Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:28:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549101.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_SRR1549101 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549101.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:28:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549101.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,866,452
Mapped reads	10,620,808 / 82.55%
Unmapped reads	2,245,644 / 17.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	464,927 / 3.61%
Duplication rate	2.96%
Clipped reads	938,632 / 7.3%

2.2. ACGT Content

Number/percentage of A's	127,179,261 / 30.3%
Number/percentage of C's	83,132,958 / 19.8%
Number/percentage of T's	126,952,285 / 30.24%
Number/percentage of G's	82,505,069 / 19.65%
Number/percentage of N's	1,716 / 0%
GC Percentage	39.46%

2.3. Coverage

Mean	0.1356
Standard Deviation	1.2936

2.4. Mapping Quality

Mean Mapping Quality	41.72

2.5. Mismatches and indels

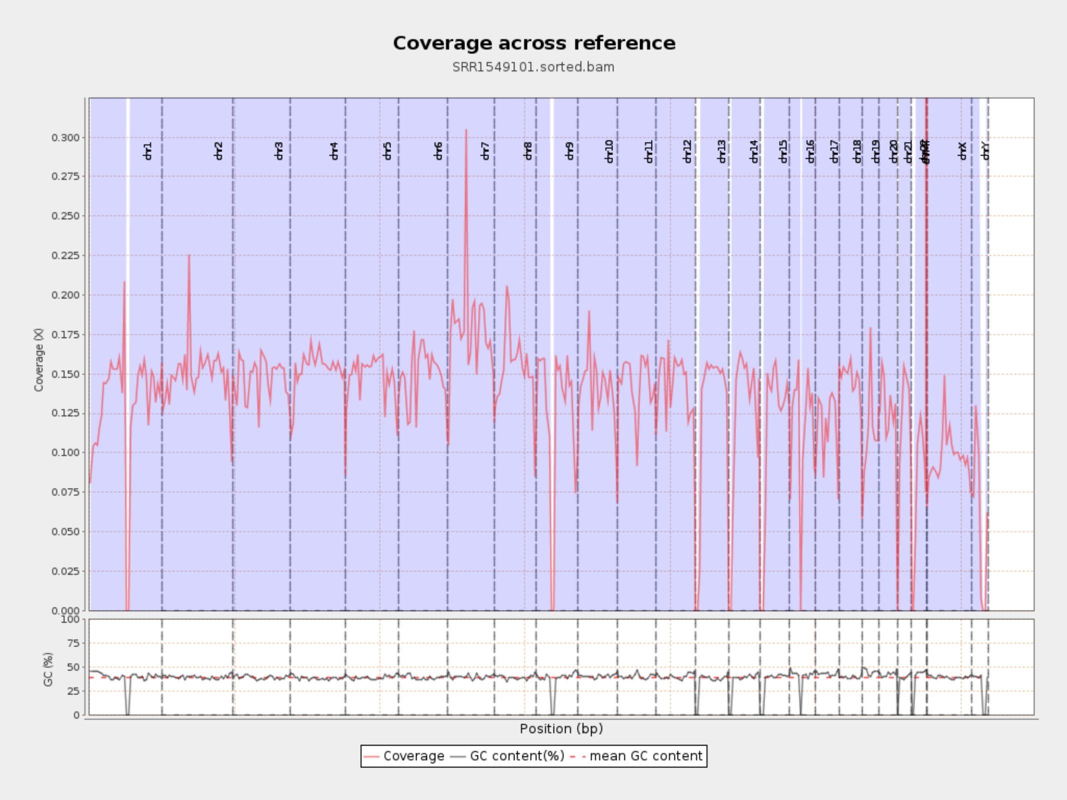
General error rate	0.37%
Mismatches	1,538,591
Insertions	16,032
Mapped reads with at least one insertion	0.15%
Deletions	38,065
Mapped reads with at least one deletion	0.36%
Homopolymer indels	43.44%

2.6. Chromosome stats

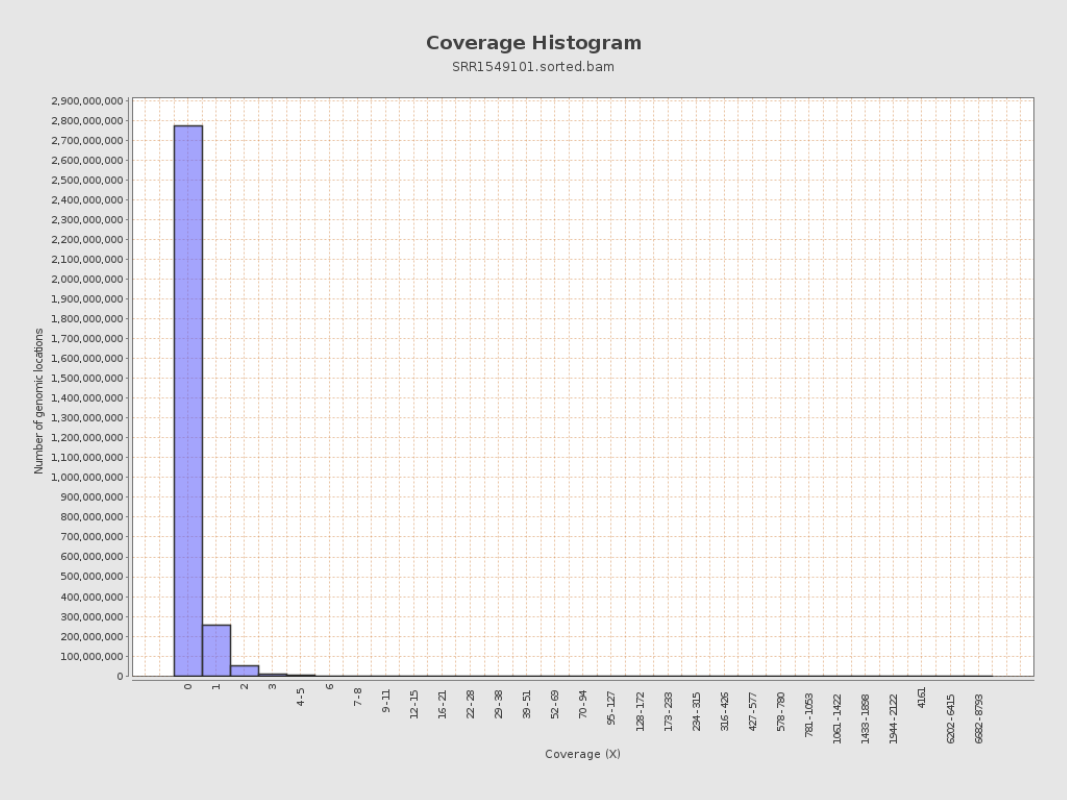
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32489490	0.1303	1.6206
chr2	243199373	36505866	0.1501	0.8874
chr3	198022430	29280006	0.1479	0.478
chr4	191154276	29265095	0.1531	0.5131
chr5	180915260	26982231	0.1491	0.498
chr6	171115067	25600577	0.1496	0.5577
chr7	159138663	28847089	0.1813	1.8467
chr8	146364022	22468147	0.1535	4.2867

chr9	141213431	17664417	0.1251	0.8947
chr10	135534747	19349191	0.1428	0.7329
chr11	135006516	19293529	0.1429	0.7857
chr12	133851895	19138192	0.143	0.5128
chr13	115169878	14300993	0.1242	0.4282
chr14	107349540	12962353	0.1207	0.7048
chr15	102531392	11730660	0.1144	0.4199
chr16	90354753	10471583	0.1159	0.545
chr17	81195210	9374312	0.1155	0.4725
chr18	78077248	11537986	0.1478	1.7504
chr19	59128983	6751361	0.1142	1.4609
chr20	63025520	7999115	0.1269	0.49
chr21	48129895	5534989	0.115	0.5455
chr22	51304566	3830577	0.0747	0.5152
chrMT	16571	84547	5.1021	5.183
chrX	155270560	15101655	0.0973	0.5479
chrY	59373566	3254463	0.0548	0.3939

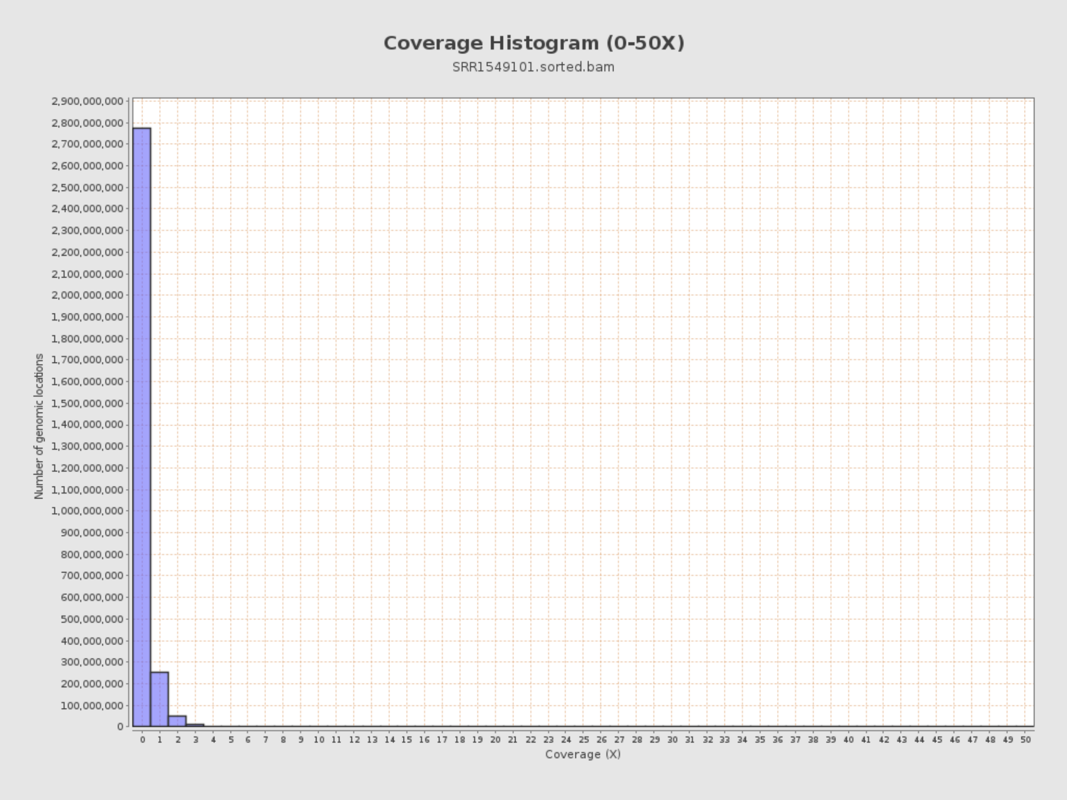
3. Results : Coverage across reference



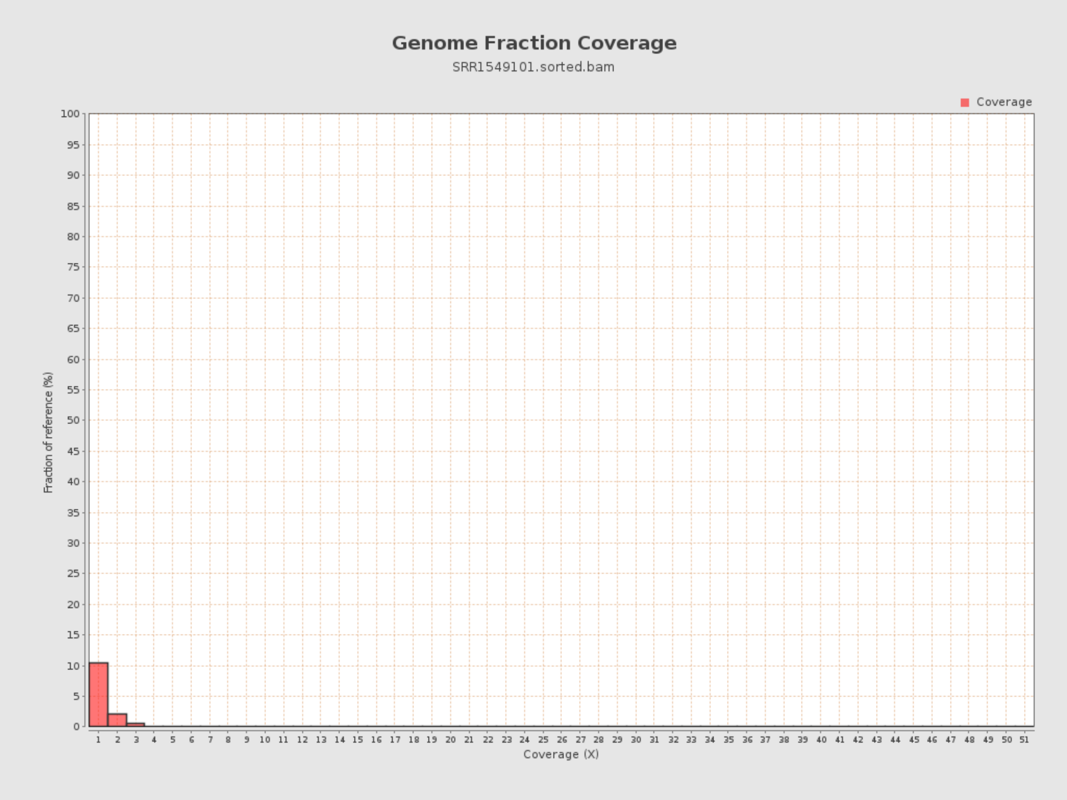
4. Results : Coverage Histogram



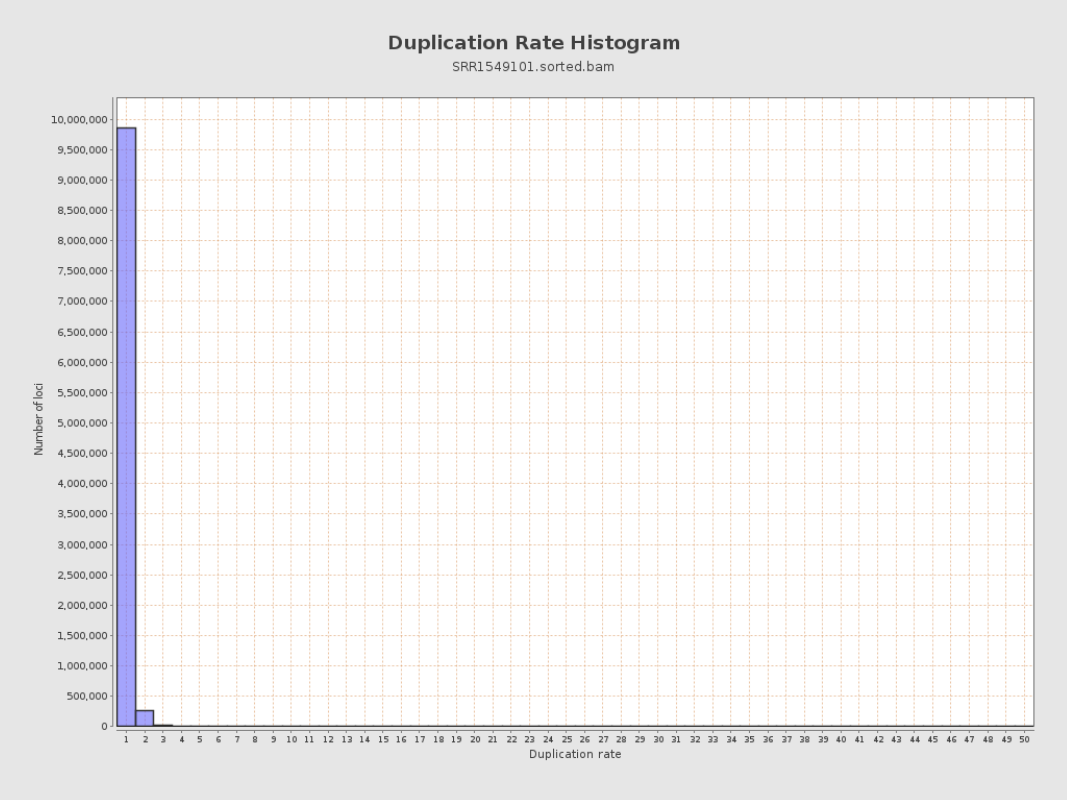
5. Results : Coverage Histogram (0-50X)



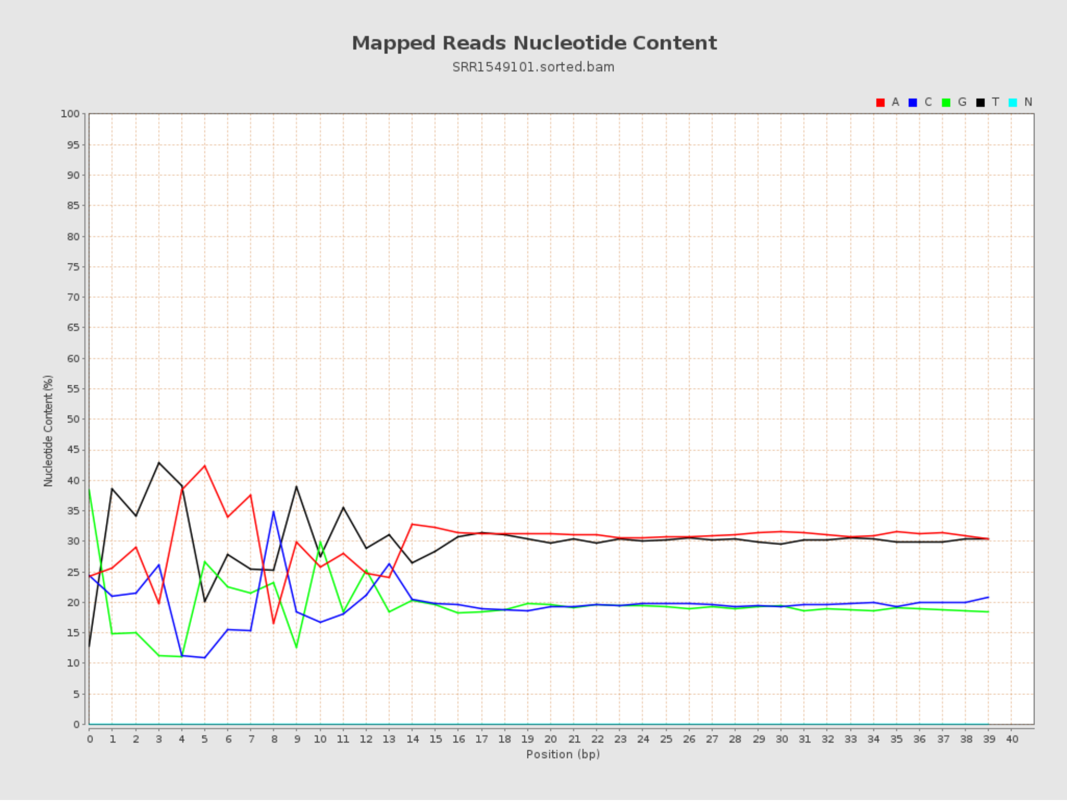
6. Results : Genome Fraction Coverage



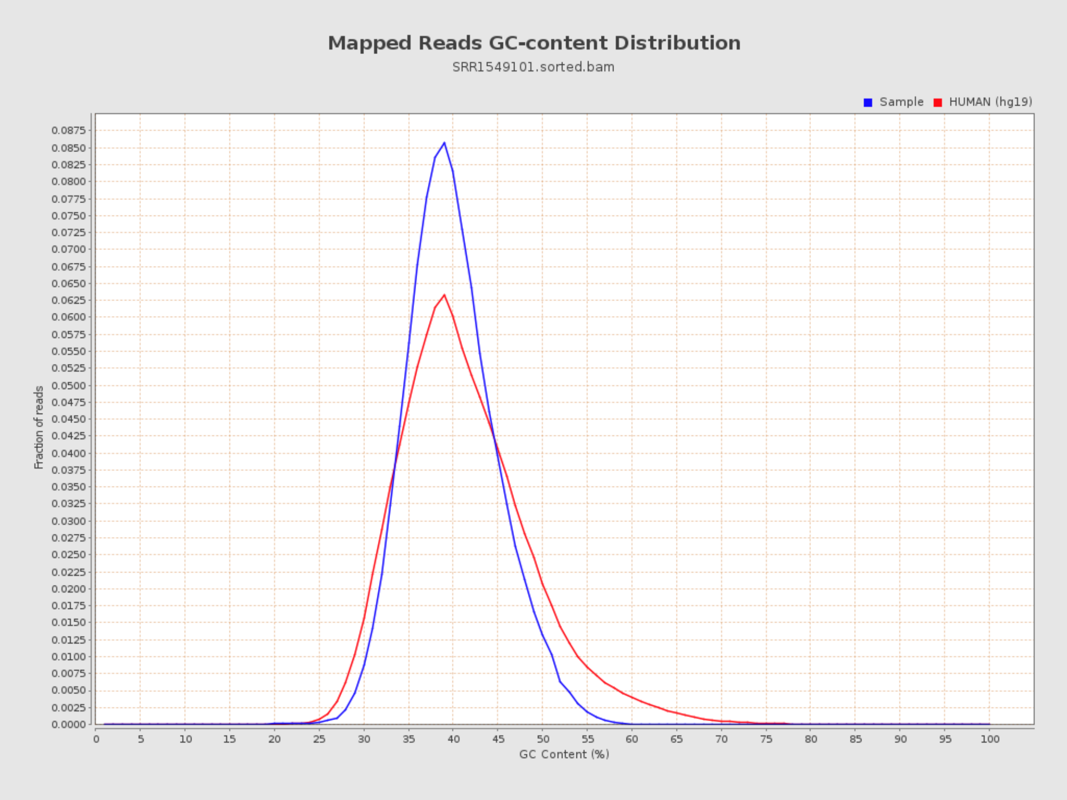
7. Results : Duplication Rate Histogram



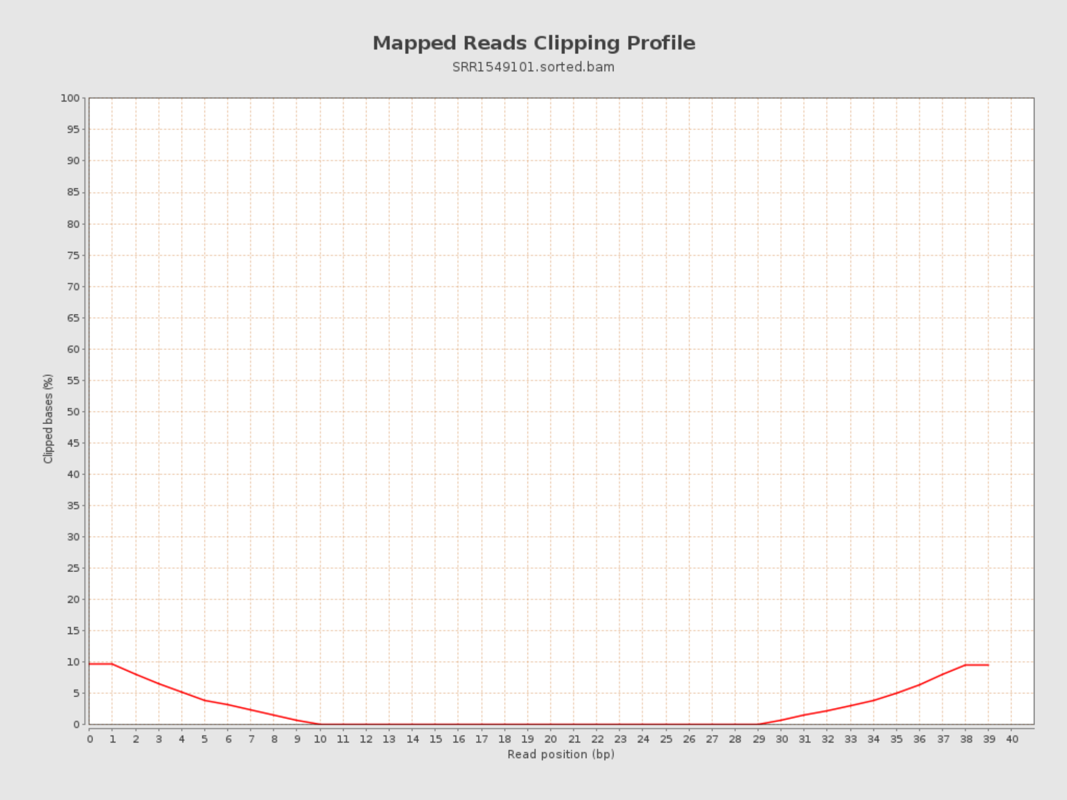
8. Results : Mapped Reads Nucleotide Content



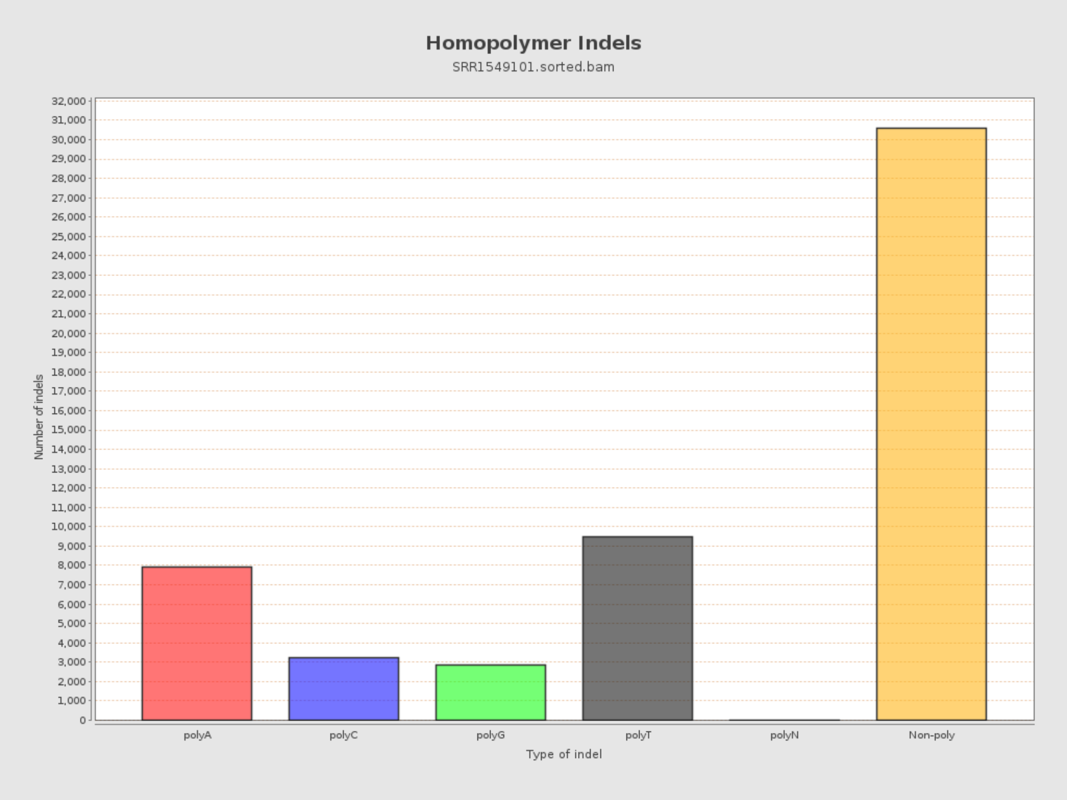
9. Results : Mapped Reads GC-content Distribution



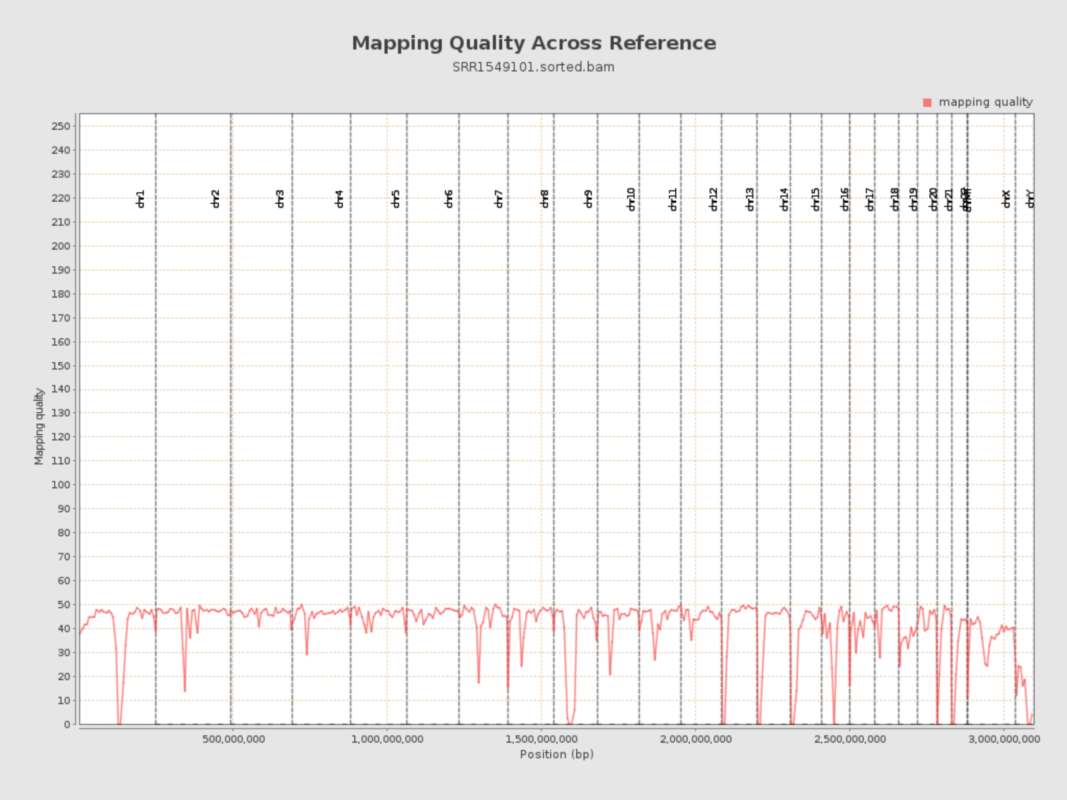
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram