Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:05:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082900.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_SRR3082900 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082900.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:05:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082900.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,072,568
Mapped reads	1,874,805 / 90.46%
Unmapped reads	197,763 / 9.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,418 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	104,703 / 5.05%
Duplication rate	4.61%
Clipped reads	802,381 / 38.71%

2.2. ACGT Content

Number/percentage of A's	34,961,312 / 27.85%
Number/percentage of C's	22,872,172 / 18.22%
Number/percentage of T's	40,403,246 / 32.19%
Number/percentage of G's	27,279,640 / 21.73%
Number/percentage of N's	5,922 / 0%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0406

Standard Deviation	0.361

2.4. Mapping Quality

Mean Mapping Quality	45.89

2.5. Mismatches and indels

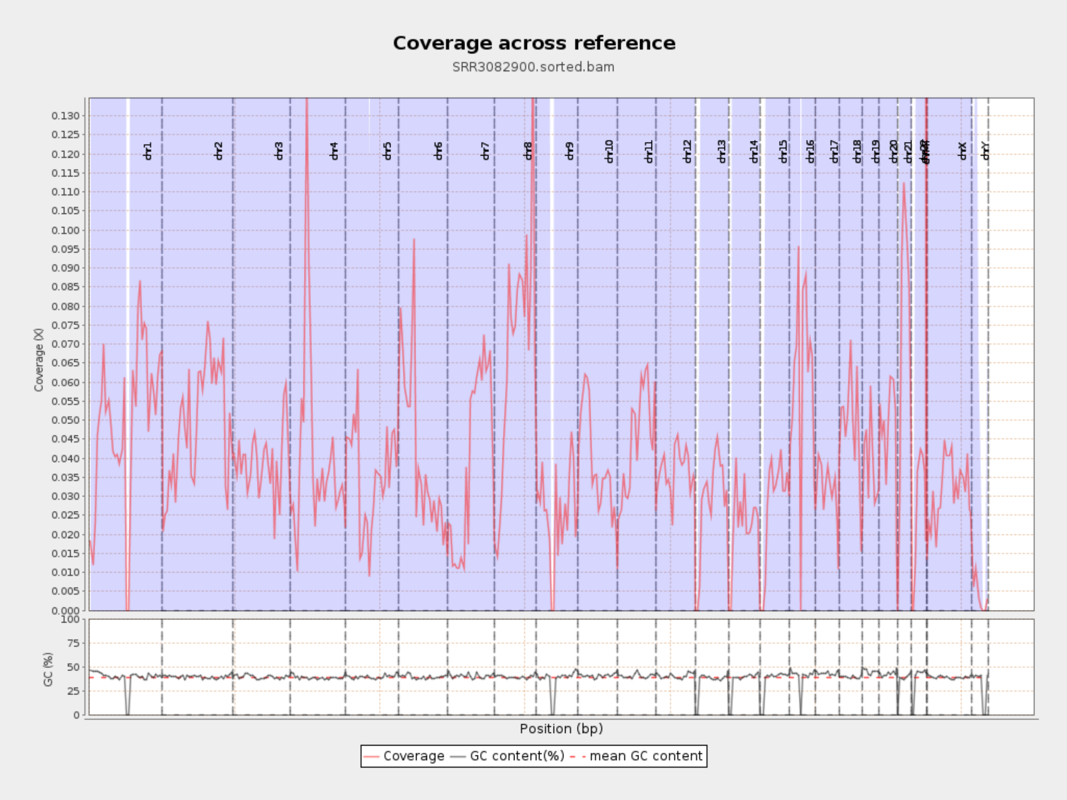
General error rate	0.74%
Mismatches	907,427
Insertions	10,286
Mapped reads with at least one insertion	0.54%
Deletions	28,857
Mapped reads with at least one deletion	1.52%
Homopolymer indels	48.55%

2.6. Chromosome stats

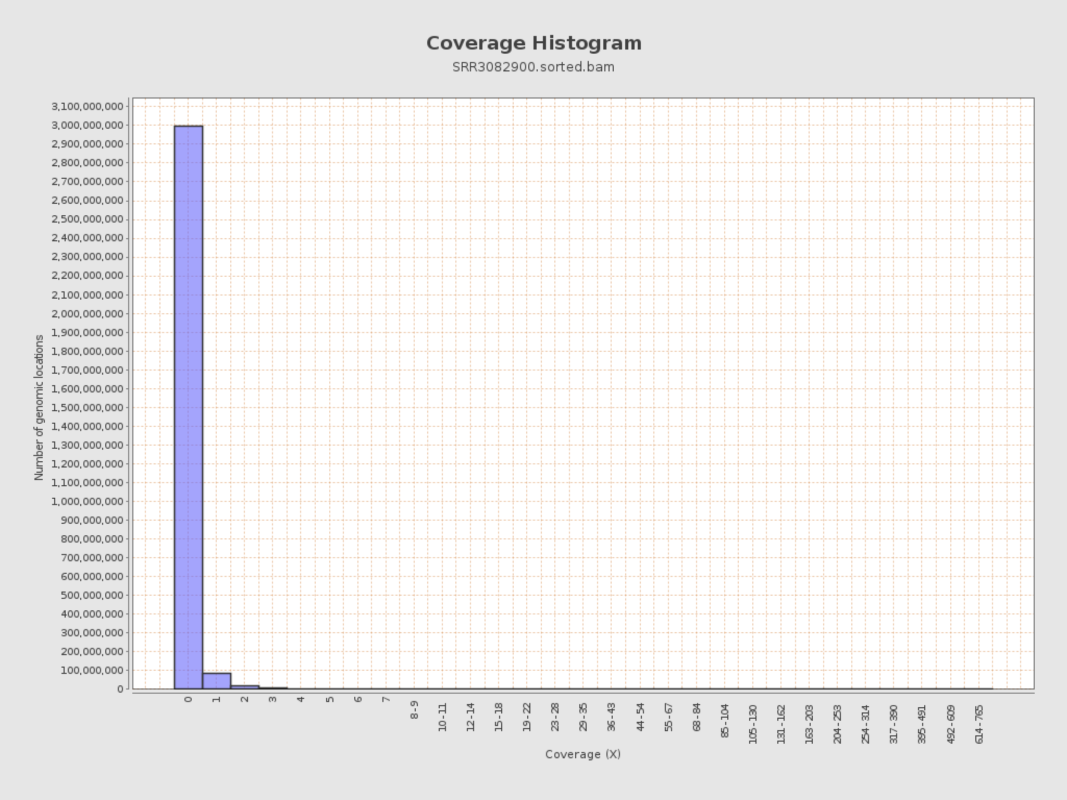
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12360847	0.0496	0.6954
chr2	243199373	11999679	0.0493	0.4527
chr3	198022430	7812465	0.0395	0.2368
chr4	191154276	7769387	0.0406	0.2488
chr5	180915260	6408274	0.0354	0.2256
chr6	171115067	7087120	0.0414	0.313
chr7	159138663	6367789	0.04	0.2965

chr8	146364022	10080021	0.0689	0.4464
chr9	141213431	3630892	0.0257	0.295
chr10	135534747	5344755	0.0394	0.2894
chr11	135006516	6005238	0.0445	0.3333
chr12	133851895	4917364	0.0367	0.2382
chr13	115169878	3242248	0.0282	0.2008
chr14	107349540	2406214	0.0224	0.2139
chr15	102531392	2825664	0.0276	0.1974
chr16	90354753	5537116	0.0613	0.314
chr17	81195210	2576399	0.0317	0.234
chr18	78077248	3858424	0.0494	0.6603
chr19	59128983	2304322	0.039	0.4498
chr20	63025520	3095620	0.0491	0.2904
chr21	48129895	3451163	0.0717	0.3296
chr22	51304566	1343100	0.0262	0.1917
chrMT	16571	19080	1.1514	1.3703
chrX	155270560	4875710	0.0314	0.2338
chrY	59373566	250524	0.0042	0.0866

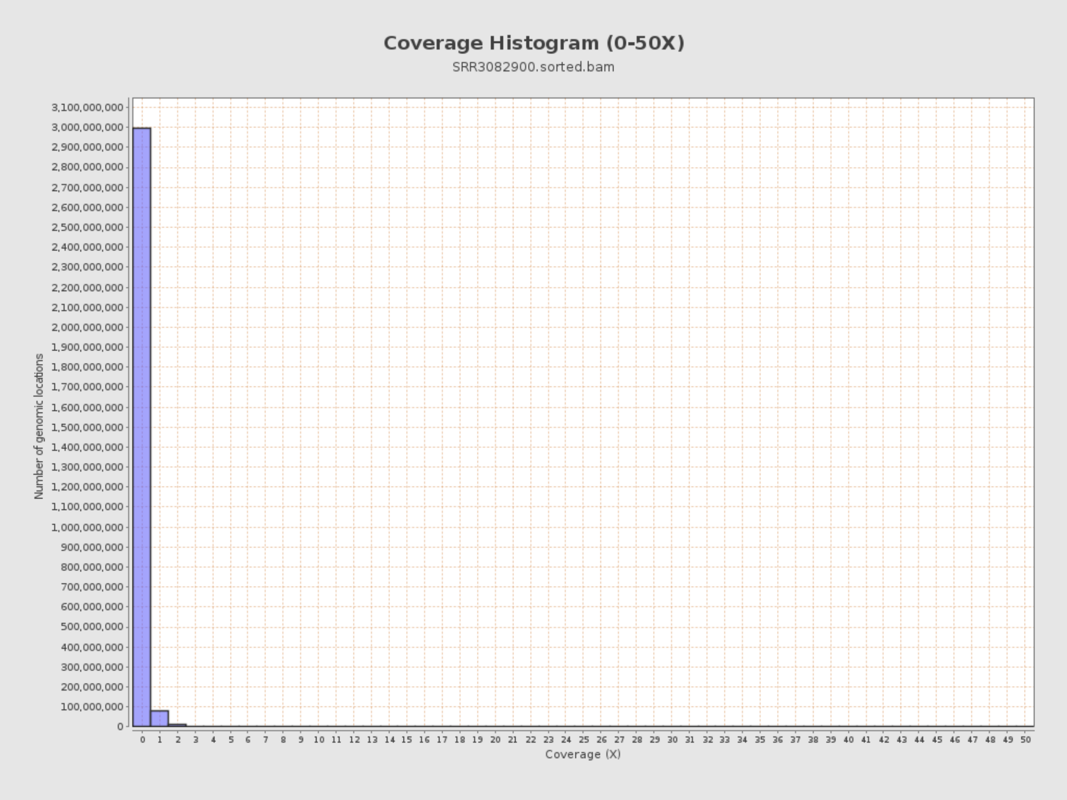
3. Results : Coverage across reference



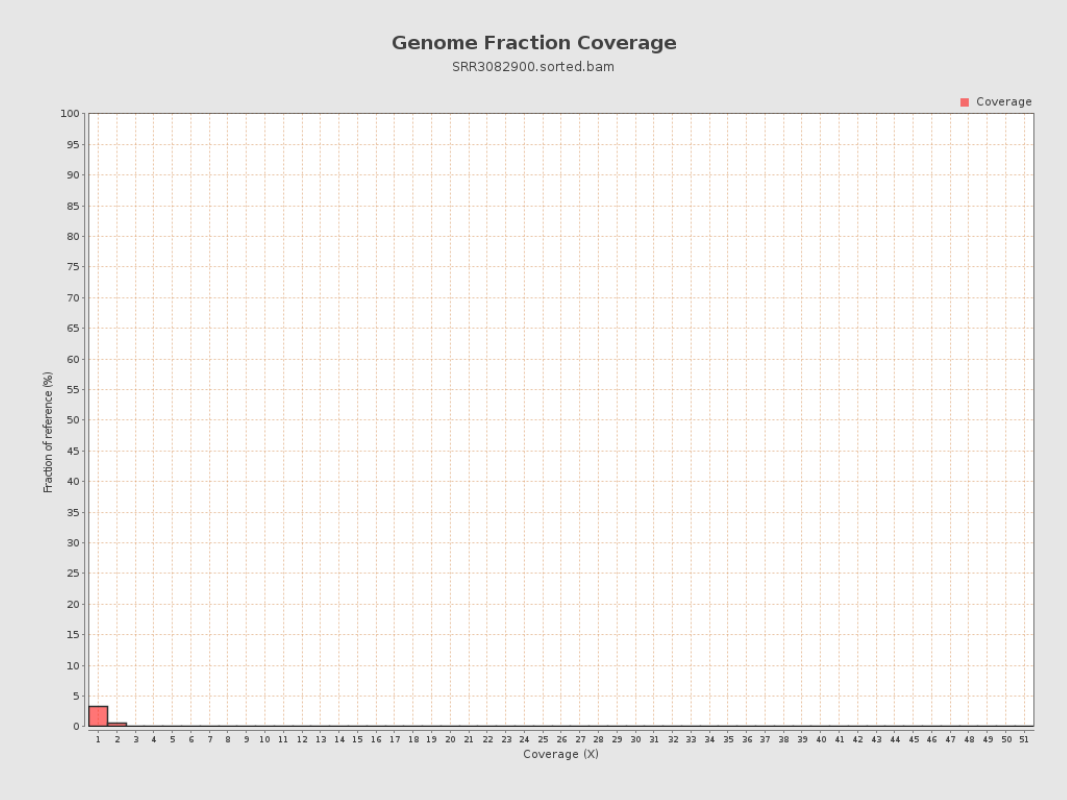
4. Results : Coverage Histogram



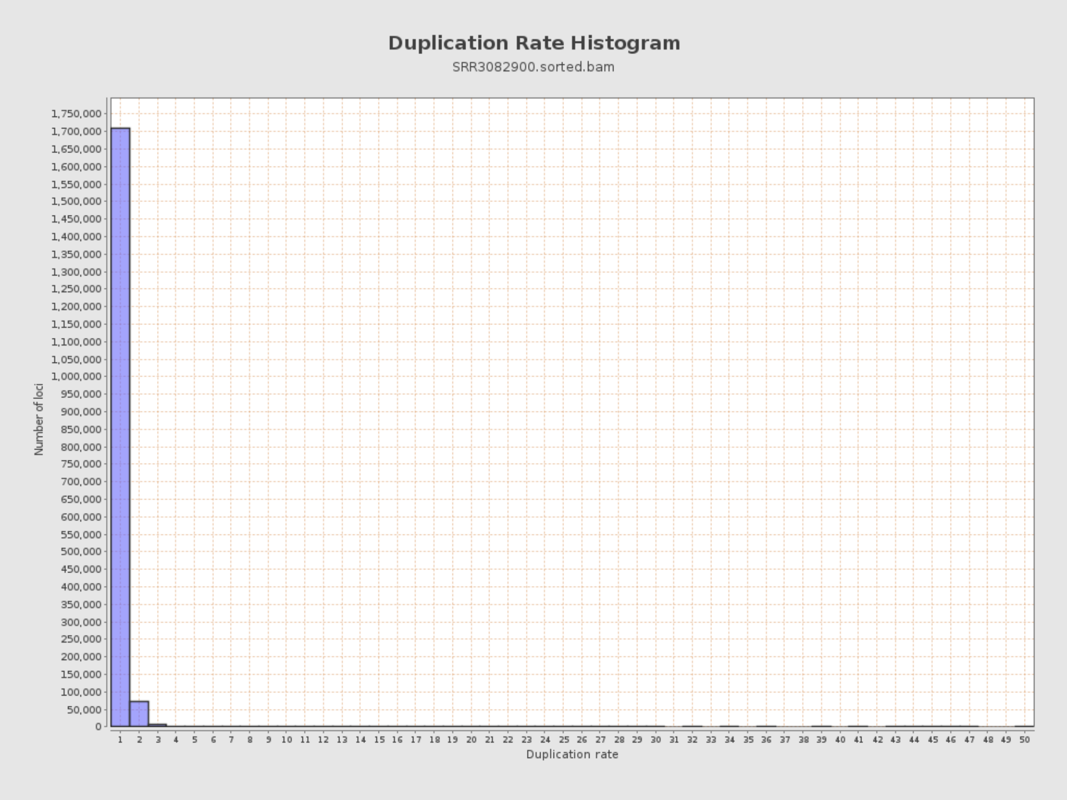
5. Results : Coverage Histogram (0-50X)



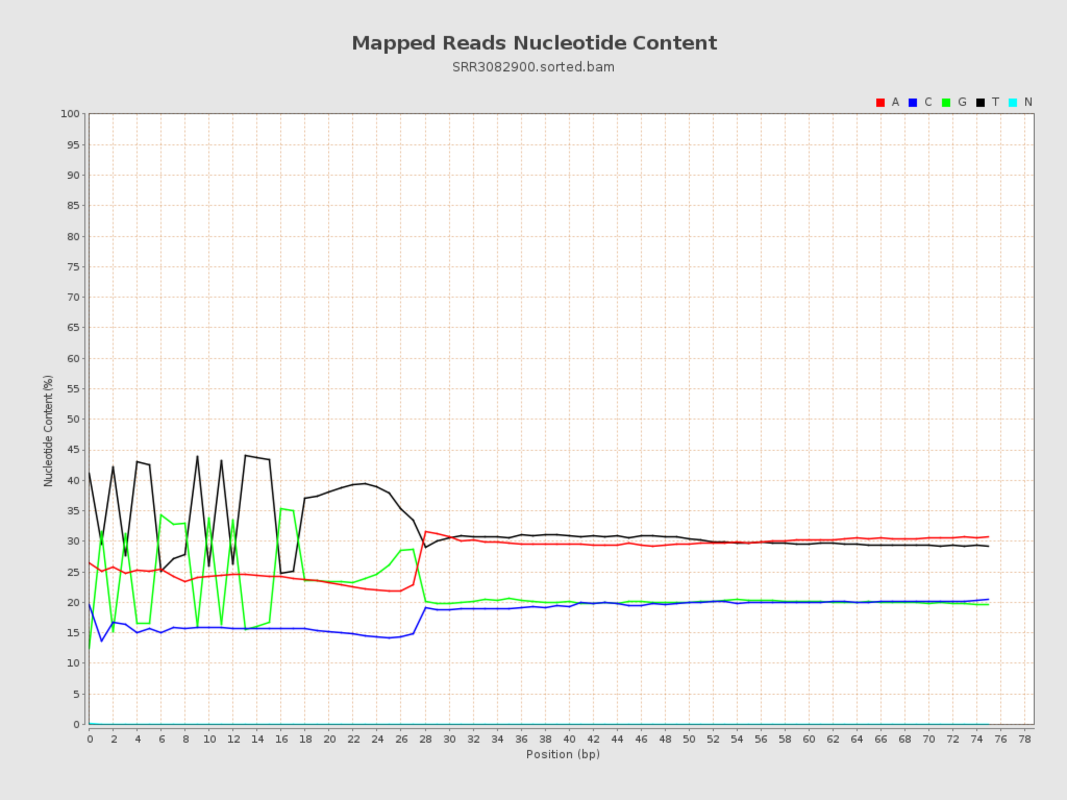
6. Results : Genome Fraction Coverage



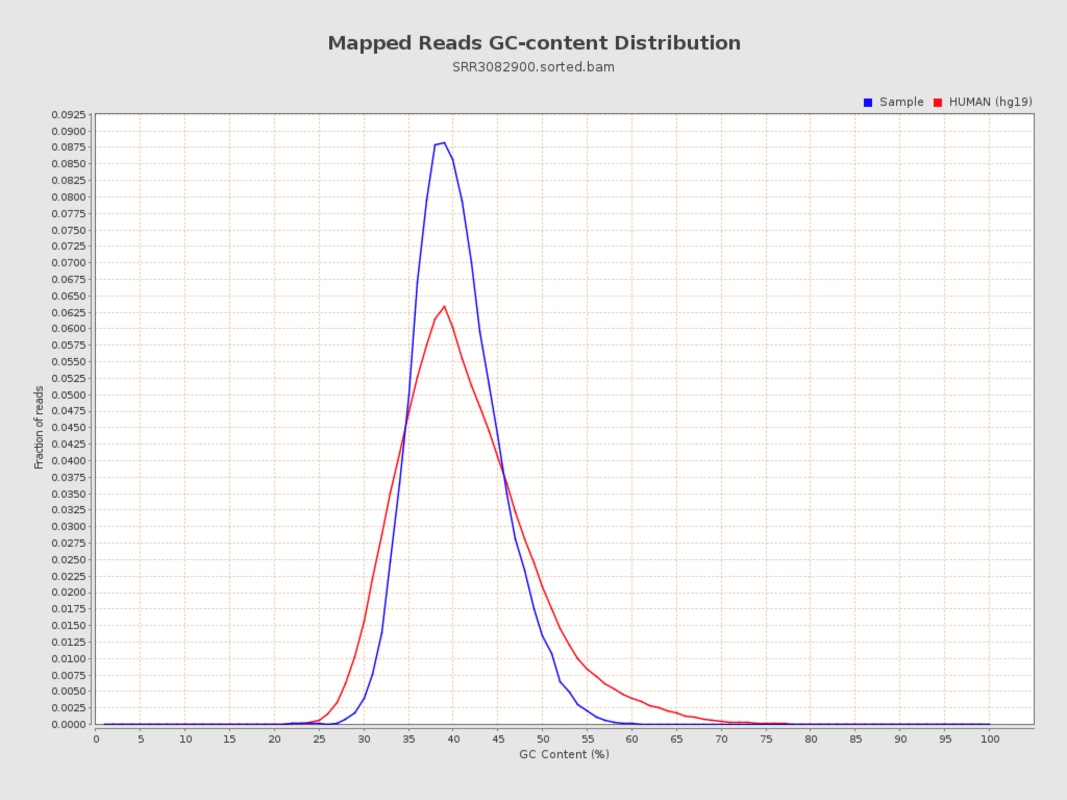
7. Results : Duplication Rate Histogram



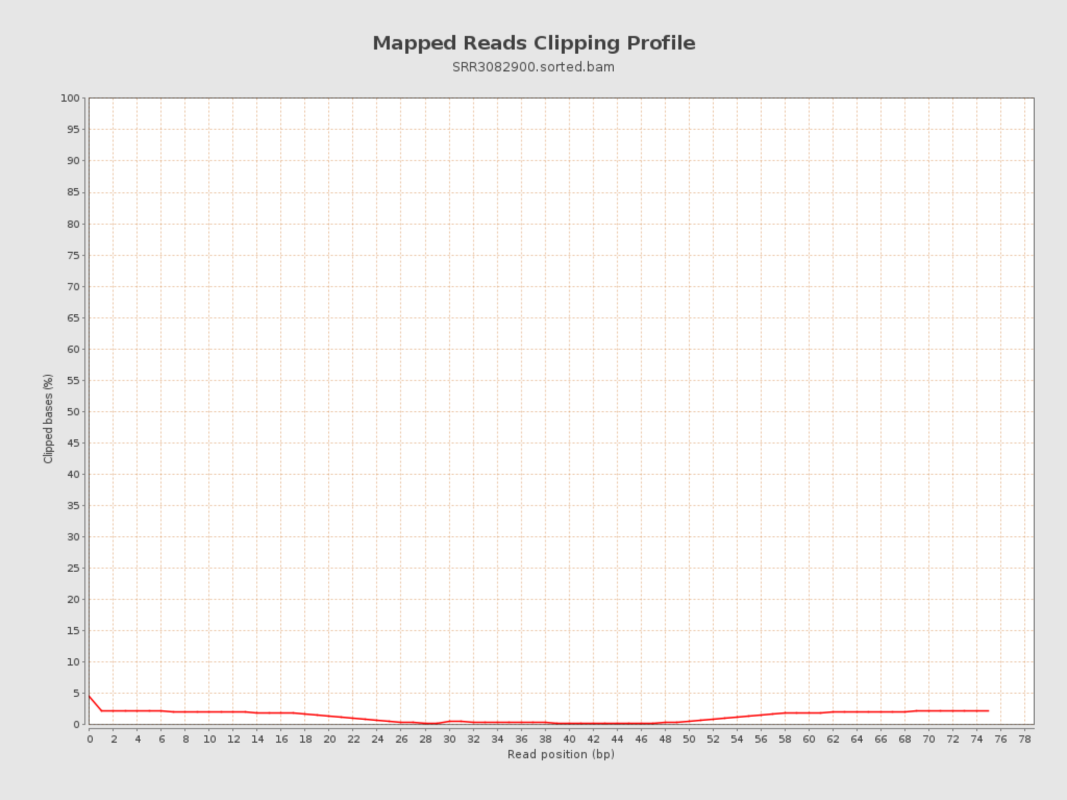
8. Results : Mapped Reads Nucleotide Content



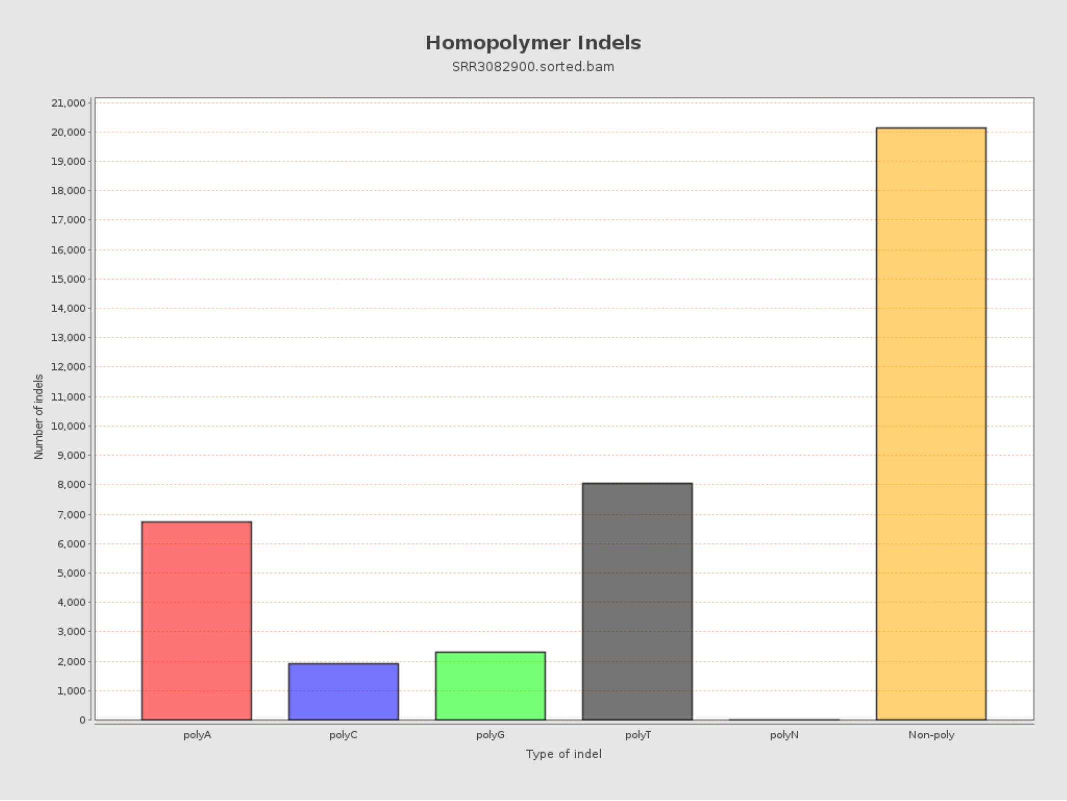
9. Results : Mapped Reads GC-content Distribution



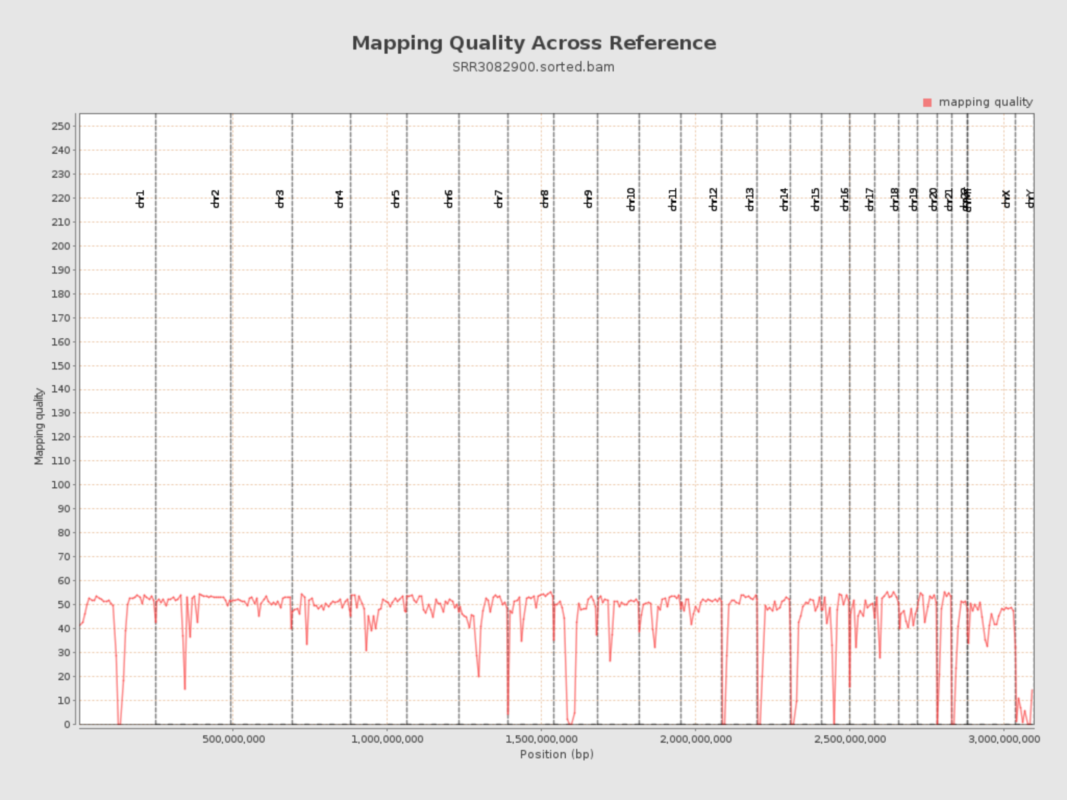
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram