Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 15:00:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124802.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_SRR3124802 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124802.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 15:00:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124802.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	703,389
Mapped reads	702,727 / 99.91%
Unmapped reads	662 / 0.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	319,620 / 45.44%
Read min/max/mean length	30 / 151 / 180.19
Duplicated reads (estimated)	1,020,869 / 145.14%
Duplication rate	44.99%
Clipped reads	661,173 / 94%

2.2. ACGT Content

Number/percentage of A's	30,608,485 / 28.96%
Number/percentage of C's	20,865,650 / 19.74%
Number/percentage of T's	33,321,929 / 31.52%
Number/percentage of G's	20,911,336 / 19.78%
Number/percentage of N's	1 / 0%
GC Percentage	39.52%

2.3. Coverage

Mean	0.0342

Standard Deviation	57.0228

2.4. Mapping Quality

Mean Mapping Quality	24.58

2.5. Mismatches and indels

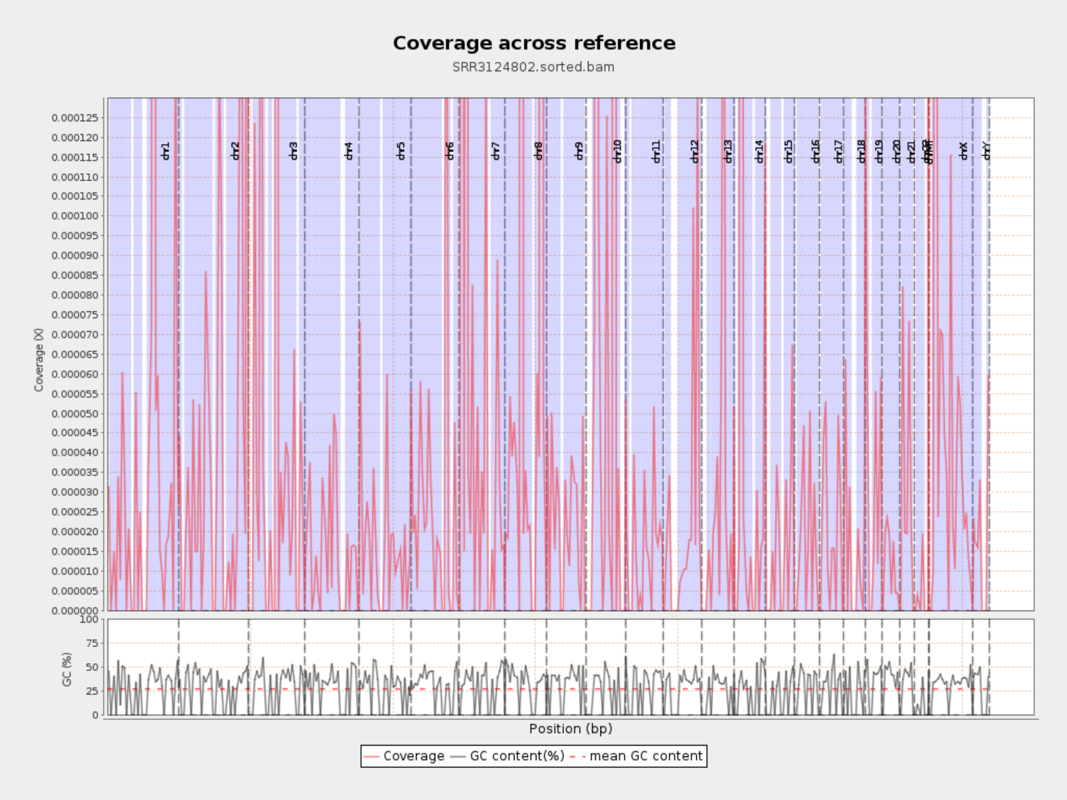
General error rate	0.76%
Mismatches	787,654
Insertions	13,023
Mapped reads with at least one insertion	1.84%
Deletions	42,887
Mapped reads with at least one deletion	5.89%
Homopolymer indels	80.38%

2.6. Chromosome stats

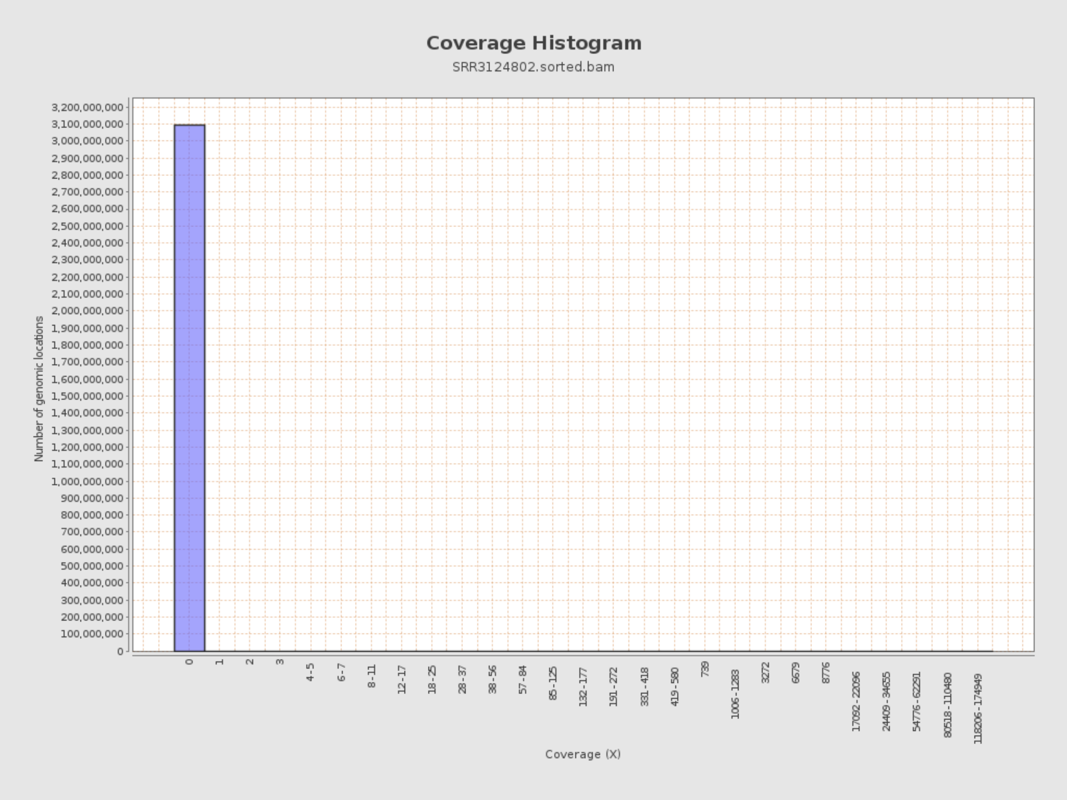
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	61824	0.0002	0.2091
chr2	243199373	11814	0	0.0383
chr3	198022430	10245	0.0001	0.0472
chr4	191154276	2924	0	0.0064
chr5	180915260	3044	0	0.0071
chr6	171115067	5207	0	0.0238
chr7	159138663	14772	0.0001	0.091

chr8	146364022	77367264	0.5286	237.5012
chr9	141213431	3112	0	0.0049
chr10	135534747	28233800	0.2083	115.5604
chr11	135006516	2239	0	0.0043
chr12	133851895	3067	0	0.0131
chr13	115169878	3574	0	0.0285
chr14	107349540	11893	0.0001	0.1542
chr15	102531392	1650	0	0.0045
chr16	90354753	1440	0	0.0049
chr17	81195210	1698	0	0.0065
chr18	78077248	1081	0	0.0038
chr19	59128983	1880	0	0.0083
chr20	63025520	721	0	0.0034
chr21	48129895	1670	0	0.0135
chr22	51304566	181	0	0.0019
chrMT	16571	113	0.0068	0.0823
chrX	155270560	7351	0	0.0224
chrY	59373566	1100	0	0.0043

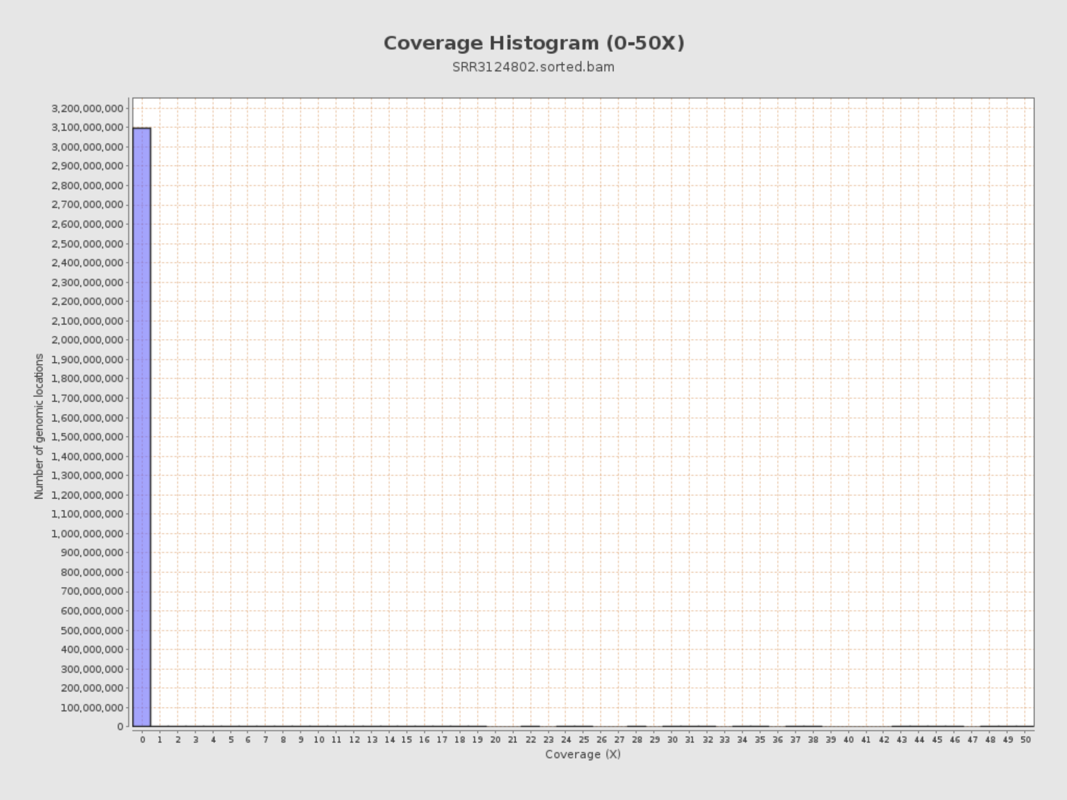
3. Results : Coverage across reference



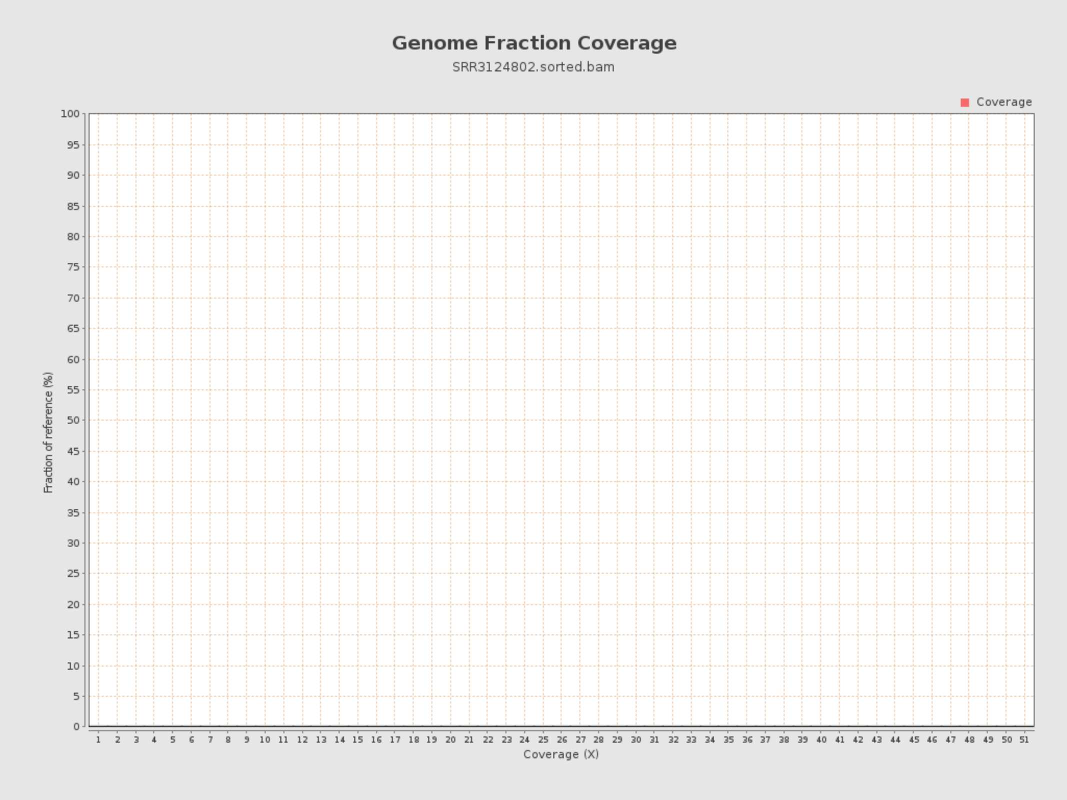
4. Results : Coverage Histogram



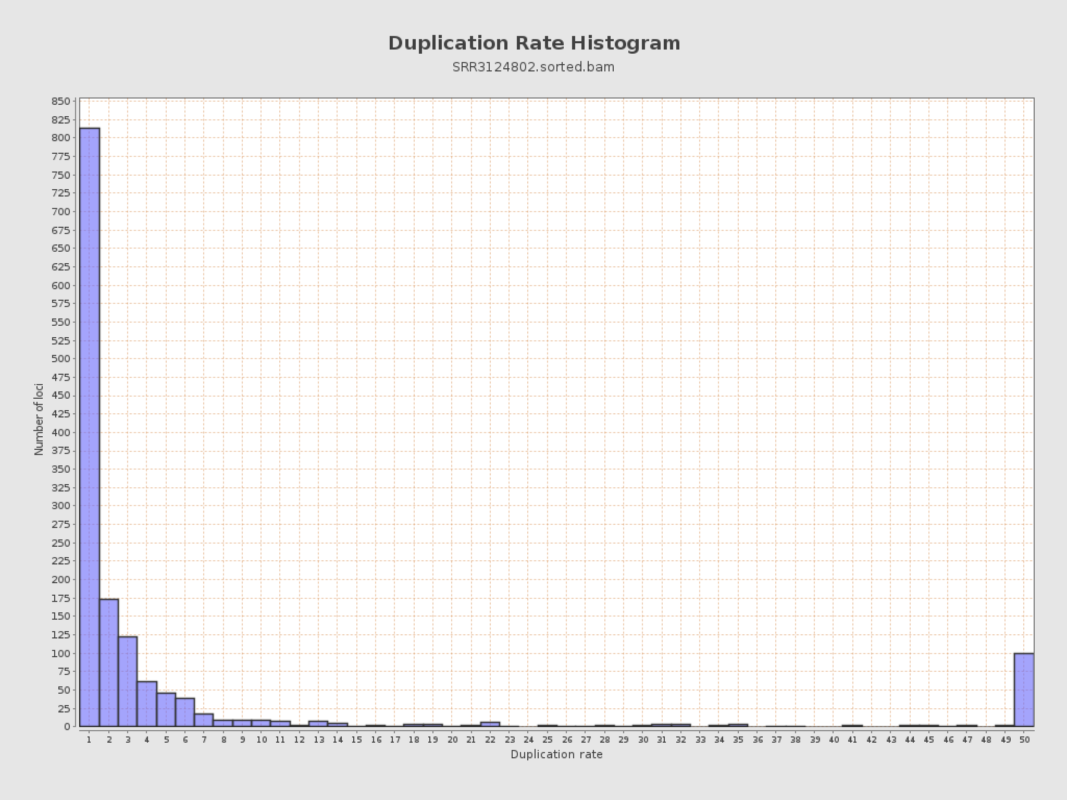
5. Results : Coverage Histogram (0-50X)



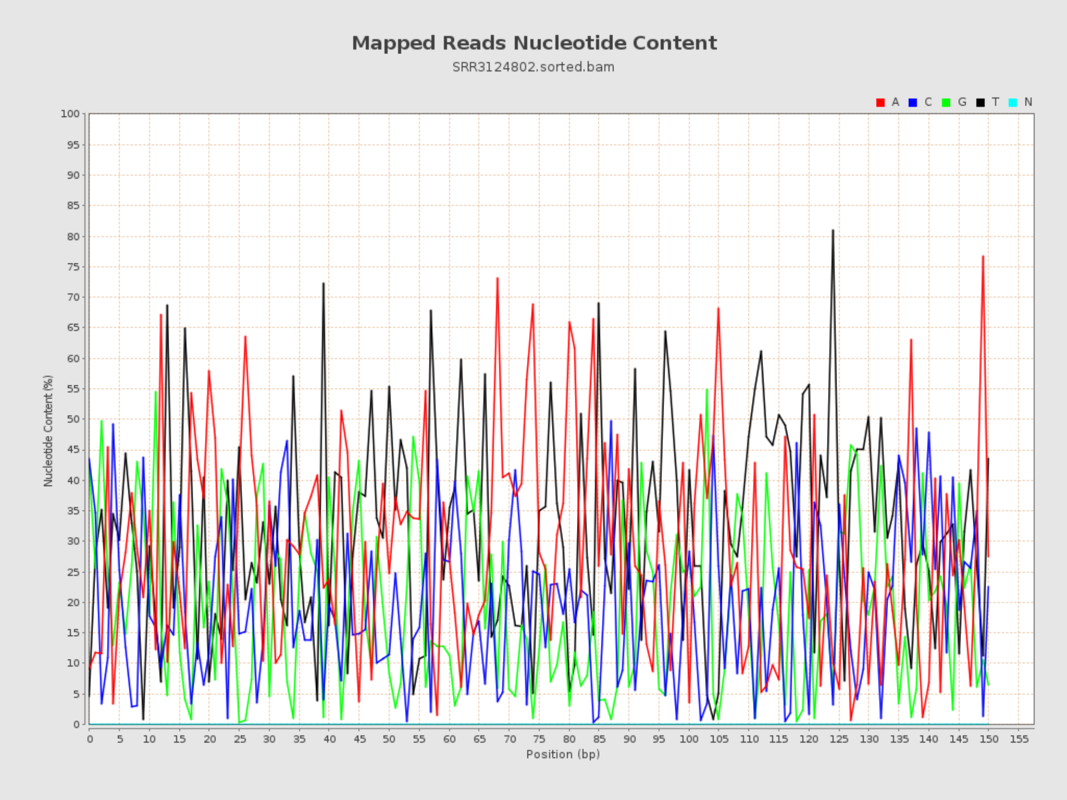
6. Results : Genome Fraction Coverage



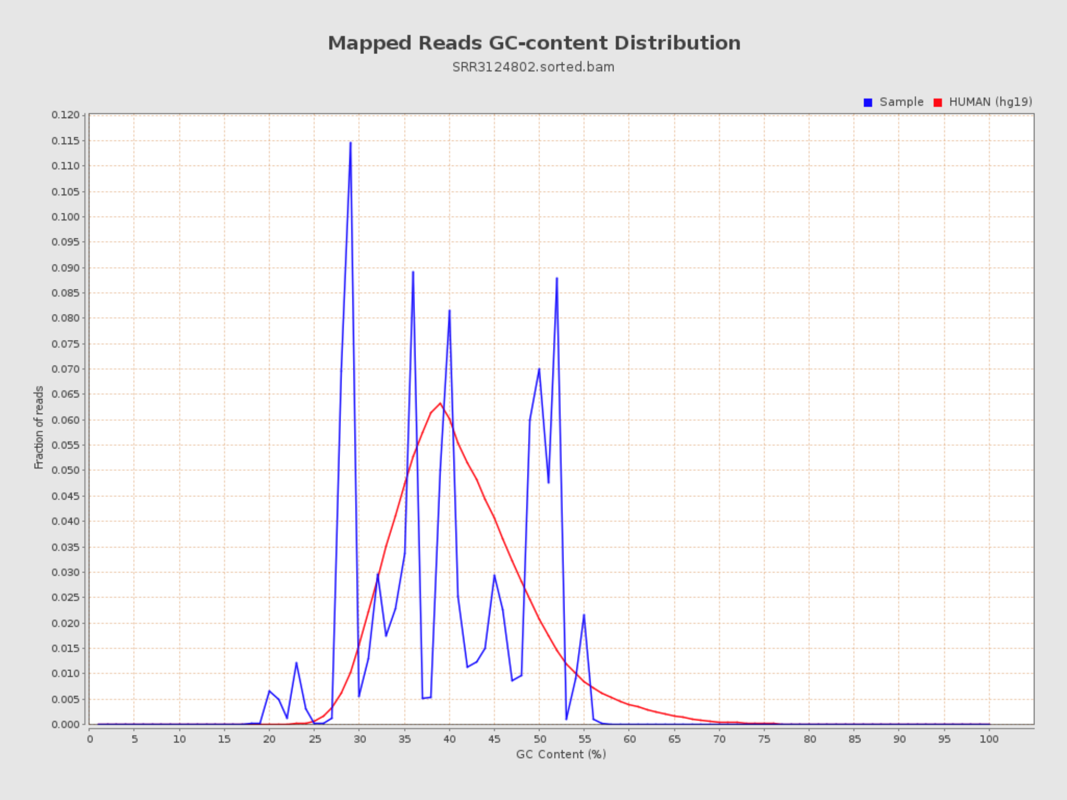
7. Results : Duplication Rate Histogram



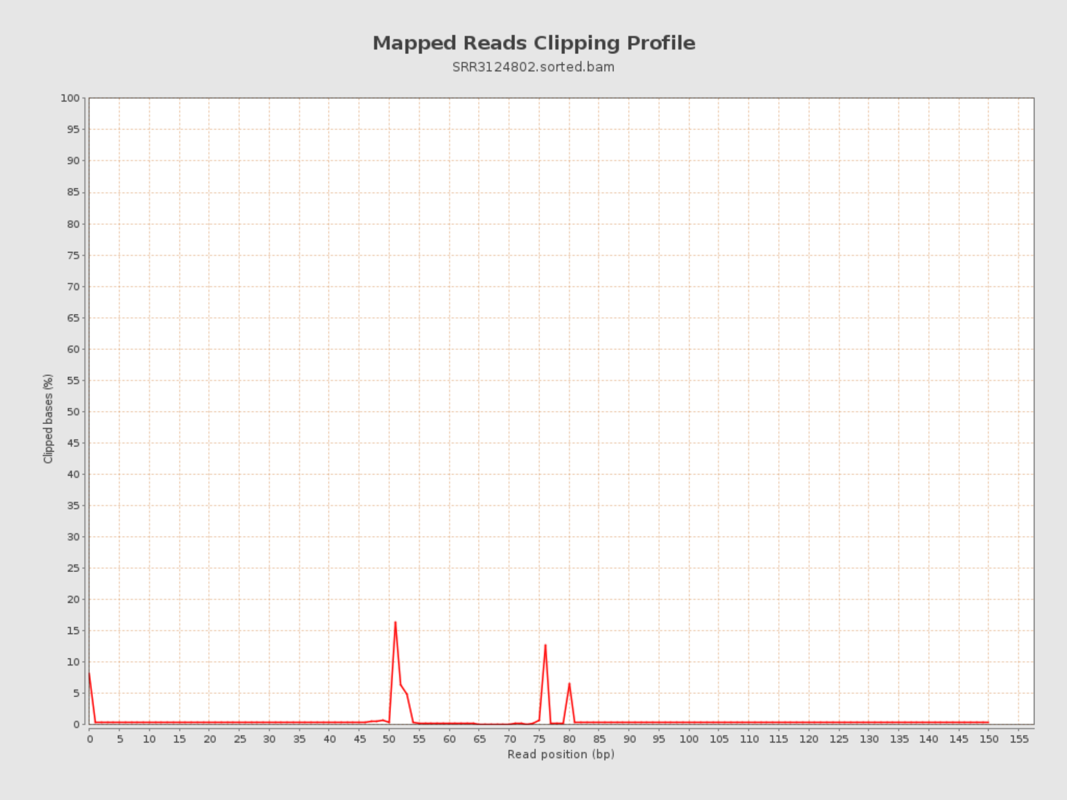
8. Results : Mapped Reads Nucleotide Content



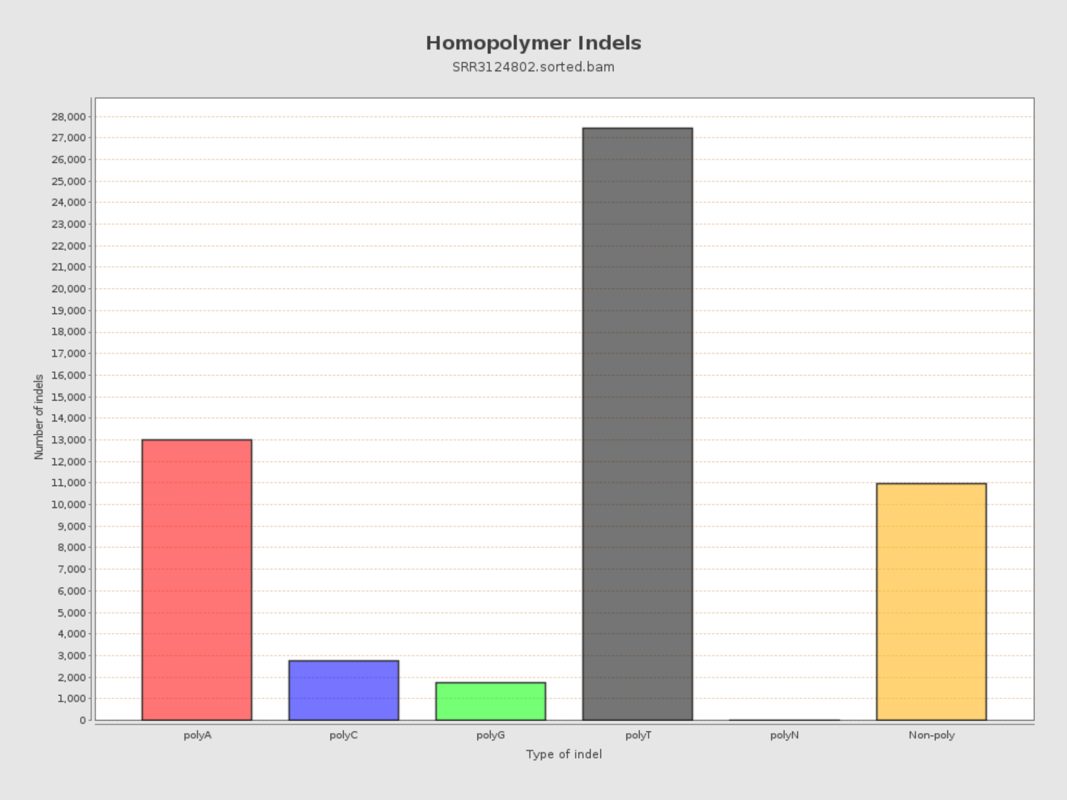
9. Results : Mapped Reads GC-content Distribution



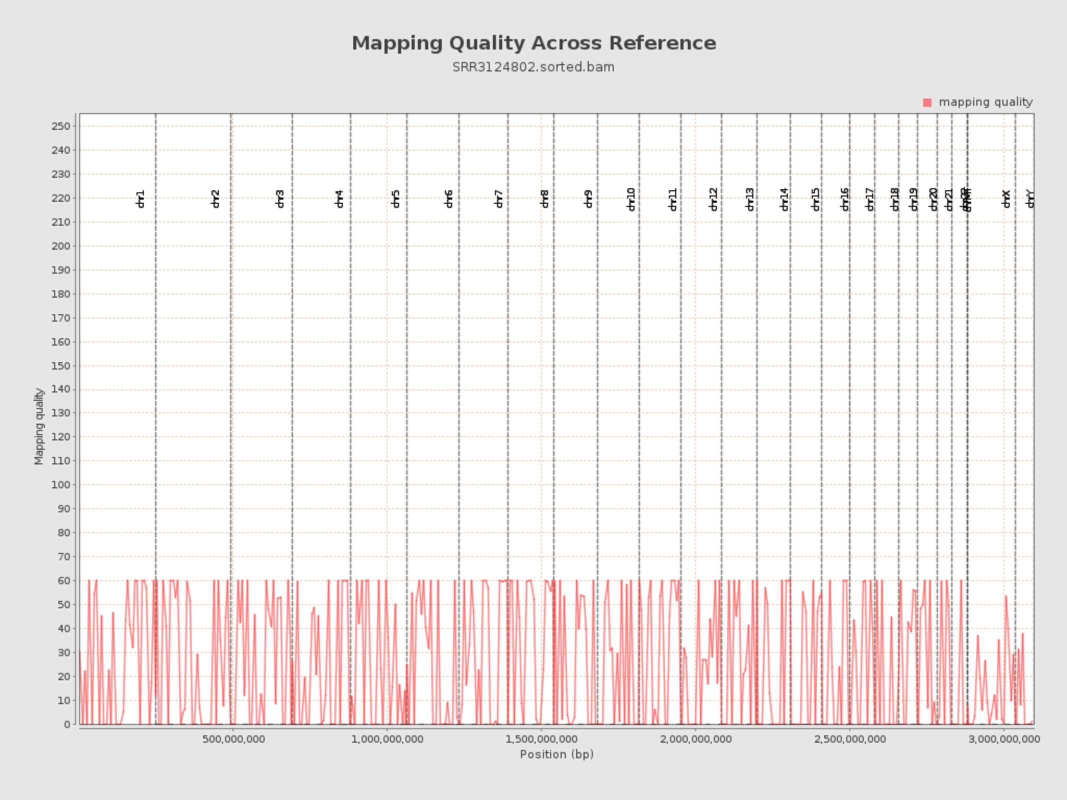
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram