Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:50:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549115.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_SRR1549115 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:50:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,044,333
Mapped reads	5,361,907 / 59.28%
Unmapped reads	3,682,426 / 40.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	153,415 / 1.7%
Duplication rate	2.07%
Clipped reads	267,934 / 2.96%

2.2. ACGT Content

Number/percentage of A's	61,680,137 / 28.98%
Number/percentage of C's	44,651,746 / 20.98%
Number/percentage of T's	61,906,574 / 29.08%
Number/percentage of G's	44,612,783 / 20.96%
Number/percentage of N's	8,600 / 0%
GC Percentage	41.94%

2.3. Coverage

Mean	0.0688
Standard Deviation	0.4346

2.4. Mapping Quality

Mean Mapping Quality	43.33

2.5. Mismatches and indels

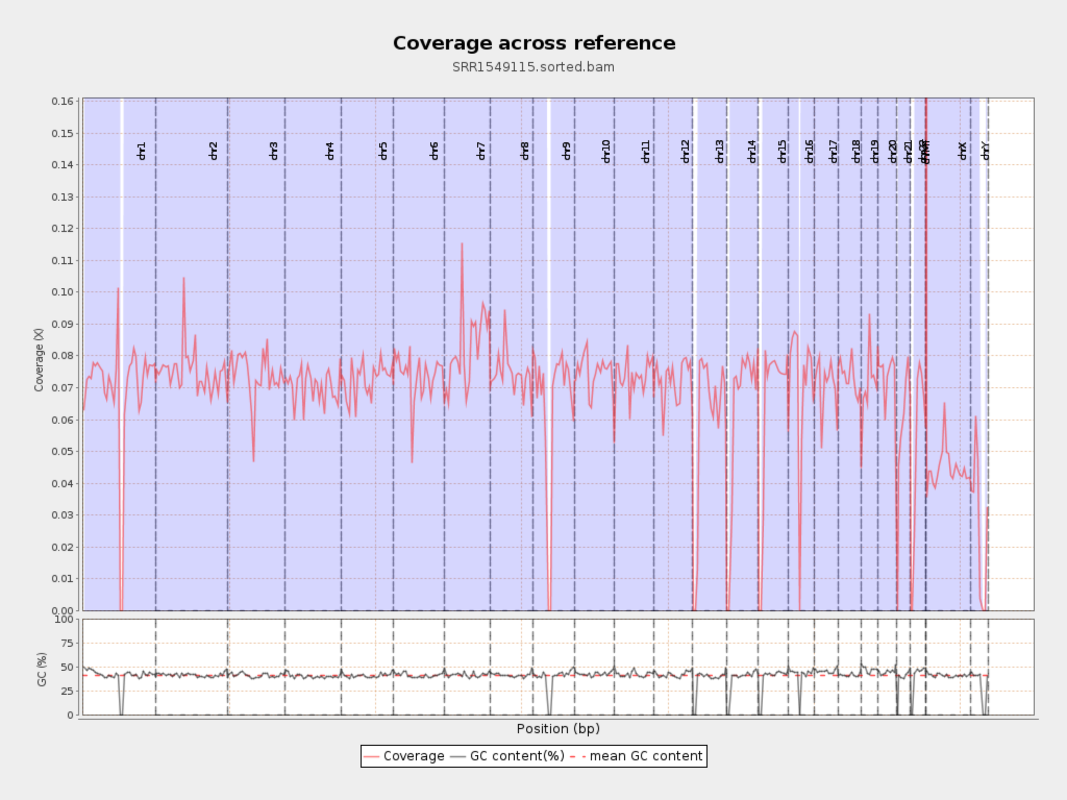
General error rate	0.31%
Mismatches	644,526
Insertions	5,420
Mapped reads with at least one insertion	0.1%
Deletions	16,039
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.45%

2.6. Chromosome stats

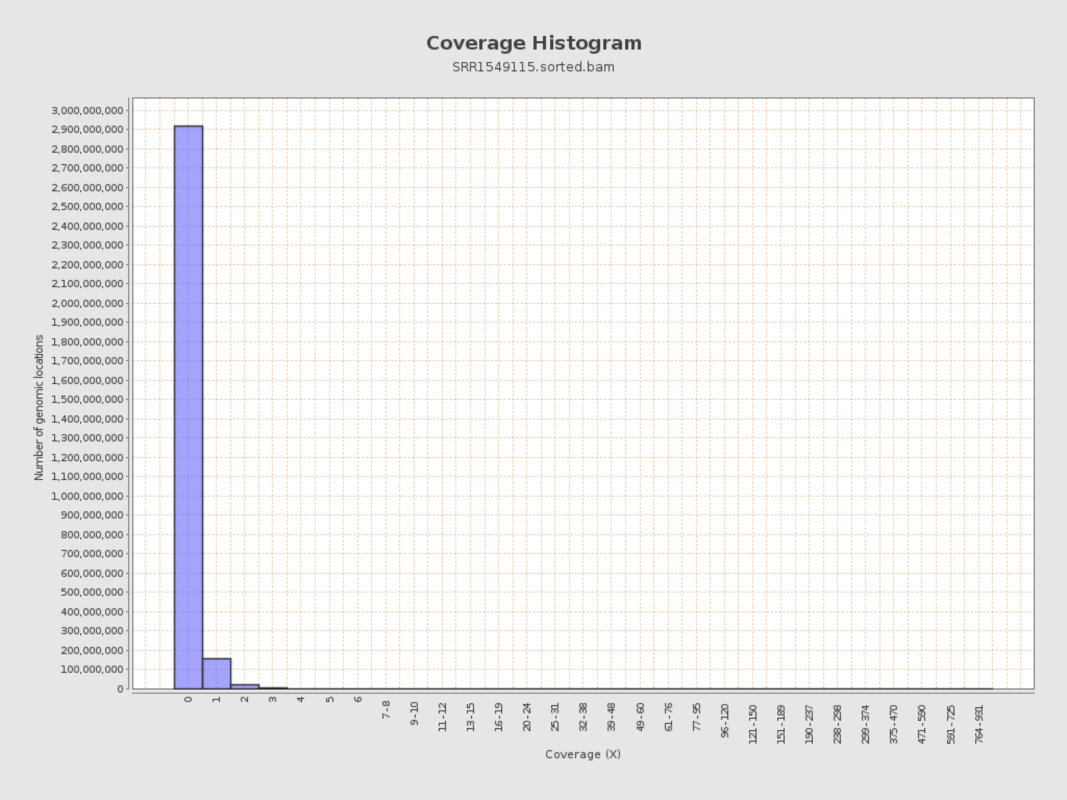
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17366137	0.0697	0.7464
chr2	243199373	18308705	0.0753	0.4293
chr3	198022430	14606035	0.0738	0.3101
chr4	191154276	13488592	0.0706	0.3099
chr5	180915260	13156616	0.0727	0.3132
chr6	171115067	12601269	0.0736	0.3424
chr7	159138663	13159835	0.0827	0.6608
chr8	146364022	10871683	0.0743	0.4198

chr9	141213431	9076044	0.0643	0.4069
chr10	135534747	10168857	0.075	0.399
chr11	135006516	9919561	0.0735	0.4041
chr12	133851895	9736890	0.0727	0.3174
chr13	115169878	6782712	0.0589	0.2744
chr14	107349540	6673696	0.0622	0.3401
chr15	102531392	6371088	0.0621	0.2833
chr16	90354753	6262256	0.0693	0.3278
chr17	81195210	5799958	0.0714	0.3227
chr18	78077248	5727598	0.0734	0.7847
chr19	59128983	4257925	0.072	0.621
chr20	63025520	4630059	0.0735	0.3225
chr21	48129895	2766694	0.0575	0.3037
chr22	51304566	2561508	0.0499	0.2655
chrMT	16571	58523	3.5317	5.25
chrX	155270560	6922410	0.0446	0.2885
chrY	59373566	1605225	0.027	0.228

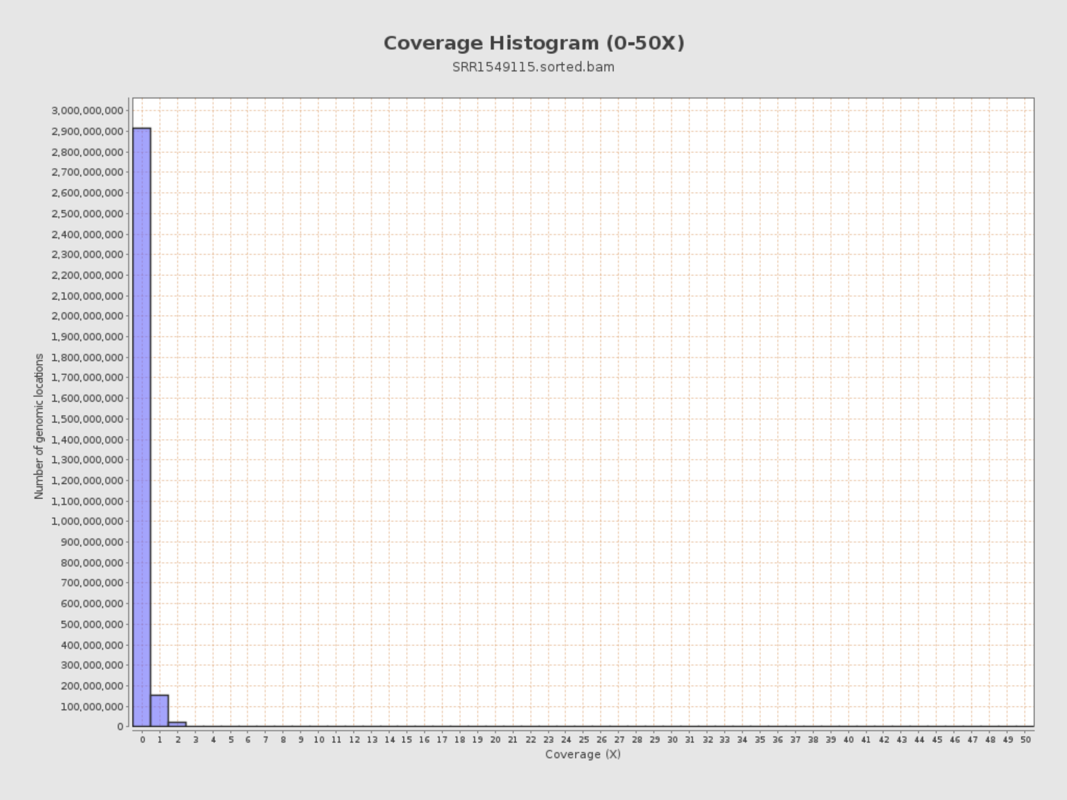
3. Results : Coverage across reference



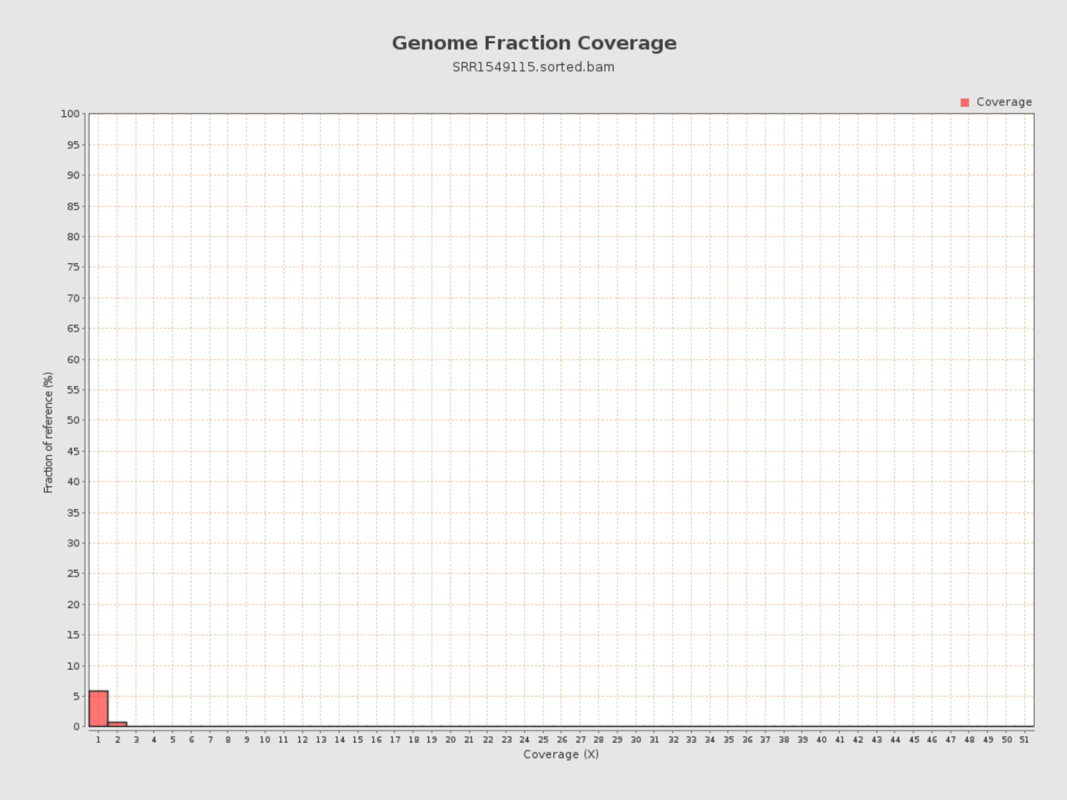
4. Results : Coverage Histogram



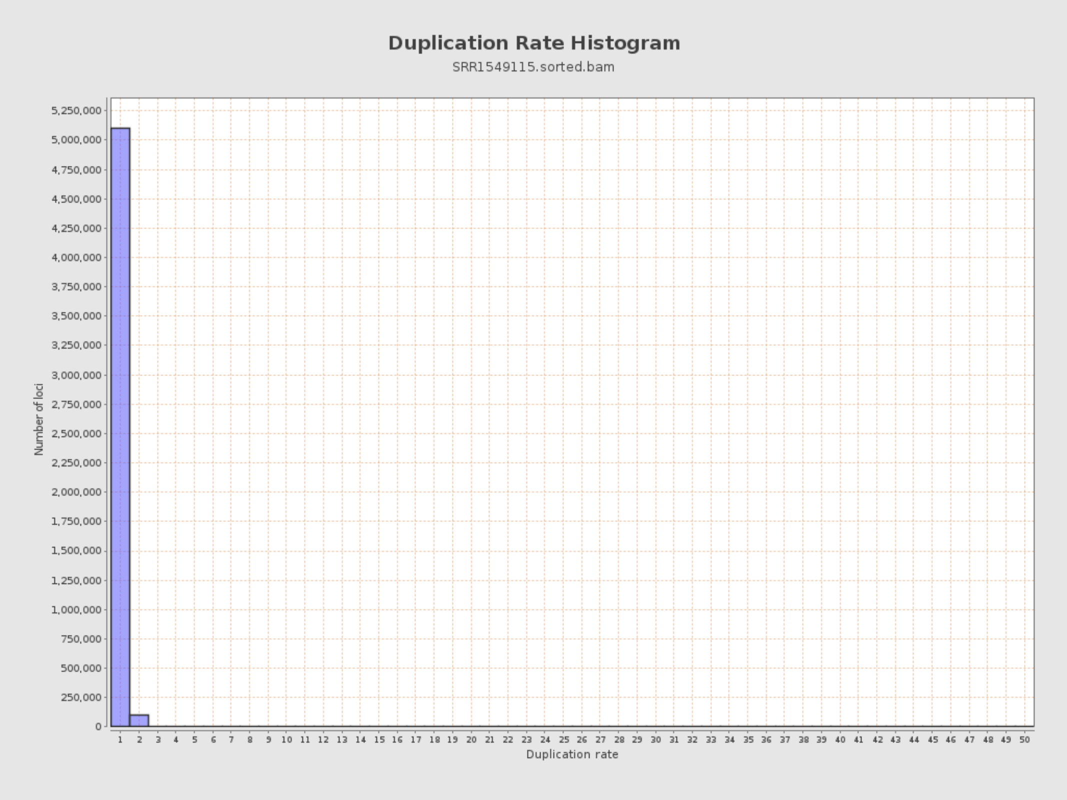
5. Results : Coverage Histogram (0-50X)



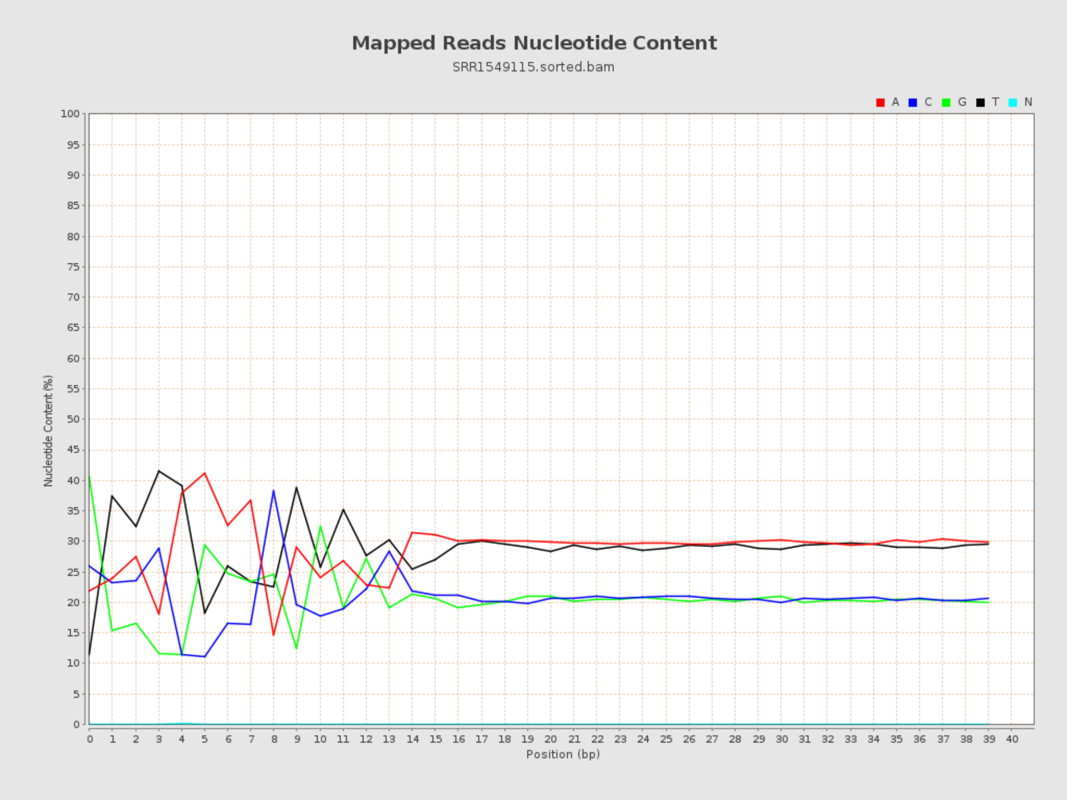
6. Results : Genome Fraction Coverage



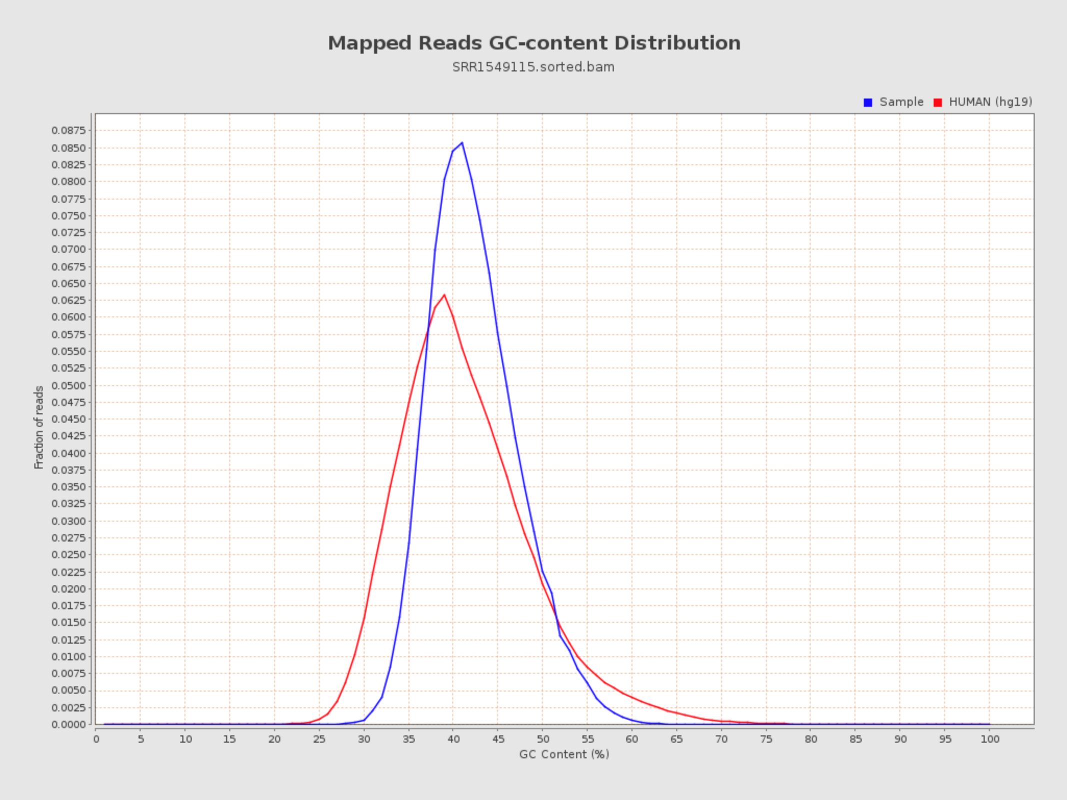
7. Results : Duplication Rate Histogram



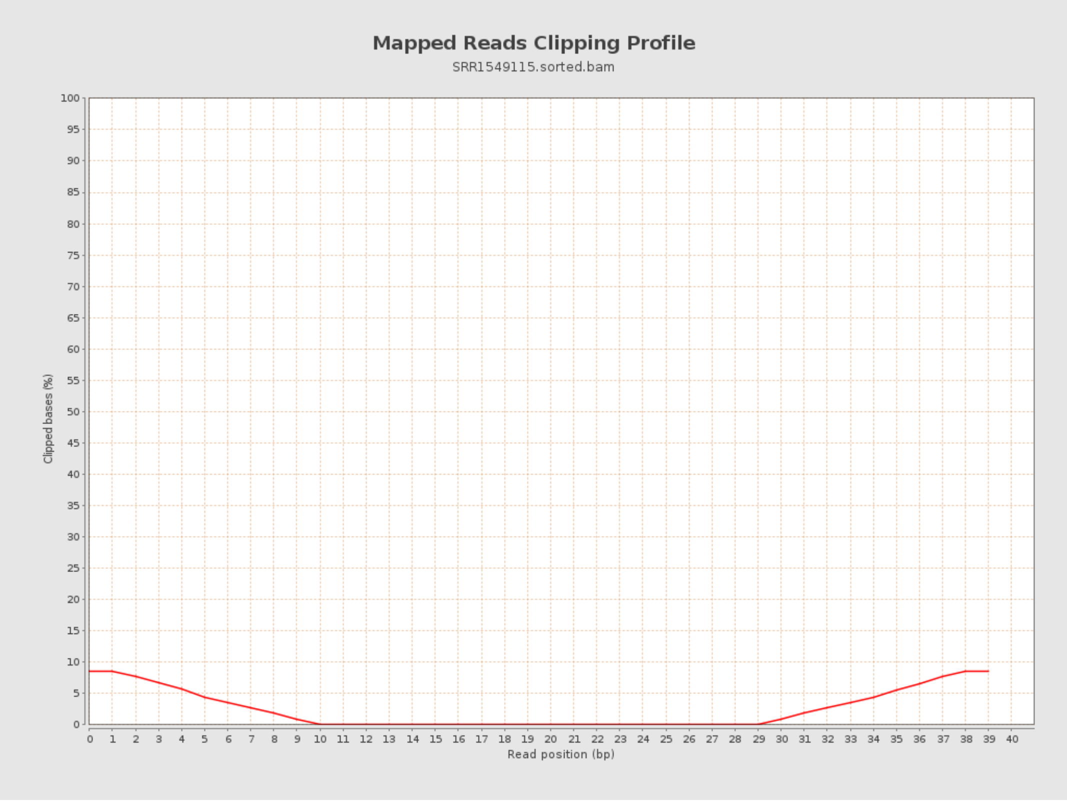
8. Results : Mapped Reads Nucleotide Content



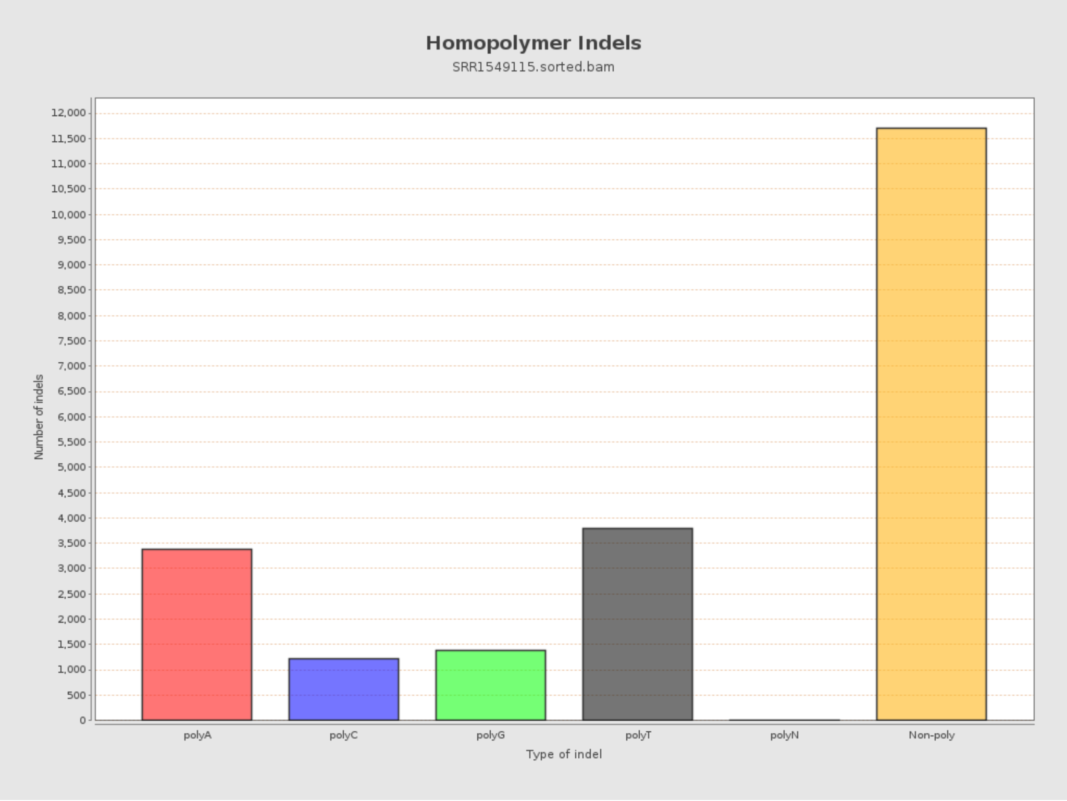
9. Results : Mapped Reads GC-content Distribution



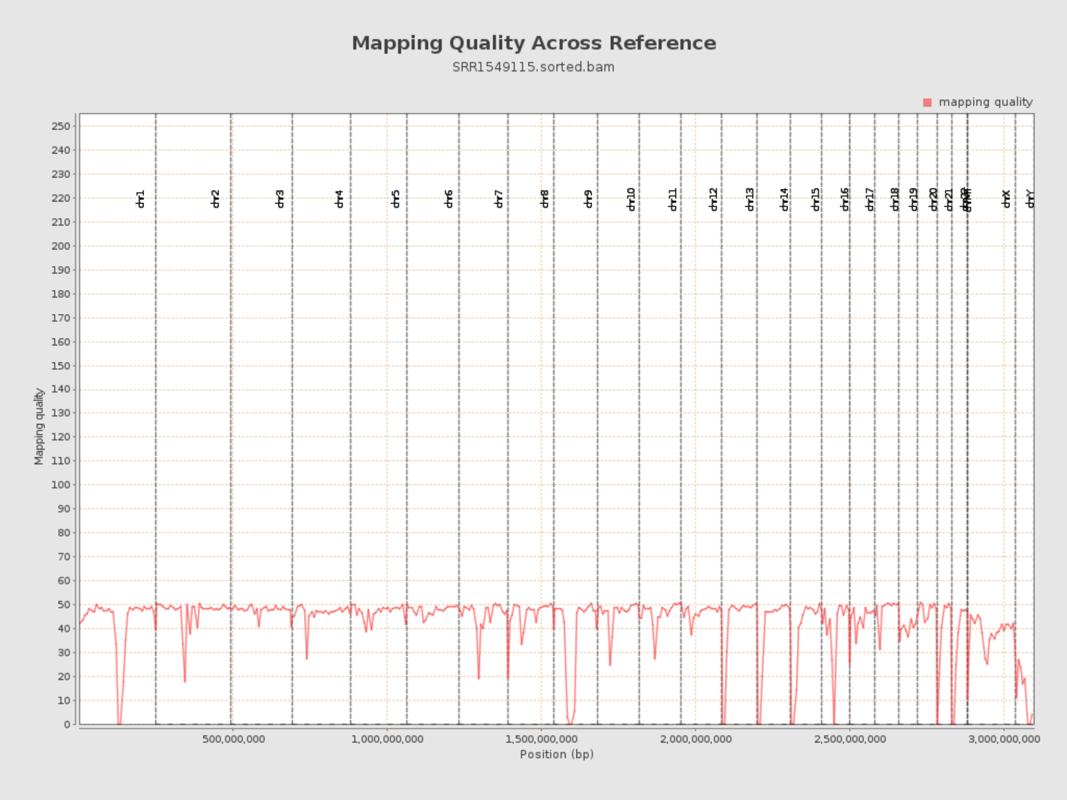
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram