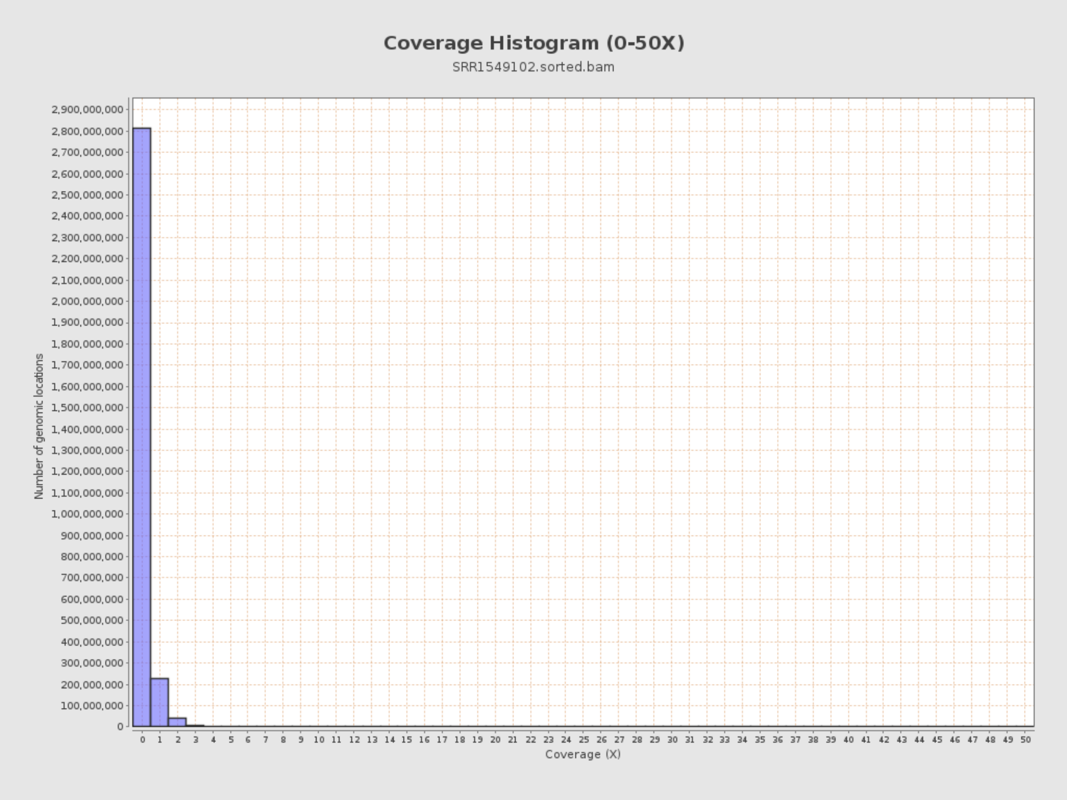
3. Results : Coverage across reference



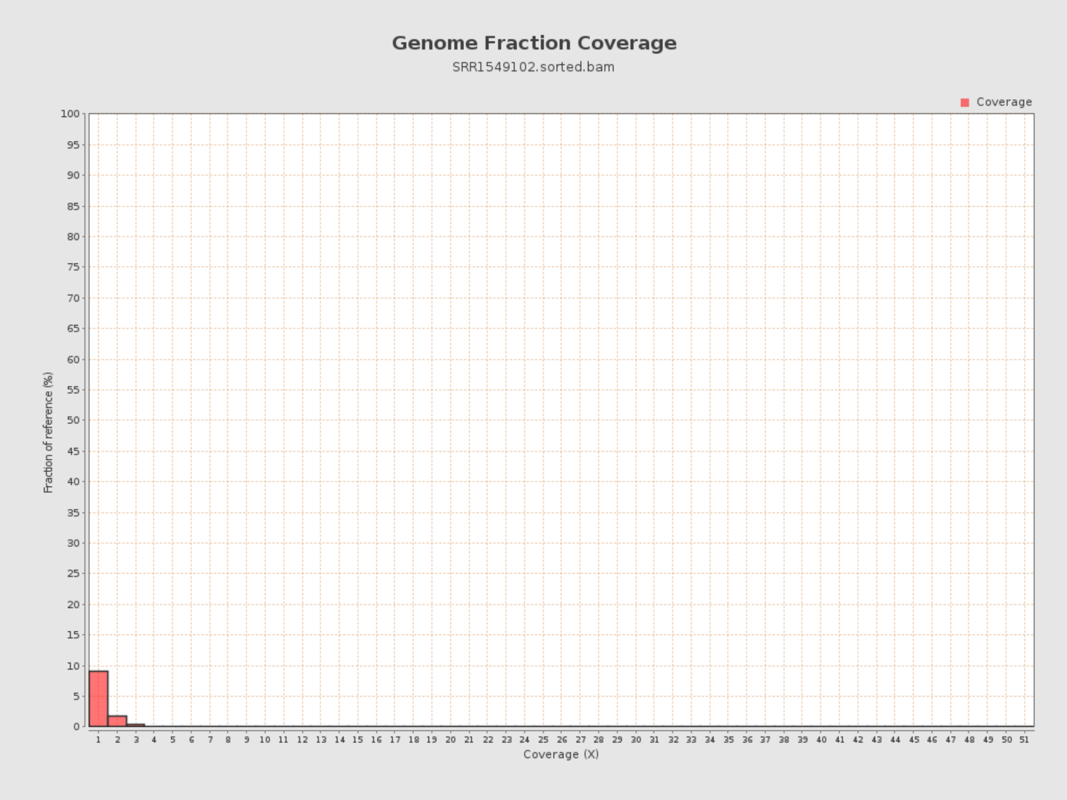
4. Results : Coverage Histogram



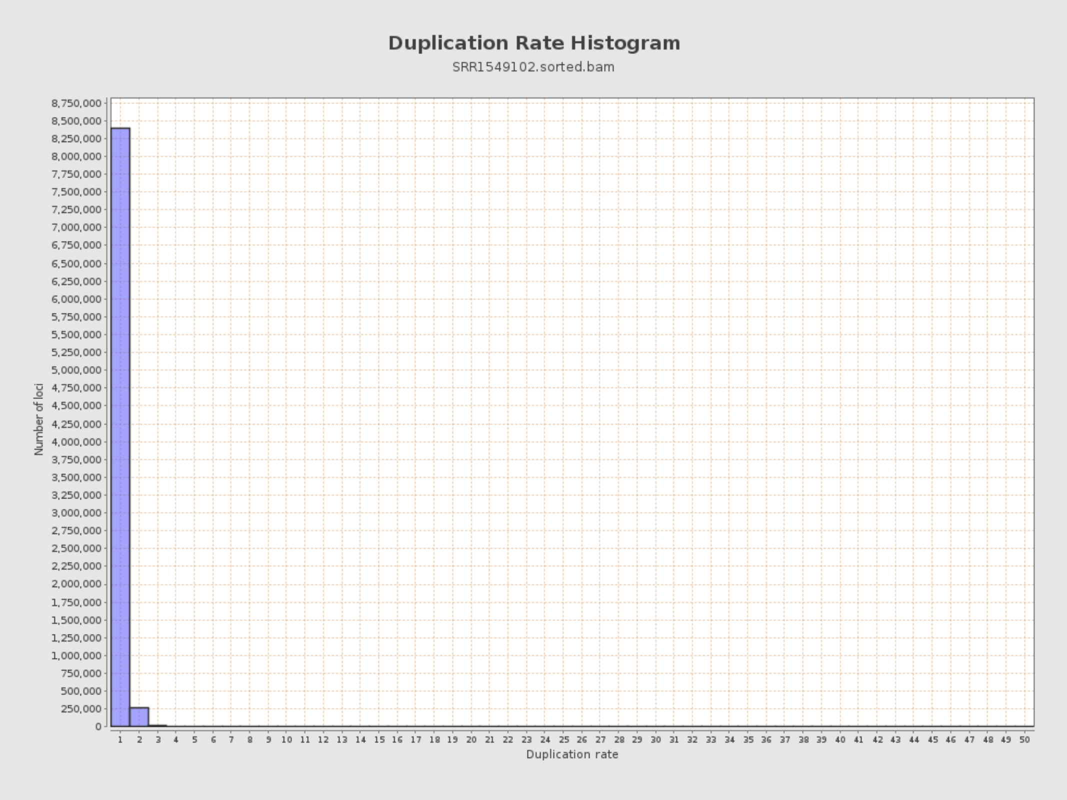
5. Results : Coverage Histogram (0-50X)



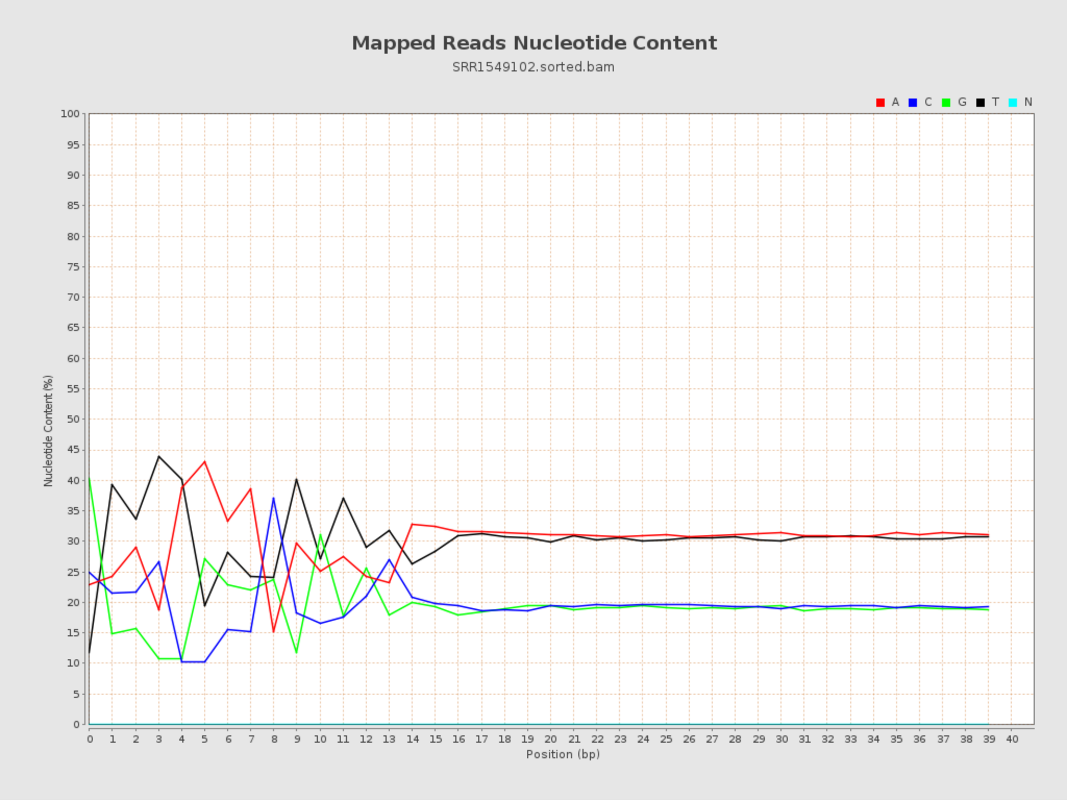
6. Results : Genome Fraction Coverage



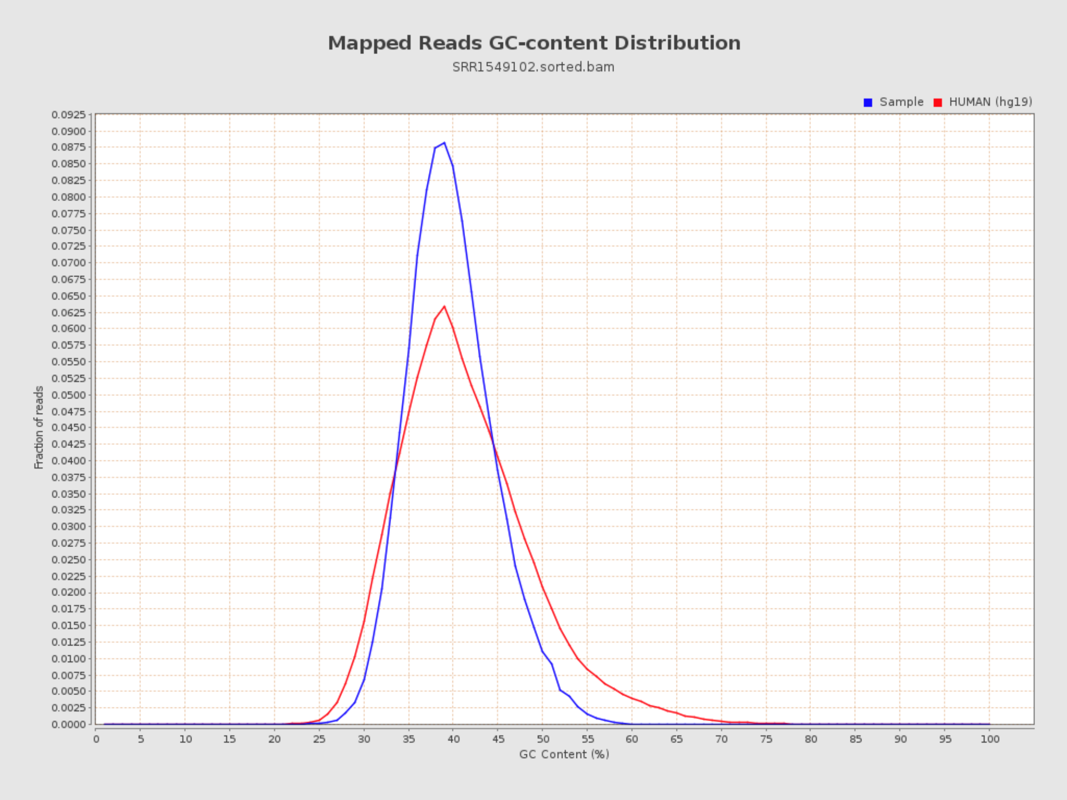
7. Results : Duplication Rate Histogram



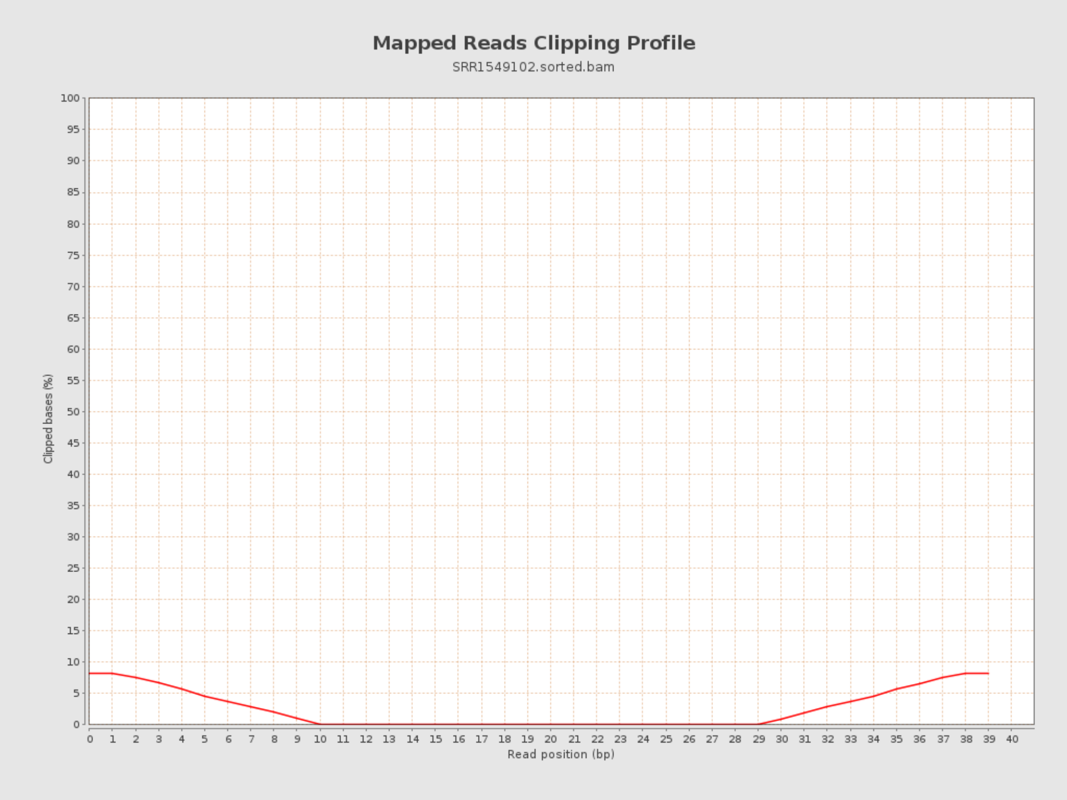
8. Results : Mapped Reads Nucleotide Content



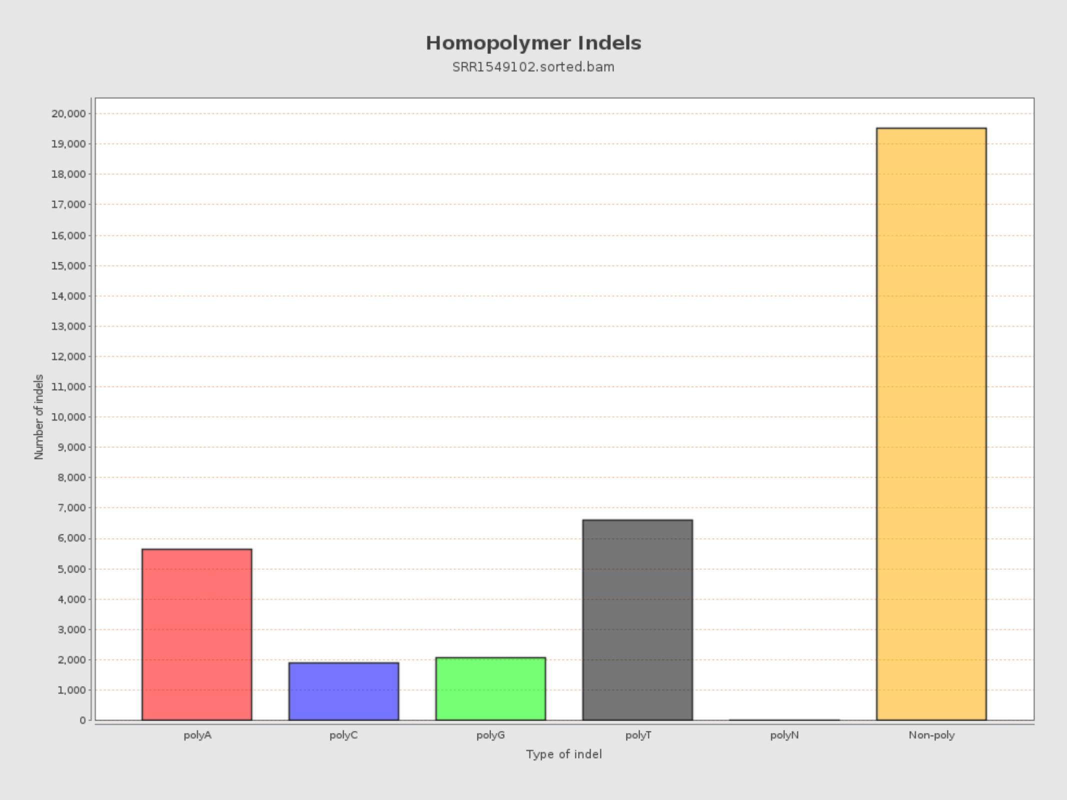
9. Results : Mapped Reads GC-content Distribution



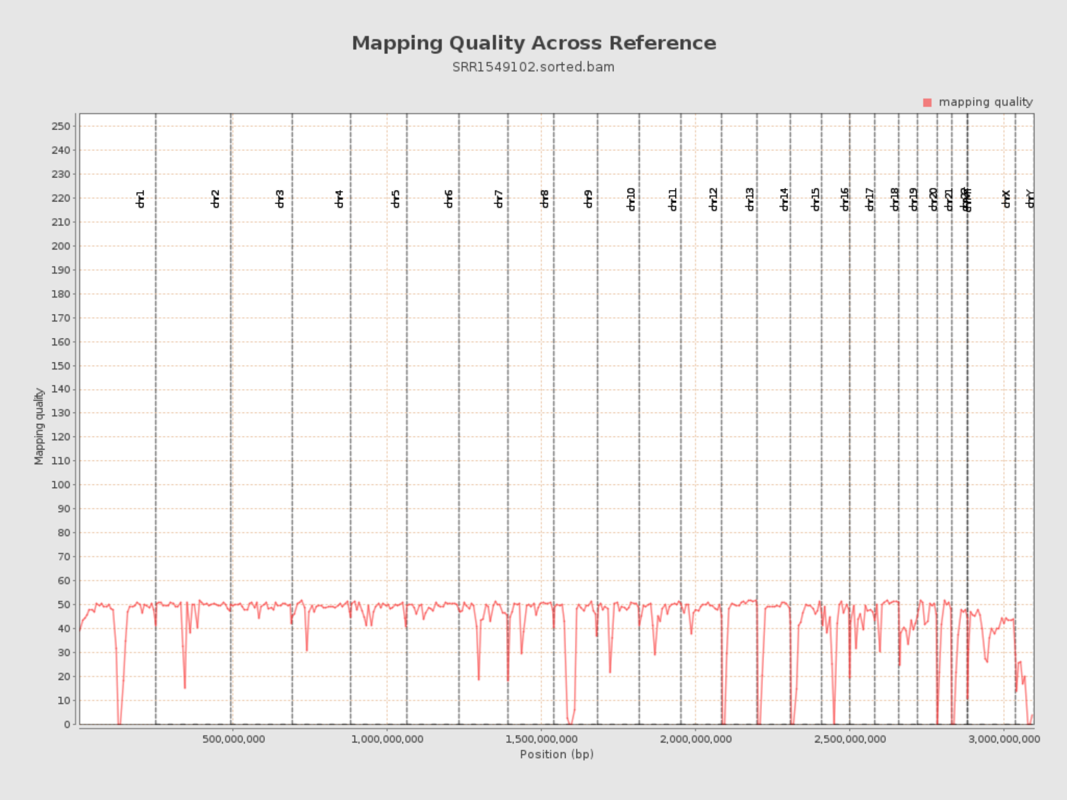
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram