Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:52:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124797.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_SRR3124797 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124797.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:52:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124797.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	140,977
Mapped reads	134,586 / 95.47%
Unmapped reads	6,391 / 4.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,490 / 5.31%
Read min/max/mean length	30 / 151 / 153.43
Duplicated reads (estimated)	17,859 / 12.67%
Duplication rate	1.44%
Clipped reads	96,628 / 68.54%

2.2. ACGT Content

Number/percentage of A's	5,028,096 / 28.91%
Number/percentage of C's	3,375,300 / 19.4%
Number/percentage of T's	5,020,753 / 28.86%
Number/percentage of G's	3,970,750 / 22.83%
Number/percentage of N's	0 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0056

Standard Deviation	1.2541

2.4. Mapping Quality

Mean Mapping Quality	51.21

2.5. Mismatches and indels

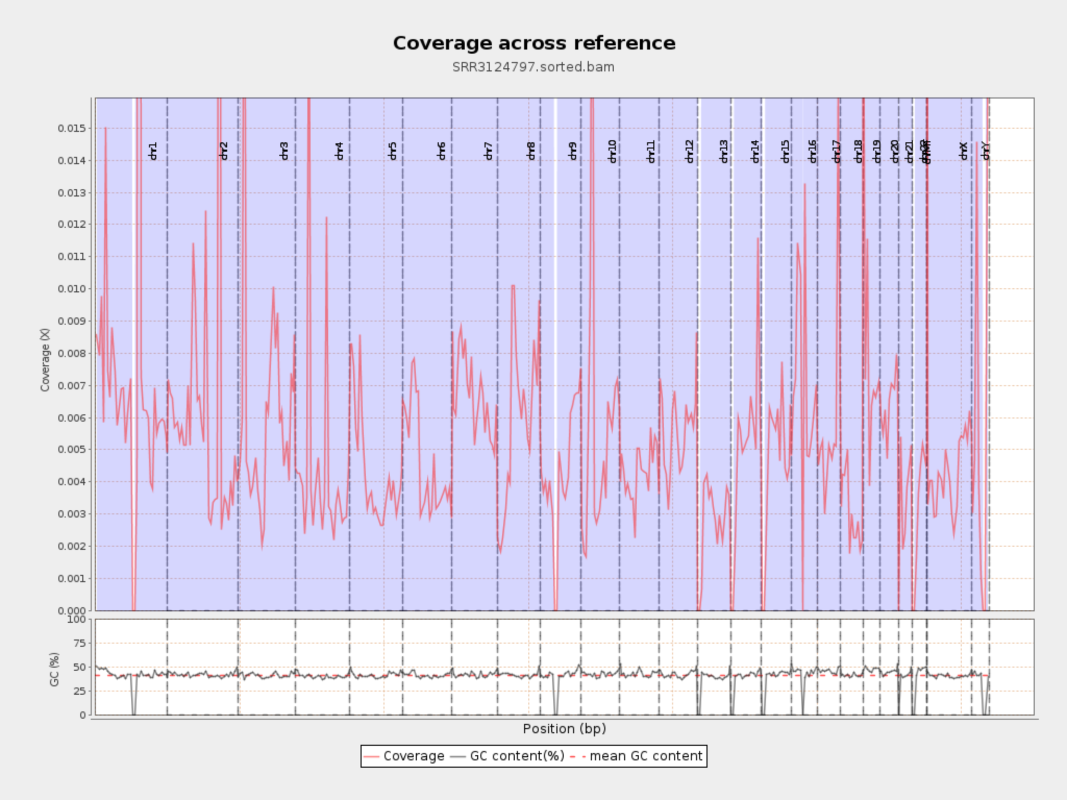
General error rate	1.49%
Mismatches	243,878
Insertions	4,513
Mapped reads with at least one insertion	3.07%
Deletions	8,841
Mapped reads with at least one deletion	6.23%
Homopolymer indels	43.07%

2.6. Chromosome stats

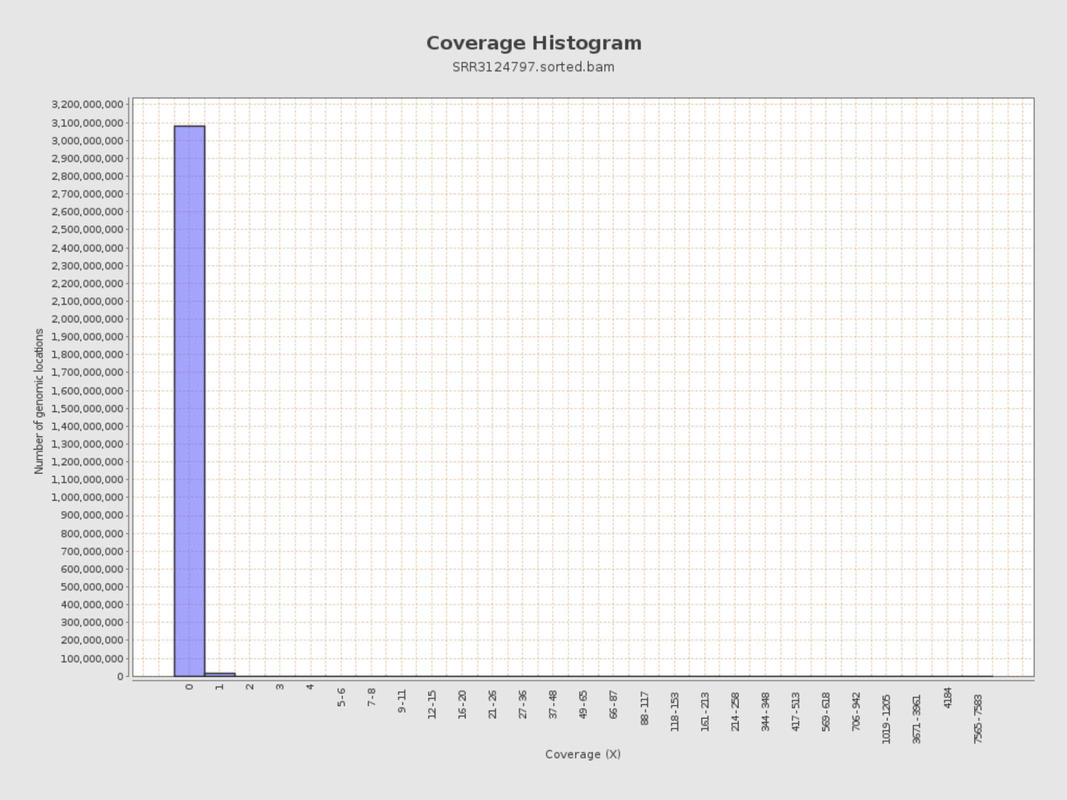
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2625556	0.0105	4.1728
chr2	243199373	1571126	0.0065	0.9285
chr3	198022430	1251652	0.0063	1.0038
chr4	191154276	864733	0.0045	0.3263
chr5	180915260	779160	0.0043	0.0712
chr6	171115067	785966	0.0046	0.0732
chr7	159138663	1065896	0.0067	0.0887

chr8	146364022	871746	0.006	0.0853
chr9	141213431	598699	0.0042	0.076
chr10	135534747	801677	0.0059	0.1844
chr11	135006516	585540	0.0043	0.0678
chr12	133851895	738202	0.0055	0.1379
chr13	115169878	313670	0.0027	0.0534
chr14	107349540	541411	0.005	0.511
chr15	102531392	467172	0.0046	0.1546
chr16	90354753	619713	0.0069	0.473
chr17	81195210	477163	0.0059	0.444
chr18	78077248	233839	0.003	0.066
chr19	59128983	459824	0.0078	0.509
chr20	63025520	405924	0.0064	0.0938
chr21	48129895	166727	0.0035	0.0843
chr22	51304566	160934	0.0031	0.0589
chrMT	16571	1348	0.0813	0.2755
chrX	155270560	662430	0.0043	0.0673
chrY	59373566	364281	0.0061	0.191

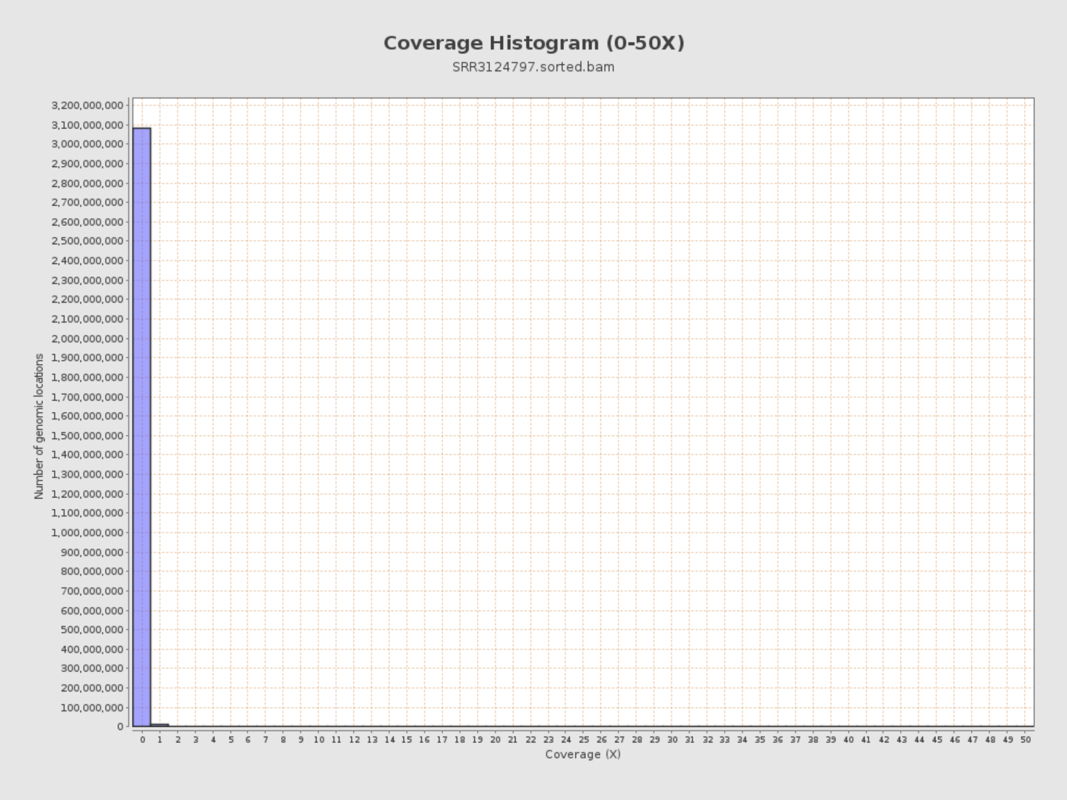
3. Results : Coverage across reference



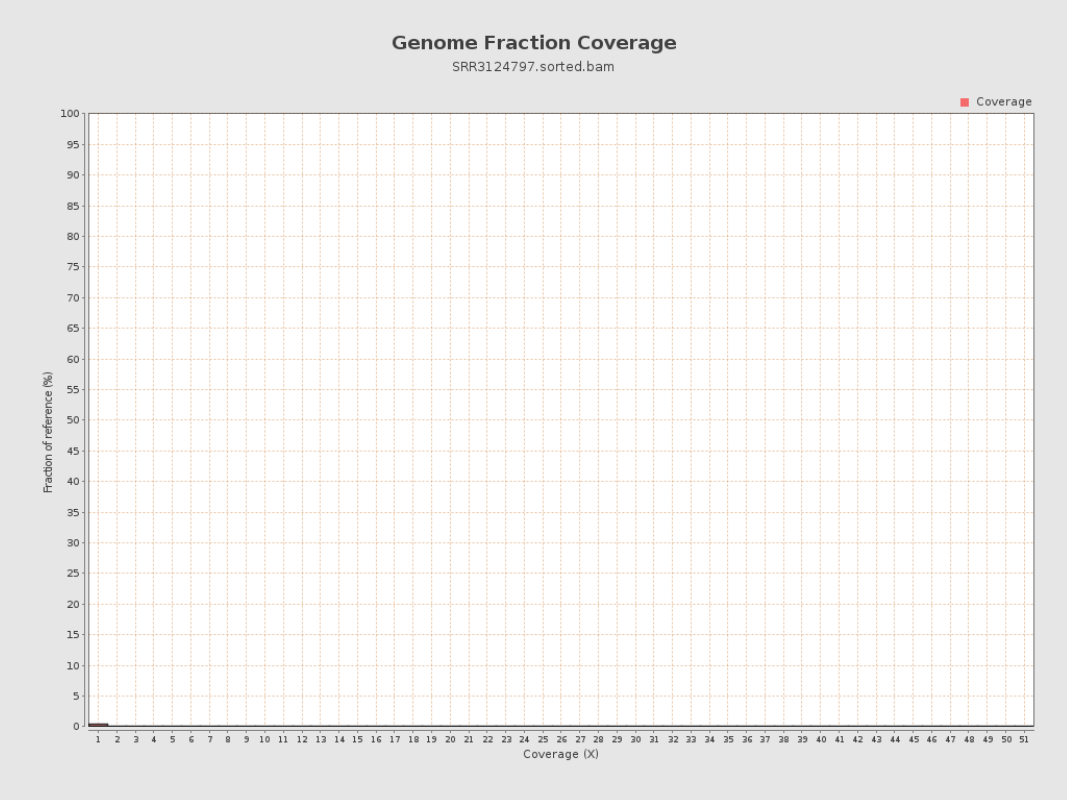
4. Results : Coverage Histogram



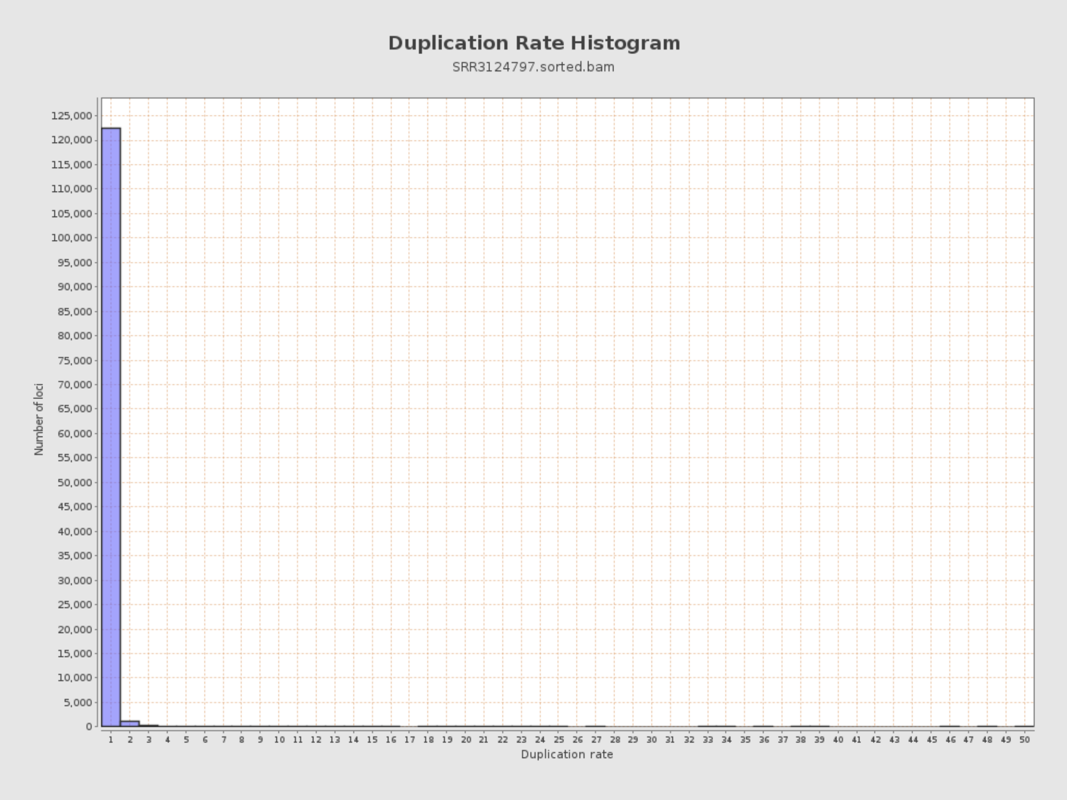
5. Results : Coverage Histogram (0-50X)



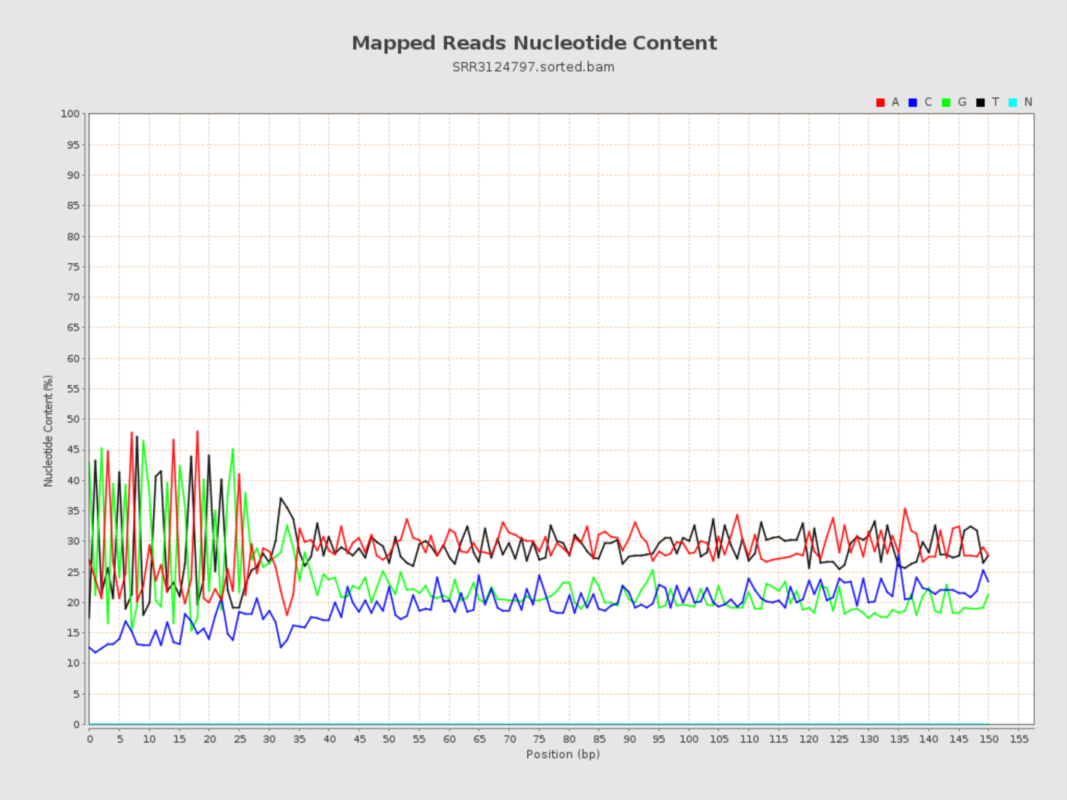
6. Results : Genome Fraction Coverage



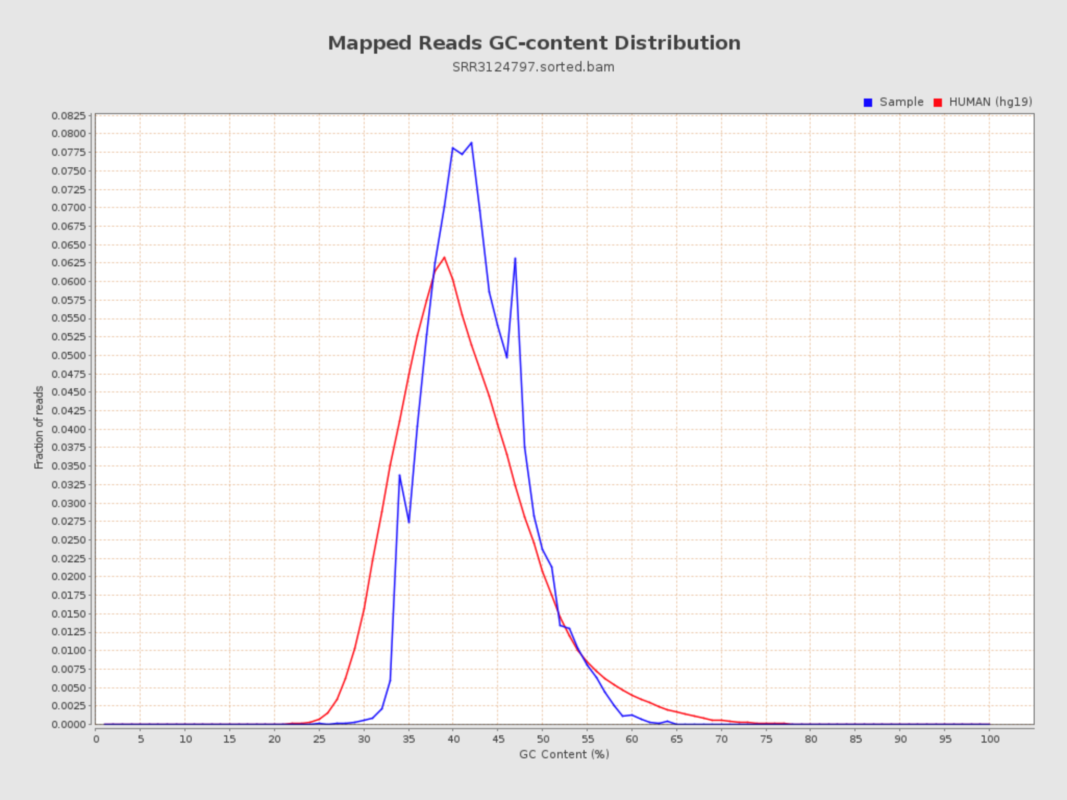
7. Results : Duplication Rate Histogram



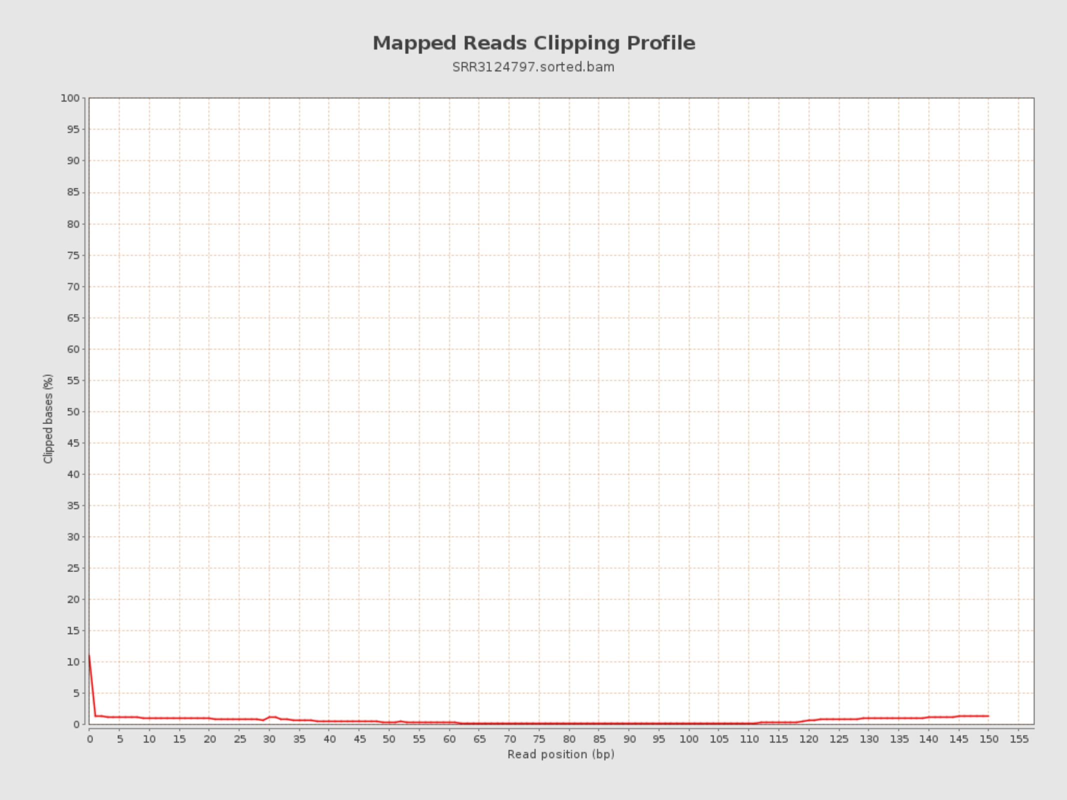
8. Results : Mapped Reads Nucleotide Content



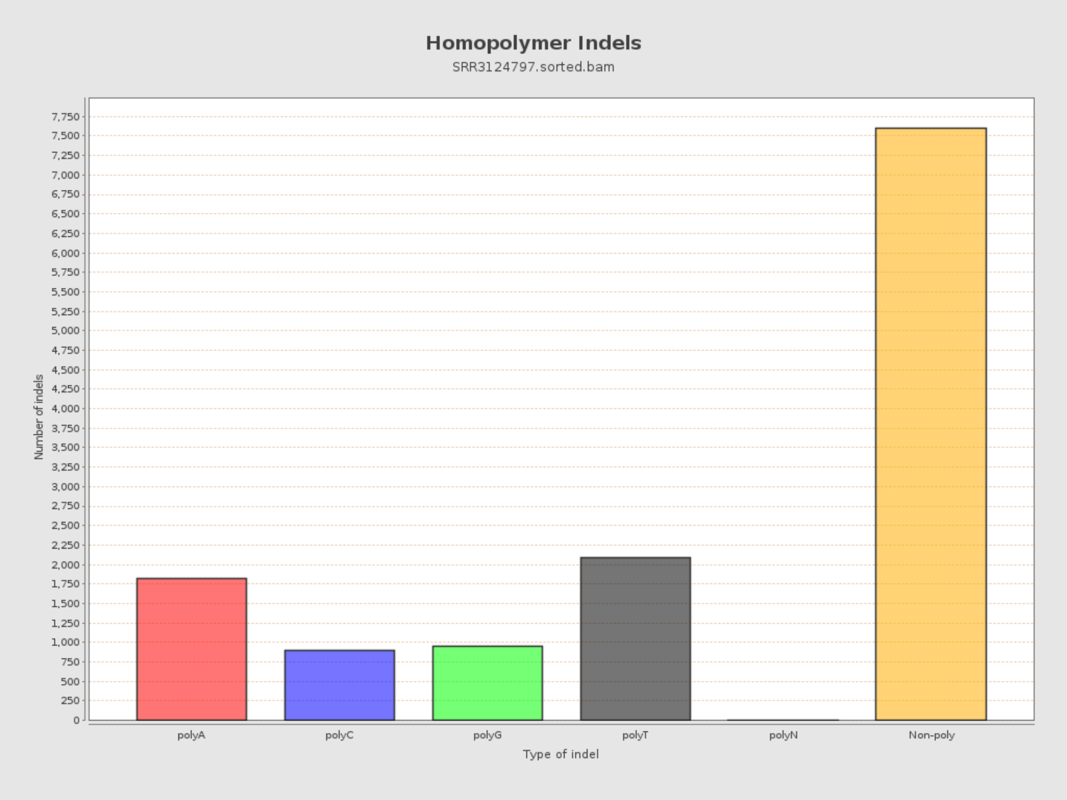
9. Results : Mapped Reads GC-content Distribution



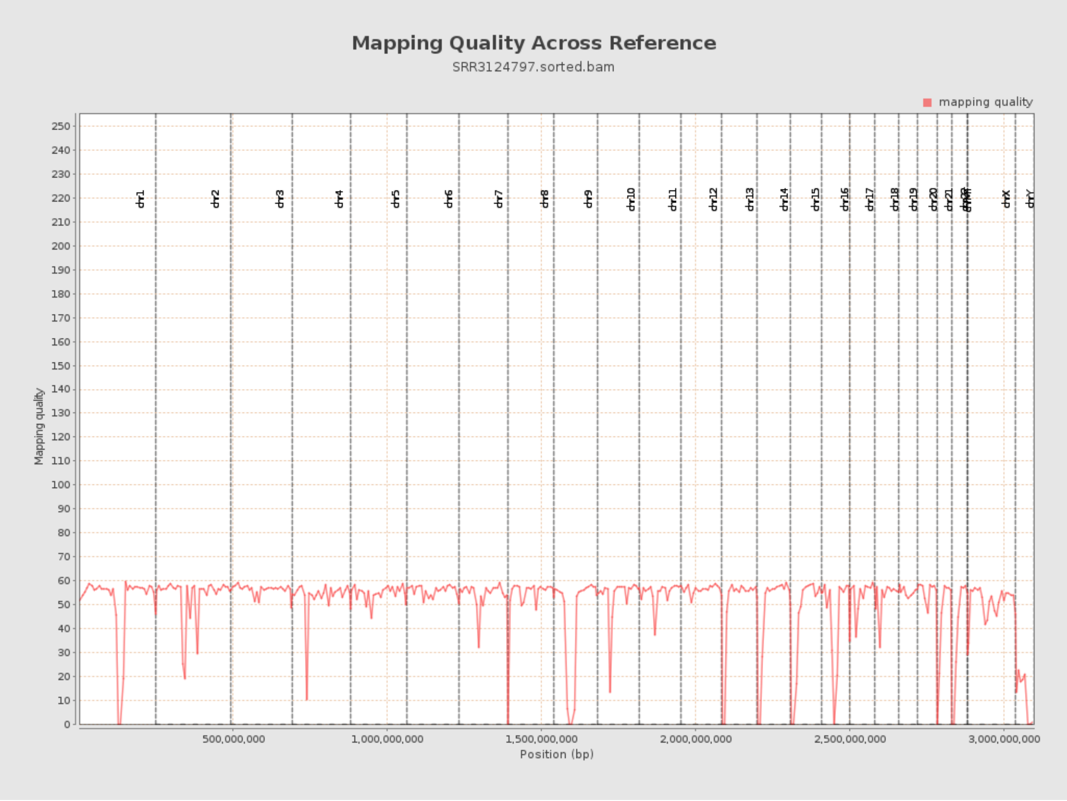
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram