Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:08:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082901.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_SRR3082901 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082901.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:08:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082901.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,863,661
Mapped reads	1,690,167 / 90.69%
Unmapped reads	173,494 / 9.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,823 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	87,796 / 4.71%
Duplication rate	4.36%
Clipped reads	749,870 / 40.24%

2.2. ACGT Content

Number/percentage of A's	31,169,161 / 27.64%
Number/percentage of C's	20,753,502 / 18.41%
Number/percentage of T's	36,034,215 / 31.96%
Number/percentage of G's	24,790,347 / 21.99%
Number/percentage of N's	5,356 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0364

Standard Deviation	0.3027

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

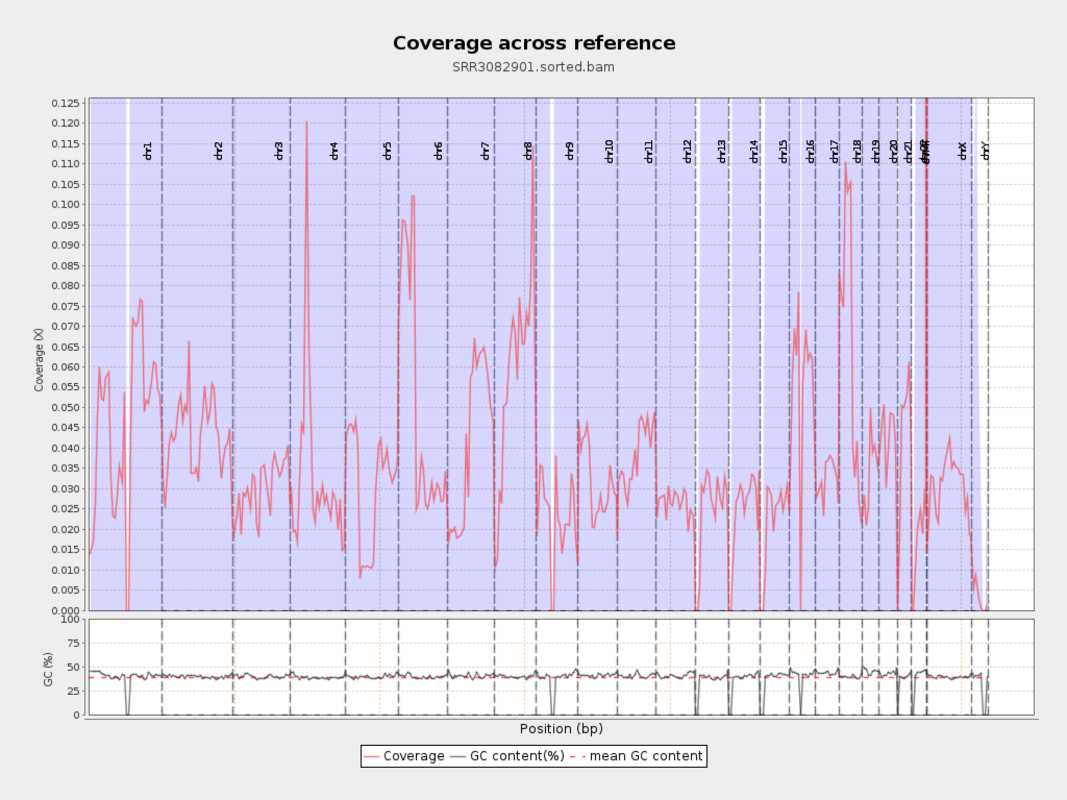
General error rate	0.72%
Mismatches	790,214
Insertions	9,588
Mapped reads with at least one insertion	0.56%
Deletions	26,139
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.52%

2.6. Chromosome stats

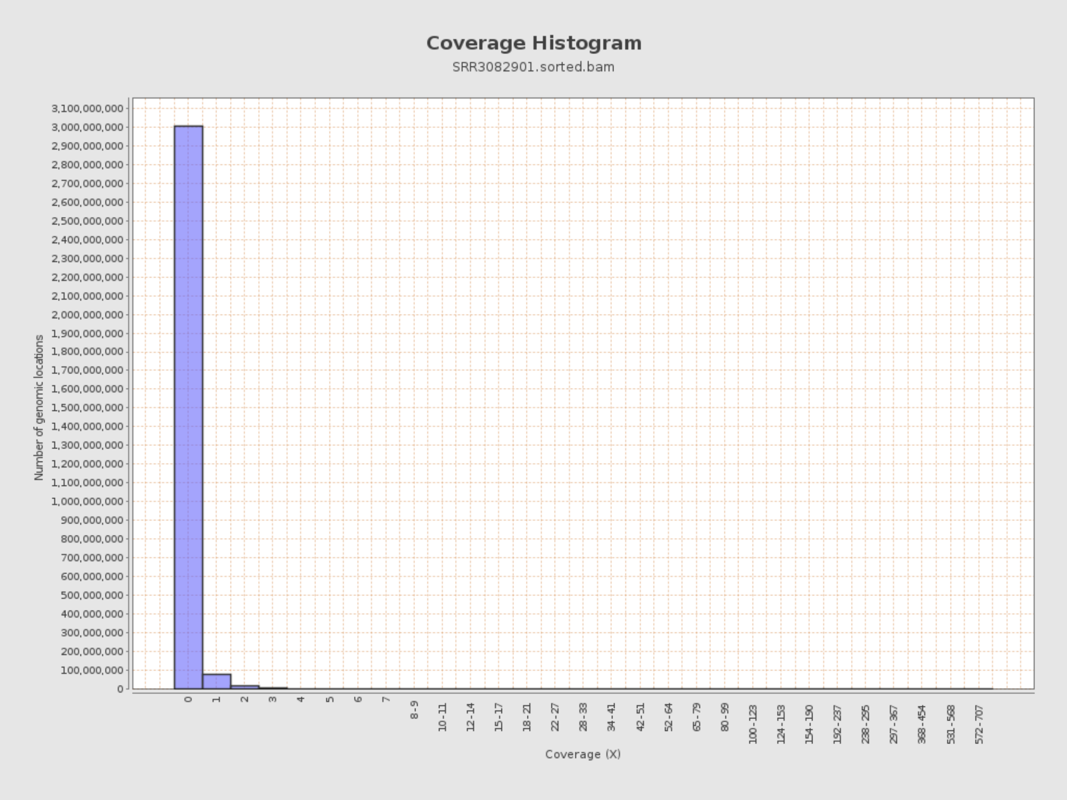
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11350716	0.0455	0.4824
chr2	243199373	10531081	0.0433	0.4503
chr3	198022430	5947834	0.03	0.2043
chr4	191154276	6200901	0.0324	0.2176
chr5	180915260	5509818	0.0305	0.2077
chr6	171115067	8652469	0.0506	0.3186
chr7	159138663	6706806	0.0421	0.3244

chr8	146364022	8593253	0.0587	0.3517
chr9	141213431	3256492	0.0231	0.2612
chr10	135534747	4350530	0.0321	0.2368
chr11	135006516	5176668	0.0383	0.2556
chr12	133851895	3507529	0.0262	0.1971
chr13	115169878	2809680	0.0244	0.1859
chr14	107349540	2556170	0.0238	0.1995
chr15	102531392	2251418	0.022	0.1754
chr16	90354753	5020233	0.0556	0.2899
chr17	81195210	2640488	0.0325	0.2204
chr18	78077248	5141514	0.0659	0.4786
chr19	59128983	1999295	0.0338	0.3887
chr20	63025520	2661061	0.0422	0.2494
chr21	48129895	2009844	0.0418	0.2476
chr22	51304566	852382	0.0166	0.1501
chrMT	16571	134096	8.0922	6.3958
chrX	155270560	4732680	0.0305	0.2177
chrY	59373566	201986	0.0034	0.0741

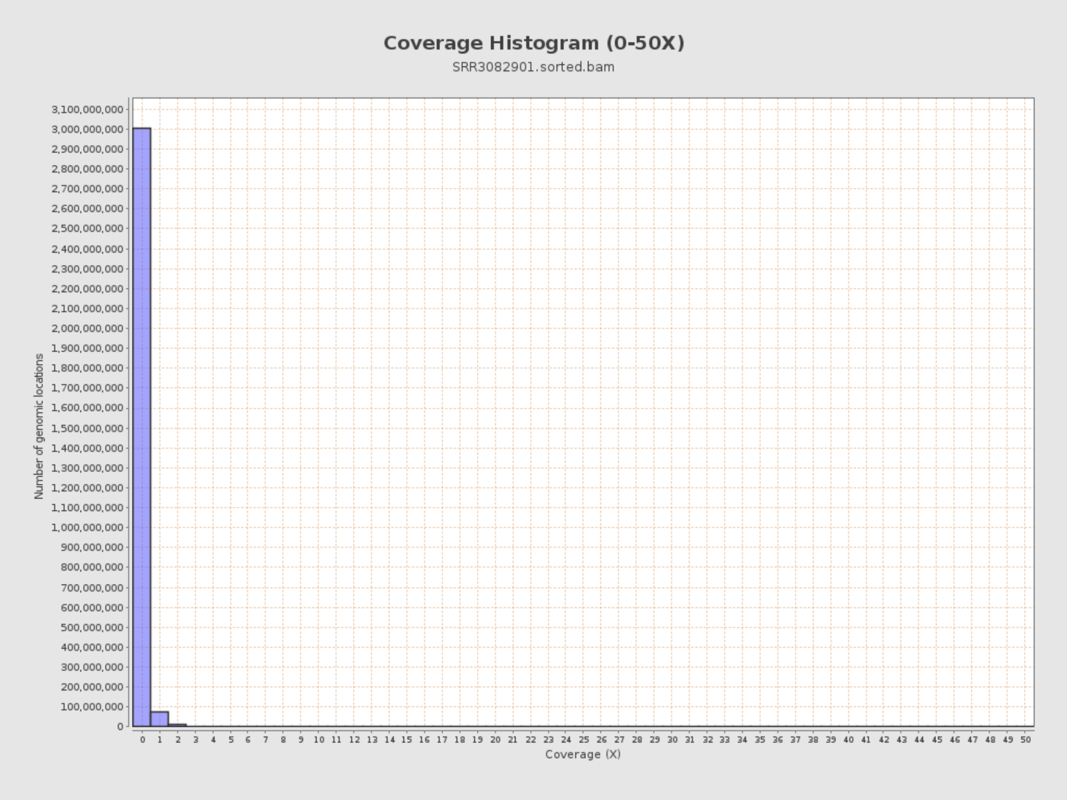
3. Results : Coverage across reference



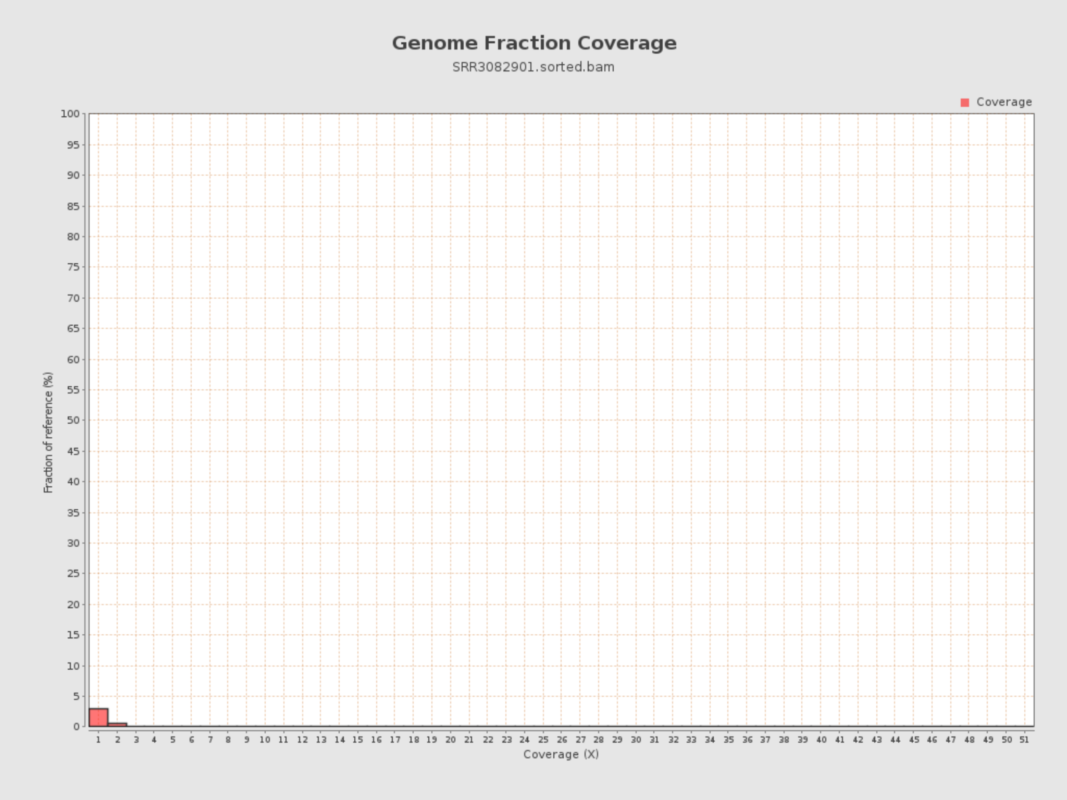
4. Results : Coverage Histogram



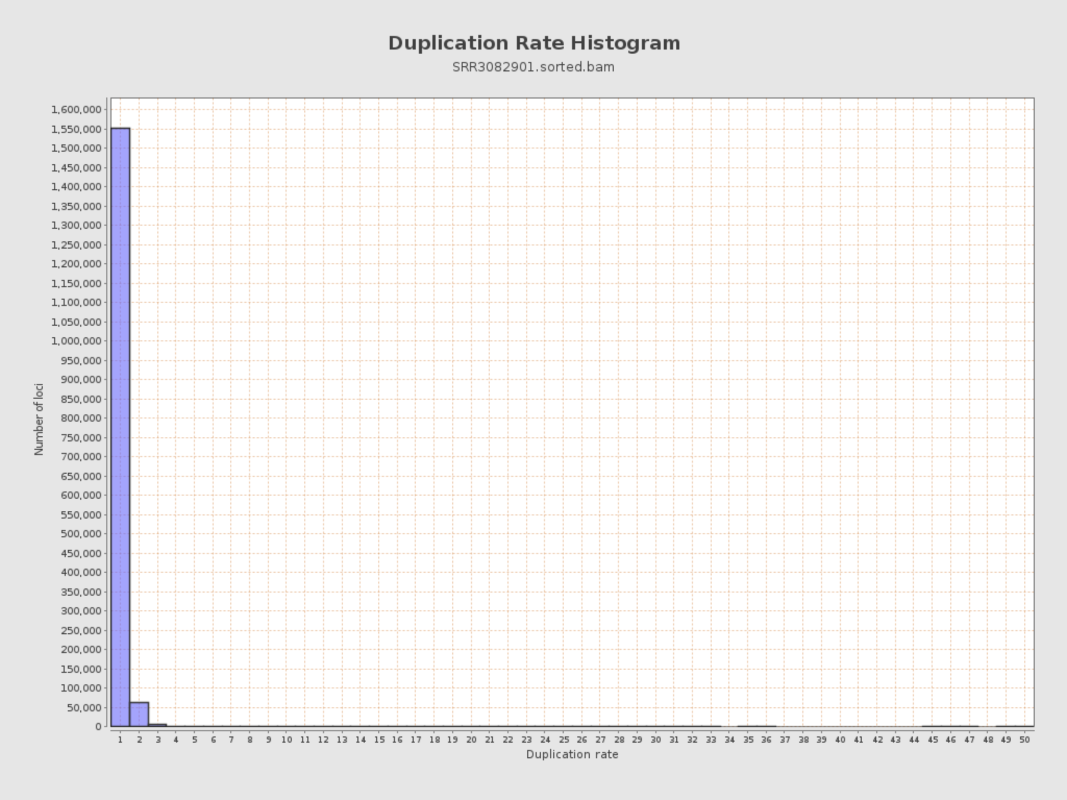
5. Results : Coverage Histogram (0-50X)



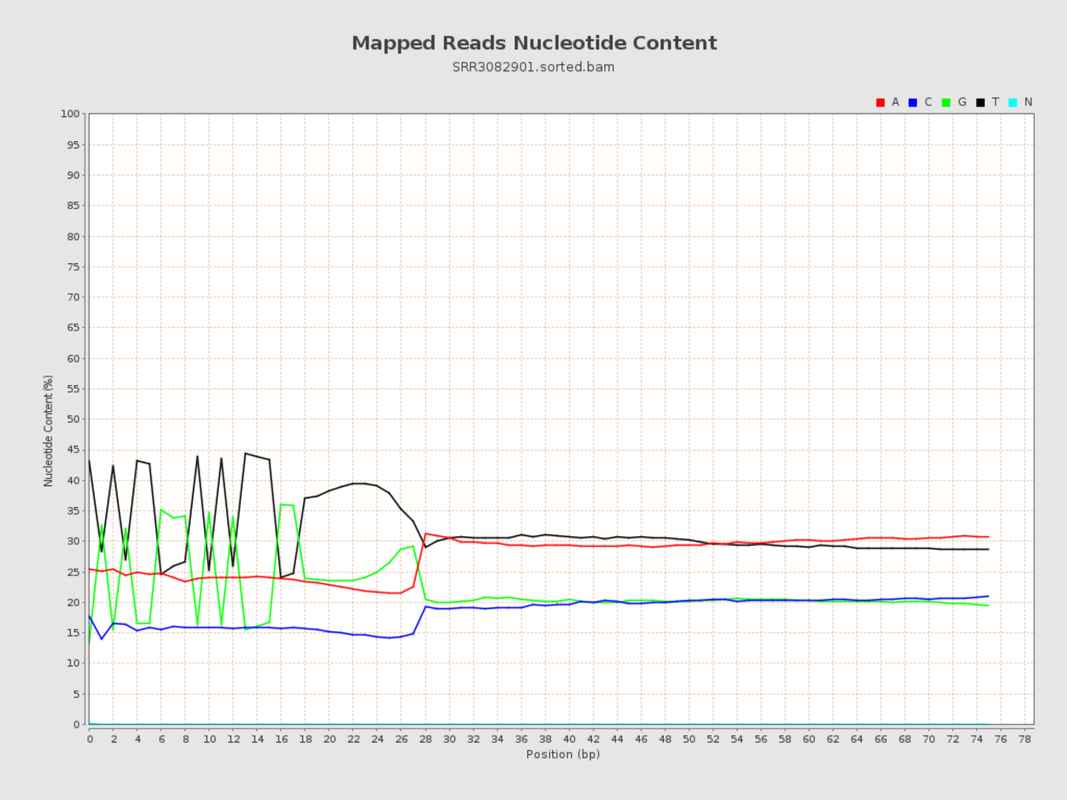
6. Results : Genome Fraction Coverage



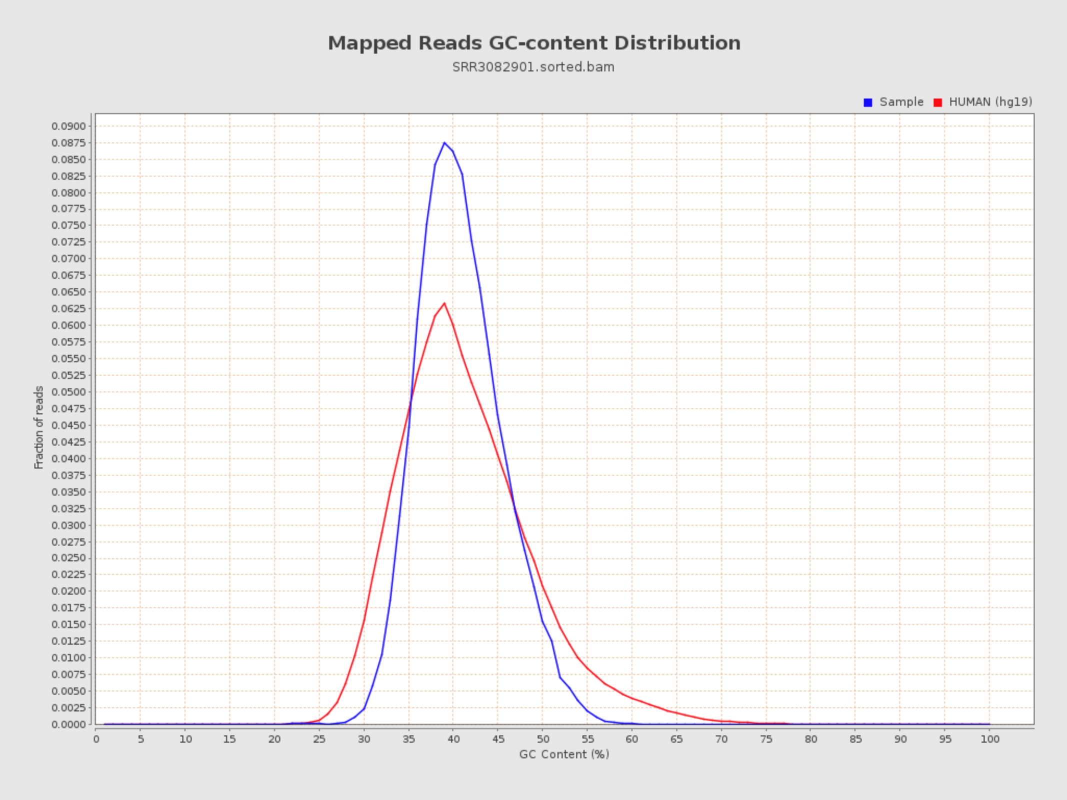
7. Results : Duplication Rate Histogram



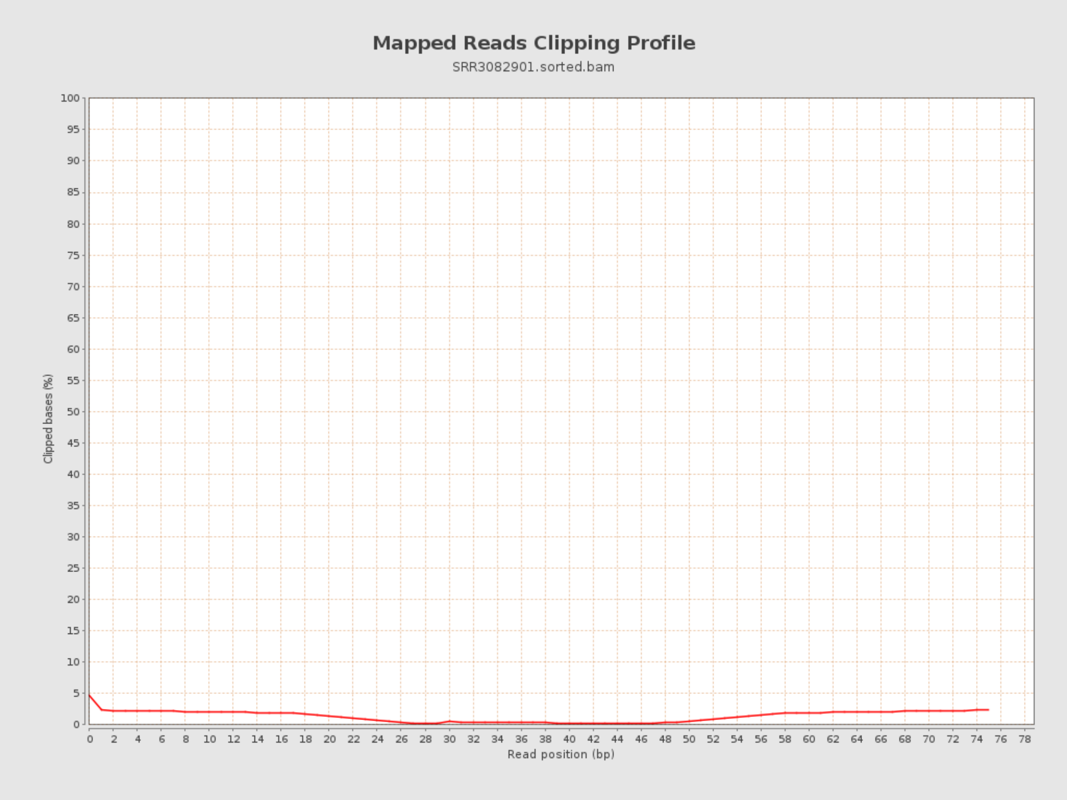
8. Results : Mapped Reads Nucleotide Content



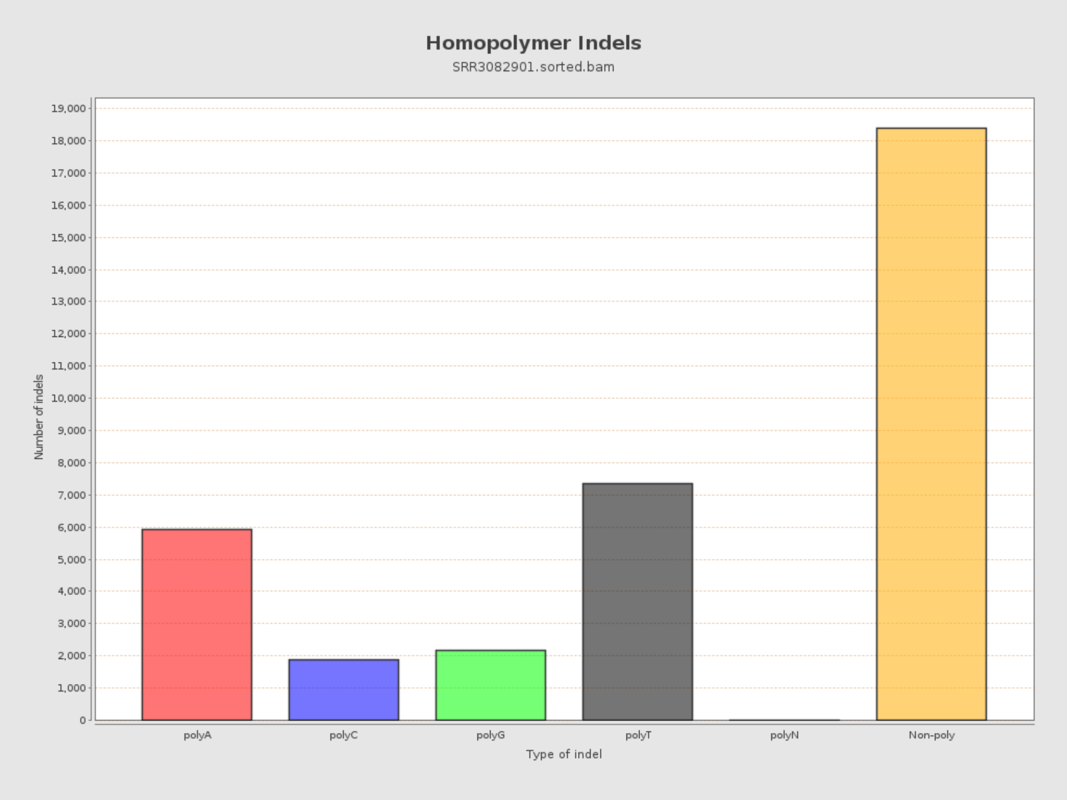
9. Results : Mapped Reads GC-content Distribution



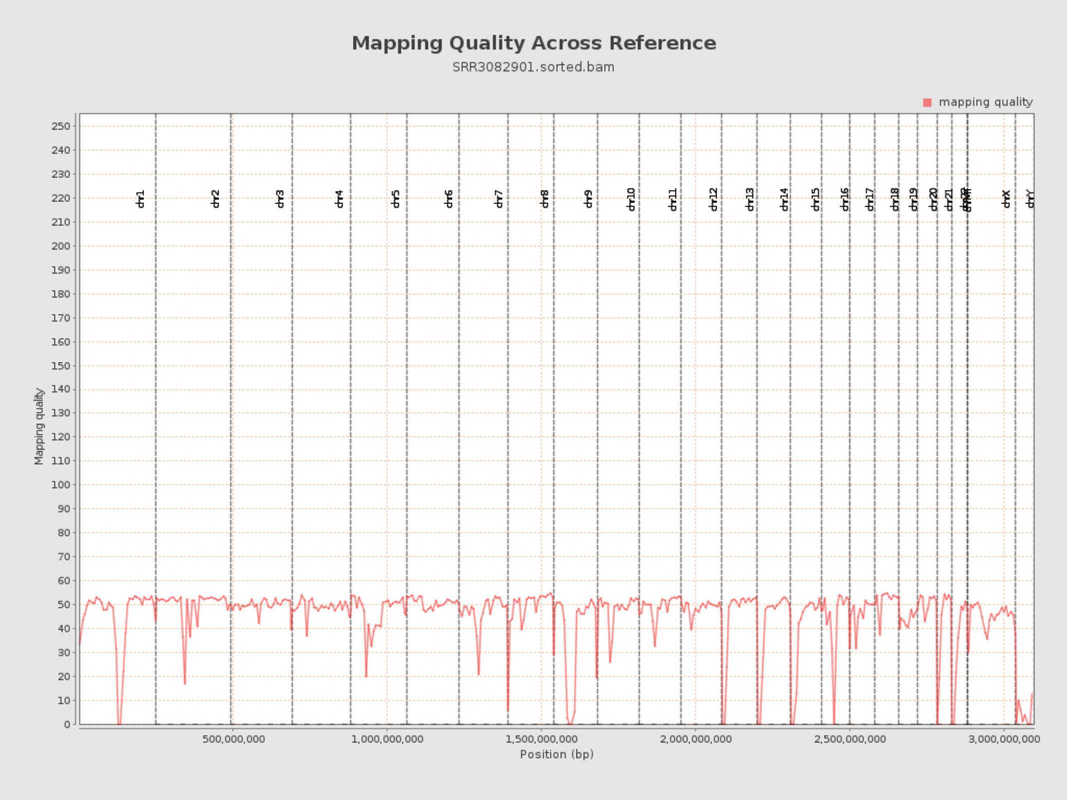
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram