Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:16:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549037.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_SRR1549037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549037.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:15:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,175,614
Mapped reads	7,072,380 / 86.51%
Unmapped reads	1,103,234 / 13.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	311,559 / 3.81%
Duplication rate	3.74%
Clipped reads	458,597 / 5.61%

2.2. ACGT Content

Number/percentage of A's	79,155,664 / 28.24%
Number/percentage of C's	59,756,175 / 21.32%
Number/percentage of T's	80,702,697 / 28.8%
Number/percentage of G's	60,642,692 / 21.64%
Number/percentage of N's	227 / 0%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0905
Standard Deviation	0.5128

2.4. Mapping Quality

Mean Mapping Quality	41.42

2.5. Mismatches and indels

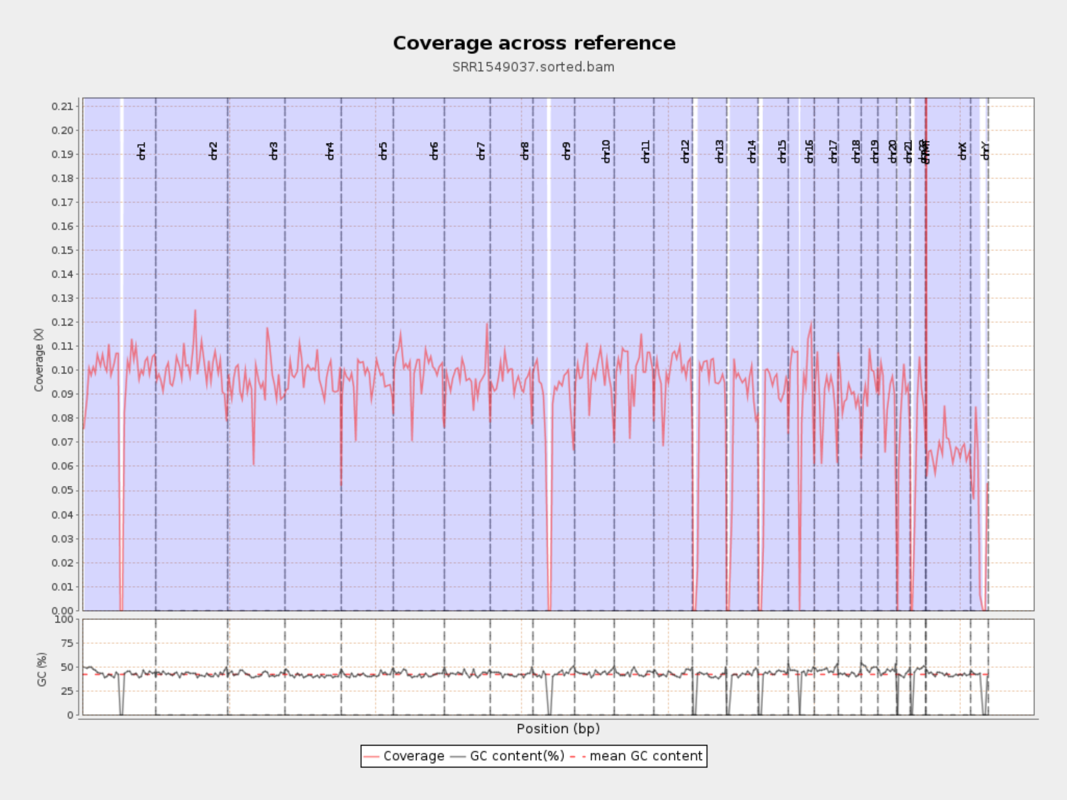
General error rate	0.25%
Mismatches	699,412
Insertions	7,623
Mapped reads with at least one insertion	0.11%
Deletions	19,426
Mapped reads with at least one deletion	0.27%
Homopolymer indels	42.7%

2.6. Chromosome stats

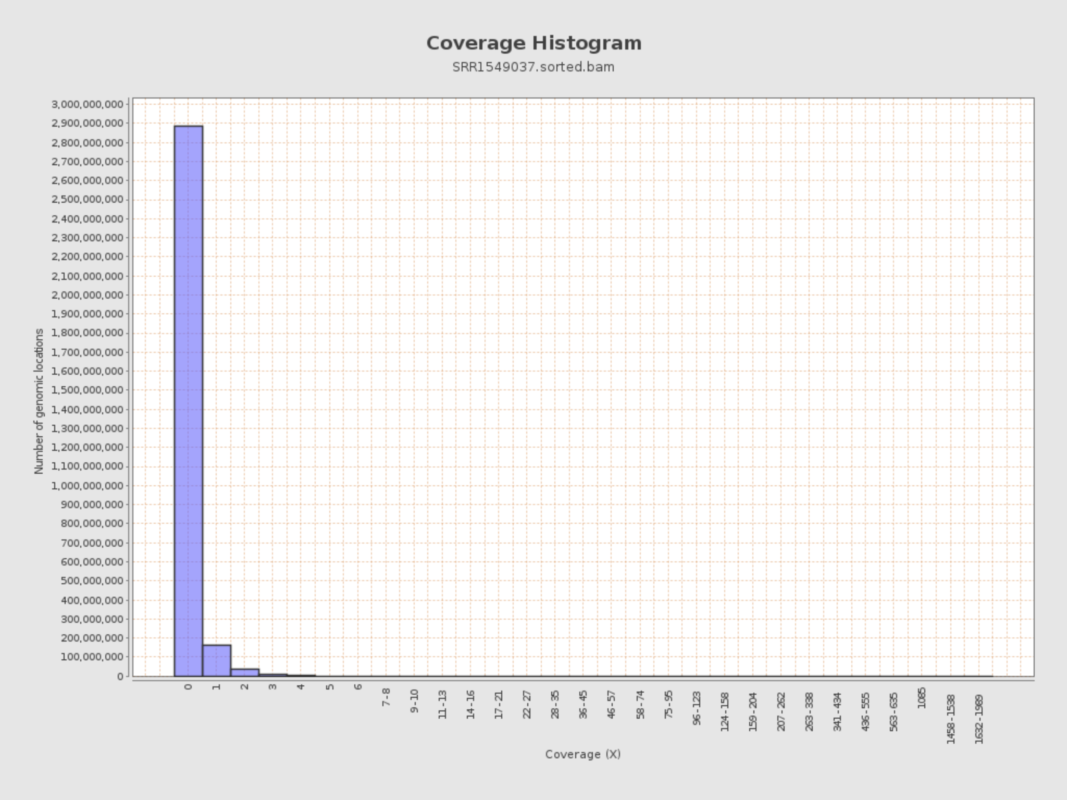
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23653572	0.0949	0.6456
chr2	243199373	24458587	0.1006	0.5131
chr3	198022430	18707925	0.0945	0.3948
chr4	191154276	18820547	0.0985	0.4249
chr5	180915260	17318081	0.0957	0.3991
chr6	171115067	17282457	0.101	0.4284
chr7	159138663	15380023	0.0966	0.5398
chr8	146364022	14044467	0.096	1.0559

chr9	141213431	11518416	0.0816	0.4689
chr10	135534747	13312992	0.0982	0.4838
chr11	135006516	13565171	0.1005	0.4485
chr12	133851895	13278421	0.0992	0.4121
chr13	115169878	9532296	0.0828	0.3727
chr14	107349540	8481293	0.079	0.4044
chr15	102531392	7855520	0.0766	0.3566
chr16	90354753	8146737	0.0902	0.4146
chr17	81195210	7251552	0.0893	0.389
chr18	78077248	7023120	0.09	0.7496
chr19	59128983	5540824	0.0937	0.6364
chr20	63025520	5584059	0.0886	0.3918
chr21	48129895	3670944	0.0763	0.432
chr22	51304566	3244452	0.0632	0.4279
chrMT	16571	12828	0.7741	1.3126
chrX	155270560	10328166	0.0665	0.364
chrY	59373566	2270668	0.0382	0.3433

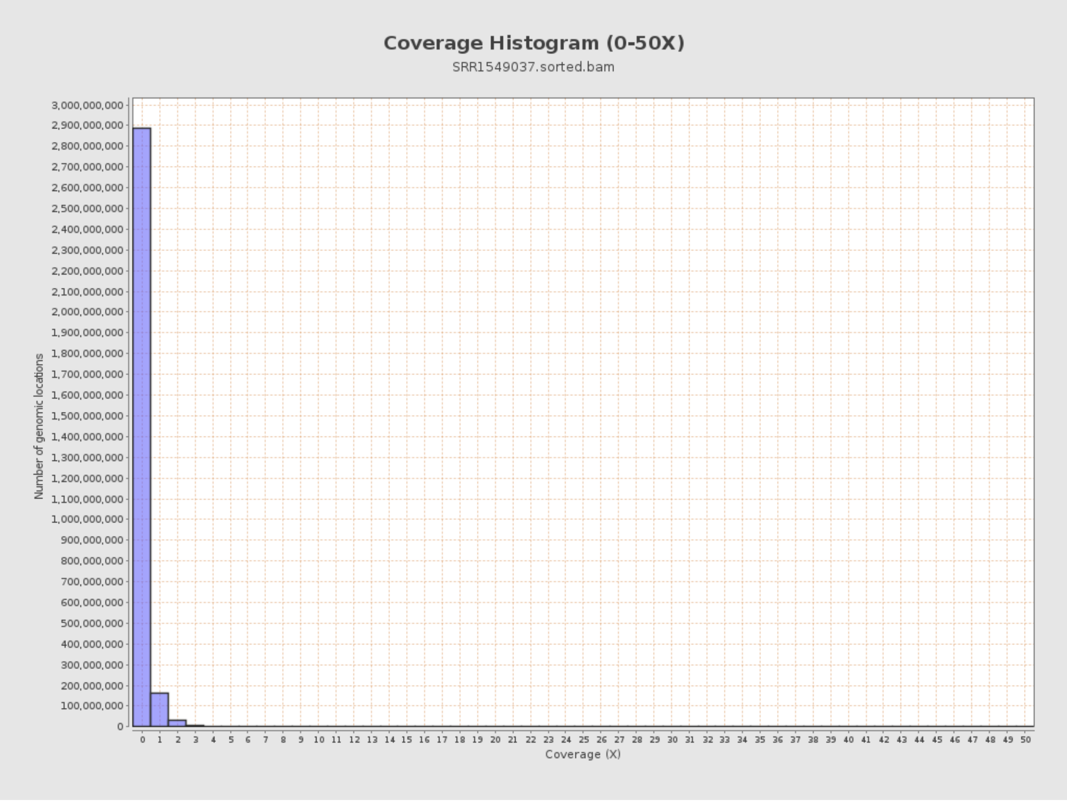
3. Results : Coverage across reference



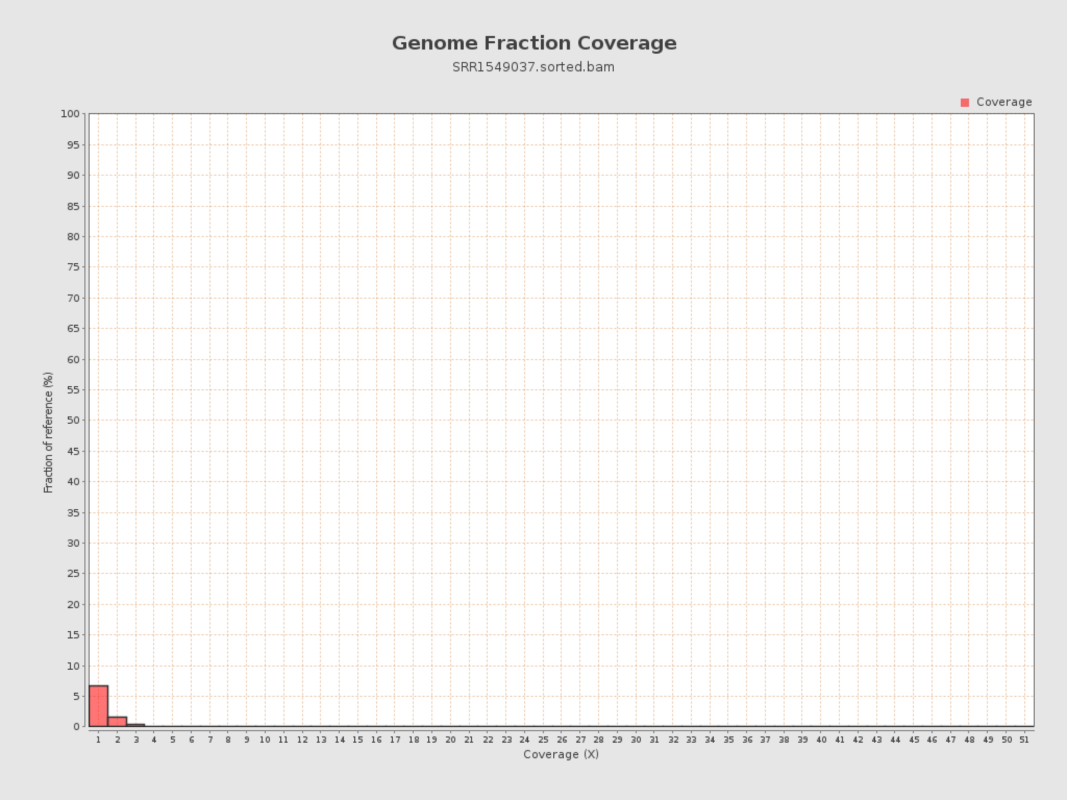
4. Results : Coverage Histogram



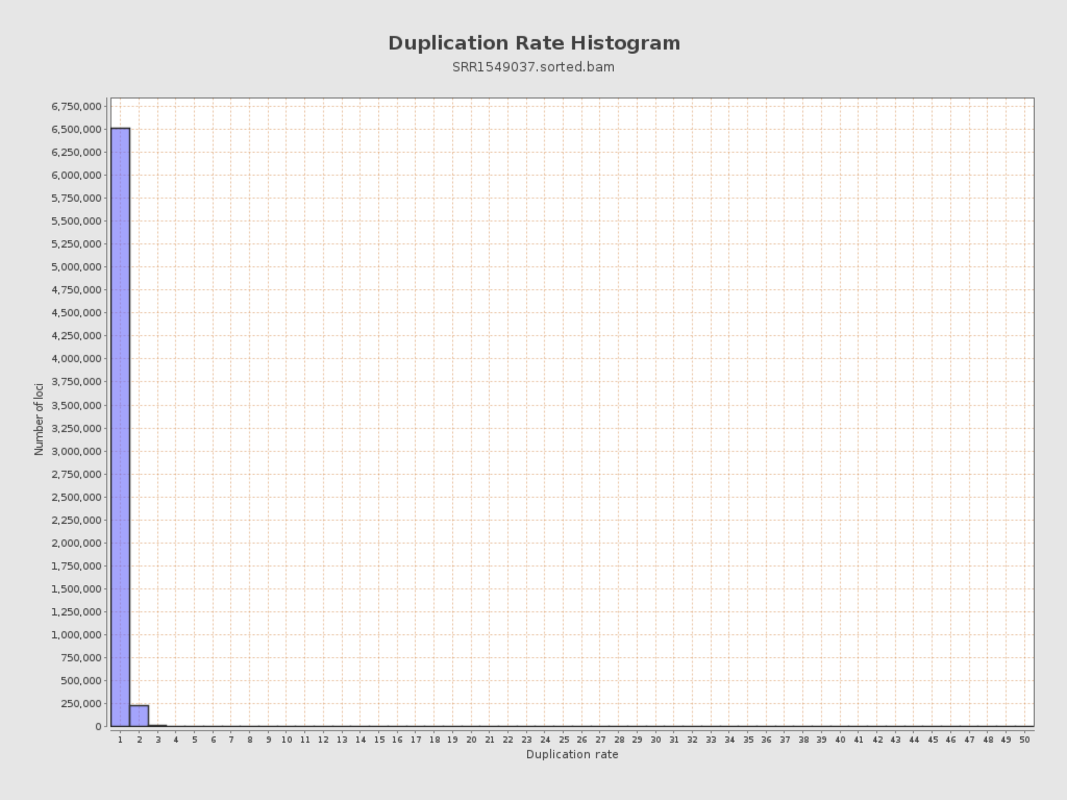
5. Results : Coverage Histogram (0-50X)



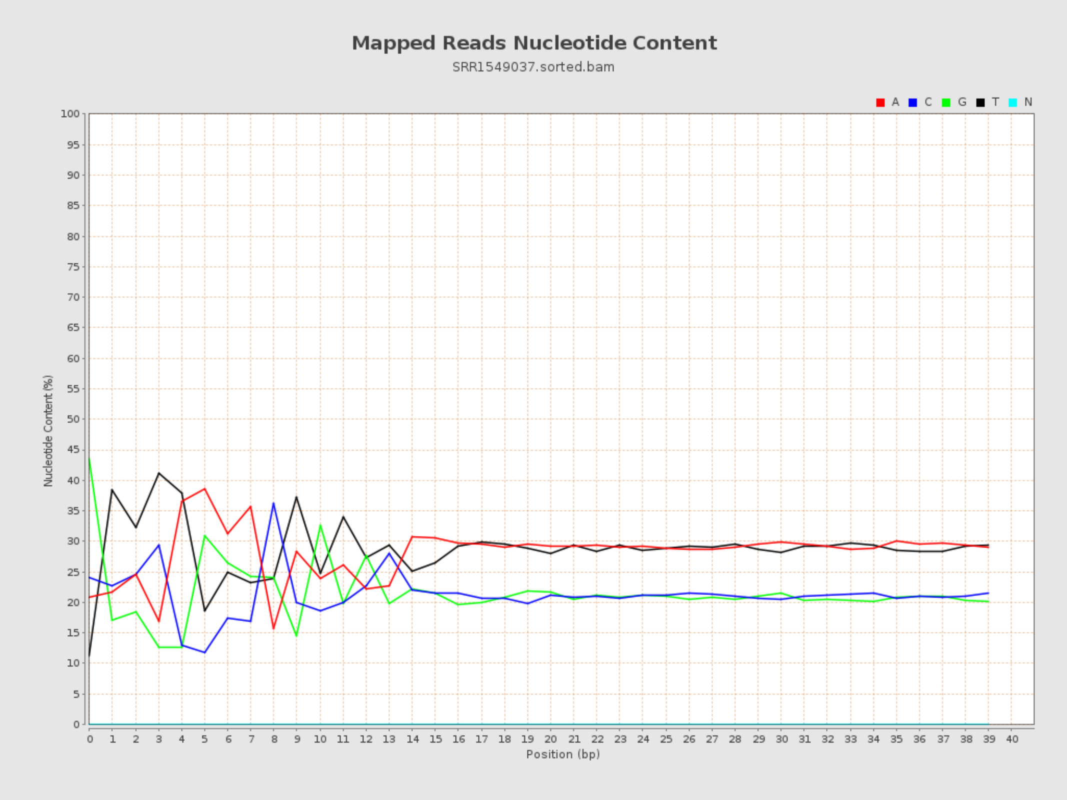
6. Results : Genome Fraction Coverage



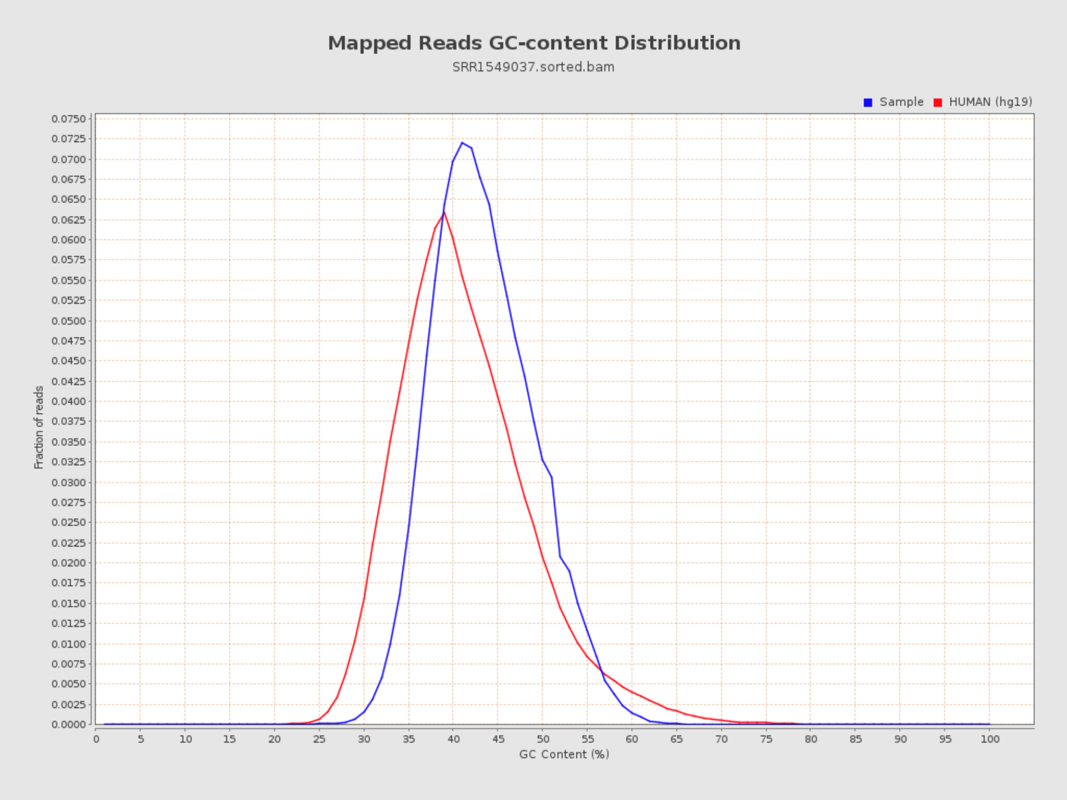
7. Results : Duplication Rate Histogram



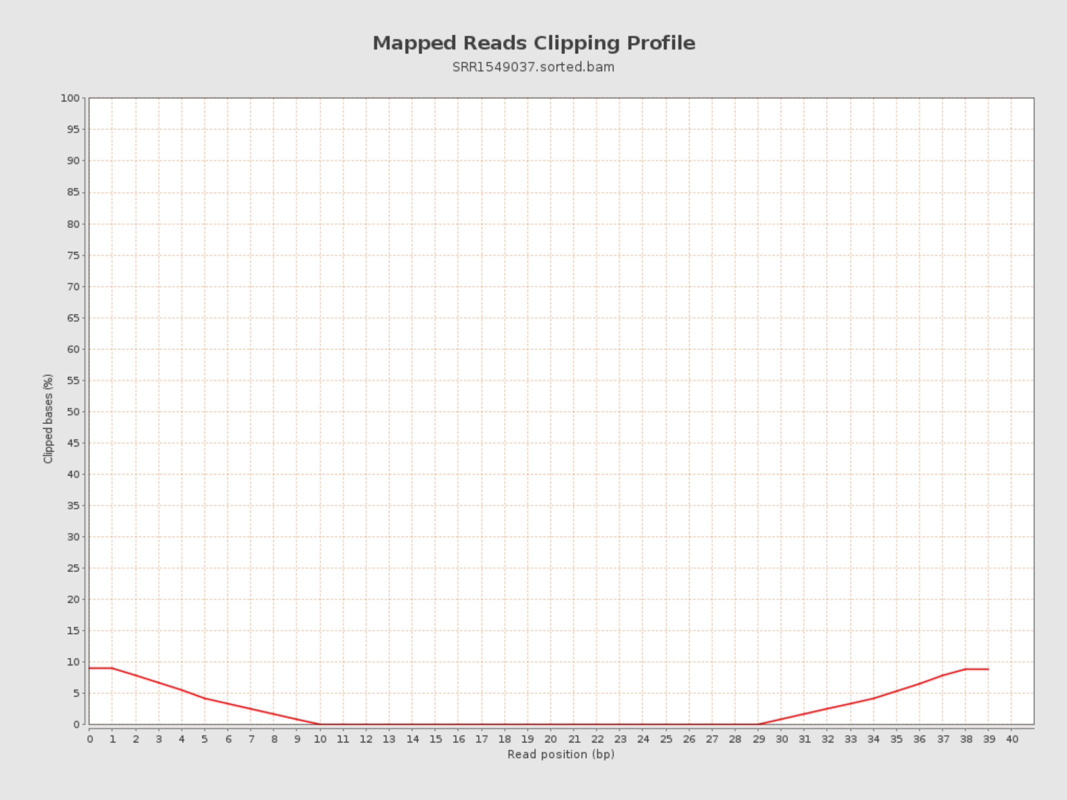
8. Results : Mapped Reads Nucleotide Content



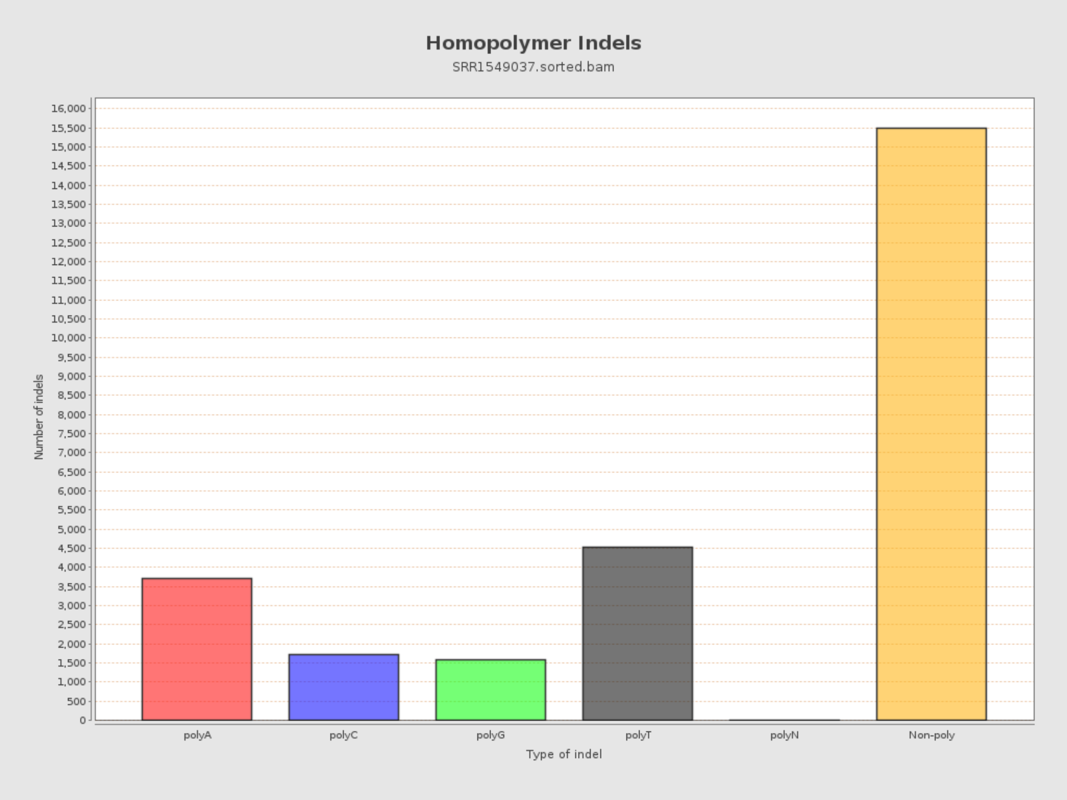
9. Results : Mapped Reads GC-content Distribution



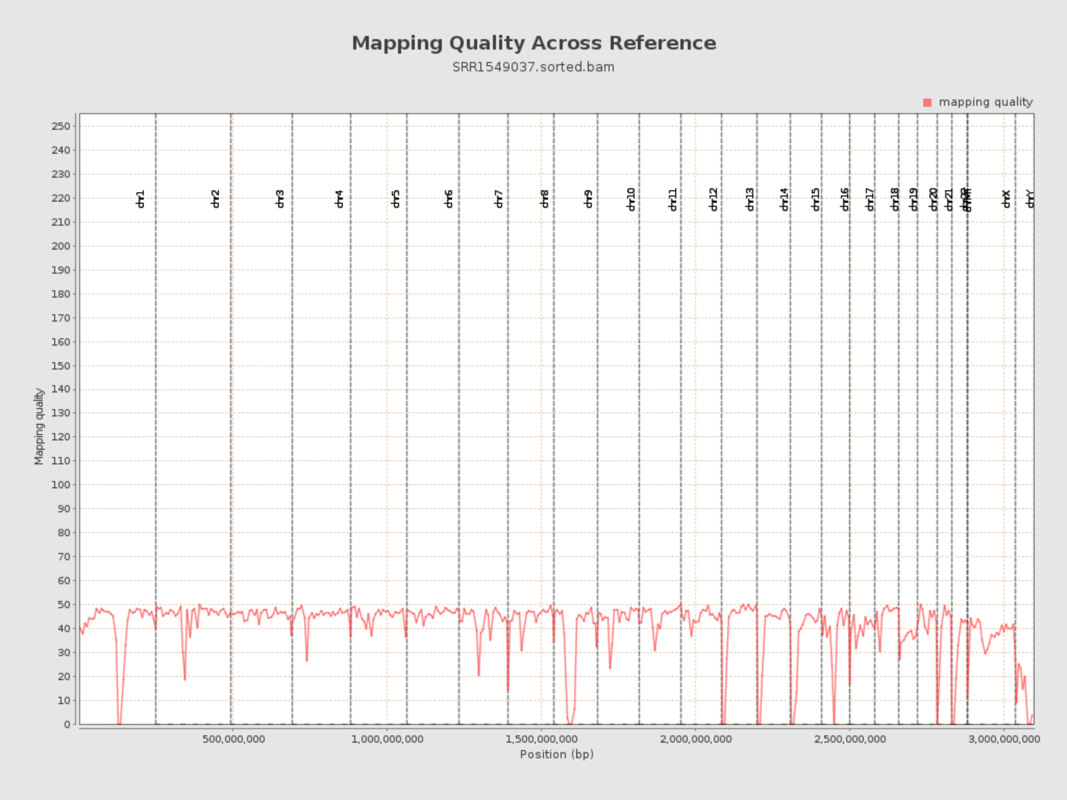
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram