

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:52:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549122.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_SRR1549122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:52:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,301,924
Mapped reads	7,237,786 / 58.83%
Unmapped reads	5,064,138 / 41.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	303,067 / 2.46%
Duplication rate	3.1%
Clipped reads	363,175 / 2.95%

2.2. ACGT Content

Number/percentage of A's	84,198,561 / 29.3%
Number/percentage of C's	59,248,358 / 20.62%
Number/percentage of T's	84,694,008 / 29.48%
Number/percentage of G's	59,168,184 / 20.59%
Number/percentage of N's	12,086 / 0%
GC Percentage	41.21%

2.3. Coverage

Mean	0.0928
Standard Deviation	0.6724

2.4. Mapping Quality

Mean Mapping Quality	44.05
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2.5. Mismatches and indels

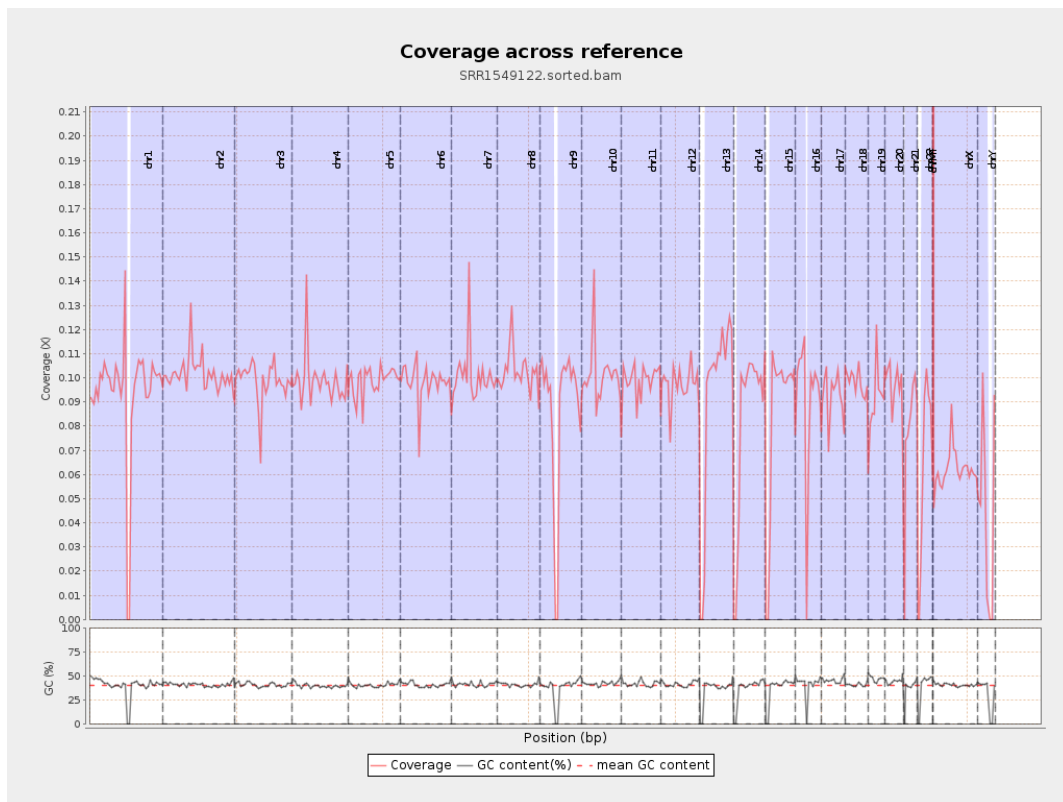
General error rate	0.31%
Mismatches	892,912
Insertions	7,145
Mapped reads with at least one insertion	0.1%
Deletions	23,124
Mapped reads with at least one deletion	0.32%
Homopolymer indels	45.04%

2.6. Chromosome stats

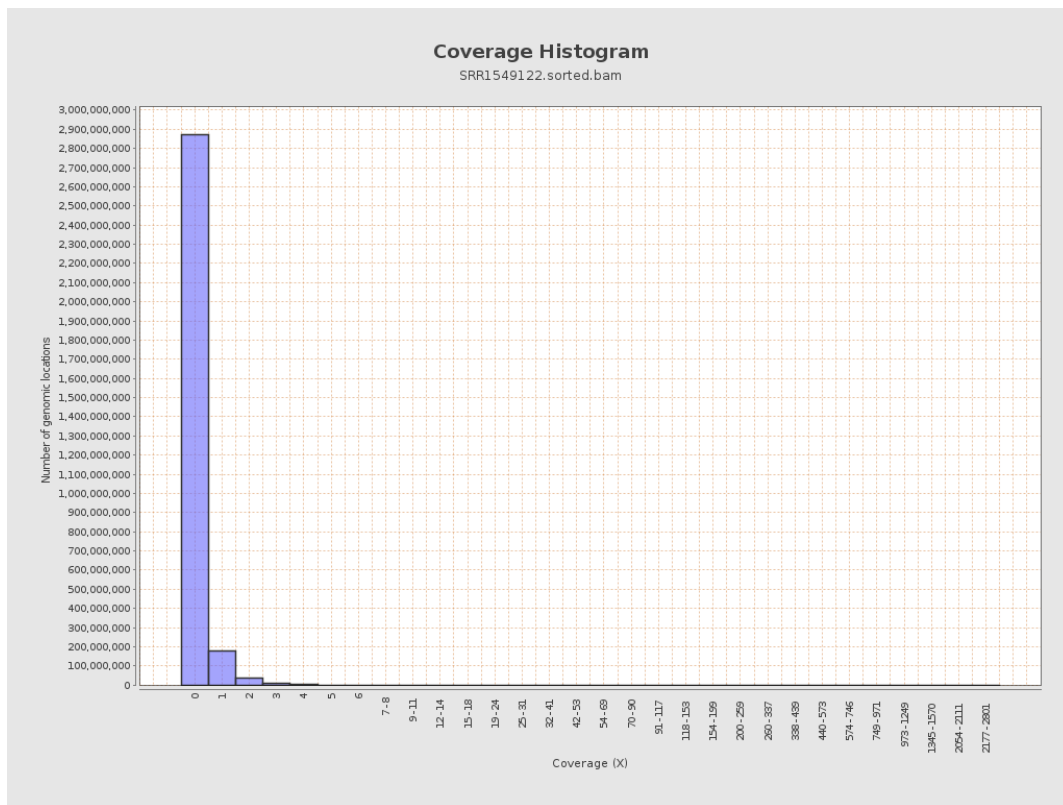
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23390169	0.0938	1.2149
chr2	243199373	24779998	0.1019	0.5621
chr3	198022430	19501181	0.0985	0.385
chr4	191154276	18950880	0.0991	0.4559
chr5	180915260	17883726	0.0989	0.3964
chr6	171115067	16849215	0.0985	0.408
chr7	159138663	16051149	0.1009	0.8068
chr8	146364022	15029262	0.1027	1.4428

chr9	141213431	12254863	0.0868	0.5064
chr10	135534747	13699644	0.1011	0.6259
chr11	135006516	13369036	0.099	0.5206
chr12	133851895	13073823	0.0977	0.4009
chr13	115169878	10594356	0.092	0.3716
chr14	107349540	8969636	0.0836	0.4389
chr15	102531392	8504914	0.0829	0.3494
chr16	90354753	8073598	0.0894	0.4133
chr17	81195210	7555242	0.0931	0.4052
chr18	78077248	7676567	0.0983	0.9842
chr19	59128983	5447884	0.0921	0.9527
chr20	63025520	6120846	0.0971	0.4136
chr21	48129895	3804054	0.079	0.4379
chr22	51304566	3284073	0.064	0.3213
chrMT	16571	128593	7.7601	9.7286
chrX	155270560	9652915	0.0622	0.3727
chrY	59373566	2705051	0.0456	0.5228

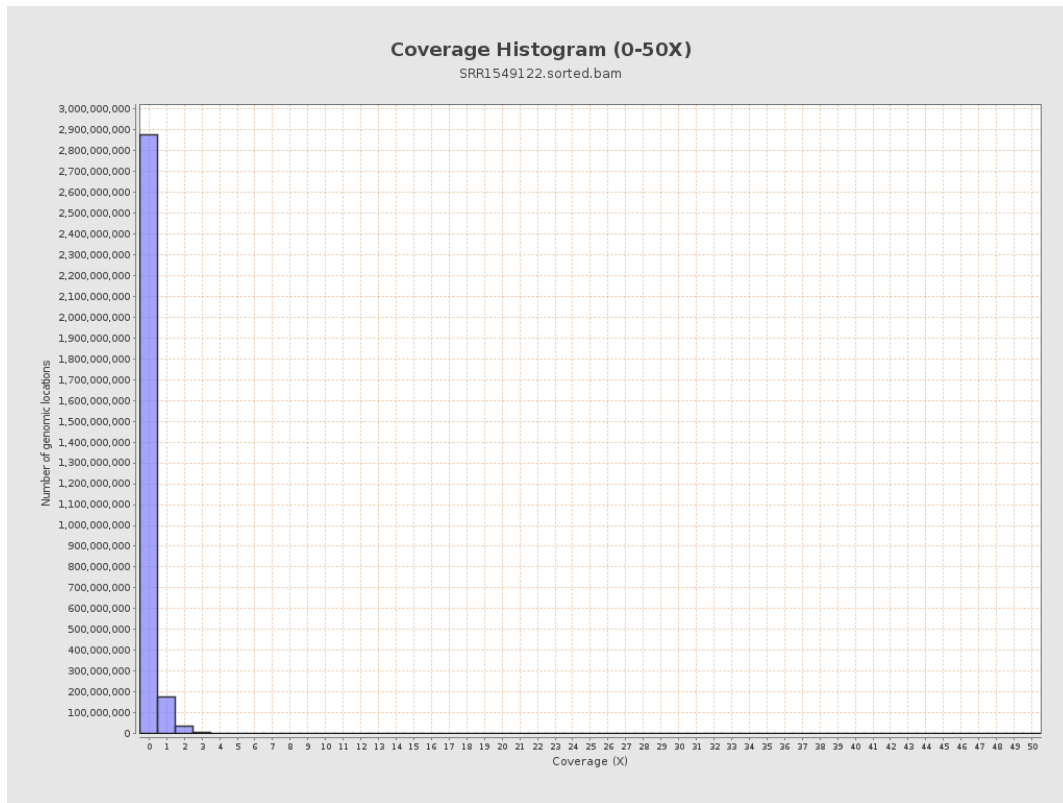
3. Results : Coverage across reference



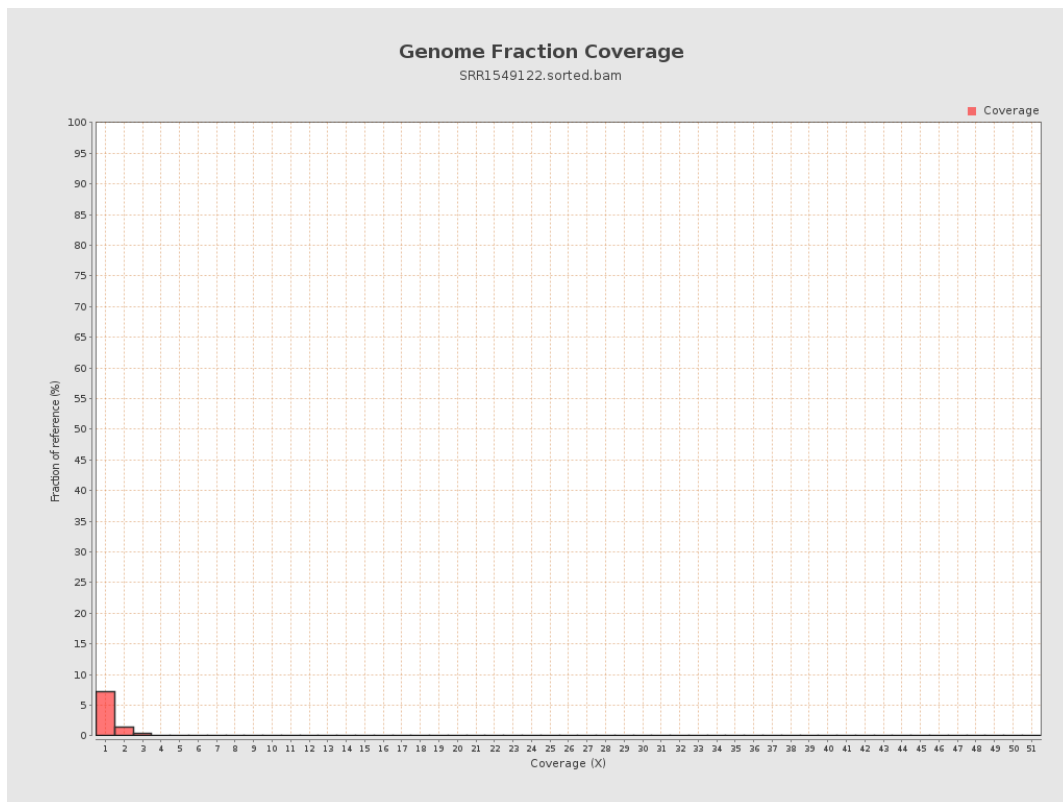
4. Results : Coverage Histogram



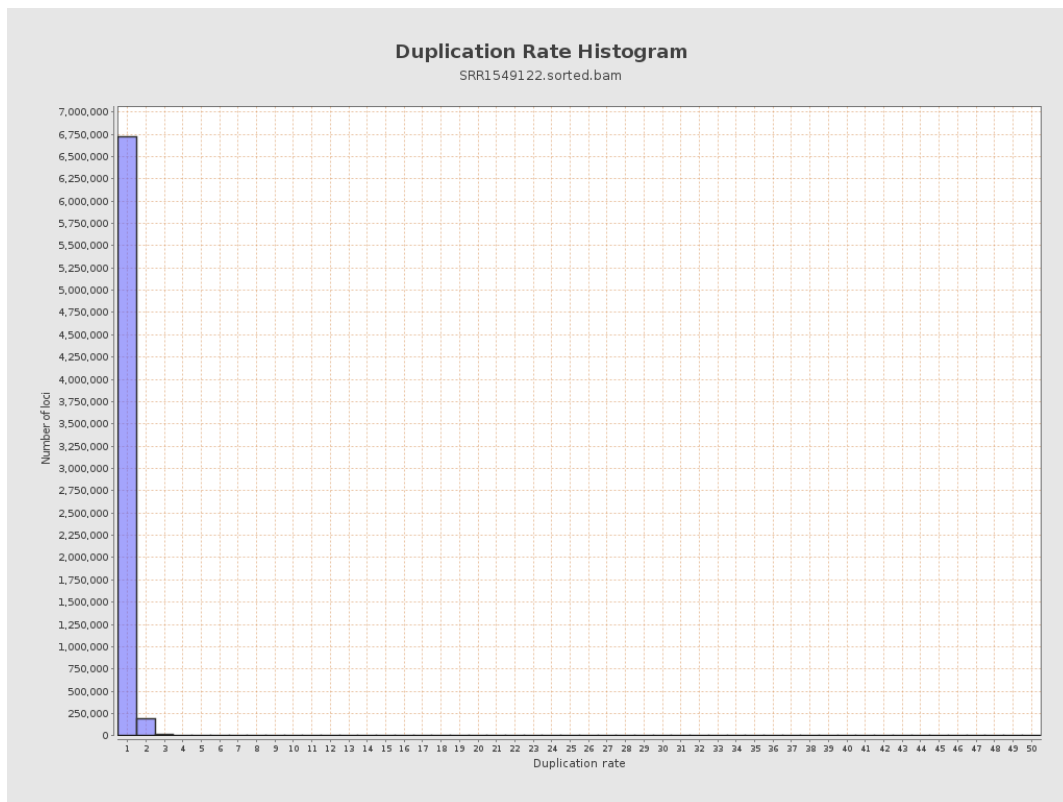
5. Results : Coverage Histogram (0-50X)



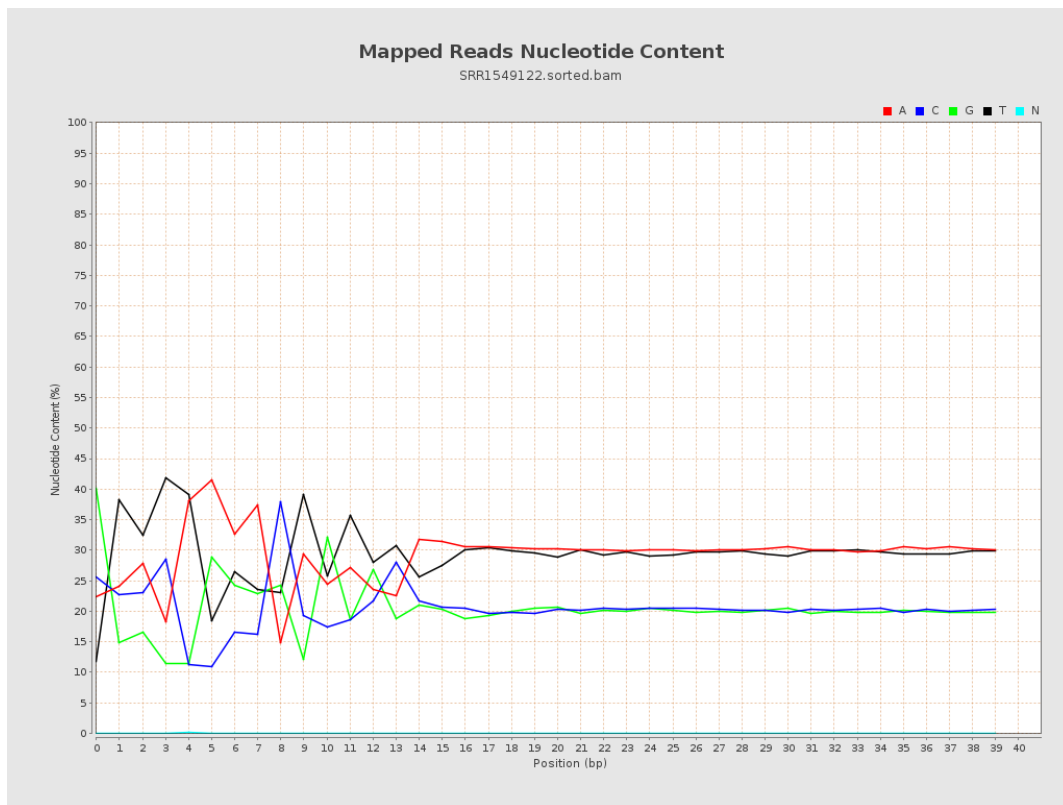
6. Results : Genome Fraction Coverage



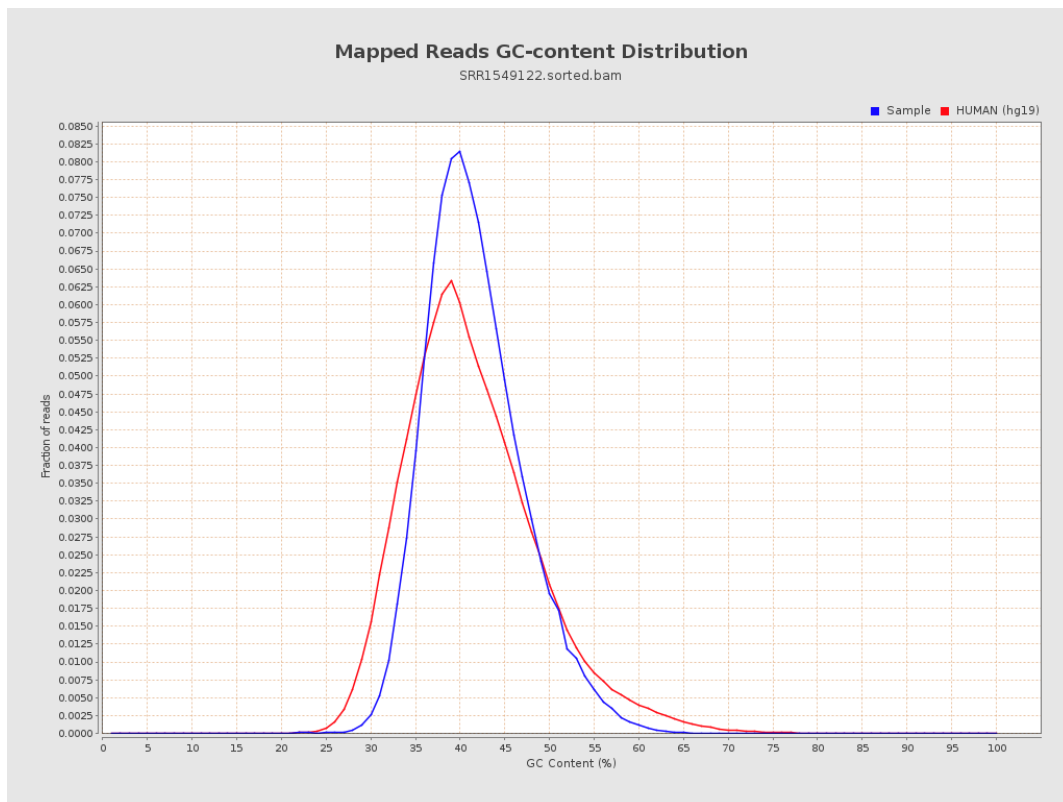
7. Results : Duplication Rate Histogram



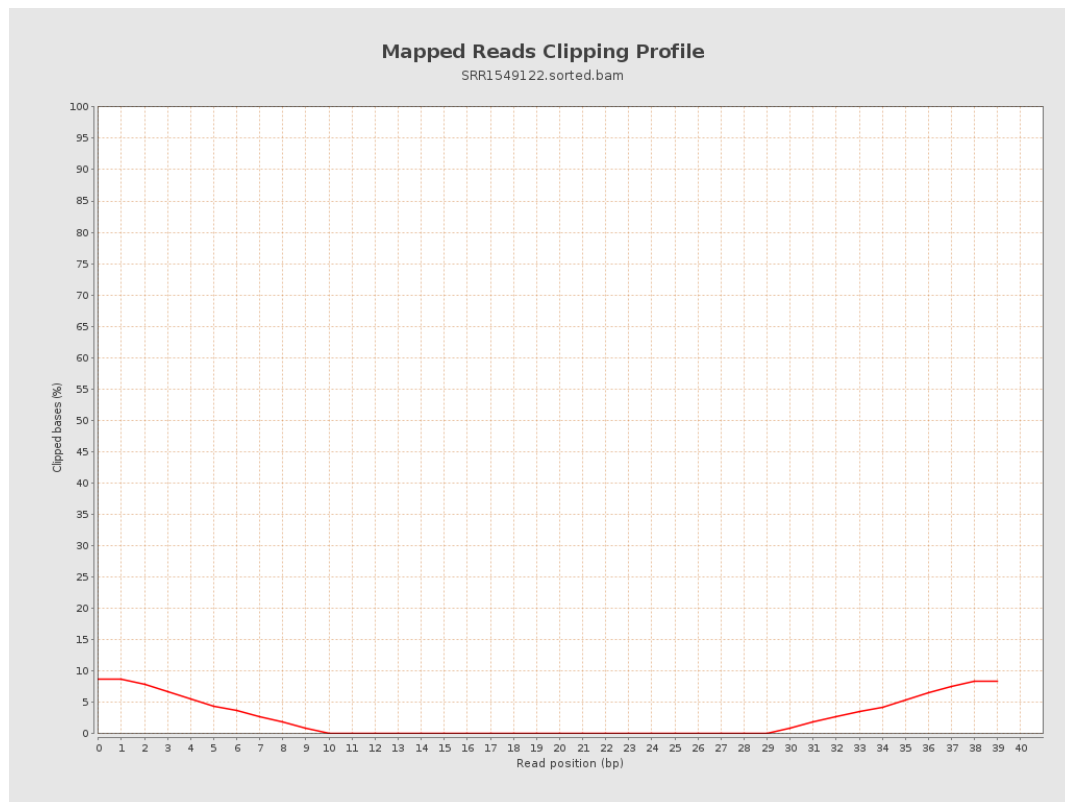
8. Results : Mapped Reads Nucleotide Content



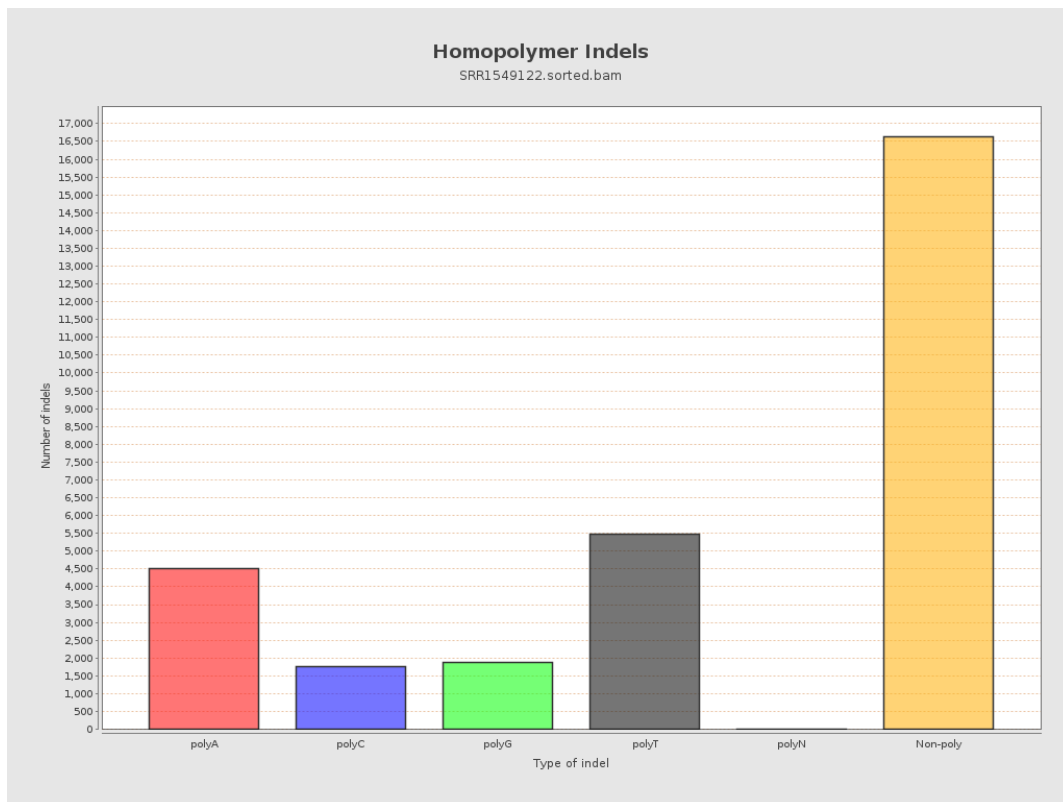
9. Results : Mapped Reads GC-content Distribution



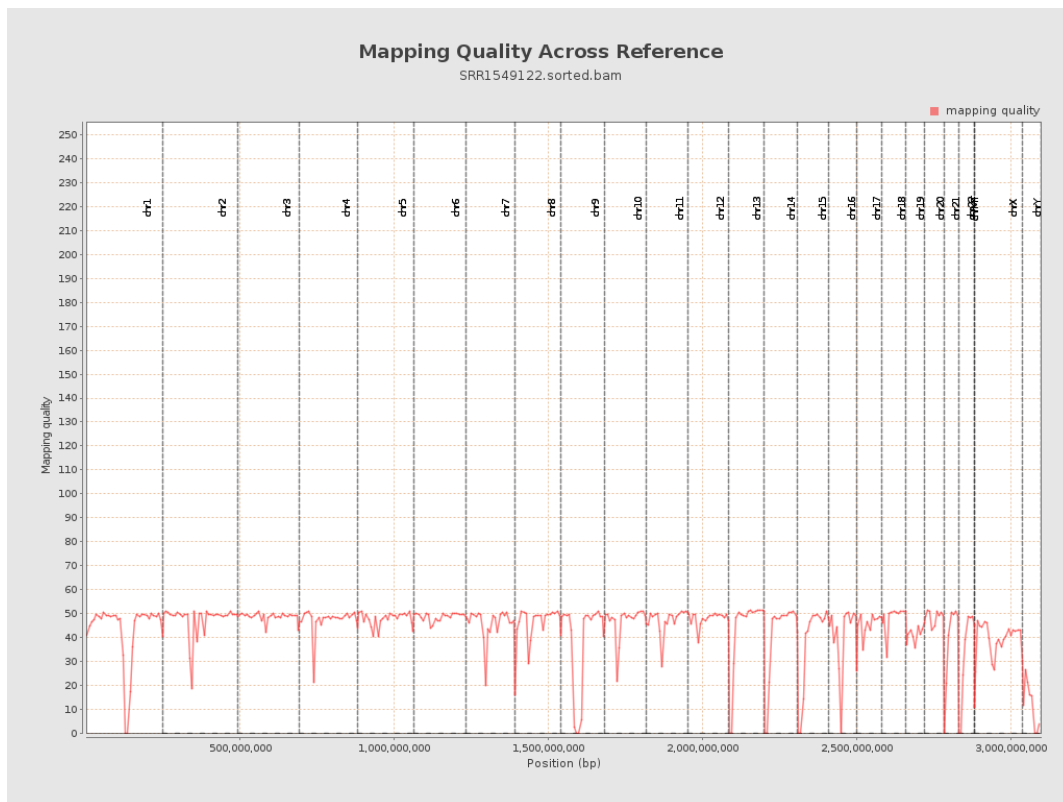
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

