Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:38:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124789.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_SRR3124789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124789.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:38:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	547,858
Mapped reads	546,888 / 99.82%
Unmapped reads	970 / 0.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	257,830 / 47.06%
Read min/max/mean length	30 / 151 / 187.31
Duplicated reads (estimated)	801,457 / 146.29%
Duplication rate	9.6%
Clipped reads	534,815 / 97.62%

2.2. ACGT Content

Number/percentage of A's	23,919,677 / 28.83%
Number/percentage of C's	12,255,374 / 14.77%
Number/percentage of T's	27,832,803 / 33.55%
Number/percentage of G's	18,946,632 / 22.84%
Number/percentage of N's	0 / 0%
GC Percentage	37.61%

2.3. Coverage

Mean	0.0268

Standard Deviation	84.0238

2.4. Mapping Quality

Mean Mapping Quality	49.1

2.5. Mismatches and indels

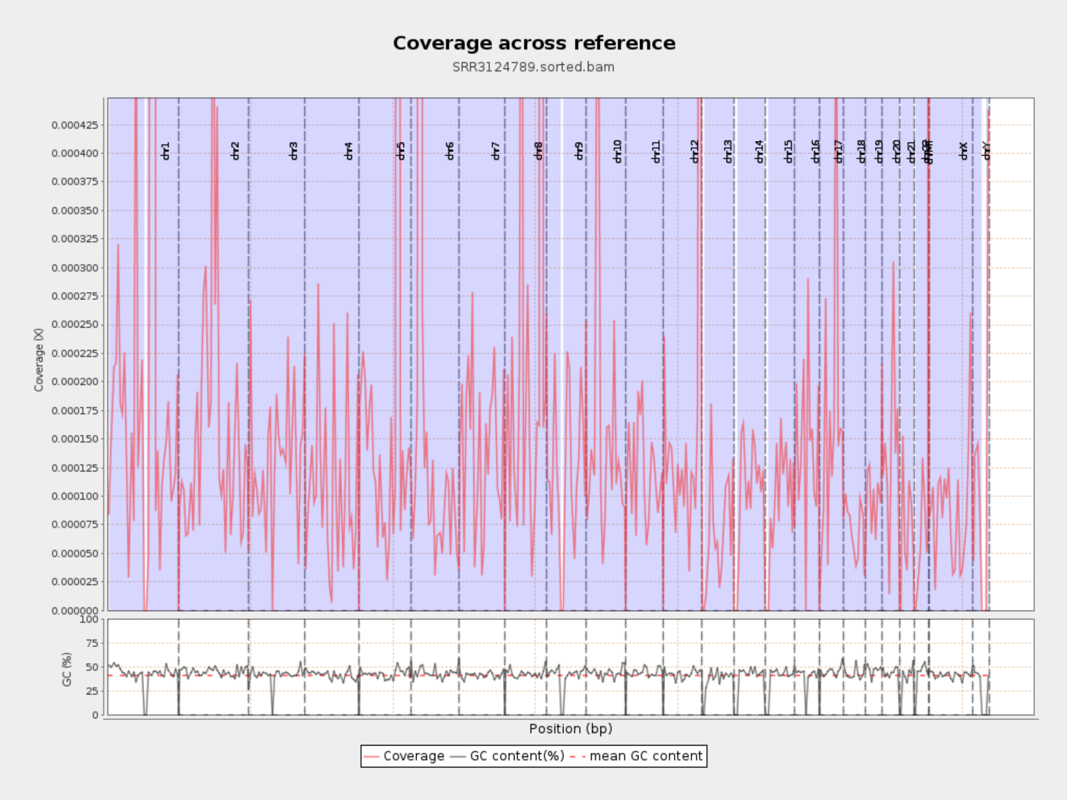
General error rate	0.88%
Mismatches	710,300
Insertions	17,684
Mapped reads with at least one insertion	3.18%
Deletions	45,417
Mapped reads with at least one deletion	8.03%
Homopolymer indels	87.18%

2.6. Chromosome stats

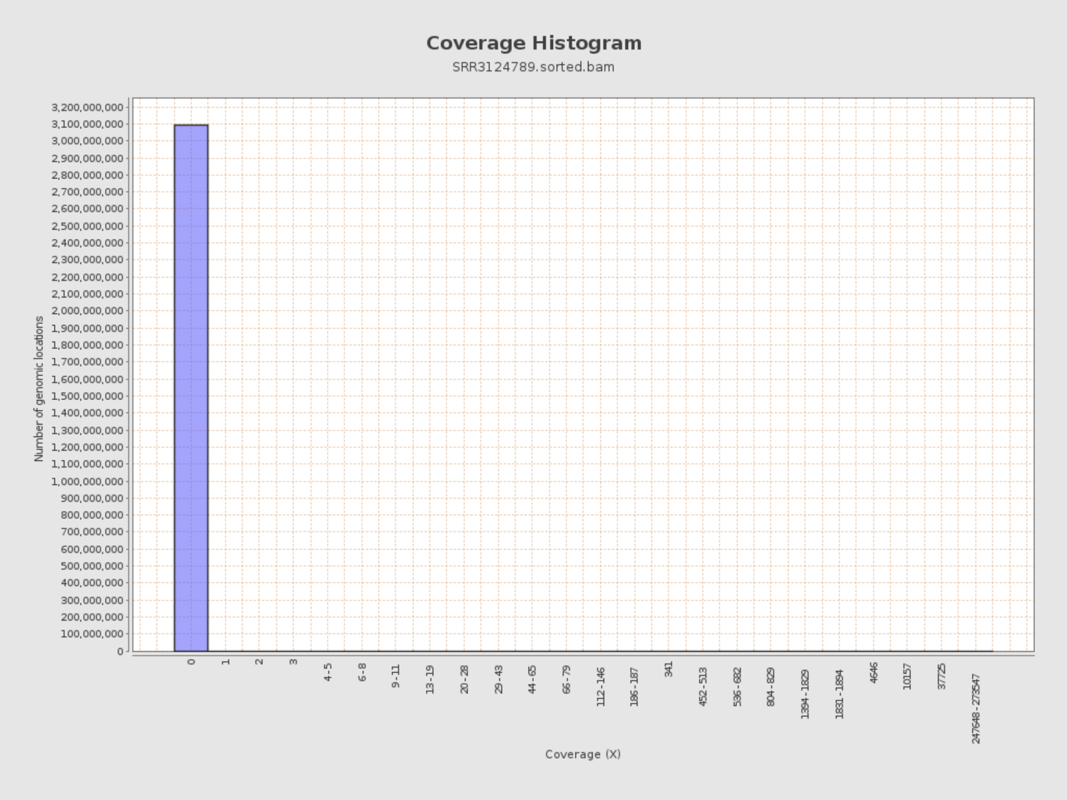
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	582973	0.0023	2.0088
chr2	243199373	39786	0.0002	0.0202
chr3	198022430	26081	0.0001	0.0119
chr4	191154276	21029	0.0001	0.0109
chr5	180915260	42216	0.0002	0.0903
chr6	171115067	42950	0.0003	0.1397
chr7	159138663	22991	0.0001	0.0121

chr8	146364022	82039396	0.5605	386.4148
chr9	141213431	17179	0.0001	0.0113
chr10	135534747	21960	0.0002	0.0176
chr11	135006516	16146	0.0001	0.0112
chr12	133851895	26422	0.0002	0.0562
chr13	115169878	7597	0.0001	0.0084
chr14	107349540	11119	0.0001	0.0102
chr15	102531392	9482	0.0001	0.0096
chr16	90354753	12959	0.0001	0.013
chr17	81195210	14627	0.0002	0.035
chr18	78077248	5510	0.0001	0.0085
chr19	59128983	5921	0.0001	0.0102
chr20	63025520	8876	0.0001	0.0137
chr21	48129895	3720	0.0001	0.0088
chr22	51304566	2837	0.0001	0.0075
chrMT	16571	371	0.0224	0.1479
chrX	155270560	13815	0.0001	0.0107
chrY	59373566	6466	0.0001	0.0109

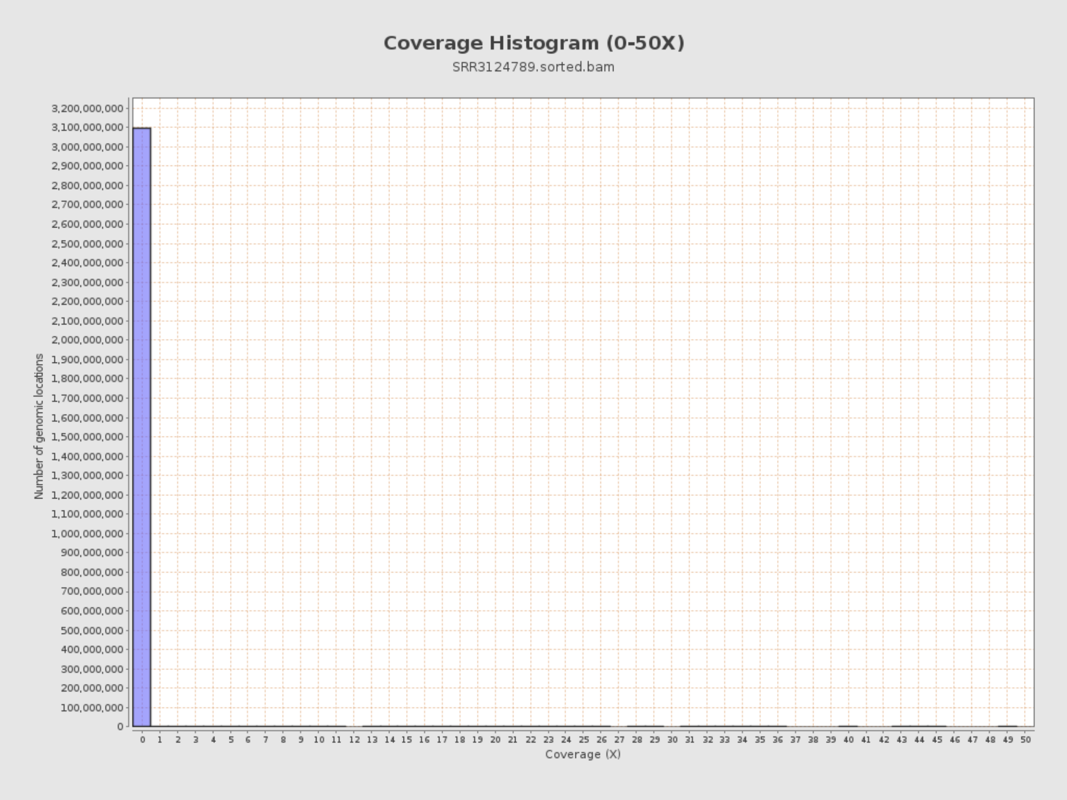
3. Results : Coverage across reference



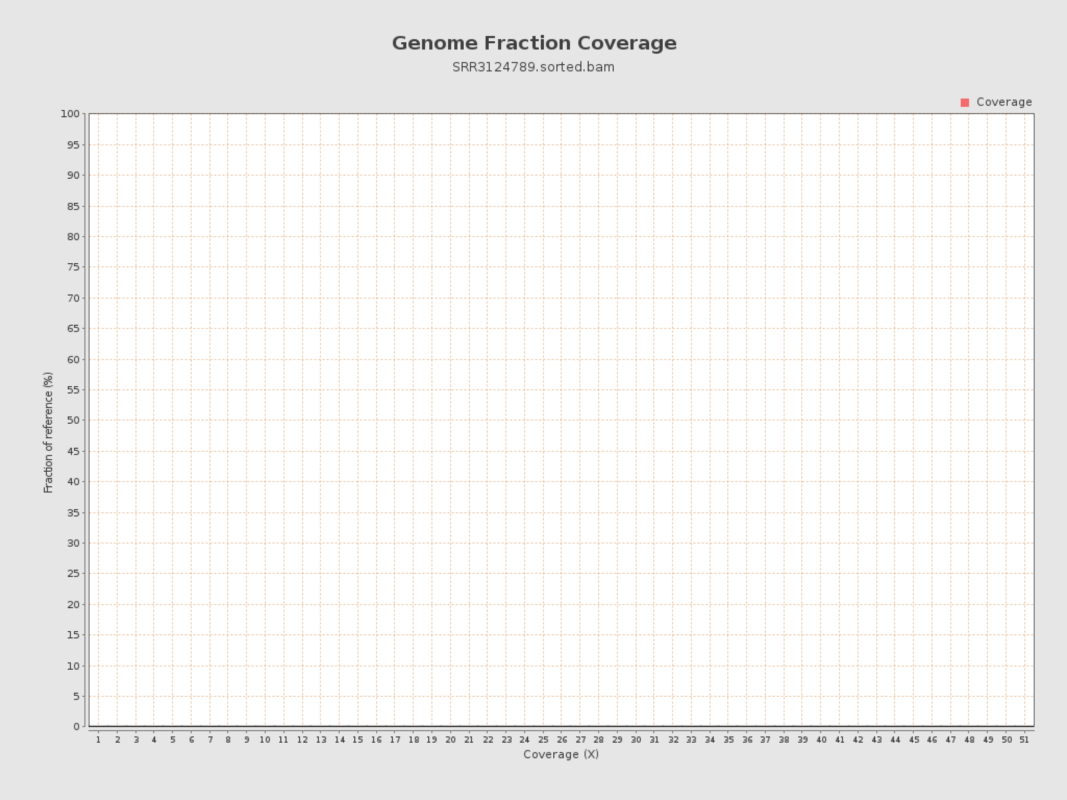
4. Results : Coverage Histogram



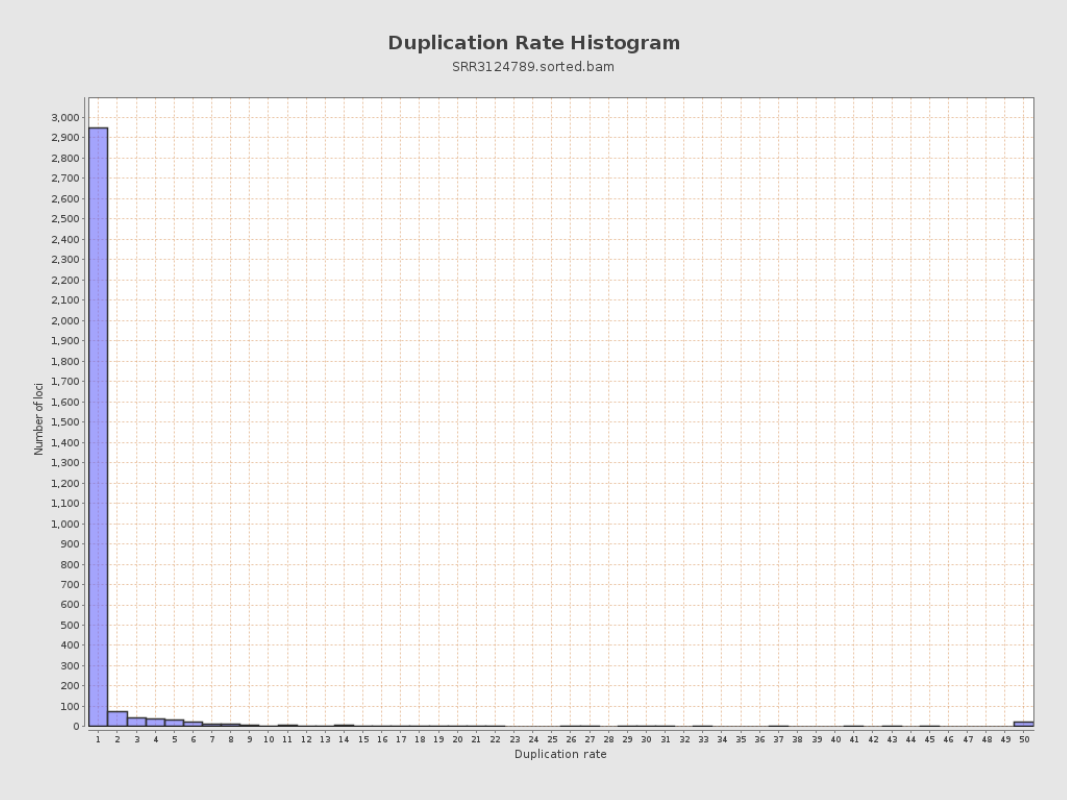
5. Results : Coverage Histogram (0-50X)



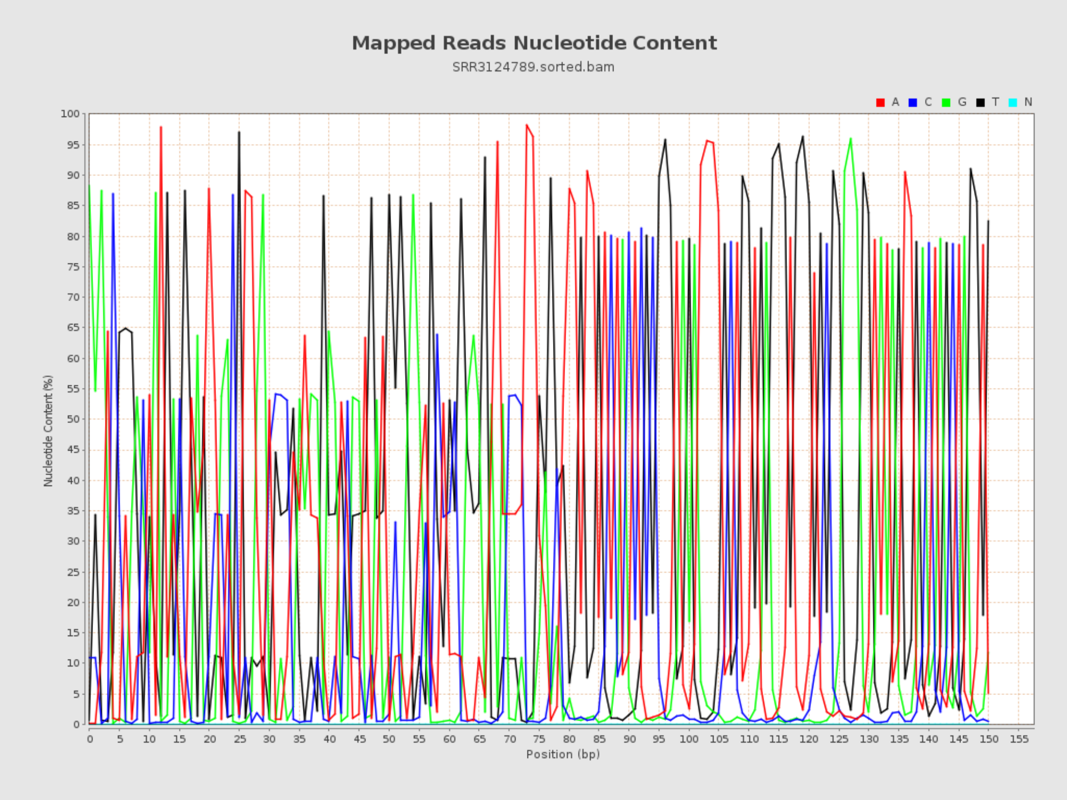
6. Results : Genome Fraction Coverage



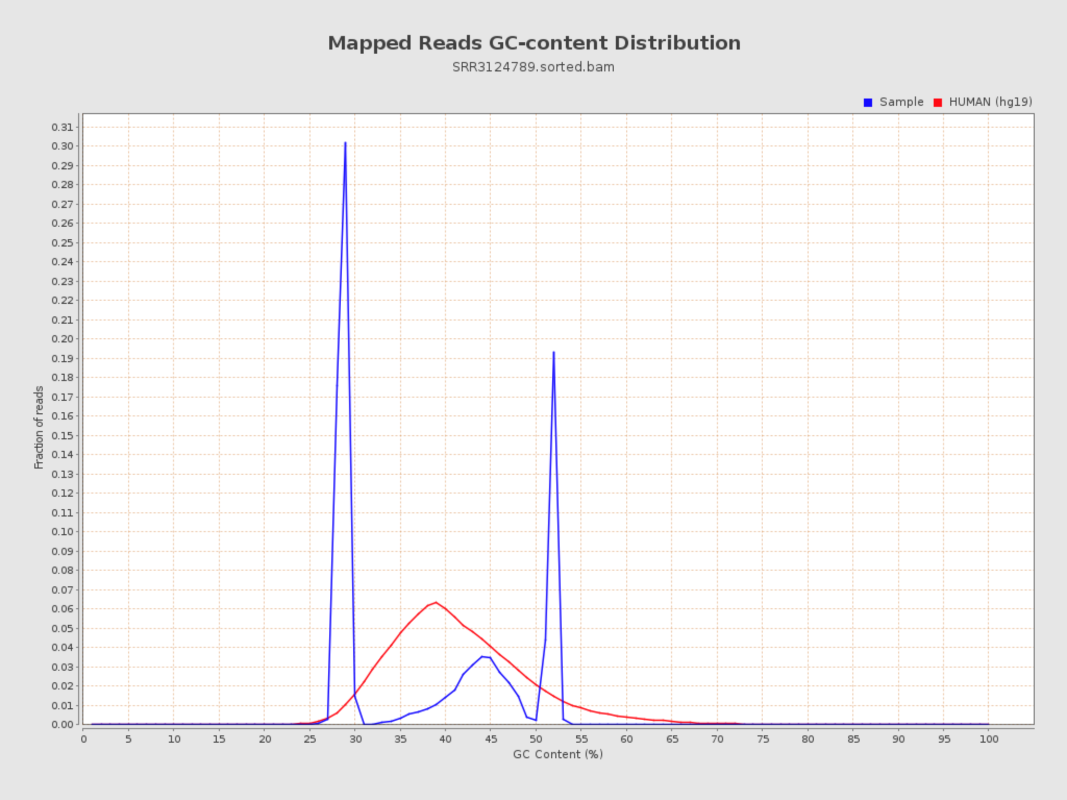
7. Results : Duplication Rate Histogram



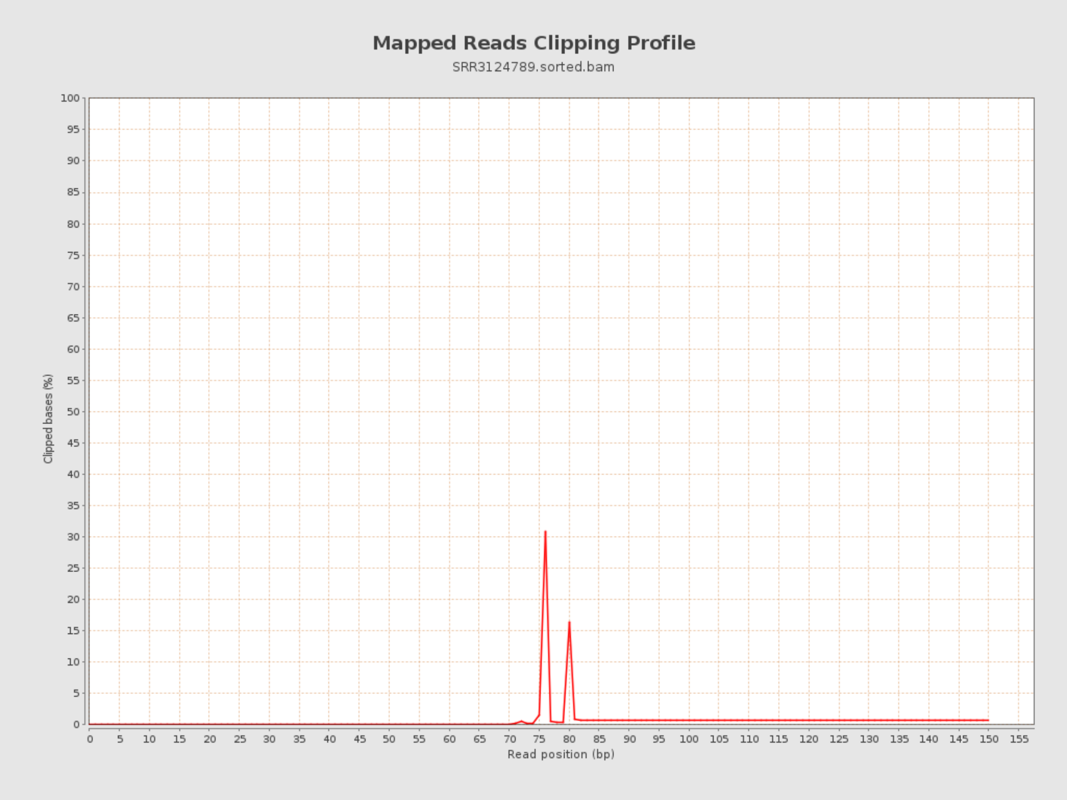
8. Results : Mapped Reads Nucleotide Content



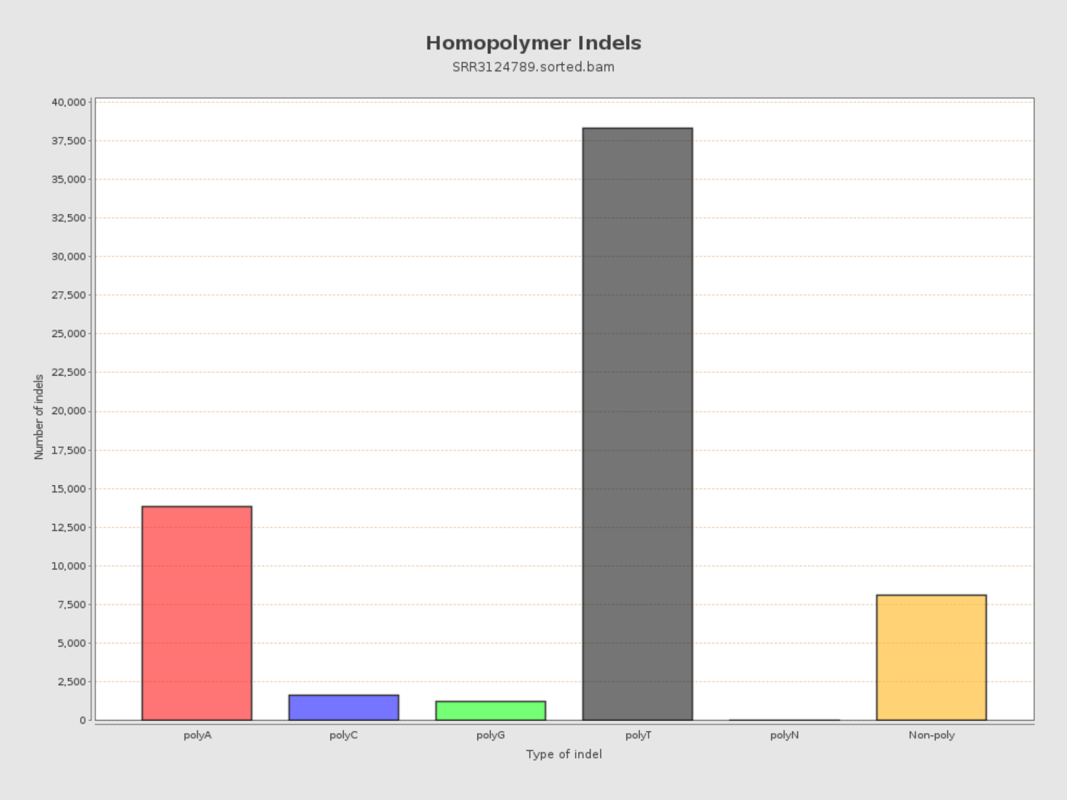
9. Results : Mapped Reads GC-content Distribution



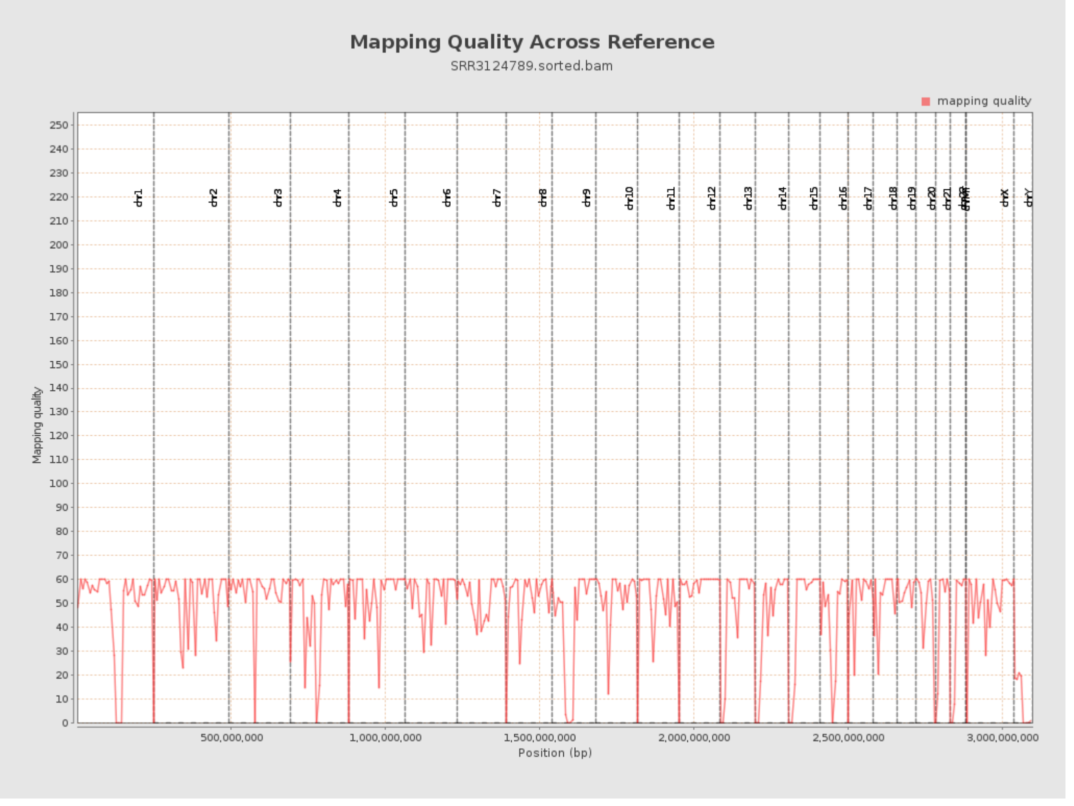
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram