Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 00:06:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506087.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_SRR1506087 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506087.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 00:06:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506087.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,933,762
Mapped reads	5,756,978 / 83.03%
Unmapped reads	1,176,784 / 16.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	107,214 / 1.55%
Read min/max/mean length	30 / 94 / 94.55
Duplicated reads (estimated)	1,311,253 / 18.91%
Duplication rate	14.4%
Clipped reads	3,551,624 / 51.22%

2.2. ACGT Content

Number/percentage of A's	119,488,345 / 26.24%
Number/percentage of C's	87,203,779 / 19.15%
Number/percentage of T's	136,903,084 / 30.06%
Number/percentage of G's	111,775,102 / 24.54%
Number/percentage of N's	76,743 / 0.02%
GC Percentage	43.69%

2.3. Coverage

Mean	0.1472

Standard Deviation	1.2523

2.4. Mapping Quality

Mean Mapping Quality	47.6

2.5. Mismatches and indels

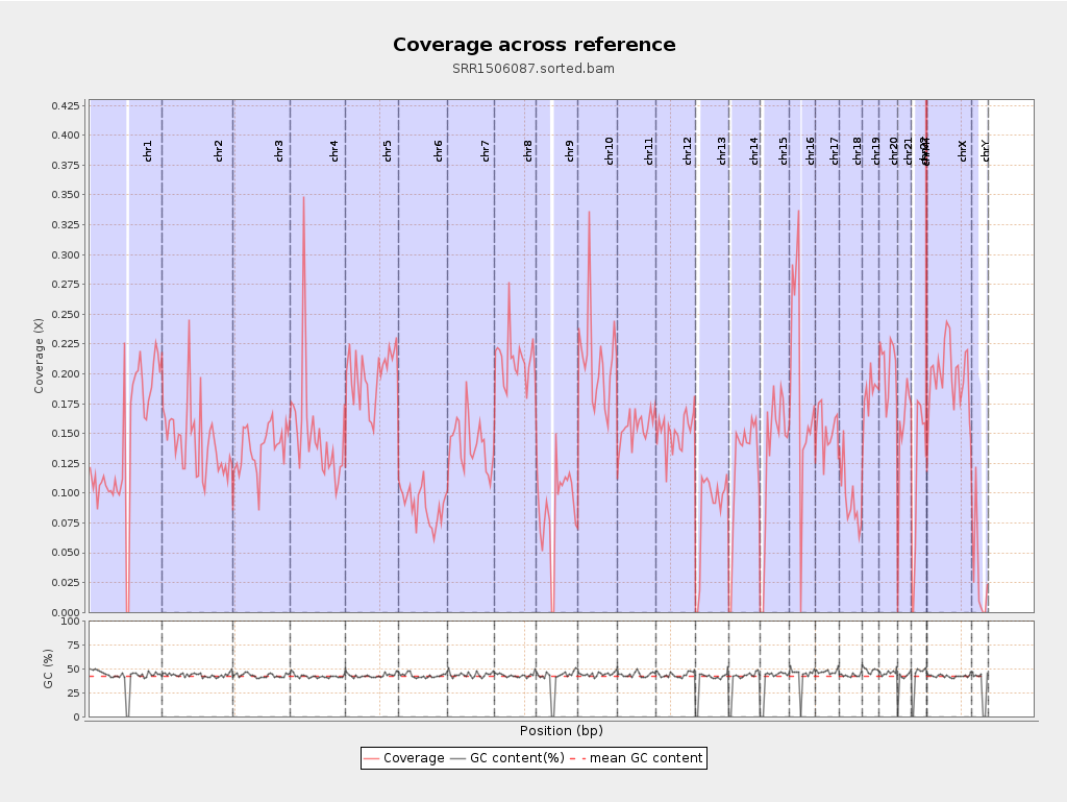
General error rate	0.83%
Mismatches	3,679,917
Insertions	39,411
Mapped reads with at least one insertion	0.67%
Deletions	94,640
Mapped reads with at least one deletion	1.61%
Homopolymer indels	42.46%

2.6. Chromosome stats

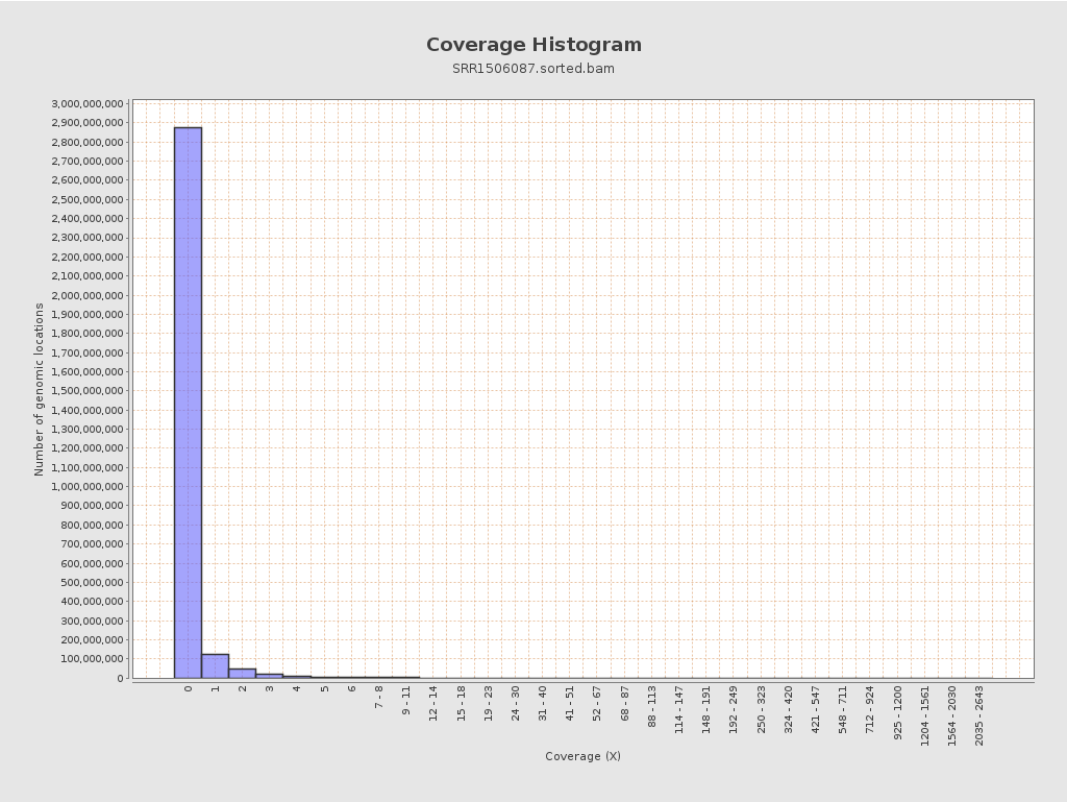
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	35531487	0.1426	2.4114
chr2	243199373	34760987	0.1429	1.2717
chr3	198022430	27332995	0.138	0.688
chr4	191154276	28462752	0.1489	1.1014
chr5	180915260	35701047	0.1973	0.8571
chr6	171115067	15382811	0.0899	0.6284
chr7	159138663	22522462	0.1415	1.2904

chr8	146364022	31034479	0.212	1.3792
chr9	141213431	12112515	0.0858	1.0707
chr10	135534747	28503457	0.2103	1.5003
chr11	135006516	20921190	0.155	1.1802
chr12	133851895	20193477	0.1509	0.7924
chr13	115169878	9896355	0.0859	0.5403
chr14	107349540	13145294	0.1225	0.7674
chr15	102531392	13596333	0.1326	0.6967
chr16	90354753	17282531	0.1913	1.0463
chr17	81195210	12368570	0.1523	0.8909
chr18	78077248	7443469	0.0953	2.1182
chr19	59128983	10815761	0.1829	1.7266
chr20	63025520	13001668	0.2063	0.9672
chr21	48129895	7371575	0.1532	1.1937
chr22	51304566	5854321	0.1141	0.7286
chrMT	16571	61657	3.7208	3.7004
chrX	155270560	30603987	0.1971	0.9456
chrY	59373566	1738625	0.0293	1.07

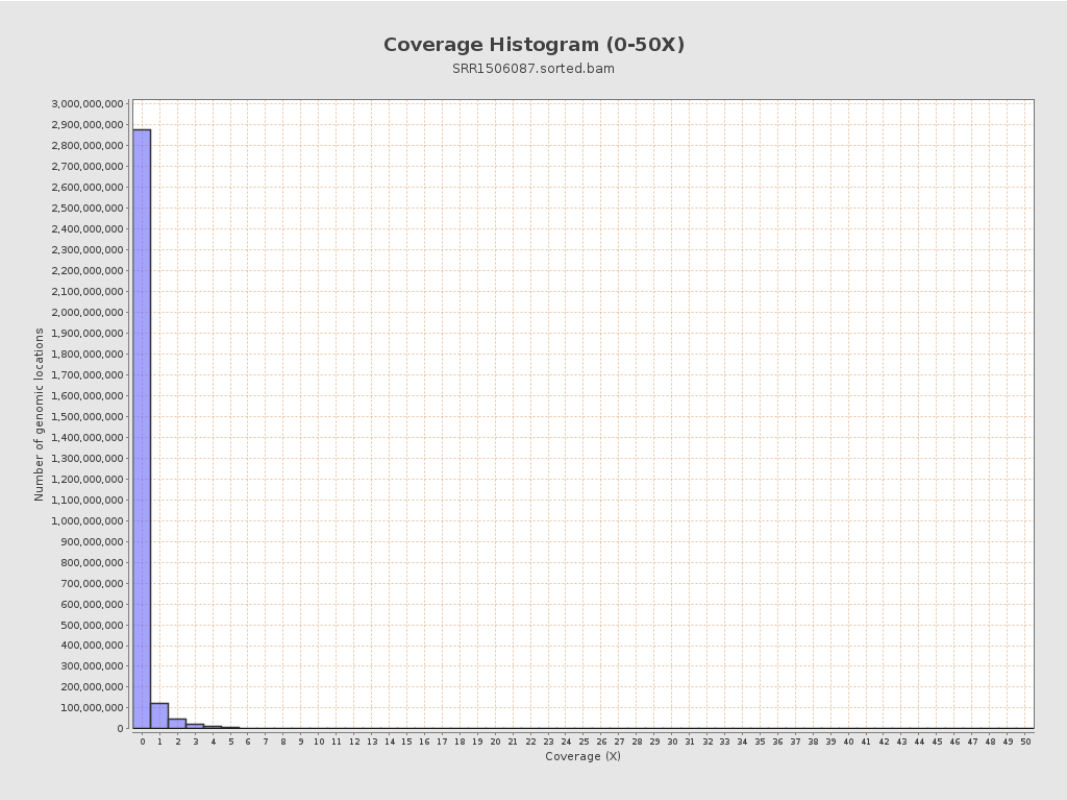
3. Results : Coverage across reference



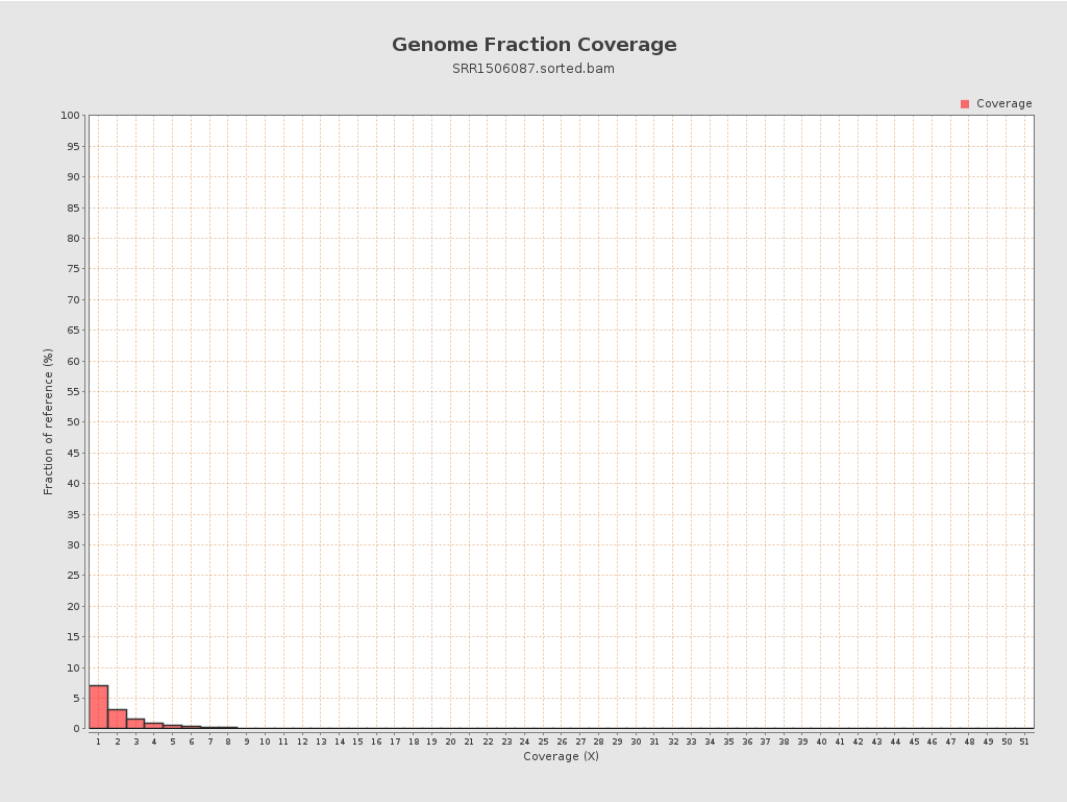
4. Results : Coverage Histogram



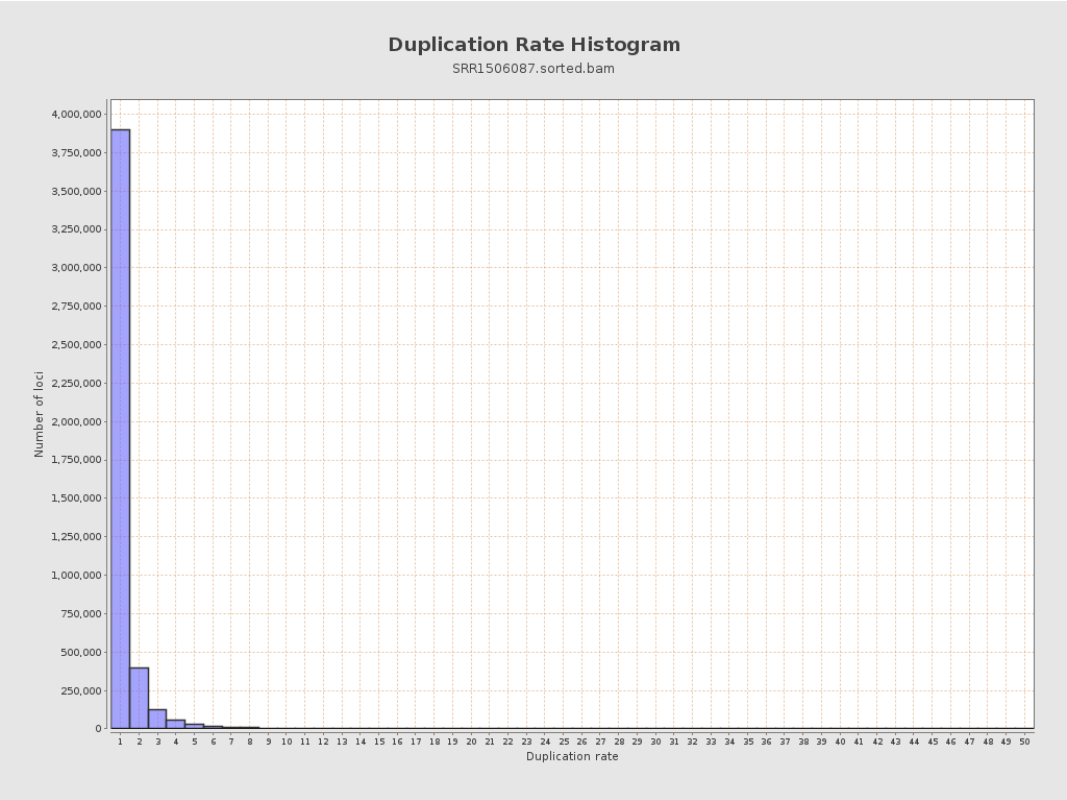
5. Results : Coverage Histogram (0-50X)



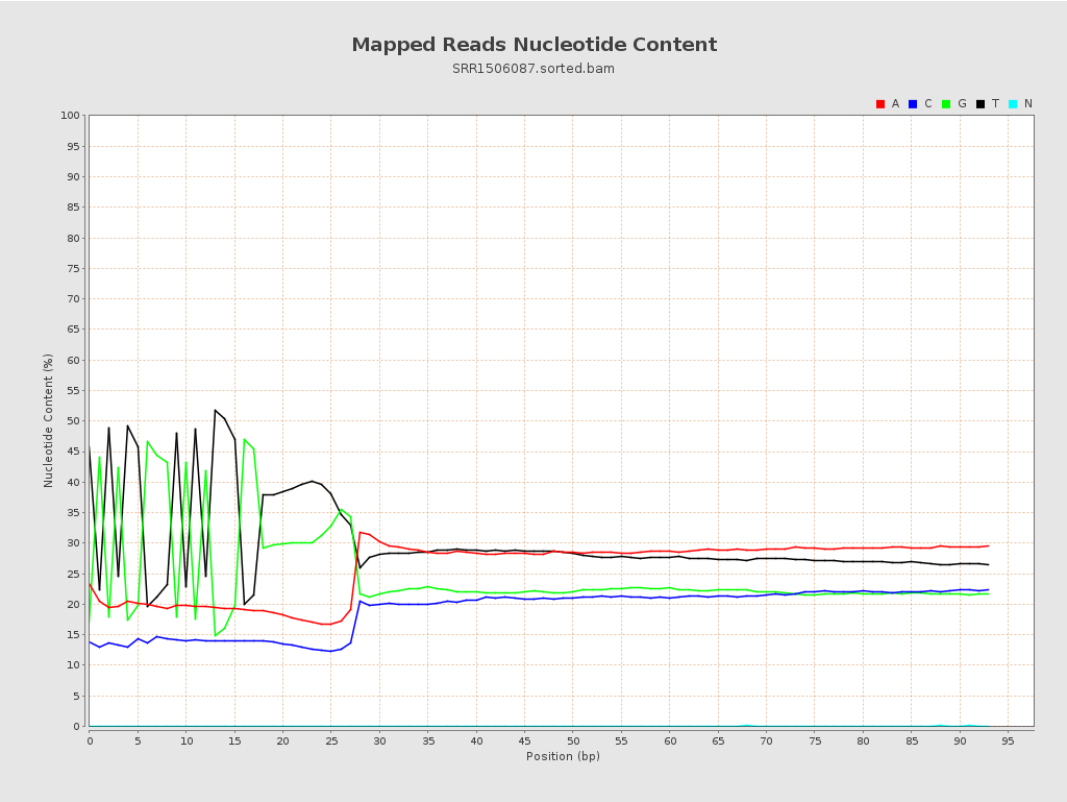
6. Results : Genome Fraction Coverage



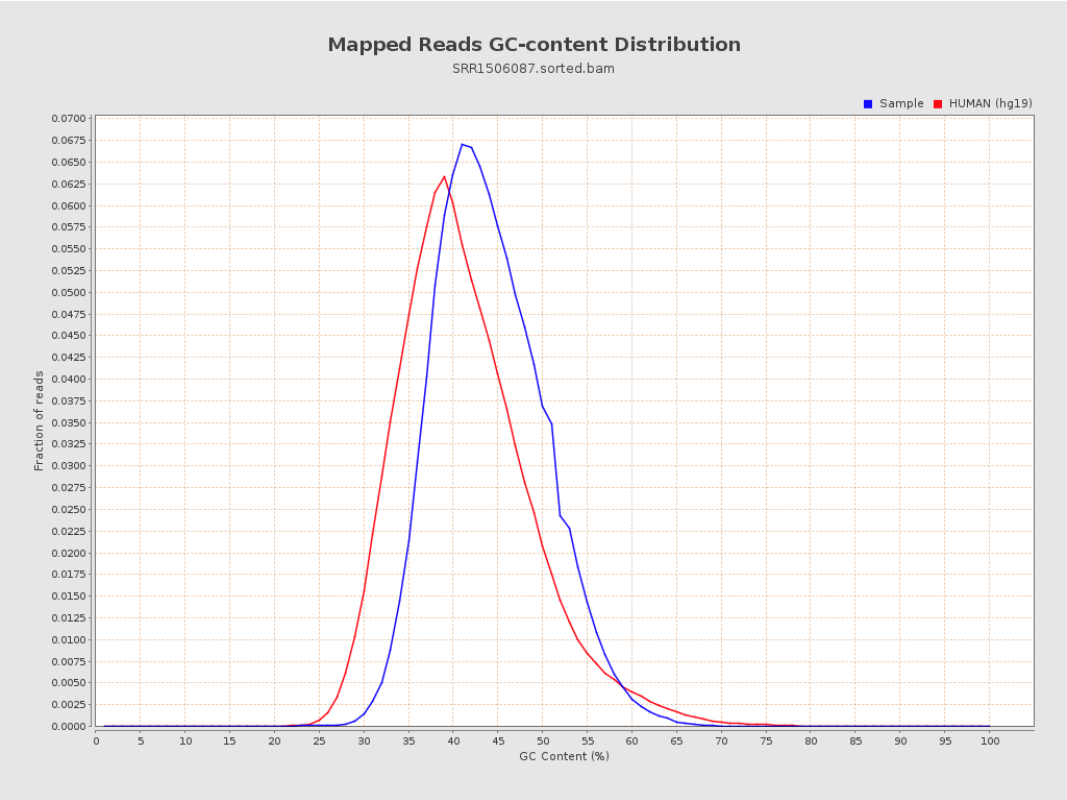
7. Results : Duplication Rate Histogram



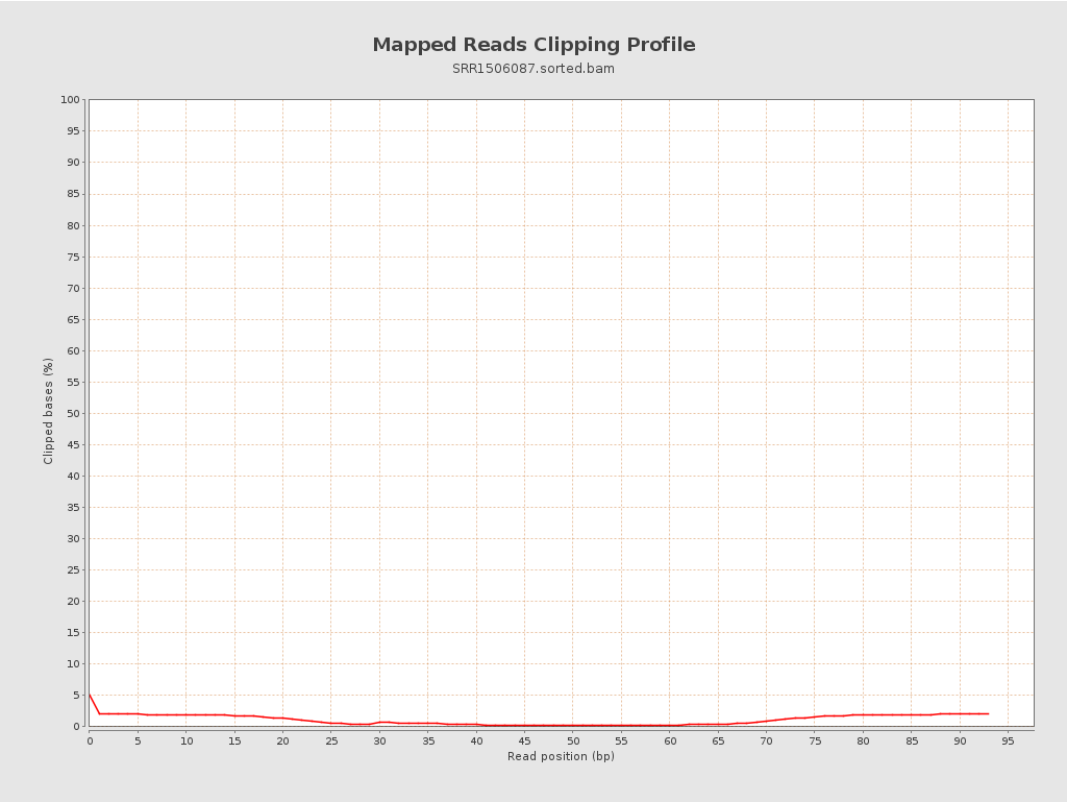
8. Results : Mapped Reads Nucleotide Content



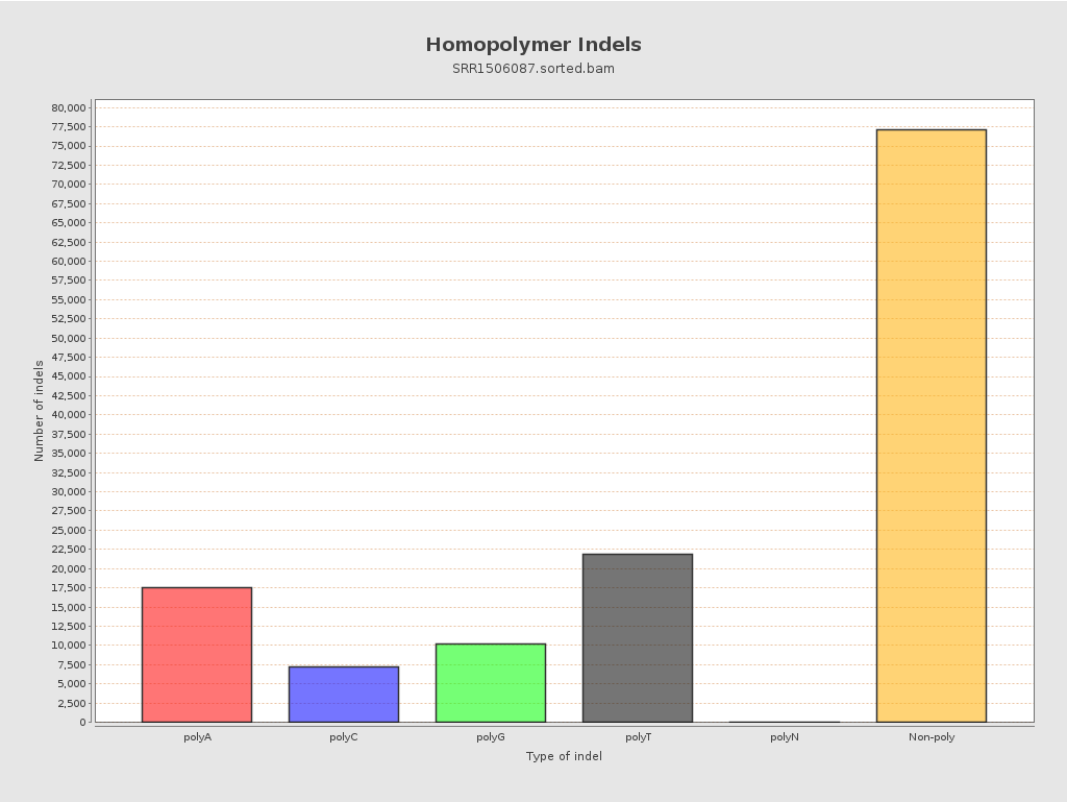
9. Results : Mapped Reads GC-content Distribution



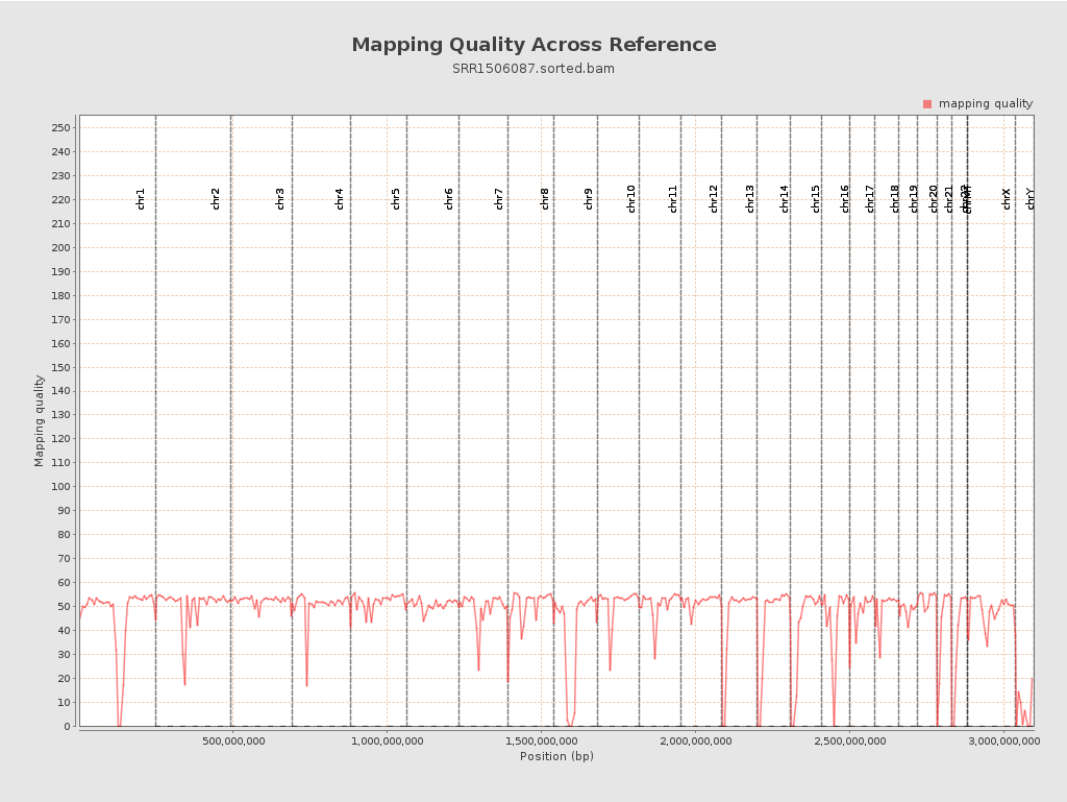
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram