Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:45:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549121.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_SRR1549121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:45:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,437,455
Mapped reads	6,794,963 / 59.41%
Unmapped reads	4,642,492 / 40.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	249,749 / 2.18%
Duplication rate	2.72%
Clipped reads	324,910 / 2.84%

2.2. ACGT Content

Number/percentage of A's	79,153,535 / 29.33%
Number/percentage of C's	55,757,790 / 20.66%
Number/percentage of T's	79,362,063 / 29.41%
Number/percentage of G's	55,550,961 / 20.59%
Number/percentage of N's	10,792 / 0%
GC Percentage	41.25%

2.3. Coverage

Mean	0.0872
Standard Deviation	0.5646

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Mismatches and indels

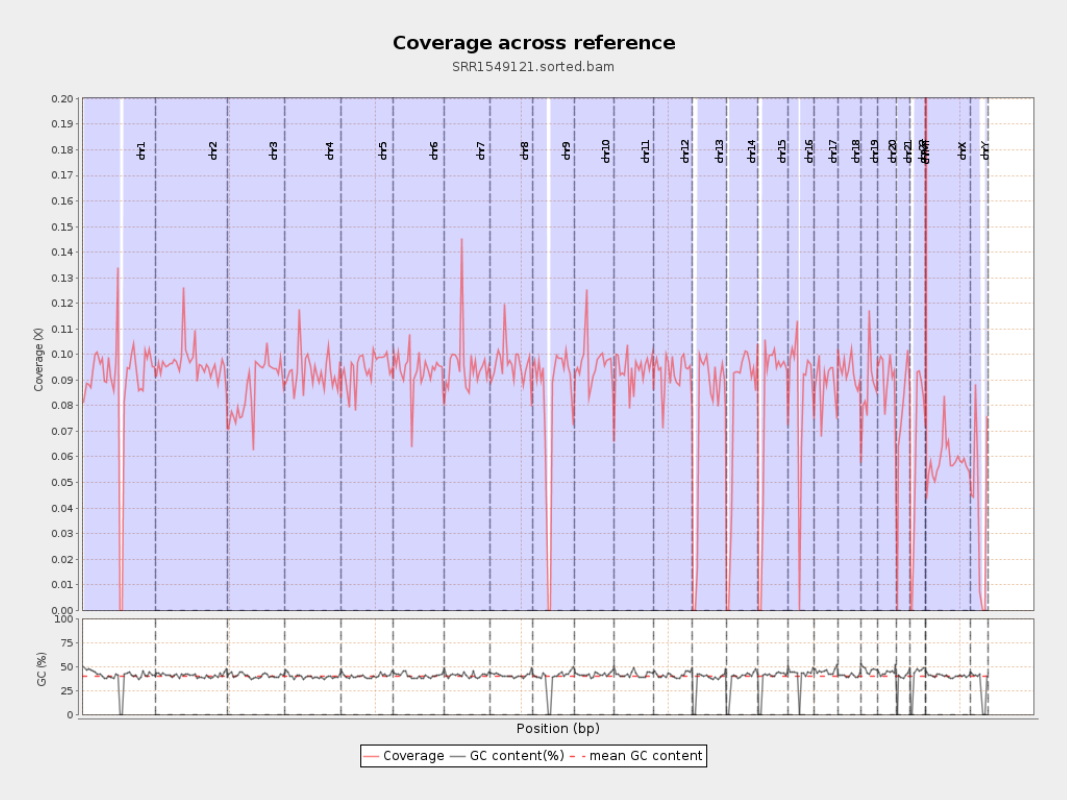
General error rate	0.31%
Mismatches	824,643
Insertions	6,591
Mapped reads with at least one insertion	0.1%
Deletions	20,204
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.82%

2.6. Chromosome stats

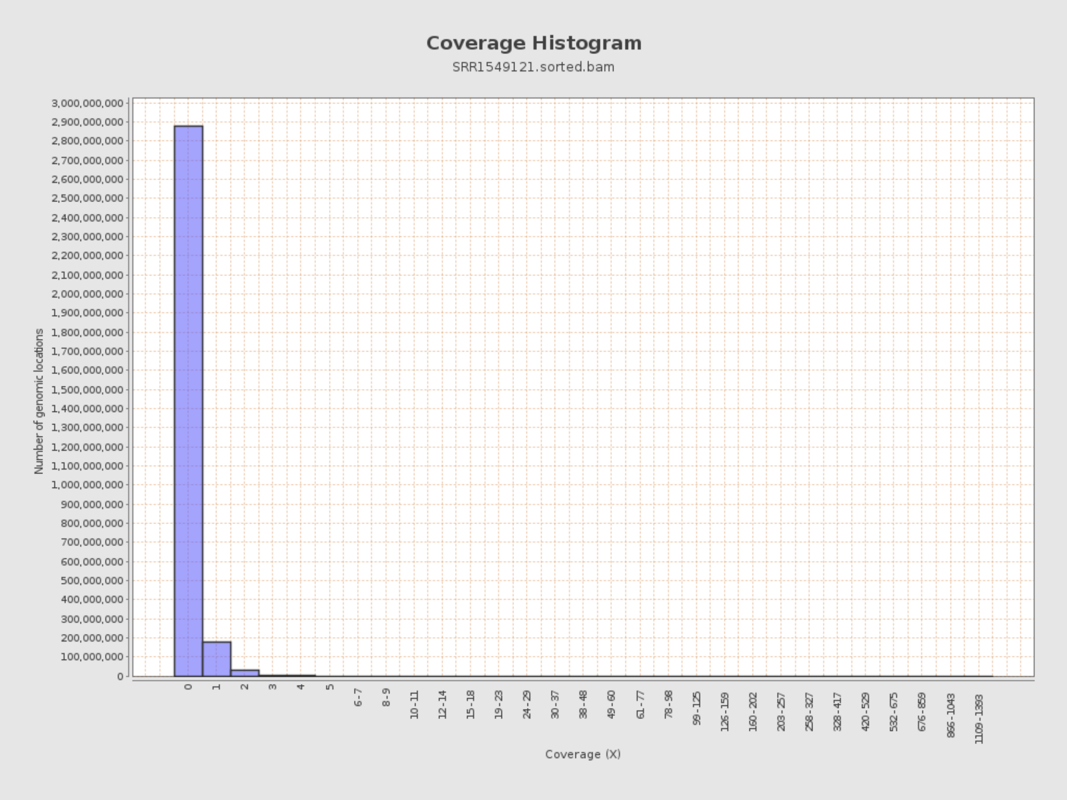
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22143414	0.0888	1.0703
chr2	243199373	23518274	0.0967	0.5166
chr3	198022430	17201278	0.0869	0.3534
chr4	191154276	17886723	0.0936	0.3948
chr5	180915260	17085647	0.0944	0.3767
chr6	171115067	16049244	0.0938	0.402
chr7	159138663	15299717	0.0961	0.8169
chr8	146364022	14056486	0.096	0.6222

chr9	141213431	11572694	0.082	0.483
chr10	135534747	13069739	0.0964	0.5348
chr11	135006516	12658189	0.0938	0.4959
chr12	133851895	12487628	0.0933	0.3827
chr13	115169878	8830224	0.0767	0.3277
chr14	107349540	8457396	0.0788	0.4446
chr15	102531392	8156310	0.0795	0.333
chr16	90354753	7642899	0.0846	0.3795
chr17	81195210	7222585	0.089	0.3785
chr18	78077248	7287526	0.0933	0.9729
chr19	59128983	5194737	0.0879	0.8744
chr20	63025520	5756974	0.0913	0.386
chr21	48129895	3615545	0.0751	0.3808
chr22	51304566	3160037	0.0616	0.3061
chrMT	16571	99394	5.9981	7.5362
chrX	155270560	9047645	0.0583	0.3561
chrY	59373566	2360283	0.0398	0.4005

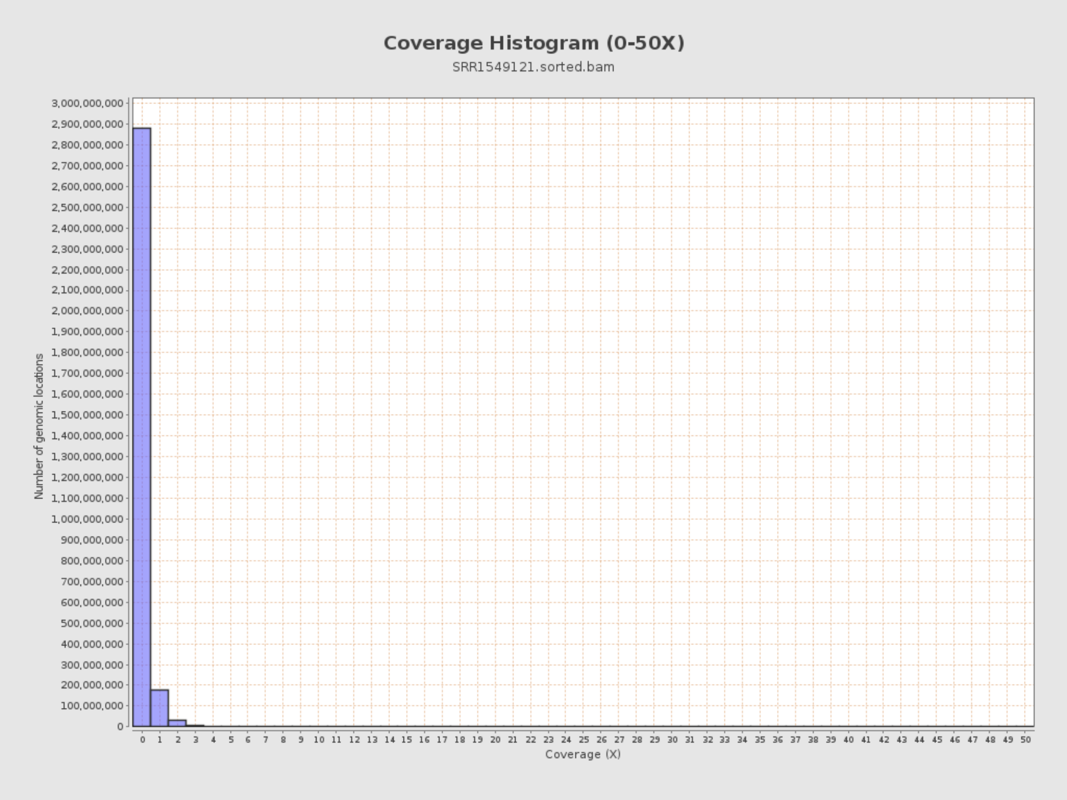
3. Results : Coverage across reference



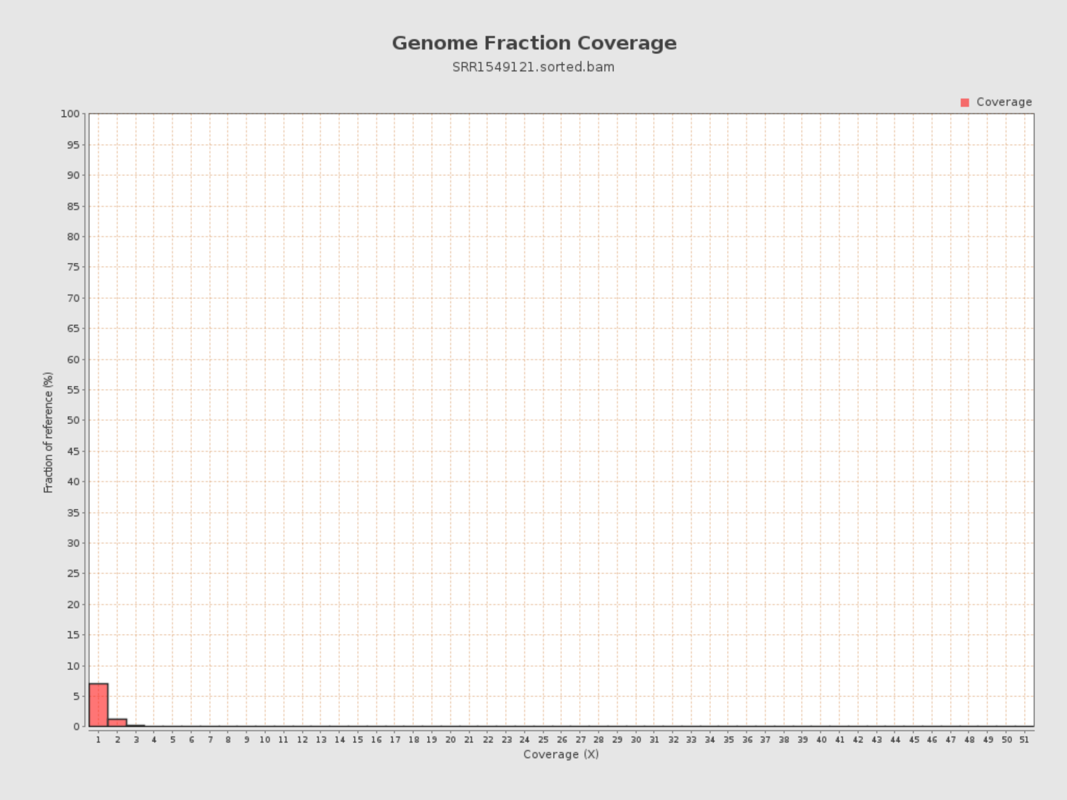
4. Results : Coverage Histogram



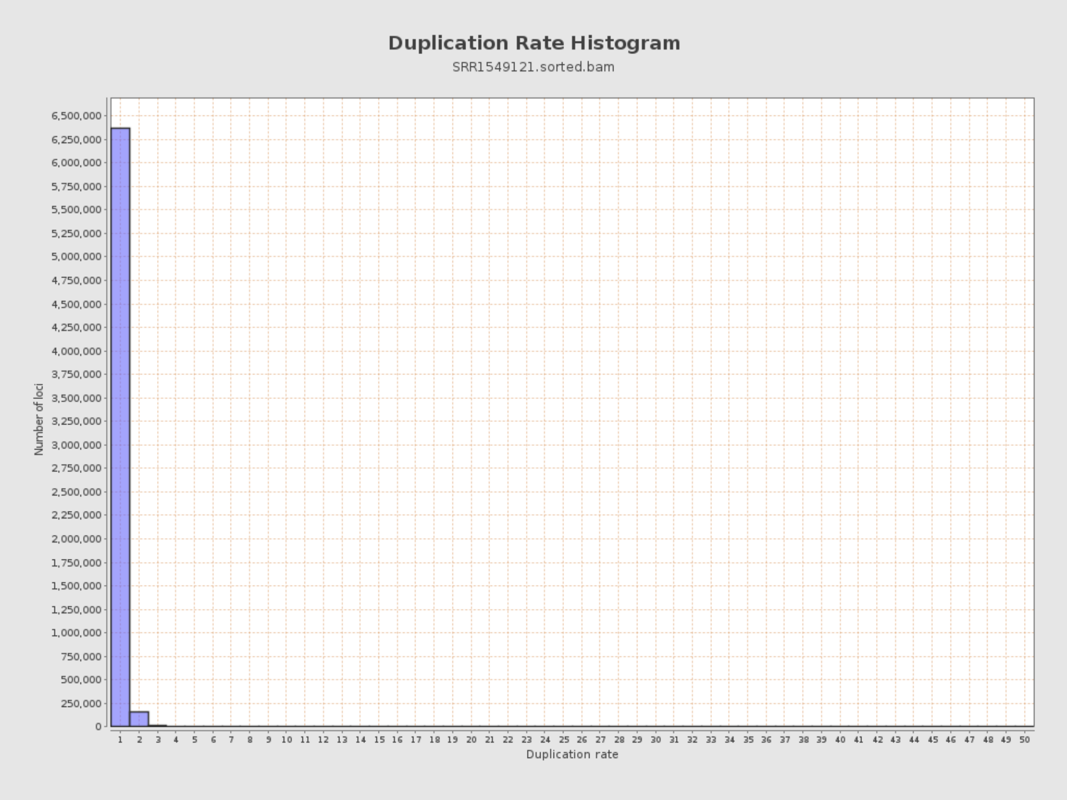
5. Results : Coverage Histogram (0-50X)



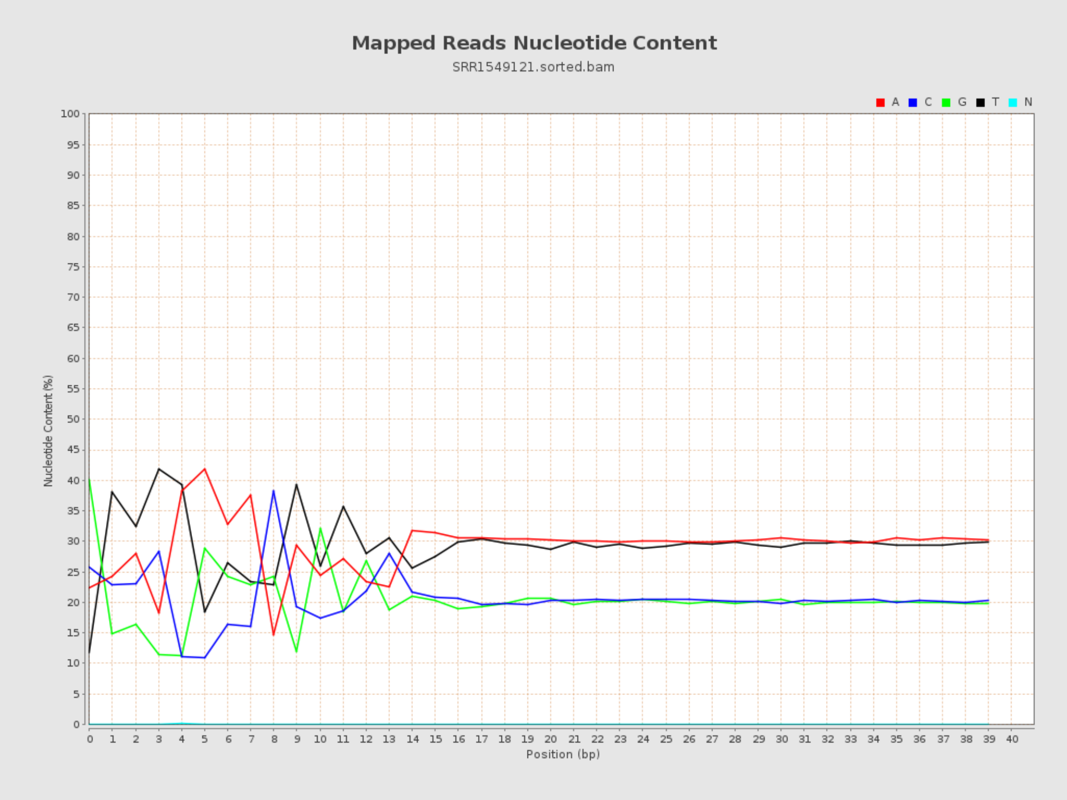
6. Results : Genome Fraction Coverage



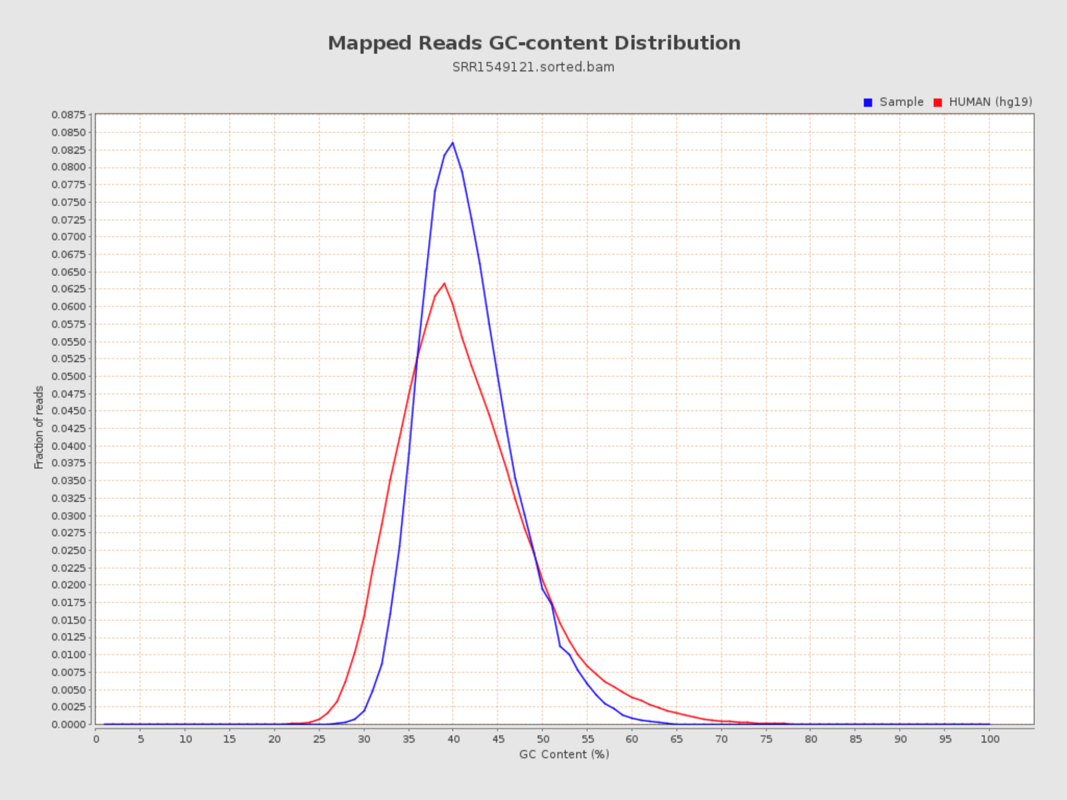
7. Results : Duplication Rate Histogram



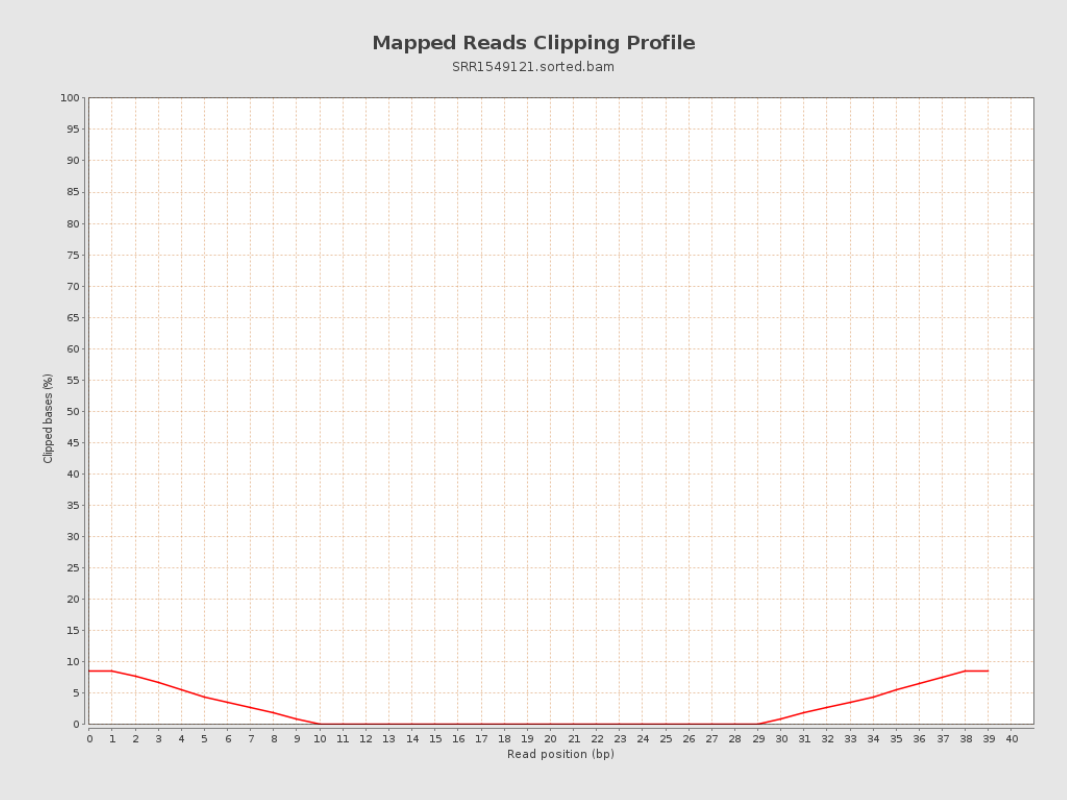
8. Results : Mapped Reads Nucleotide Content



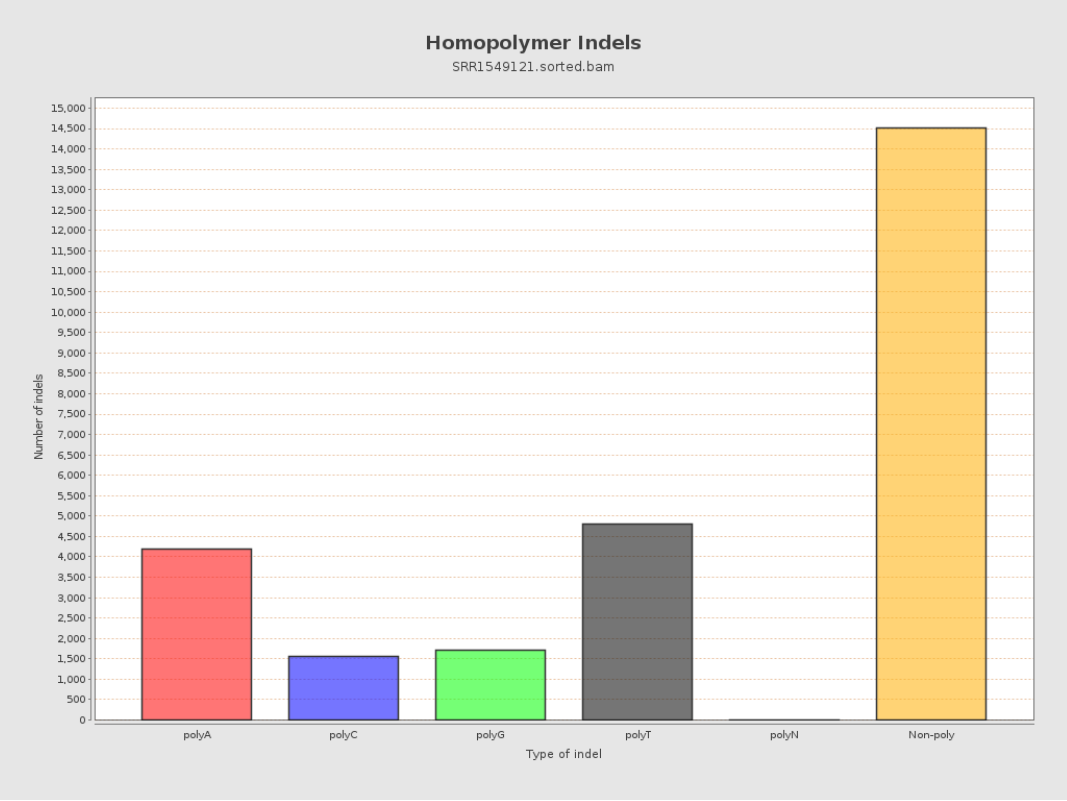
9. Results : Mapped Reads GC-content Distribution



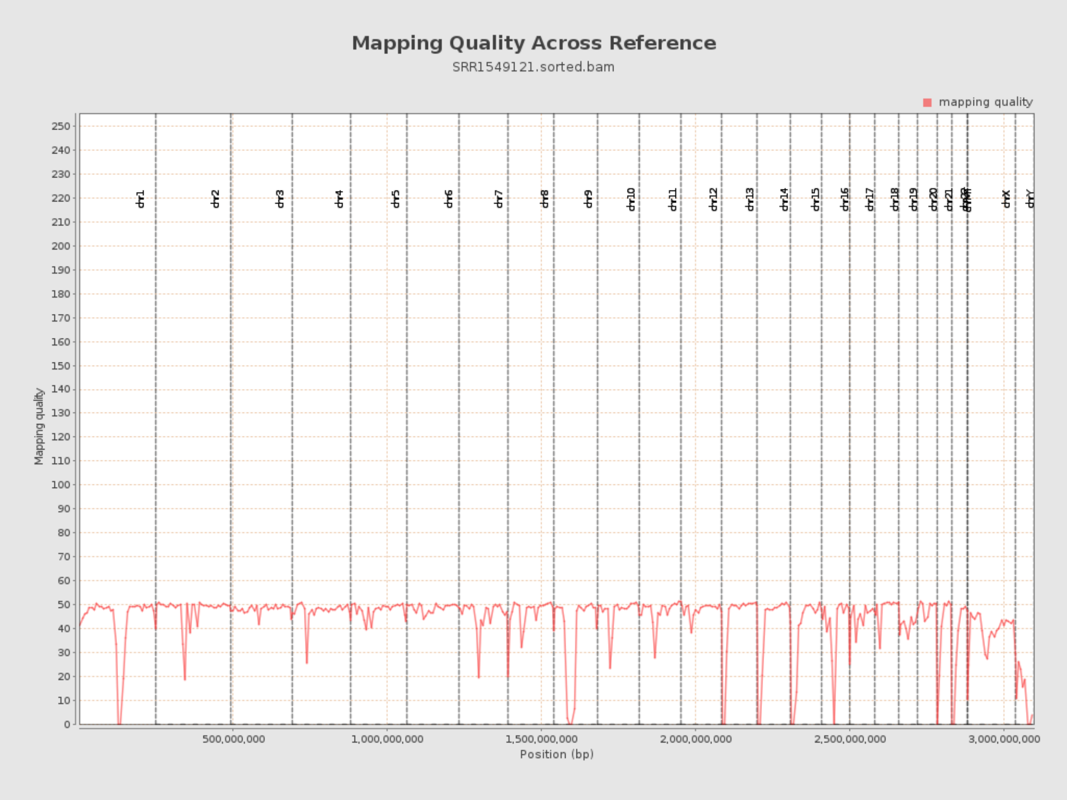
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram