Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 00:59:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506123.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_SRR1506123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 00:59:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,104,835
Mapped reads	4,821,846 / 78.98%
Unmapped reads	1,282,989 / 21.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	75,861 / 1.24%
Read min/max/mean length	30 / 94 / 94.45
Duplicated reads (estimated)	888,567 / 14.56%
Duplication rate	12.16%
Clipped reads	2,682,544 / 43.94%

2.2. ACGT Content

Number/percentage of A's	106,163,782 / 27.27%
Number/percentage of C's	72,770,971 / 18.69%
Number/percentage of T's	112,600,879 / 28.92%
Number/percentage of G's	97,734,737 / 25.1%
Number/percentage of N's	67,335 / 0.02%
GC Percentage	43.79%

2.3. Coverage

Mean	0.1258

Standard Deviation	0.9773

2.4. Mapping Quality

Mean Mapping Quality	47.92

2.5. Mismatches and indels

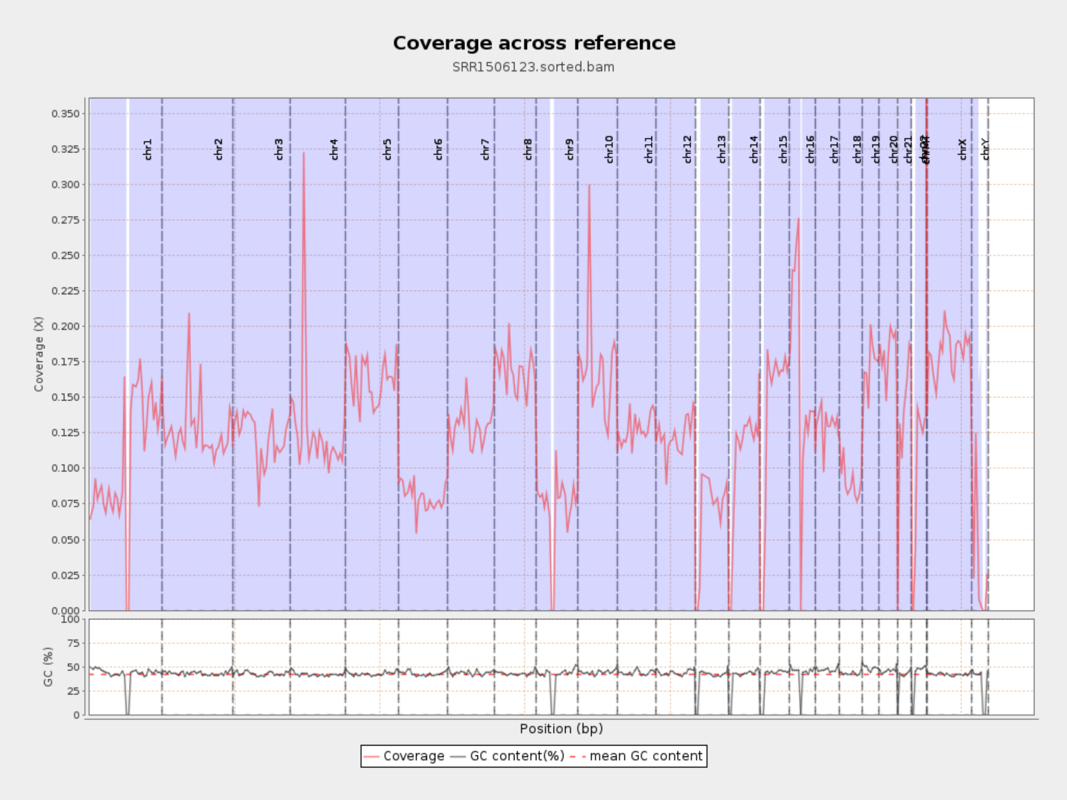
General error rate	0.79%
Mismatches	2,989,122
Insertions	34,984
Mapped reads with at least one insertion	0.71%
Deletions	85,805
Mapped reads with at least one deletion	1.74%
Homopolymer indels	42.18%

2.6. Chromosome stats

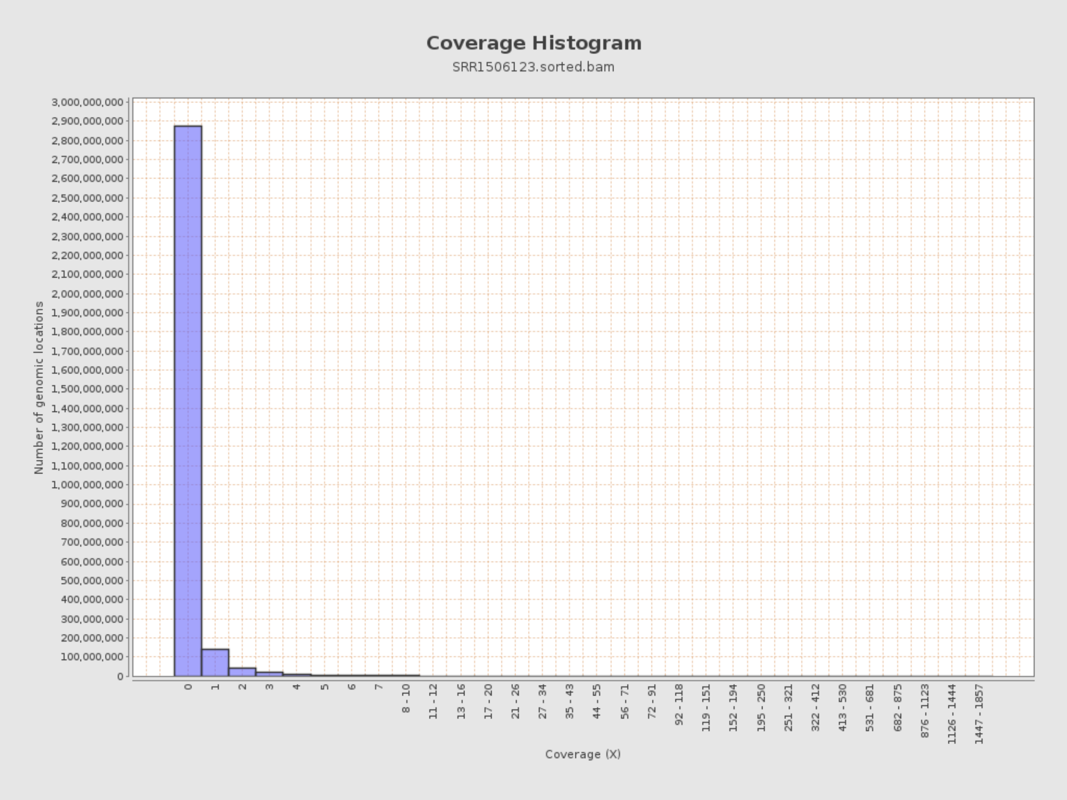
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26412833	0.106	1.7281
chr2	243199373	30799839	0.1266	1.0584
chr3	198022430	24167657	0.122	0.5703
chr4	191154276	24073460	0.1259	0.9763
chr5	180915260	29384011	0.1624	0.6721
chr6	171115067	13685621	0.08	0.4966
chr7	159138663	20605243	0.1295	1.079

chr8	146364022	24775180	0.1693	1.0771
chr9	141213431	9976964	0.0707	0.8226
chr10	135534747	23191459	0.1711	1.2868
chr11	135006516	17248134	0.1278	0.9042
chr12	133851895	16379128	0.1224	0.5904
chr13	115169878	8033305	0.0698	0.4287
chr14	107349540	11199250	0.1043	0.5972
chr15	102531392	14189882	0.1384	0.6259
chr16	90354753	14912418	0.165	0.8432
chr17	81195210	10632095	0.1309	0.7138
chr18	78077248	7080970	0.0907	1.3481
chr19	59128983	10136078	0.1714	1.2785
chr20	63025520	11412862	0.1811	0.7719
chr21	48129895	6538933	0.1359	0.8796
chr22	51304566	4744419	0.0925	0.5467
chrMT	16571	13651	0.8238	2.7157
chrX	155270560	28129318	0.1812	0.7853
chrY	59373566	1792814	0.0302	1.322

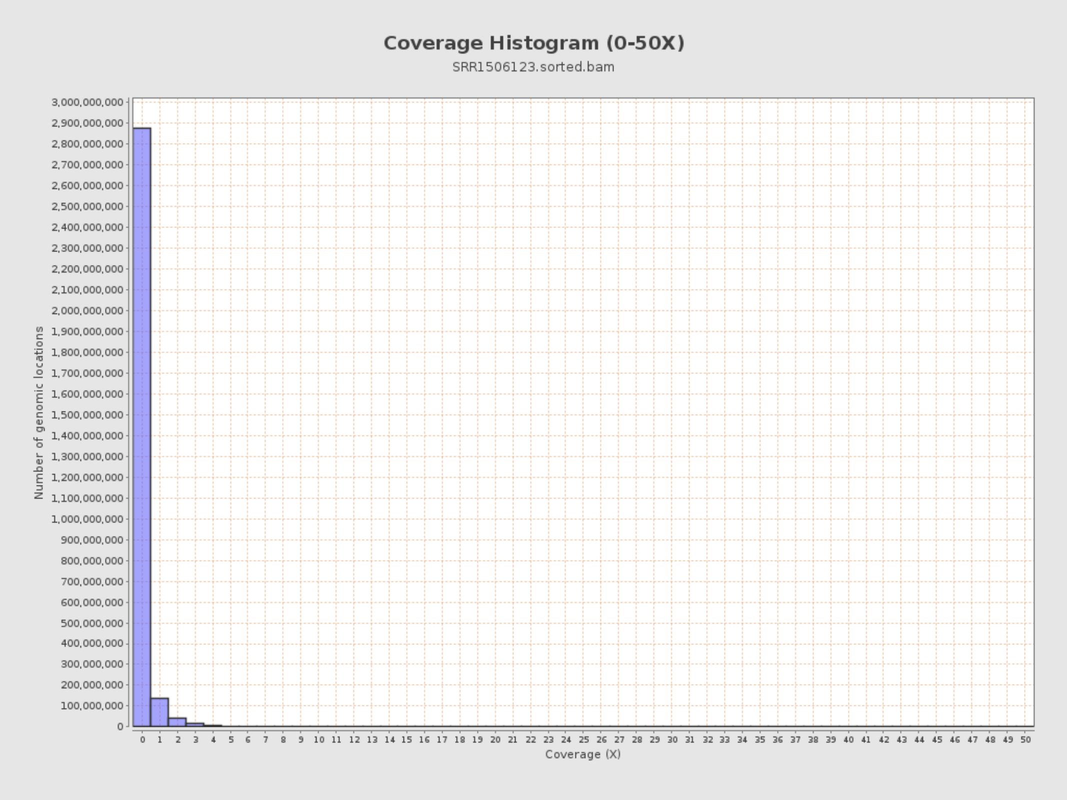
3. Results : Coverage across reference



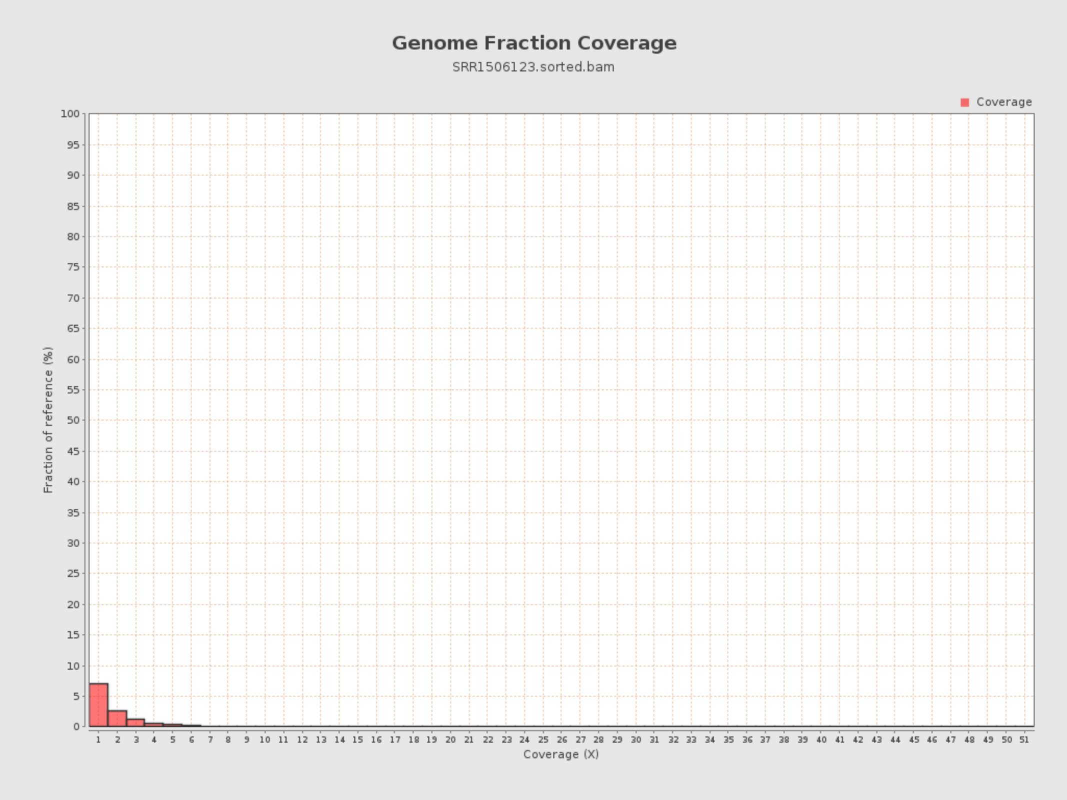
4. Results : Coverage Histogram



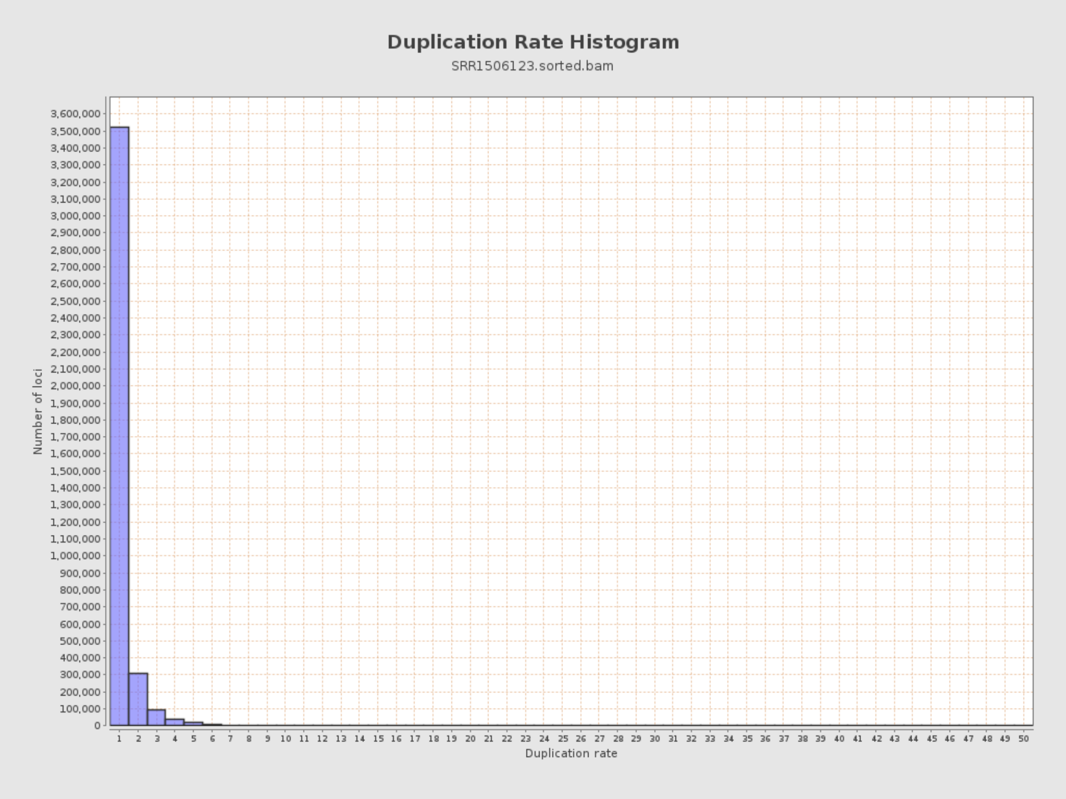
5. Results : Coverage Histogram (0-50X)



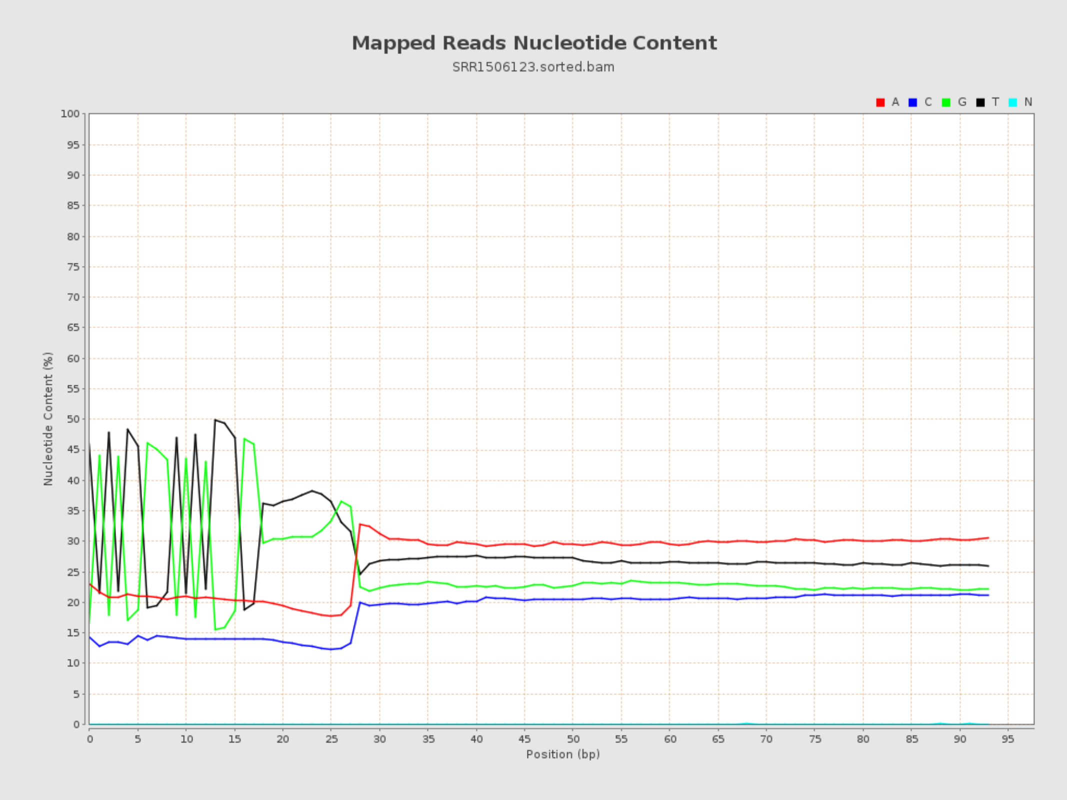
6. Results : Genome Fraction Coverage



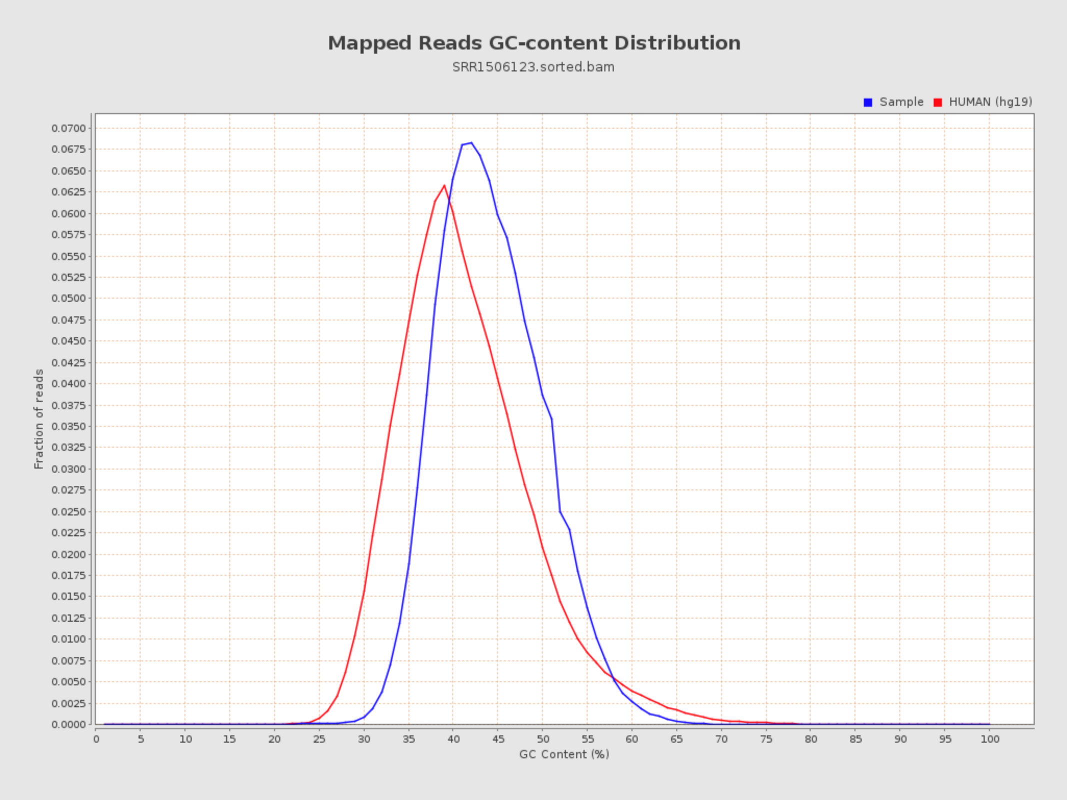
7. Results : Duplication Rate Histogram



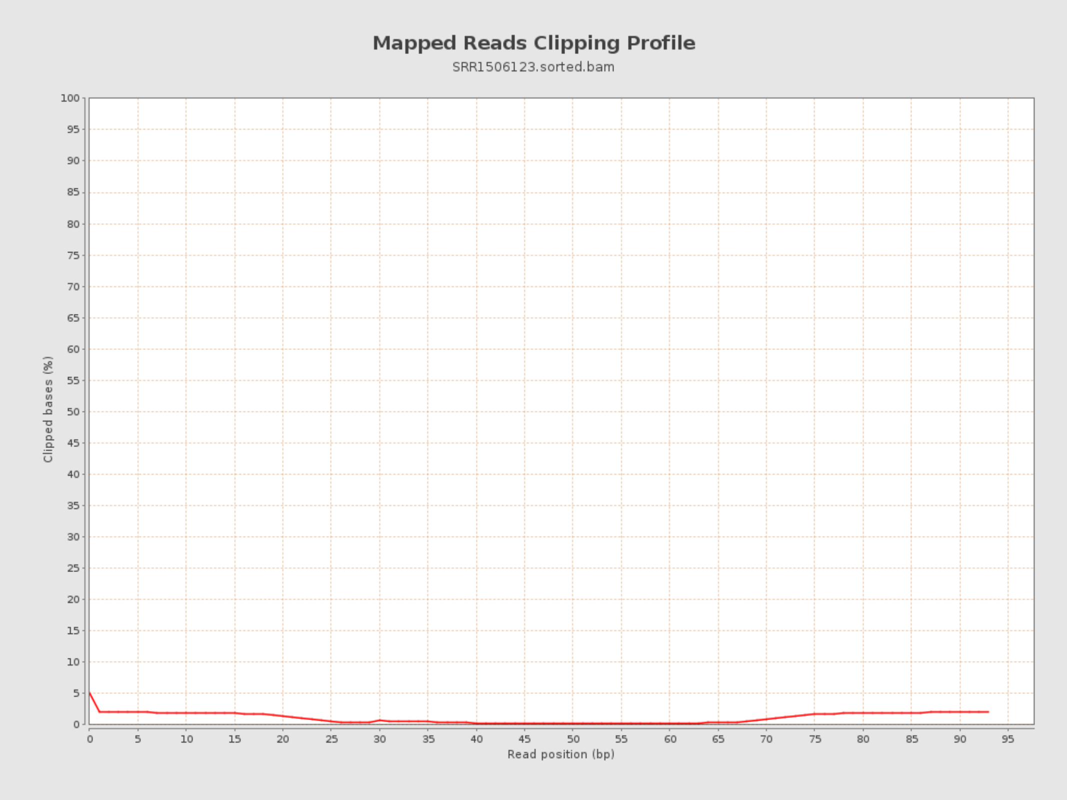
8. Results : Mapped Reads Nucleotide Content



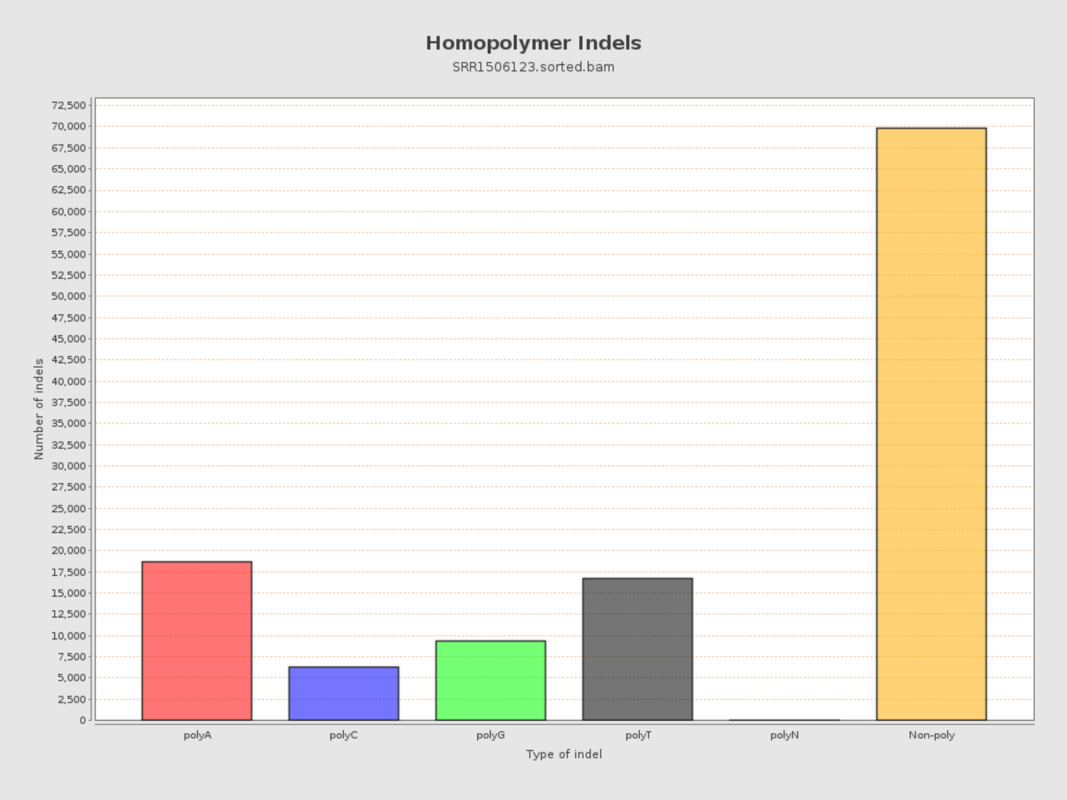
9. Results : Mapped Reads GC-content Distribution



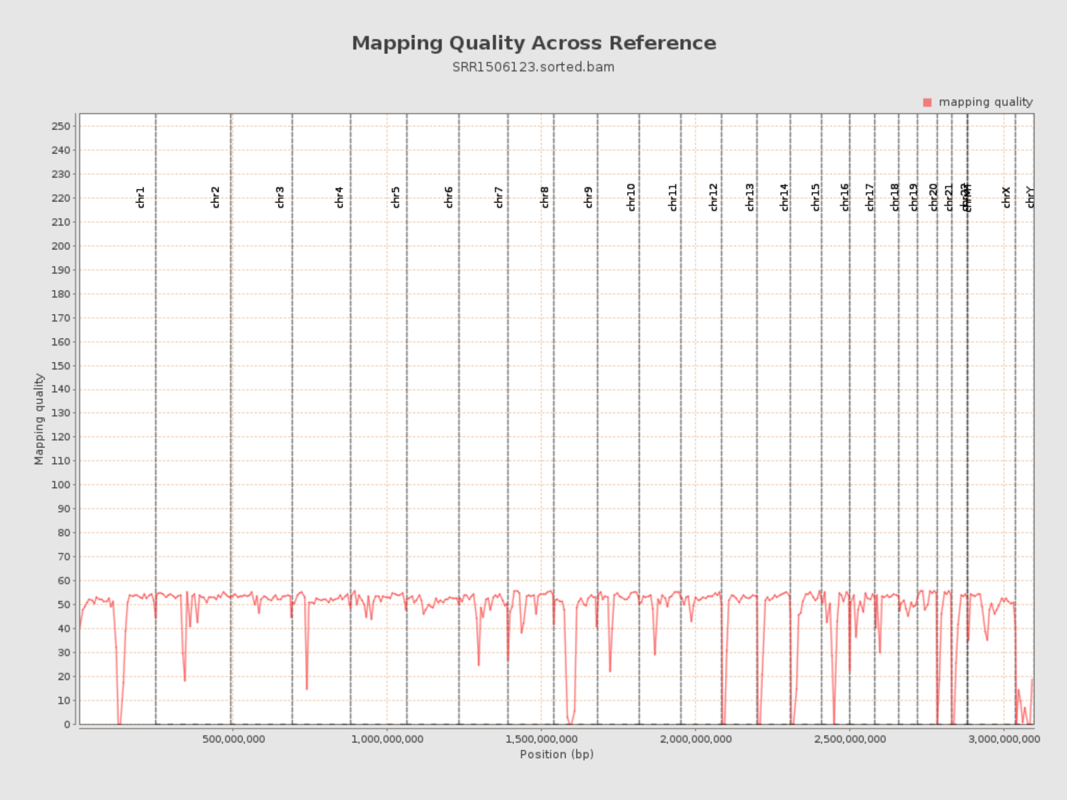
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram