Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 19:33:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549077.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_SRR1549077 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549077.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 19:33:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549077.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,332,749
Mapped reads	9,959,108 / 87.88%
Unmapped reads	1,373,641 / 12.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	395,765 / 3.49%
Duplication rate	2.21%
Clipped reads	629,008 / 5.55%

2.2. ACGT Content

Number/percentage of A's	117,733,958 / 29.83%
Number/percentage of C's	79,592,090 / 20.17%
Number/percentage of T's	119,226,185 / 30.21%
Number/percentage of G's	77,995,499 / 19.76%
Number/percentage of N's	96,246 / 0.02%
GC Percentage	39.93%

2.3. Coverage

Mean	0.1275
Standard Deviation	1.2577

2.4. Mapping Quality

Mean Mapping Quality	42.88

2.5. Mismatches and indels

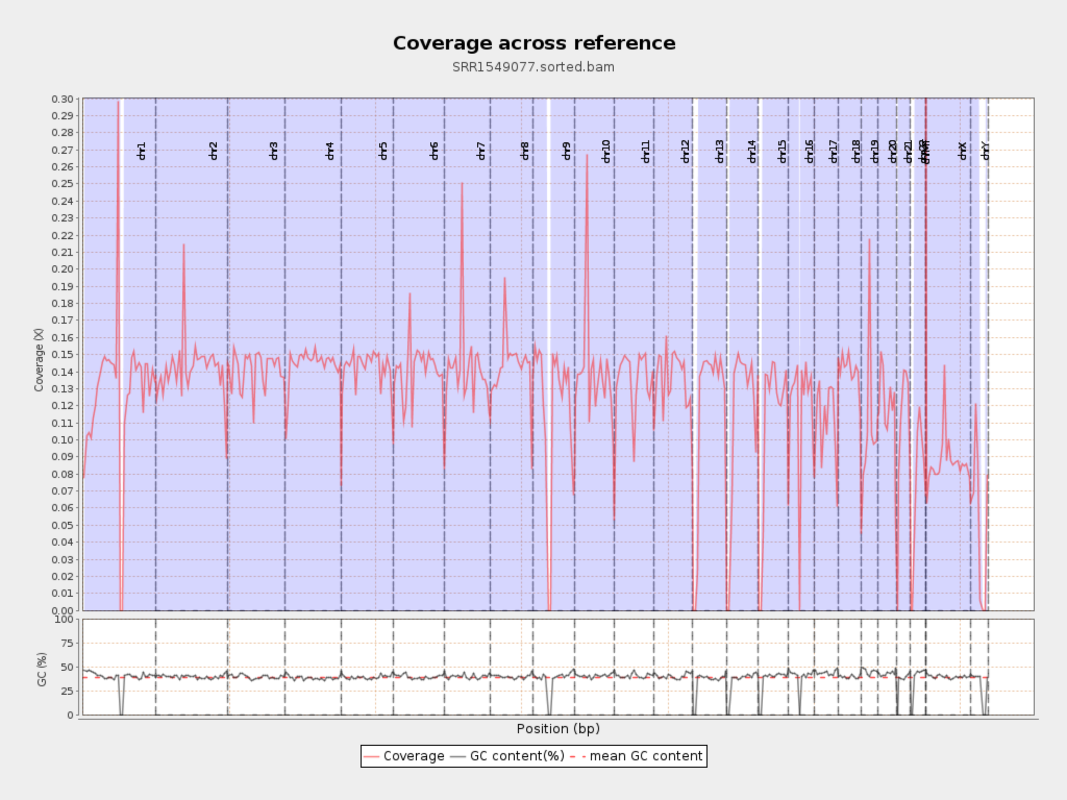
General error rate	0.42%
Mismatches	1,642,359
Insertions	10,704
Mapped reads with at least one insertion	0.11%
Deletions	30,304
Mapped reads with at least one deletion	0.3%
Homopolymer indels	44.4%

2.6. Chromosome stats

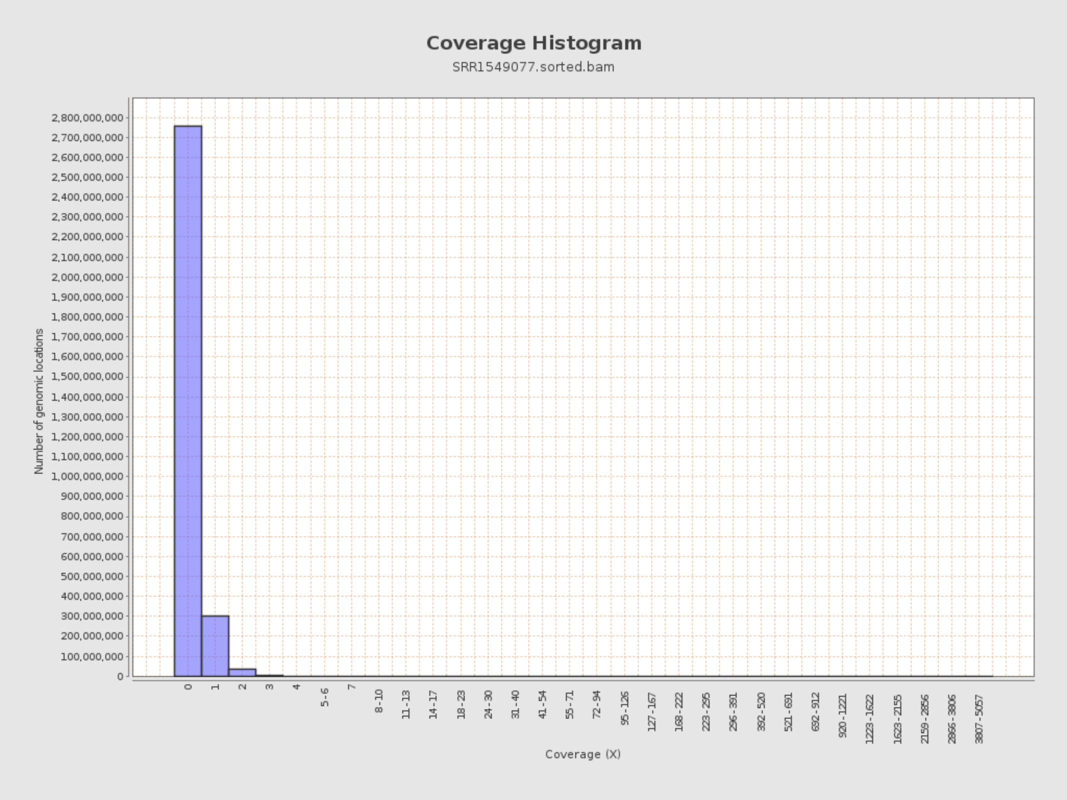
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31957457	0.1282	3.34
chr2	243199373	34532993	0.142	0.8402
chr3	198022430	28004041	0.1414	0.4509
chr4	191154276	27634496	0.1446	0.4468
chr5	180915260	25645551	0.1418	0.4497
chr6	171115067	24220322	0.1415	0.6358
chr7	159138663	22538295	0.1416	1.3684
chr8	146364022	20967327	0.1433	0.7

chr9	141213431	16653650	0.1179	0.8556
chr10	135534747	19058458	0.1406	1.1901
chr11	135006516	18213705	0.1349	0.8934
chr12	133851895	18184253	0.1359	0.4892
chr13	115169878	13493679	0.1172	0.3674
chr14	107349540	12262454	0.1142	0.5706
chr15	102531392	11062415	0.1079	0.3662
chr16	90354753	10425916	0.1154	0.6308
chr17	81195210	9168758	0.1129	0.5204
chr18	78077248	11036420	0.1414	2.0473
chr19	59128983	6461509	0.1093	2.6375
chr20	63025520	7693856	0.1221	0.4416
chr21	48129895	5093235	0.1058	0.4987
chr22	51304566	3691369	0.072	0.3805
chrMT	16571	6424	0.3877	0.717
chrX	155270560	13521379	0.0871	0.5707
chrY	59373566	3153133	0.0531	0.4314

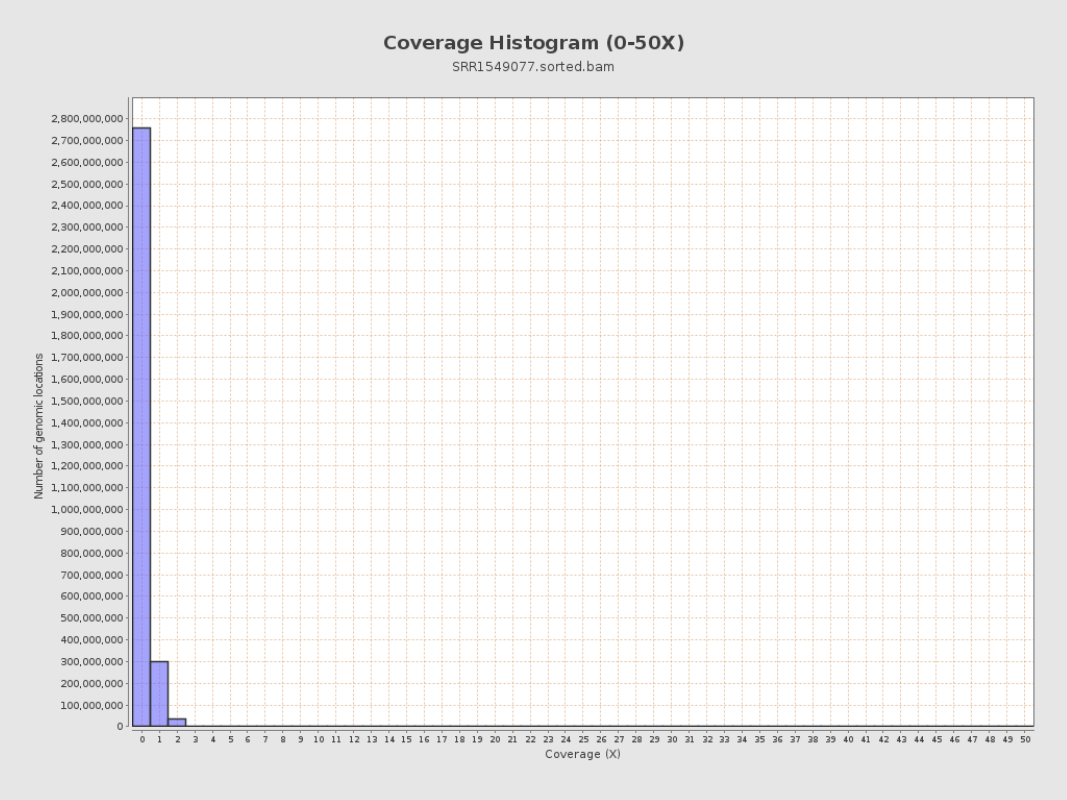
3. Results : Coverage across reference



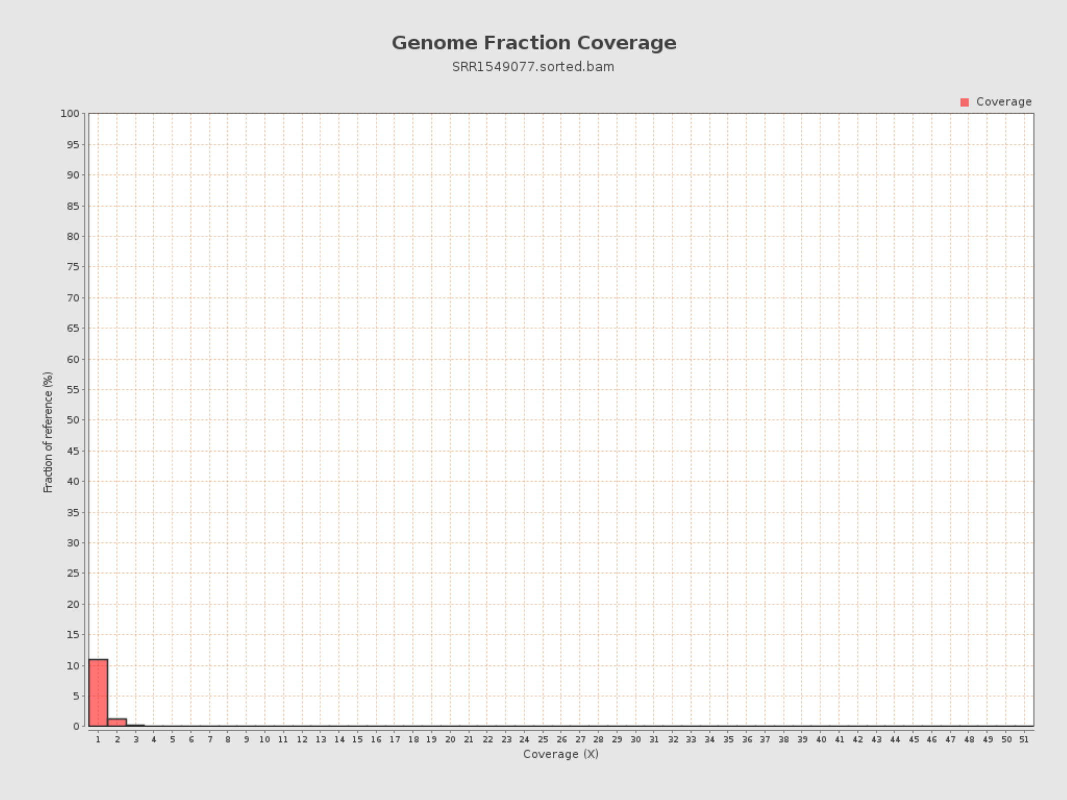
4. Results : Coverage Histogram



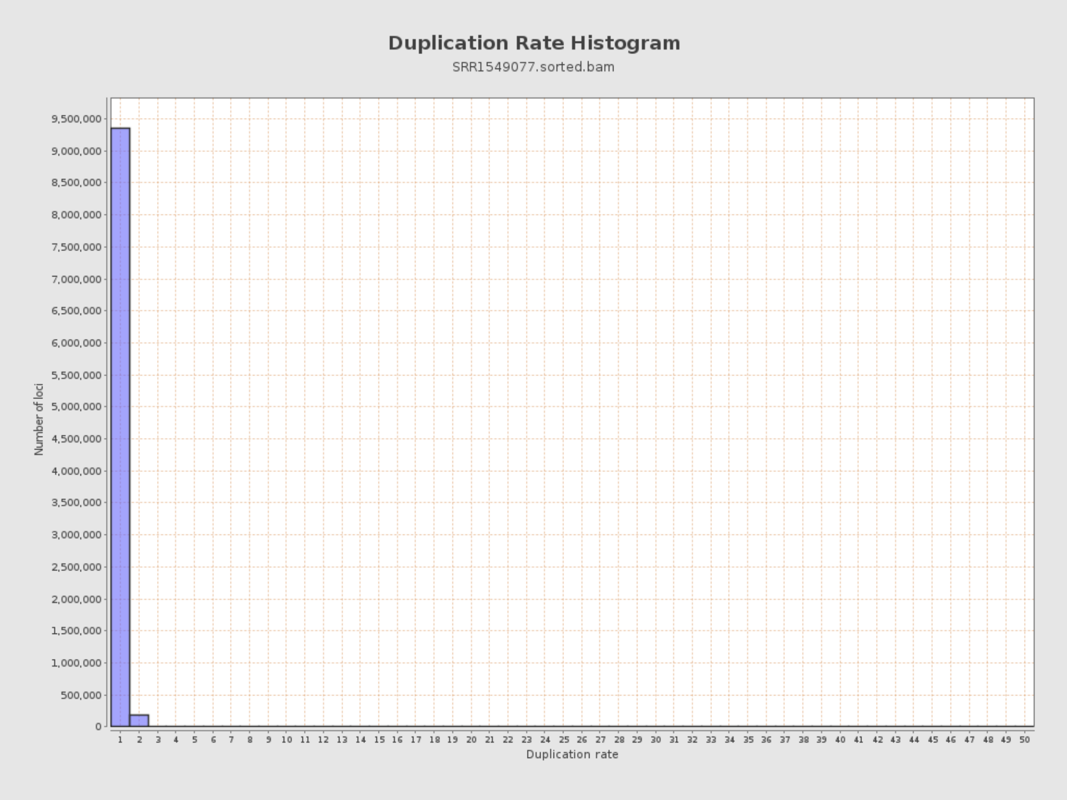
5. Results : Coverage Histogram (0-50X)



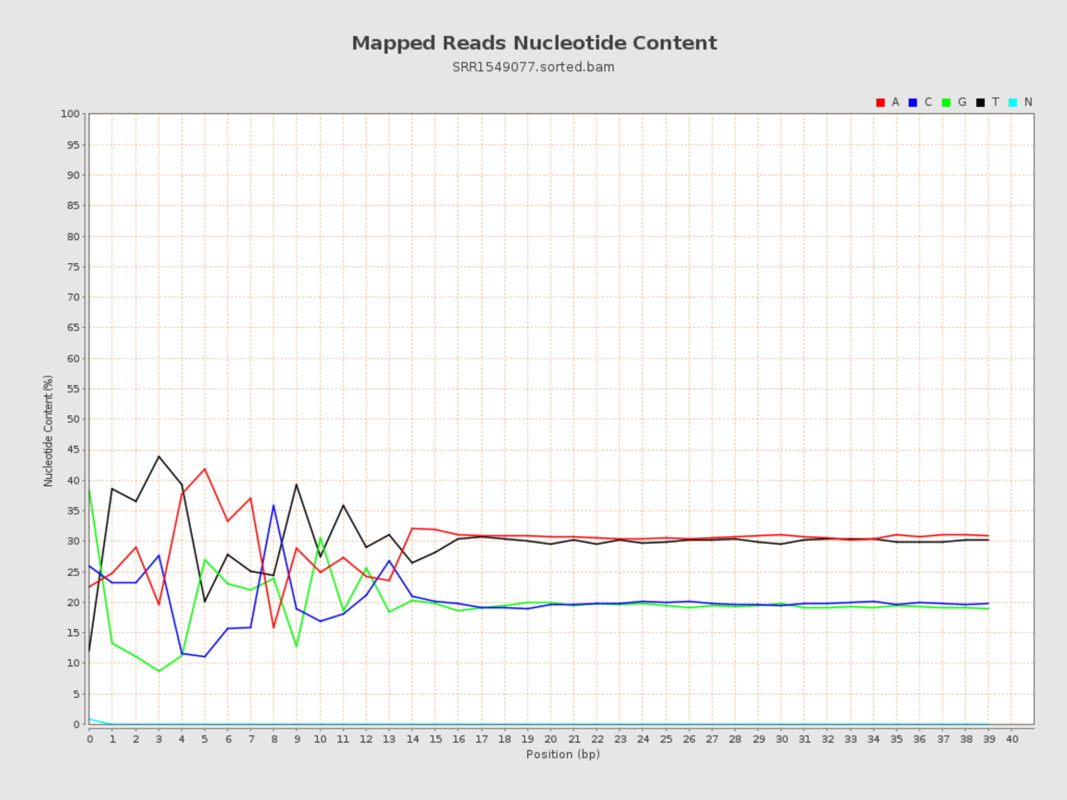
6. Results : Genome Fraction Coverage



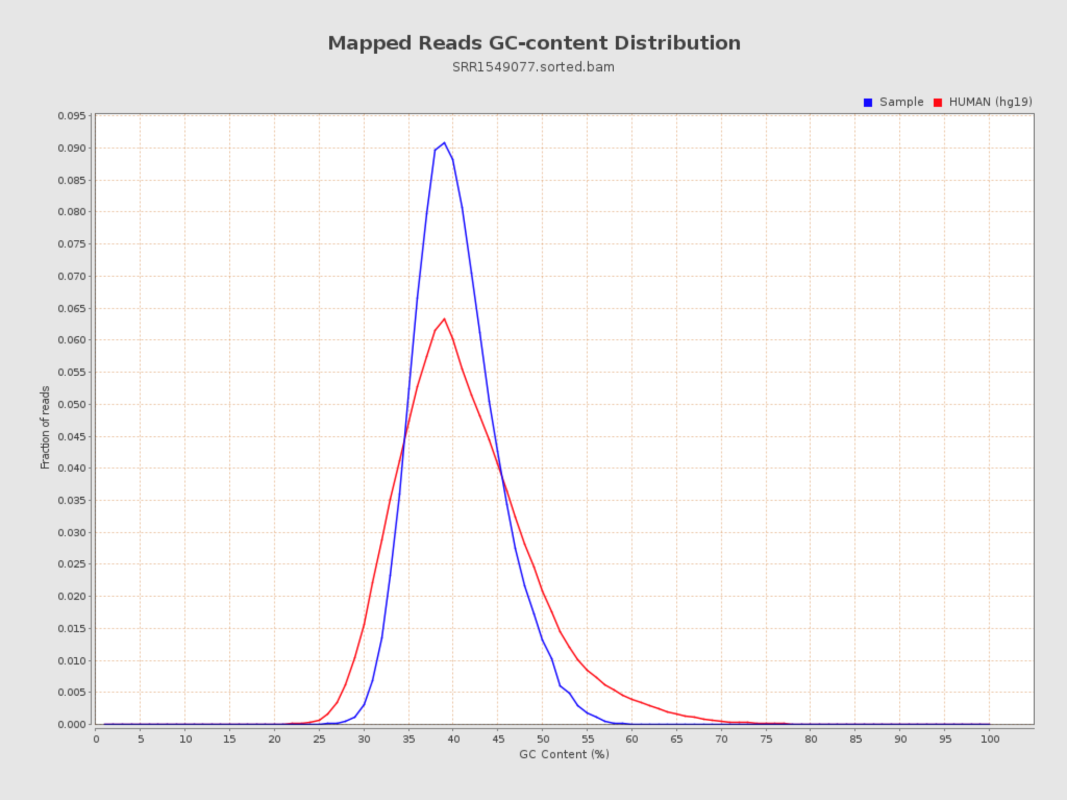
7. Results : Duplication Rate Histogram



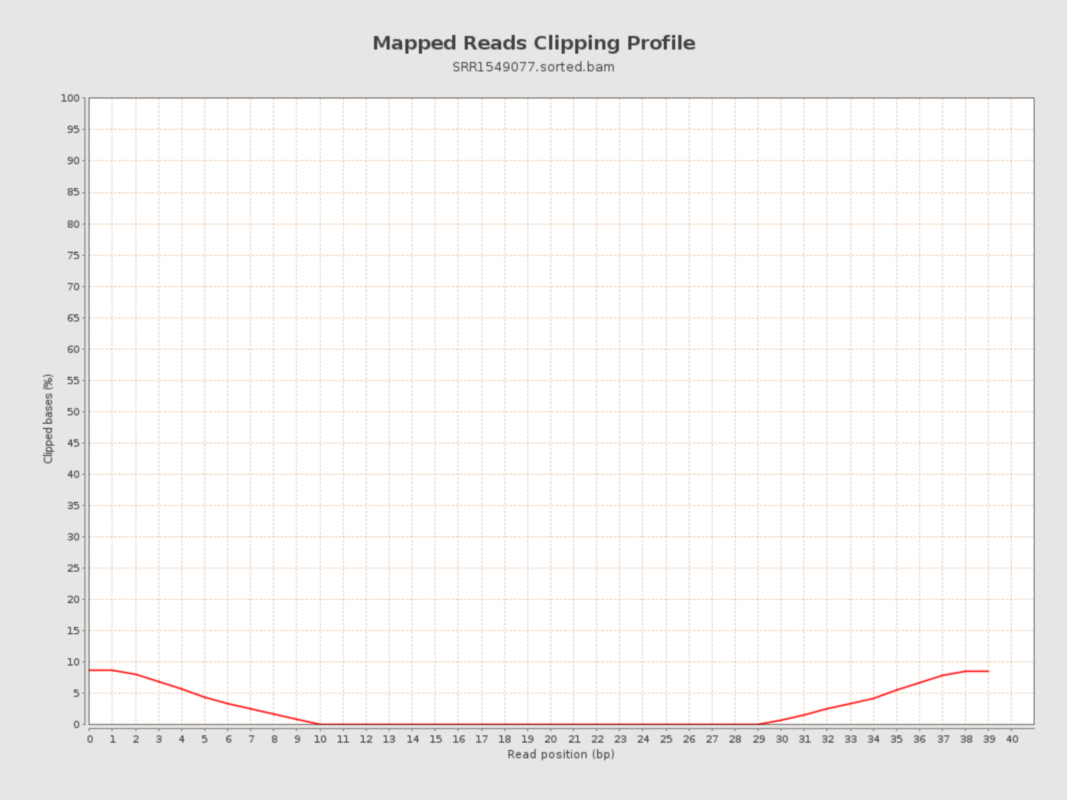
8. Results : Mapped Reads Nucleotide Content



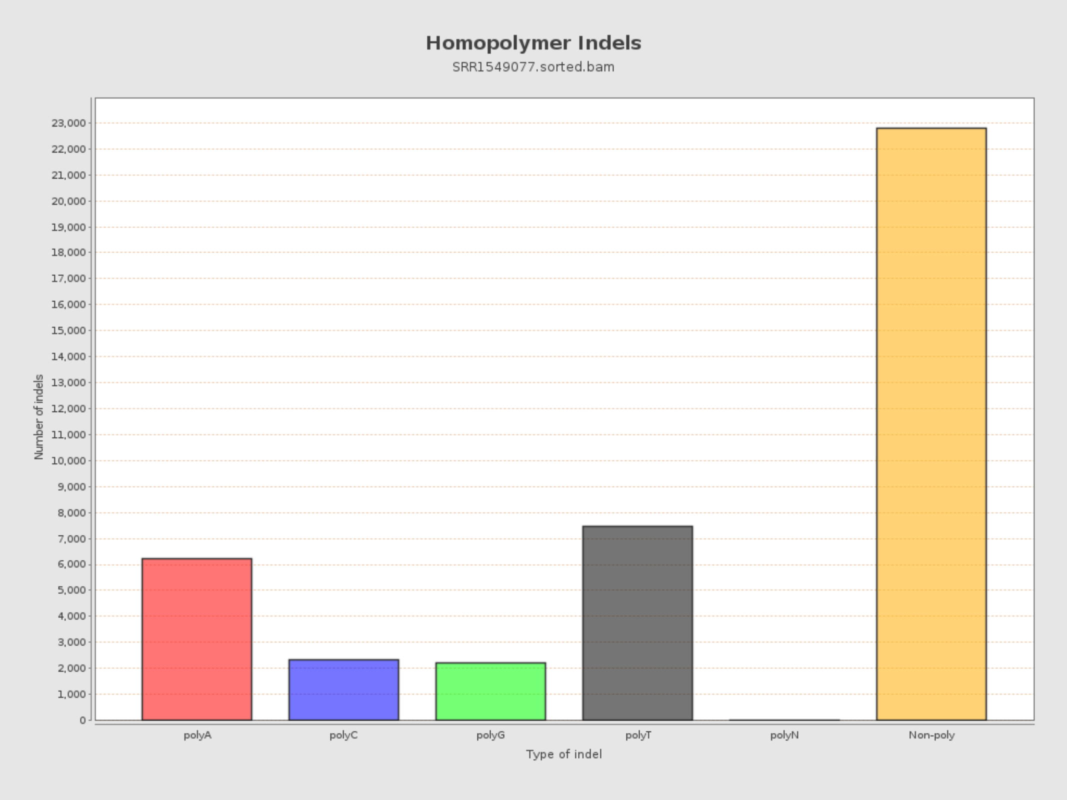
9. Results : Mapped Reads GC-content Distribution



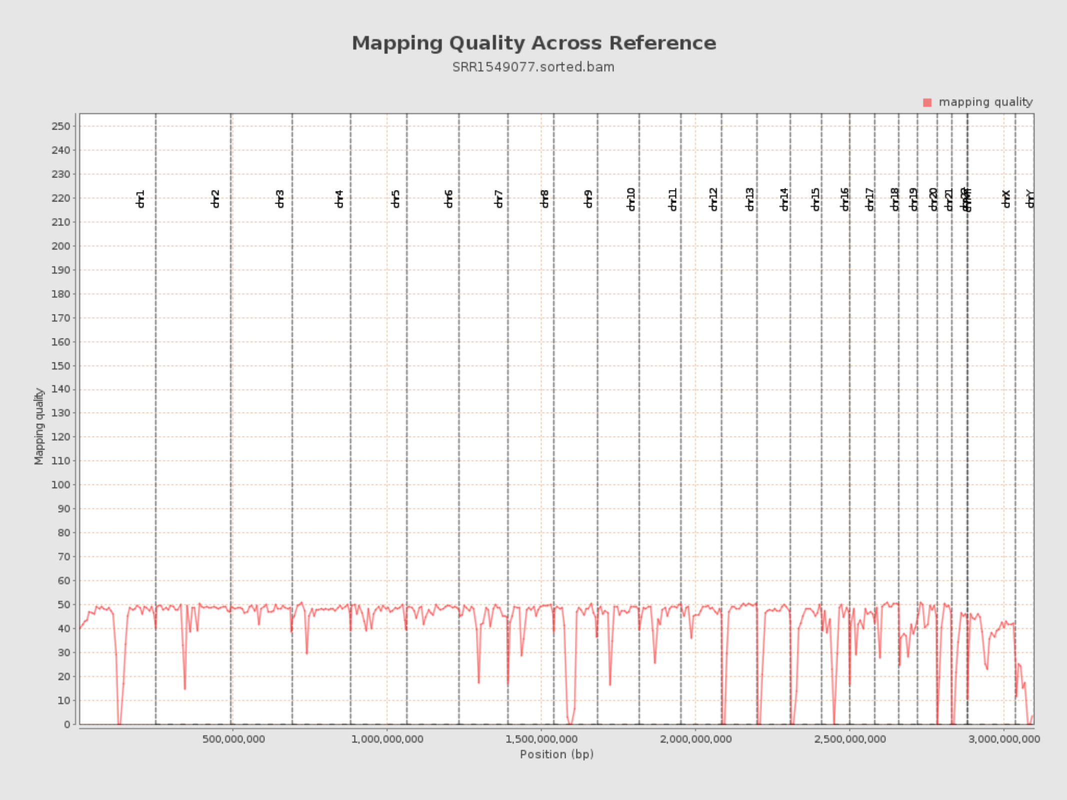
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram