Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:41:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082915.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_SRR3082915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082915.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:41:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,172,508
Mapped reads	1,947,688 / 89.65%
Unmapped reads	224,820 / 10.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,643 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	94,888 / 4.37%
Duplication rate	4.29%
Clipped reads	886,066 / 40.79%

2.2. ACGT Content

Number/percentage of A's	35,017,448 / 27.05%
Number/percentage of C's	24,184,230 / 18.68%
Number/percentage of T's	40,727,434 / 31.46%
Number/percentage of G's	29,510,968 / 22.8%
Number/percentage of N's	5,690 / 0%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0418

Standard Deviation	0.2846

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

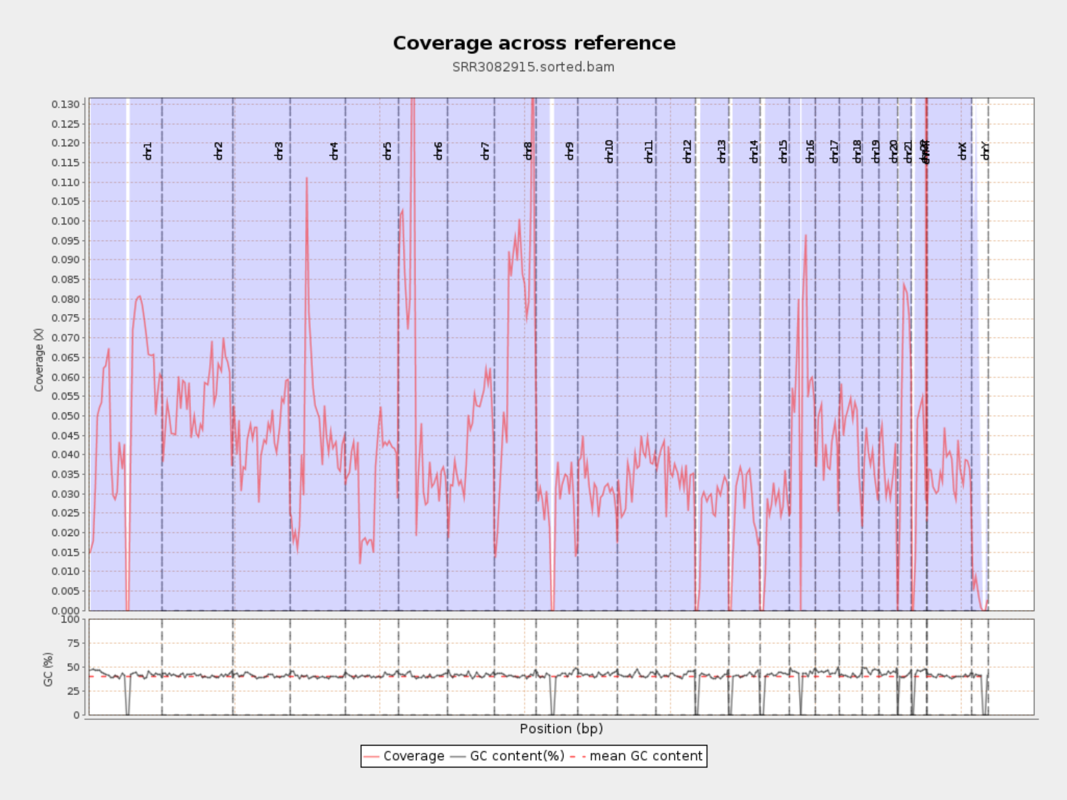
General error rate	0.72%
Mismatches	920,580
Insertions	10,227
Mapped reads with at least one insertion	0.52%
Deletions	29,600
Mapped reads with at least one deletion	1.51%
Homopolymer indels	48.13%

2.6. Chromosome stats

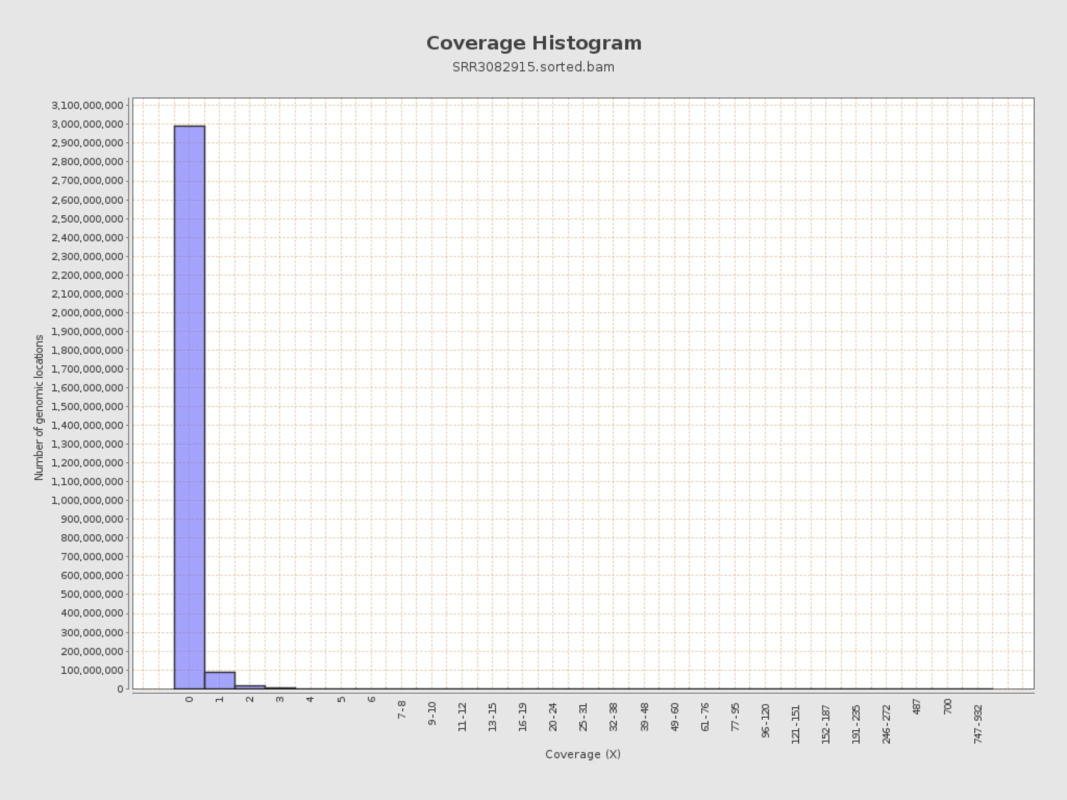
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12509998	0.0502	0.3353
chr2	243199373	13148849	0.0541	0.4755
chr3	198022430	8944148	0.0452	0.2492
chr4	191154276	8455755	0.0442	0.2523
chr5	180915260	6134639	0.0339	0.2162
chr6	171115067	9670536	0.0565	0.3296
chr7	159138663	7145981	0.0449	0.2741

chr8	146364022	10837484	0.074	0.3506
chr9	141213431	3722357	0.0264	0.223
chr10	135534747	4379789	0.0323	0.2216
chr11	135006516	4780347	0.0354	0.2341
chr12	133851895	4715202	0.0352	0.2208
chr13	115169878	2869857	0.0249	0.1877
chr14	107349540	2657355	0.0248	0.187
chr15	102531392	2370250	0.0231	0.1901
chr16	90354753	5211343	0.0577	0.2901
chr17	81195210	3366399	0.0415	0.2453
chr18	78077248	3774760	0.0483	0.3672
chr19	59128983	2210302	0.0374	0.2737
chr20	63025520	2272597	0.0361	0.2257
chr21	48129895	2767882	0.0575	0.2873
chr22	51304566	1685080	0.0328	0.2118
chrMT	16571	126379	7.6265	5.1751
chrX	155270560	5519995	0.0356	0.2267
chrY	59373566	216546	0.0036	0.0739

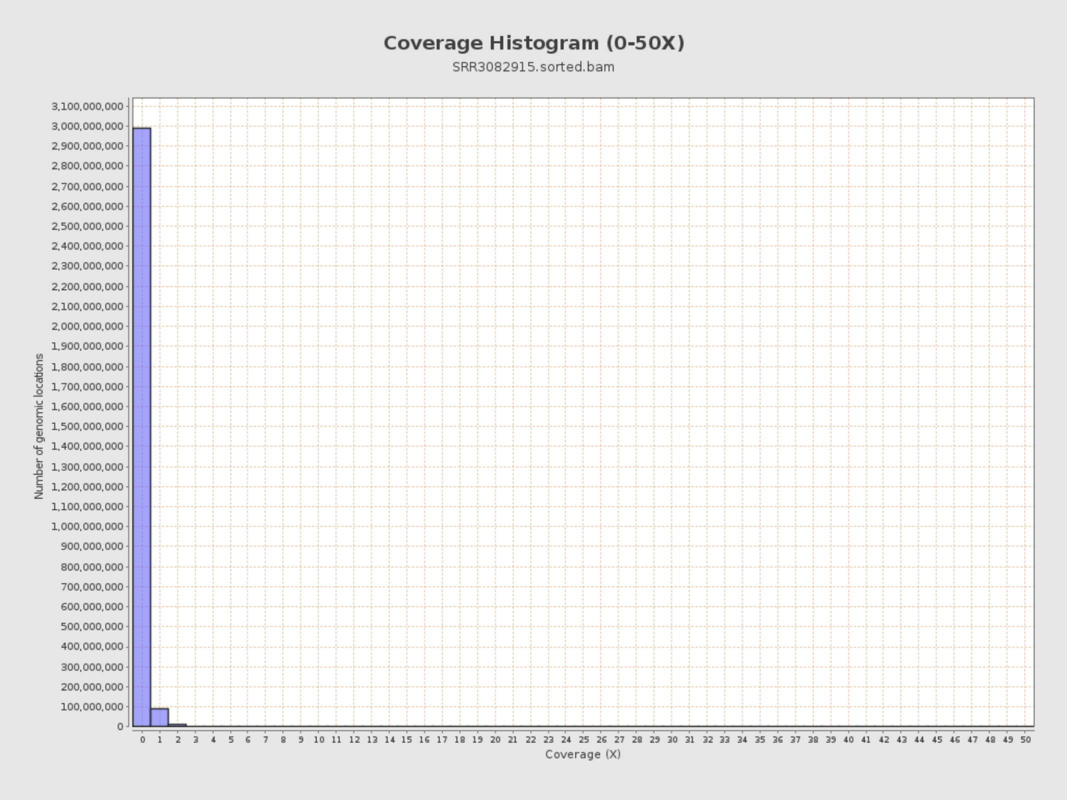
3. Results : Coverage across reference



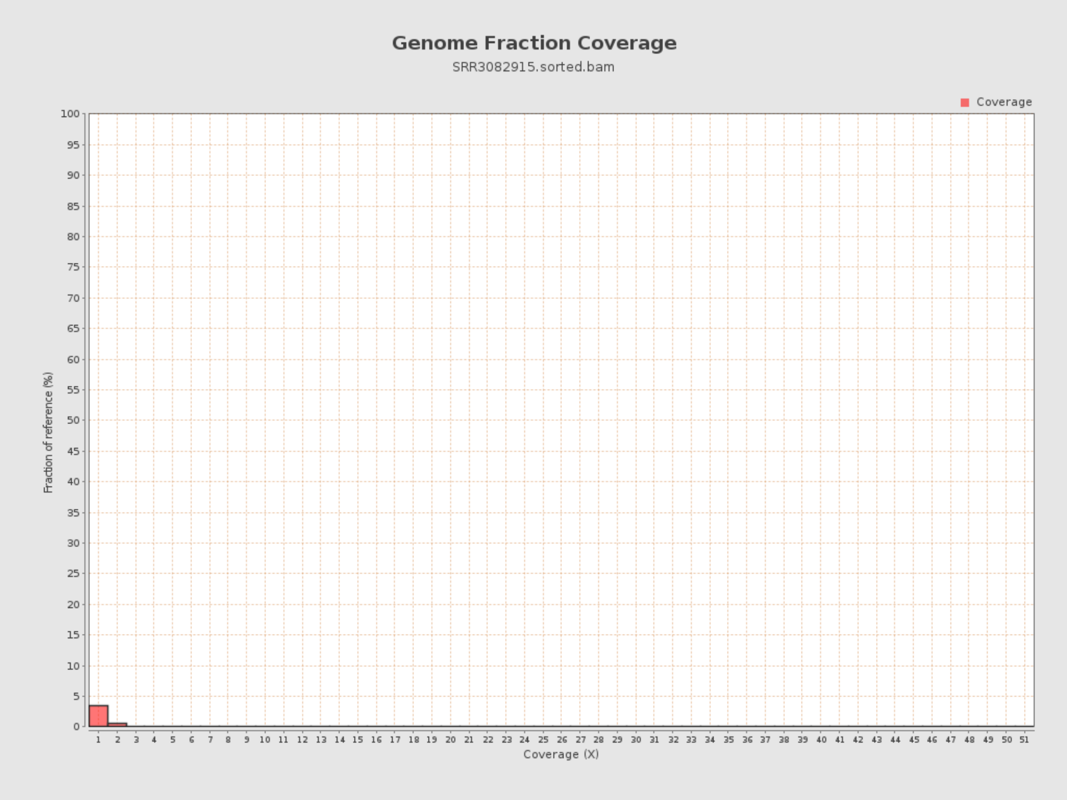
4. Results : Coverage Histogram



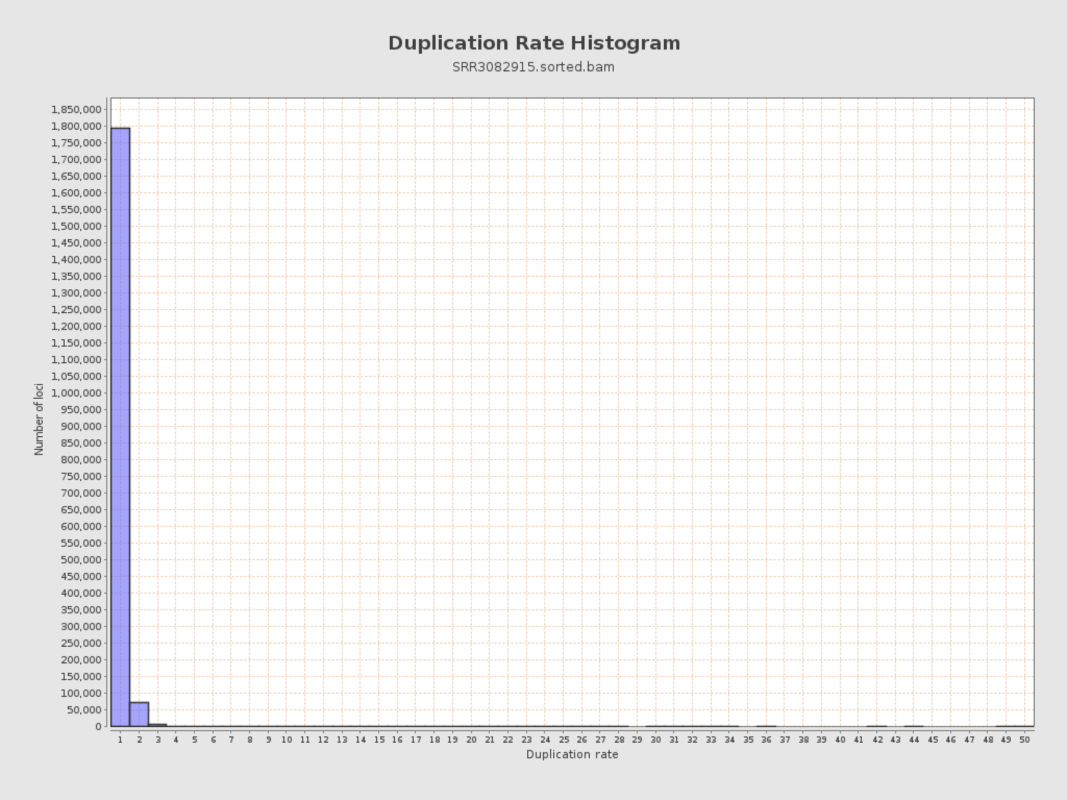
5. Results : Coverage Histogram (0-50X)



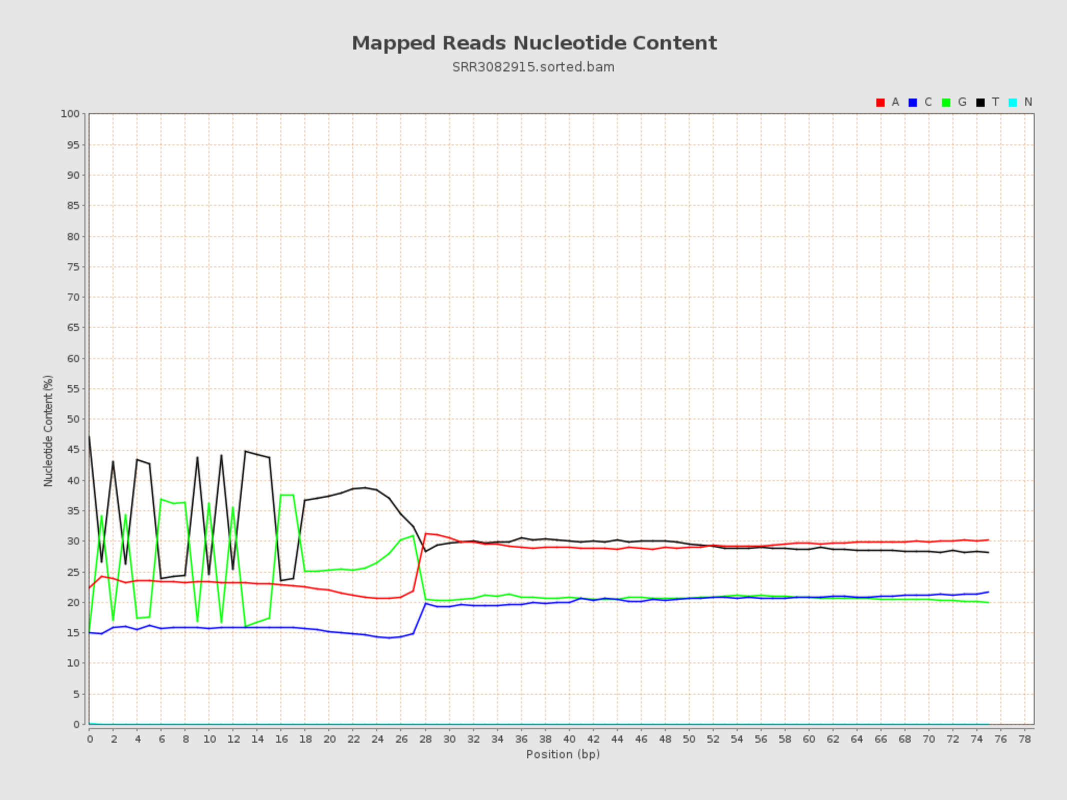
6. Results : Genome Fraction Coverage



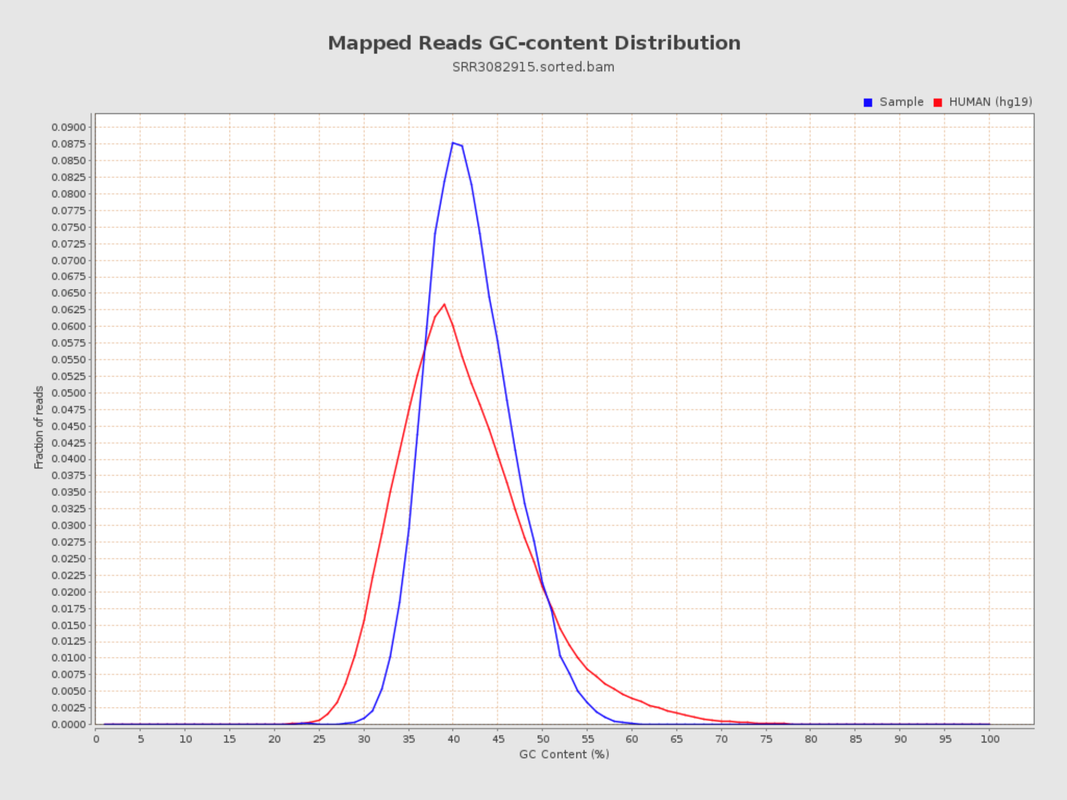
7. Results : Duplication Rate Histogram



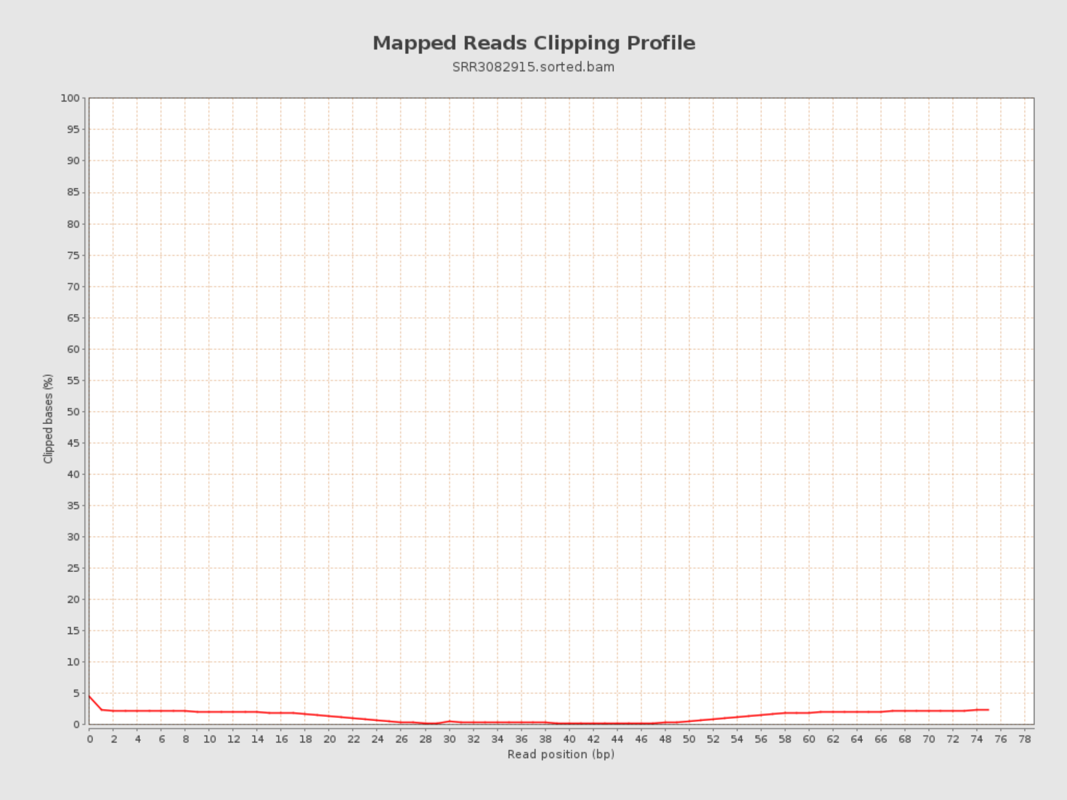
8. Results : Mapped Reads Nucleotide Content



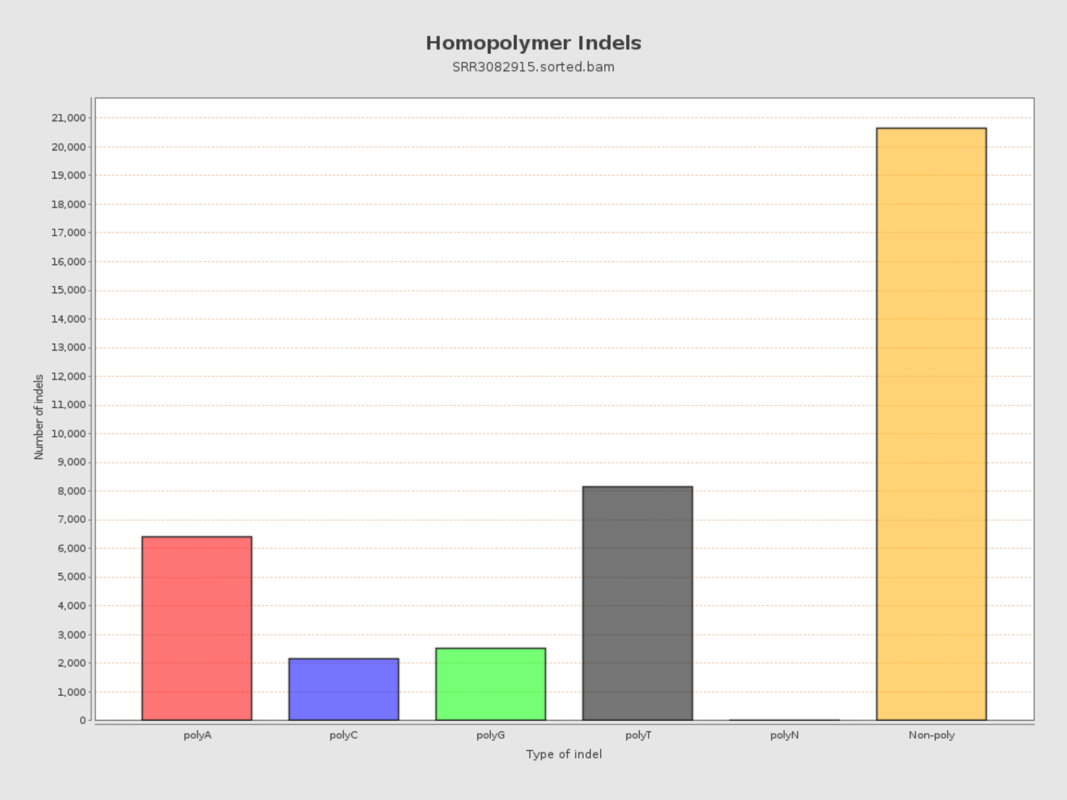
9. Results : Mapped Reads GC-content Distribution



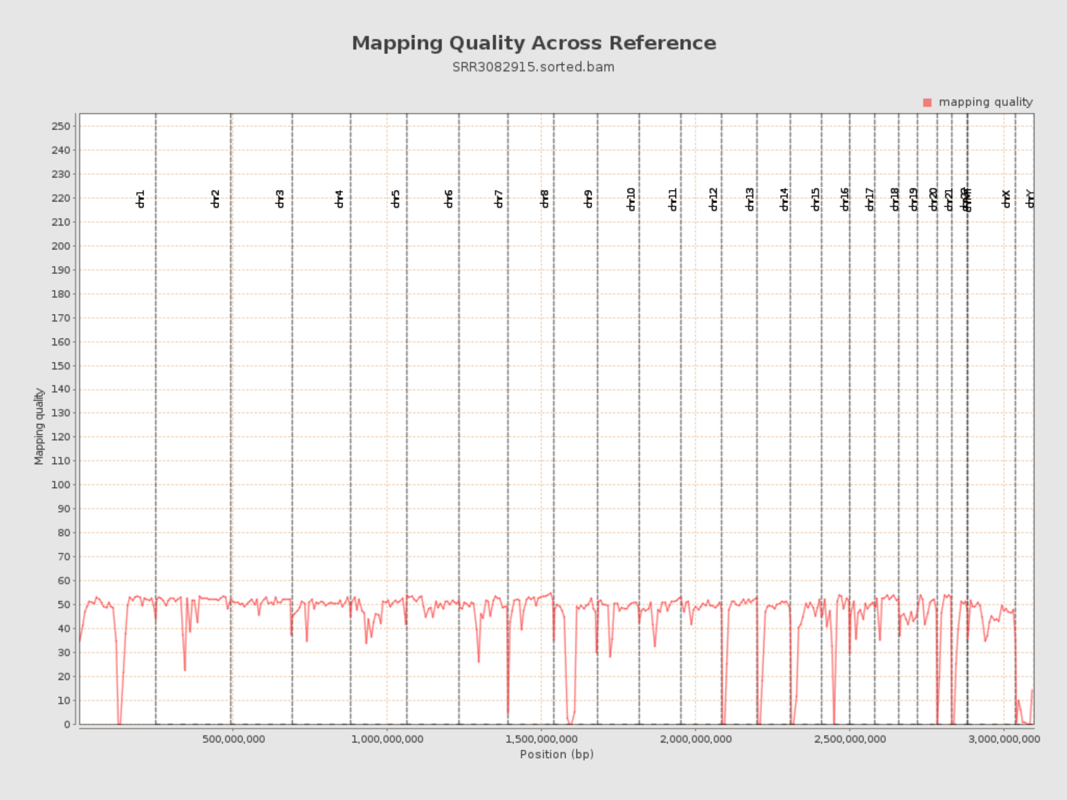
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram