Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:10:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081115.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_SRR3081115 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:10:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,506,692
Mapped reads	2,300,145 / 91.76%
Unmapped reads	206,547 / 8.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,497 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	87,850 / 3.5%
Duplication rate	2.86%
Clipped reads	790,025 / 31.52%

2.2. ACGT Content

Number/percentage of A's	46,470,383 / 29.11%
Number/percentage of C's	30,218,270 / 18.93%
Number/percentage of T's	49,860,865 / 31.23%
Number/percentage of G's	33,083,610 / 20.72%
Number/percentage of N's	1,774 / 0%
GC Percentage	39.65%

2.3. Coverage

Mean	0.0516

Standard Deviation	0.4423

2.4. Mapping Quality

Mean Mapping Quality	47.17

2.5. Mismatches and indels

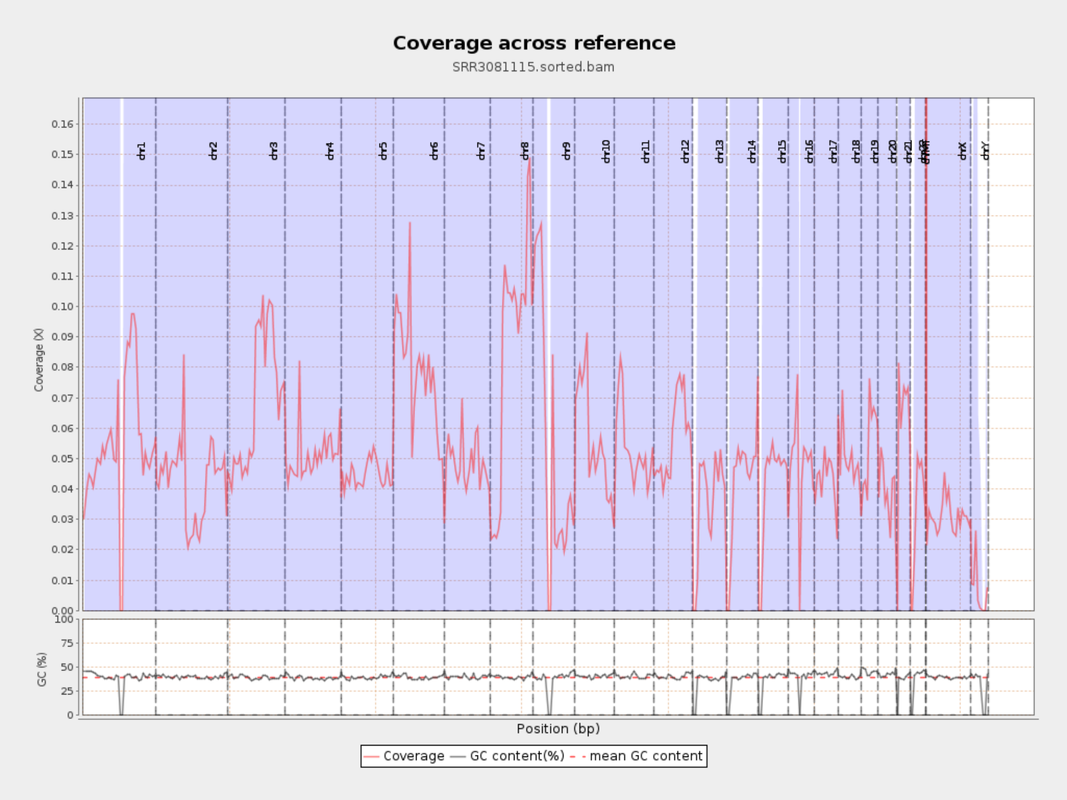
General error rate	0.89%
Mismatches	1,391,625
Insertions	12,717
Mapped reads with at least one insertion	0.55%
Deletions	35,908
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.39%

2.6. Chromosome stats

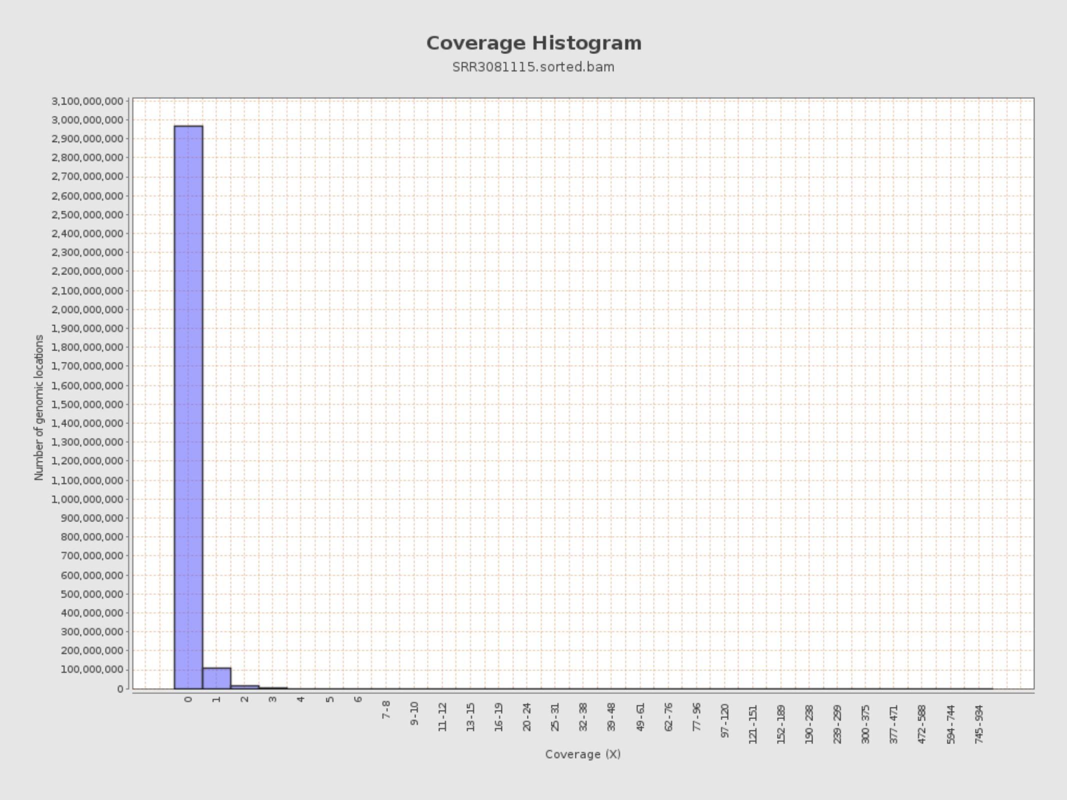
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13625847	0.0547	0.6874
chr2	243199373	10400263	0.0428	0.446
chr3	198022430	13505050	0.0682	0.3083
chr4	191154276	9787172	0.0512	0.3022
chr5	180915260	8131559	0.0449	0.2505
chr6	171115067	13532880	0.0791	0.4645
chr7	159138663	7742363	0.0487	0.4267

chr8	146364022	12720731	0.0869	0.6871
chr9	141213431	7681272	0.0544	0.5179
chr10	135534747	7659570	0.0565	0.426
chr11	135006516	7229531	0.0535	0.3729
chr12	133851895	7584990	0.0567	0.2917
chr13	115169878	4045224	0.0351	0.216
chr14	107349540	4418213	0.0412	0.3184
chr15	102531392	4154508	0.0405	0.2367
chr16	90354753	4214992	0.0466	0.3303
chr17	81195210	3508559	0.0432	0.2572
chr18	78077248	3915202	0.0501	1.049
chr19	59128983	3238985	0.0548	0.5104
chr20	63025520	2513840	0.0399	0.2515
chr21	48129895	3051171	0.0634	0.3536
chr22	51304566	1654233	0.0322	0.2065
chrMT	16571	149518	9.0229	5.7407
chrX	155270560	4827886	0.0311	0.2396
chrY	59373566	405890	0.0068	0.1815

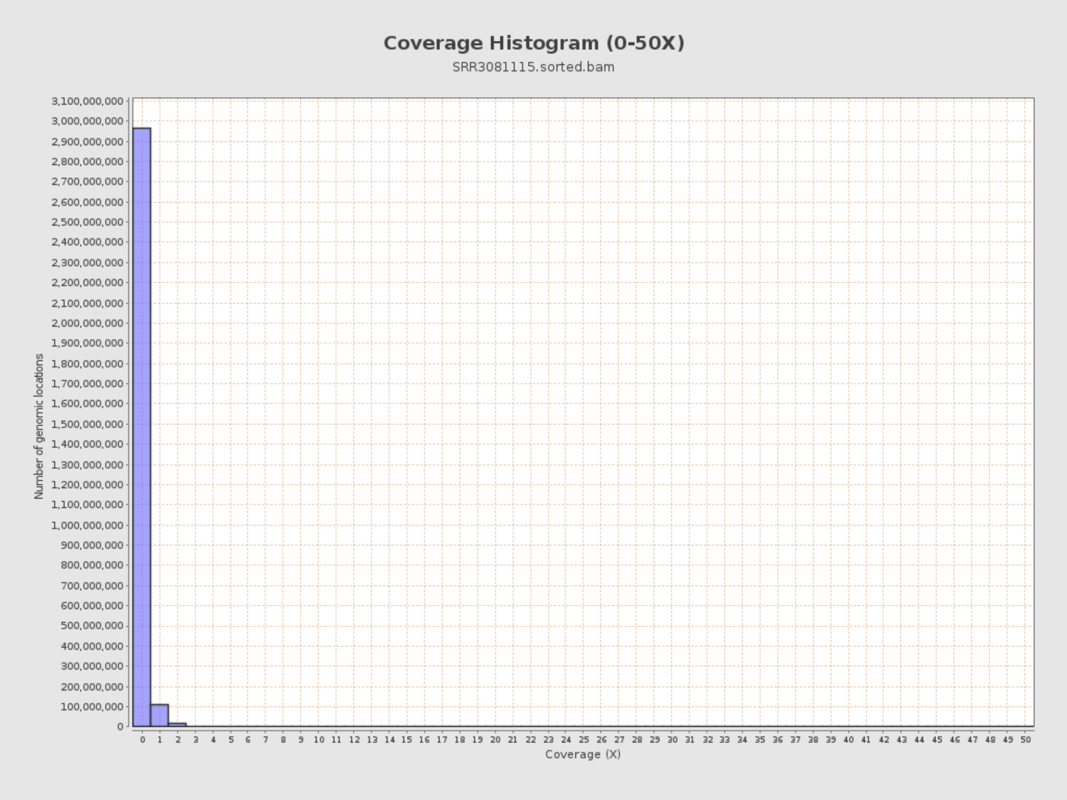
3. Results : Coverage across reference



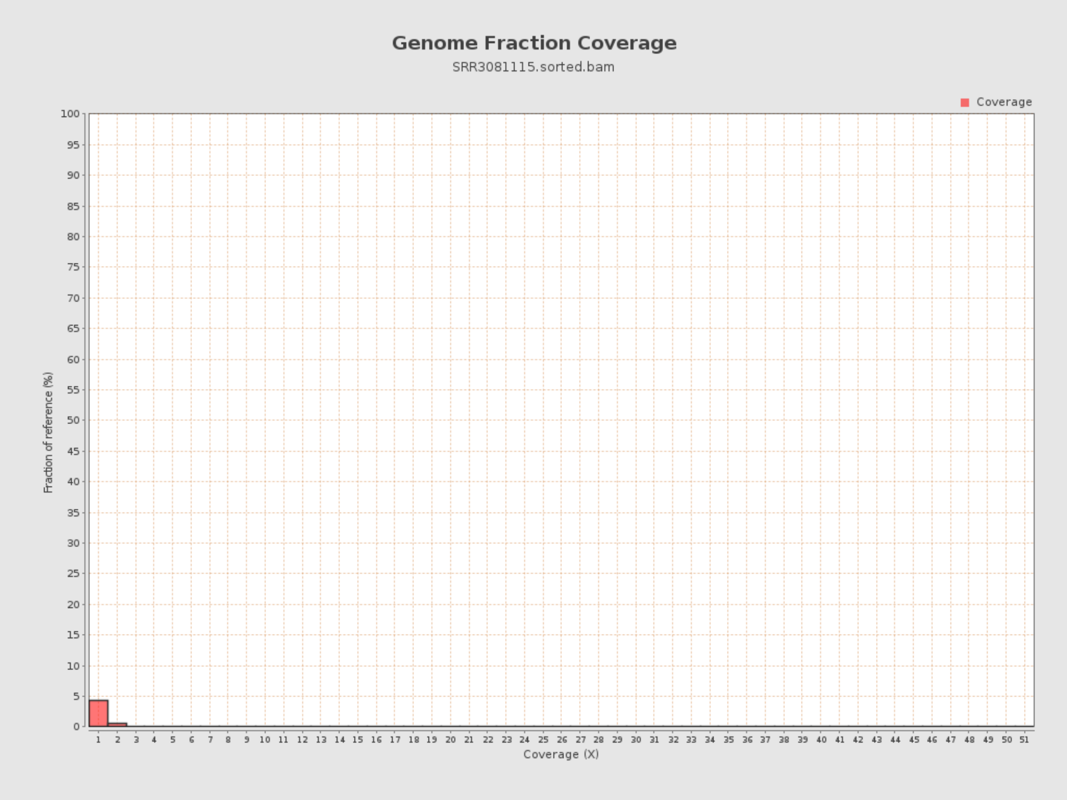
4. Results : Coverage Histogram



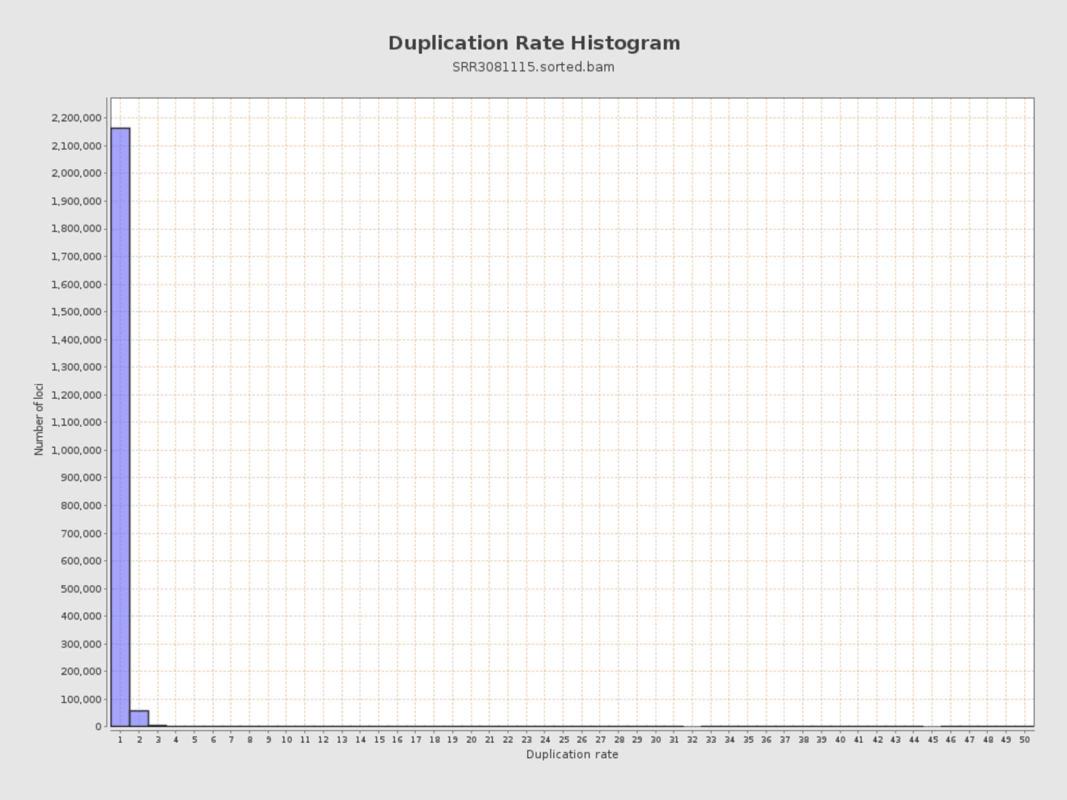
5. Results : Coverage Histogram (0-50X)



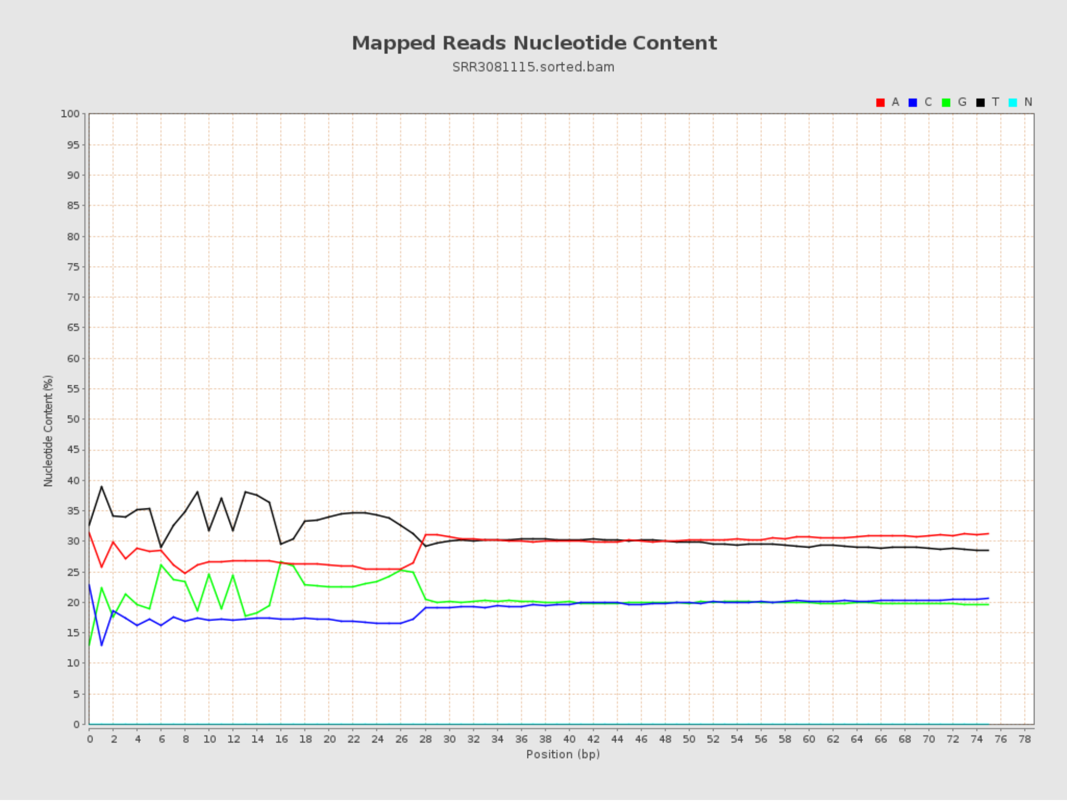
6. Results : Genome Fraction Coverage



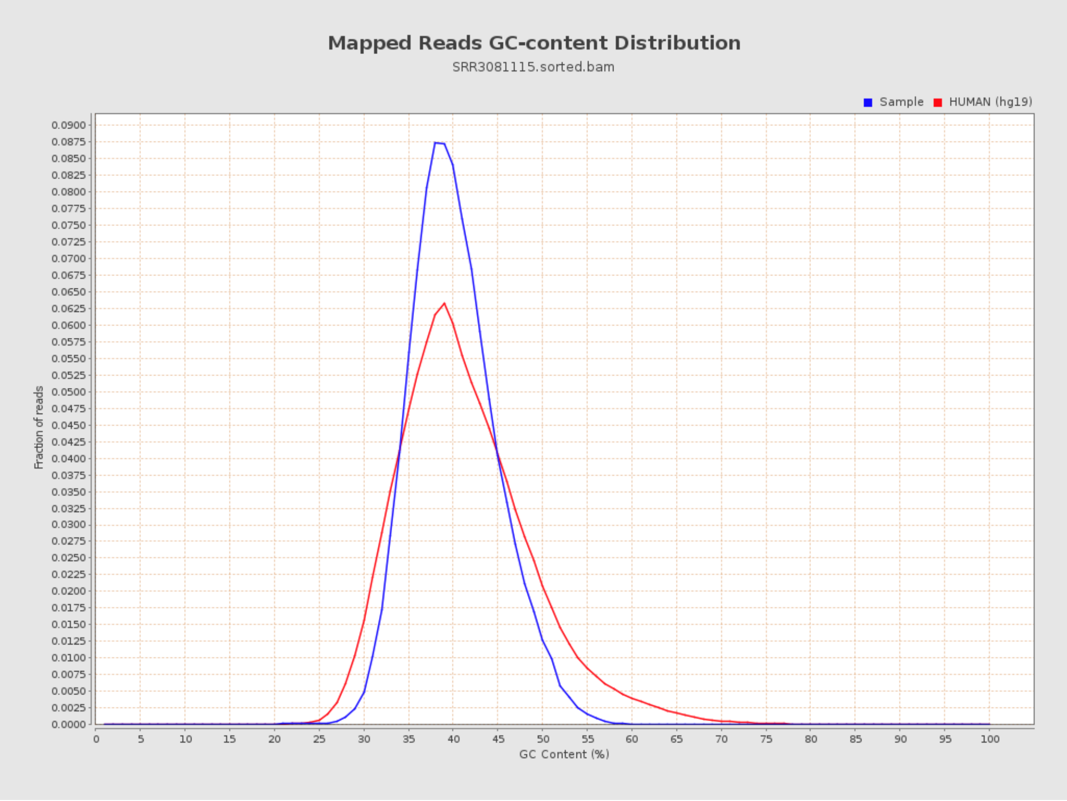
7. Results : Duplication Rate Histogram



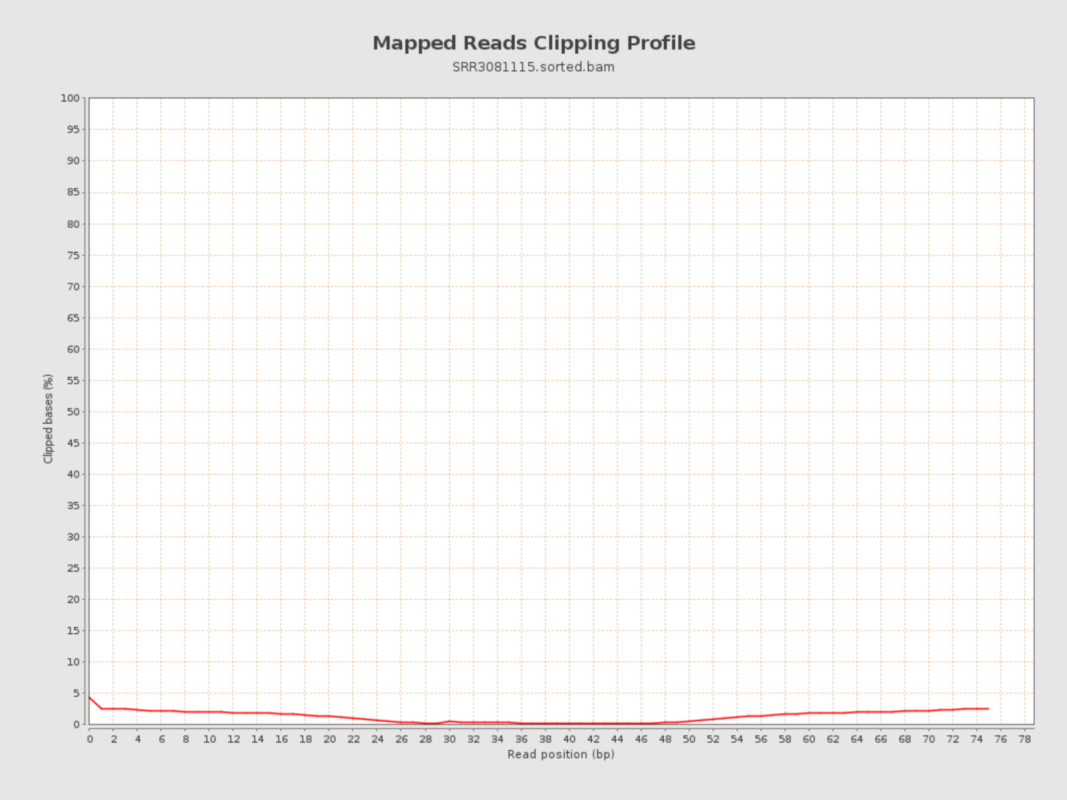
8. Results : Mapped Reads Nucleotide Content



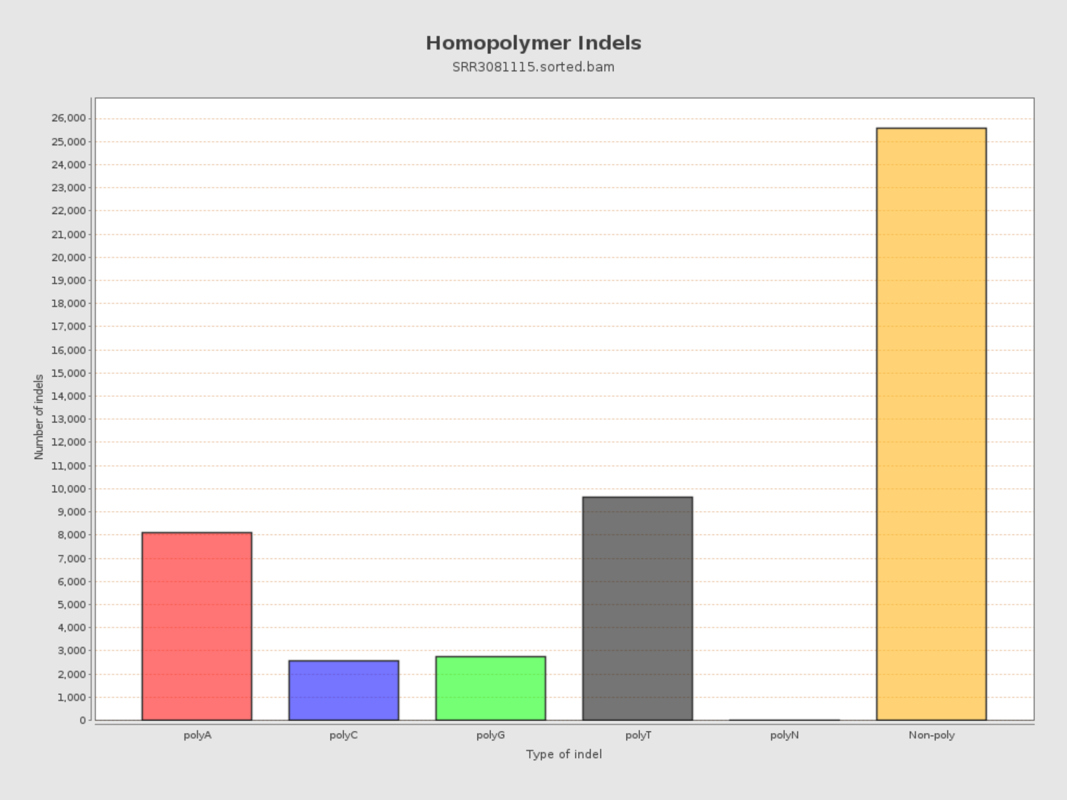
9. Results : Mapped Reads GC-content Distribution



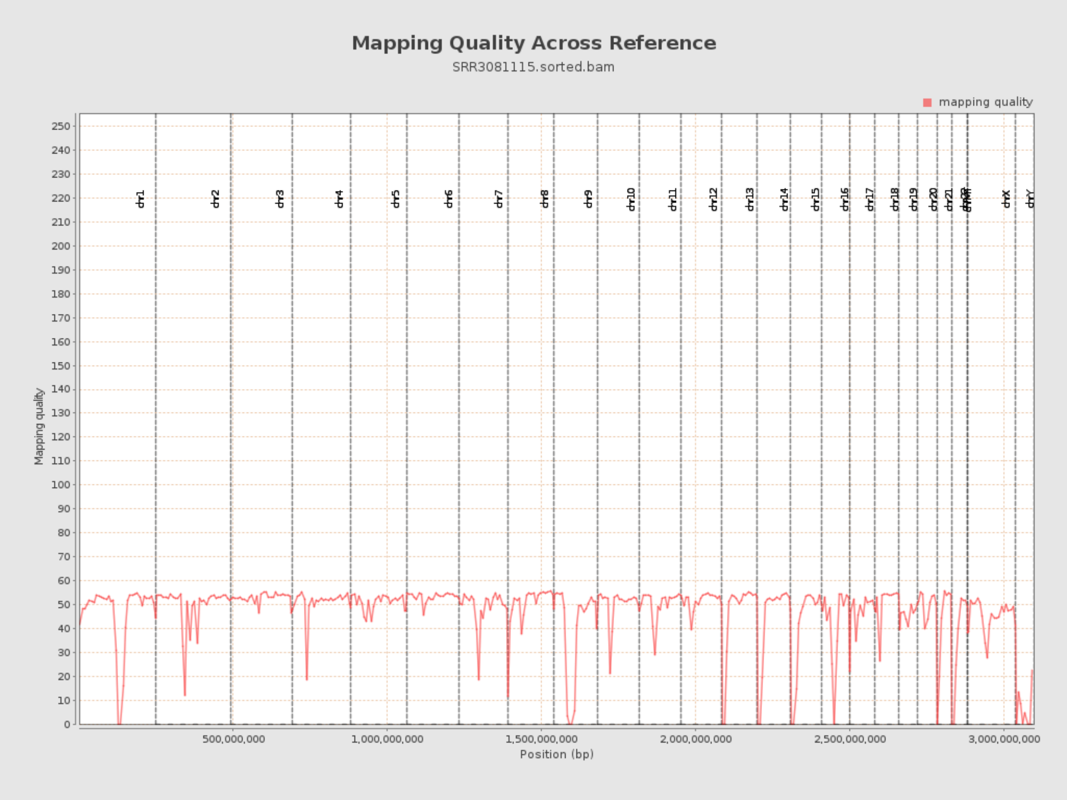
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram