Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:14:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549118.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_SRR1549118 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549118.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:14:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549118.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,669,153
Mapped reads	6,136,093 / 57.51%
Unmapped reads	4,533,060 / 42.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	212,790 / 1.99%
Duplication rate	2.74%
Clipped reads	301,519 / 2.83%

2.2. ACGT Content

Number/percentage of A's	72,510,497 / 29.76%
Number/percentage of C's	48,667,112 / 19.98%
Number/percentage of T's	73,342,014 / 30.11%
Number/percentage of G's	49,084,750 / 20.15%
Number/percentage of N's	10,147 / 0%
GC Percentage	40.13%

2.3. Coverage

Mean	0.0787
Standard Deviation	0.4662

2.4. Mapping Quality

Mean Mapping Quality	43.68

2.5. Mismatches and indels

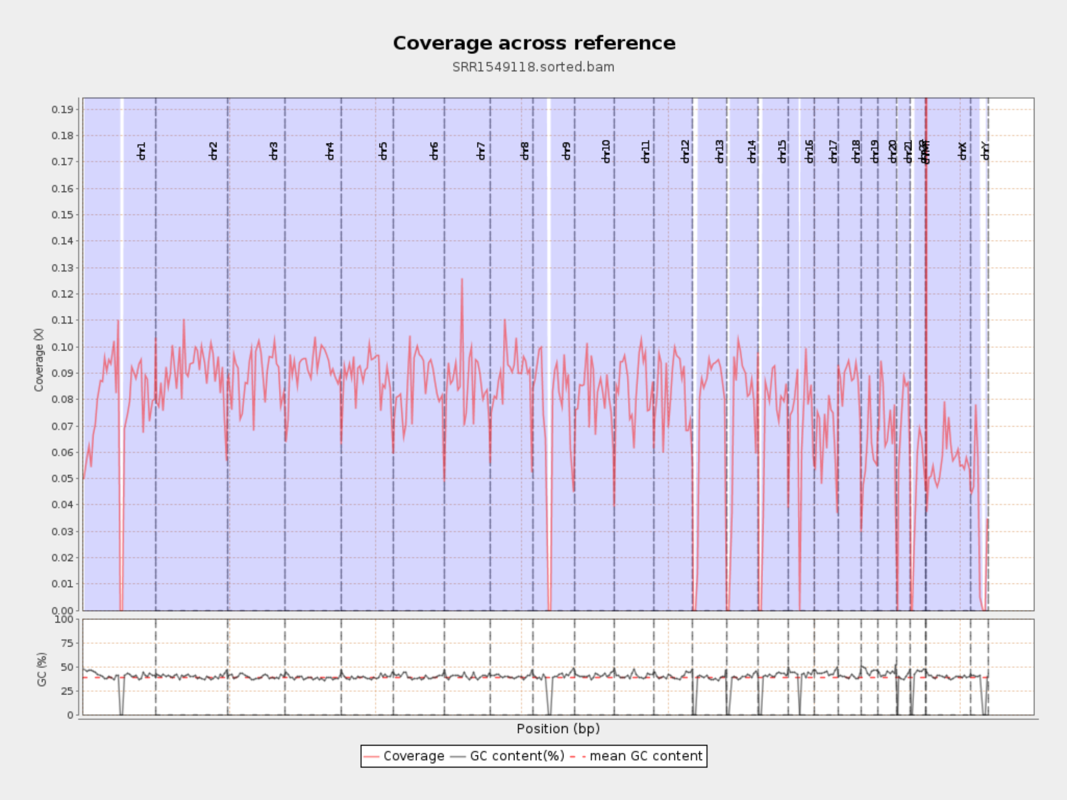
General error rate	0.3%
Mismatches	723,848
Insertions	6,020
Mapped reads with at least one insertion	0.1%
Deletions	17,966
Mapped reads with at least one deletion	0.29%
Homopolymer indels	45.91%

2.6. Chromosome stats

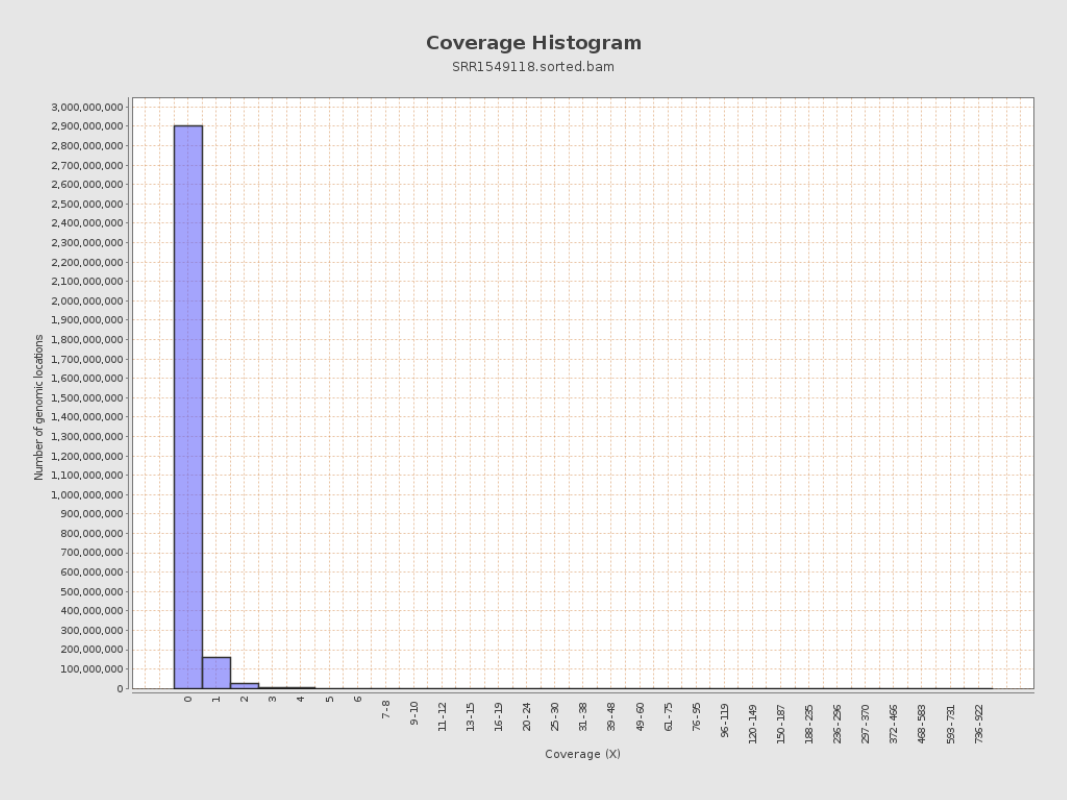
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19076529	0.0765	0.7726
chr2	243199373	21925541	0.0902	0.4524
chr3	198022430	17600461	0.0889	0.3586
chr4	191154276	17526196	0.0917	0.3722
chr5	180915260	15942391	0.0881	0.3578
chr6	171115067	14684008	0.0858	0.3837
chr7	159138663	13716266	0.0862	0.6856
chr8	146364022	12978050	0.0887	0.5578

chr9	141213431	10395717	0.0736	0.4262
chr10	135534747	11141643	0.0822	0.4388
chr11	135006516	11470907	0.085	0.4161
chr12	133851895	11118926	0.0831	0.3538
chr13	115169878	8464485	0.0735	0.3246
chr14	107349540	7790222	0.0726	0.3704
chr15	102531392	6926754	0.0676	0.3112
chr16	90354753	6269272	0.0694	0.3396
chr17	81195210	5381361	0.0663	0.3232
chr18	78077248	6867866	0.088	0.7794
chr19	59128983	3564929	0.0603	0.6097
chr20	63025520	4570232	0.0725	0.3346
chr21	48129895	3230956	0.0671	0.3412
chr22	51304566	2233079	0.0435	0.2528
chrMT	16571	41326	2.4939	3.3108
chrX	155270560	8758925	0.0564	0.3201
chrY	59373566	1960791	0.033	0.2618

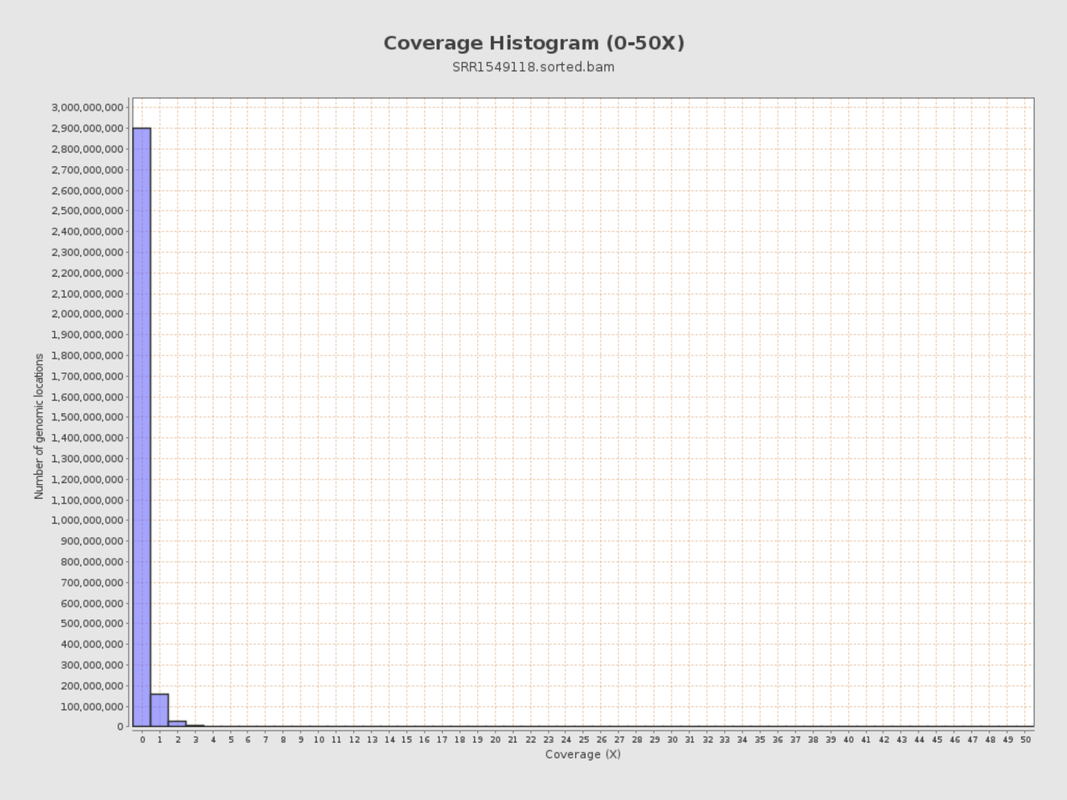
3. Results : Coverage across reference



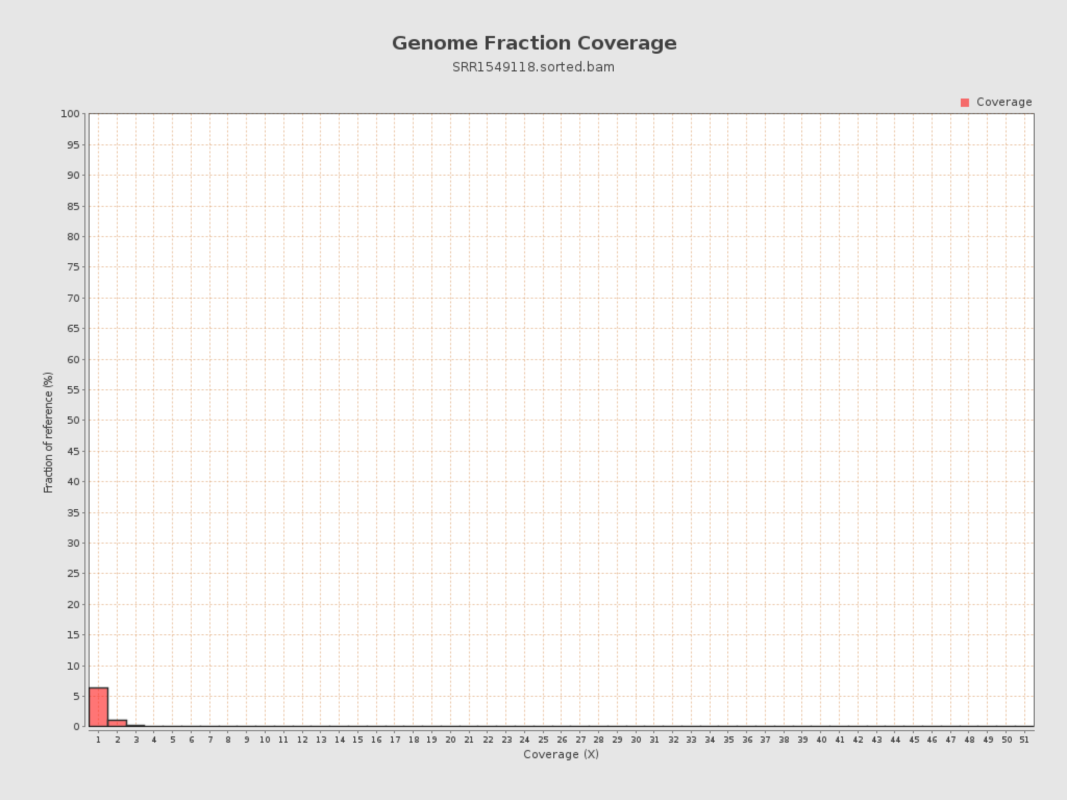
4. Results : Coverage Histogram



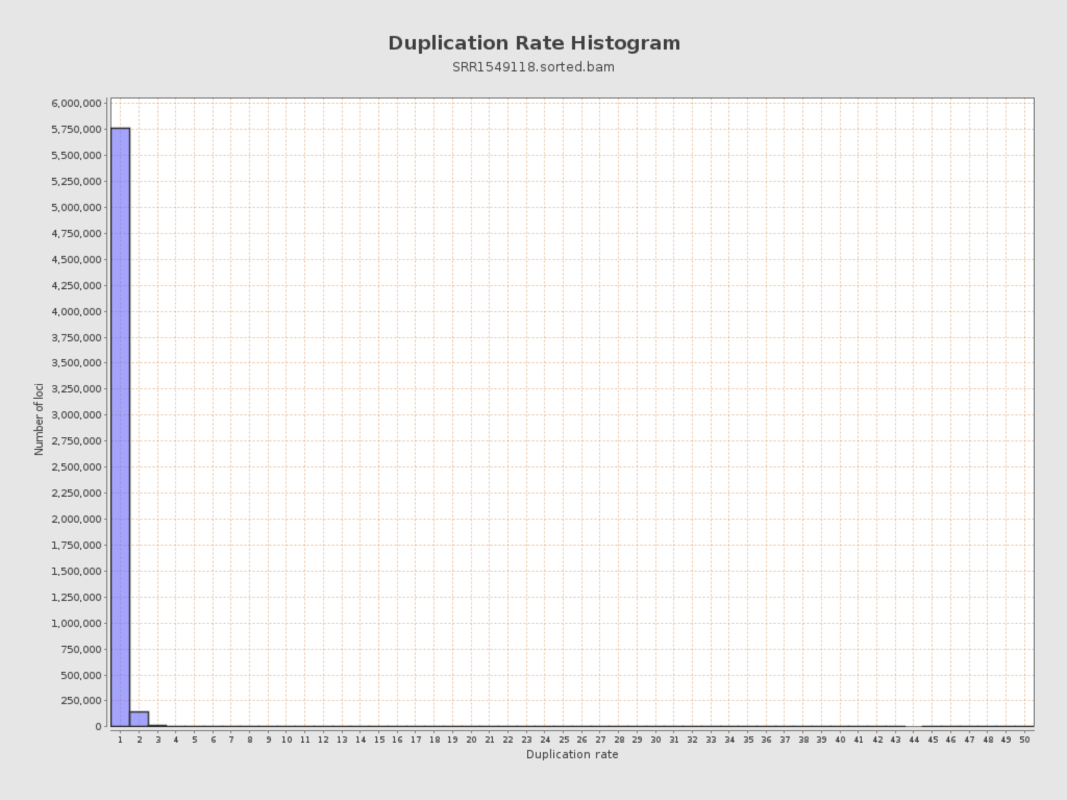
5. Results : Coverage Histogram (0-50X)



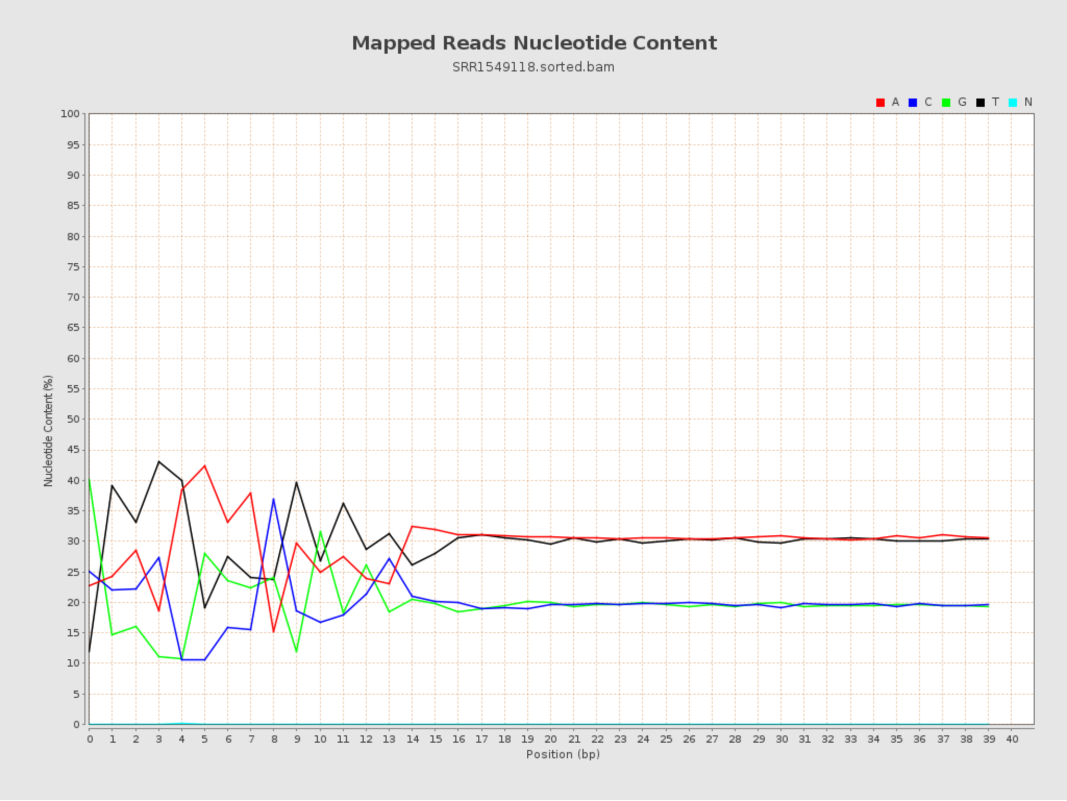
6. Results : Genome Fraction Coverage



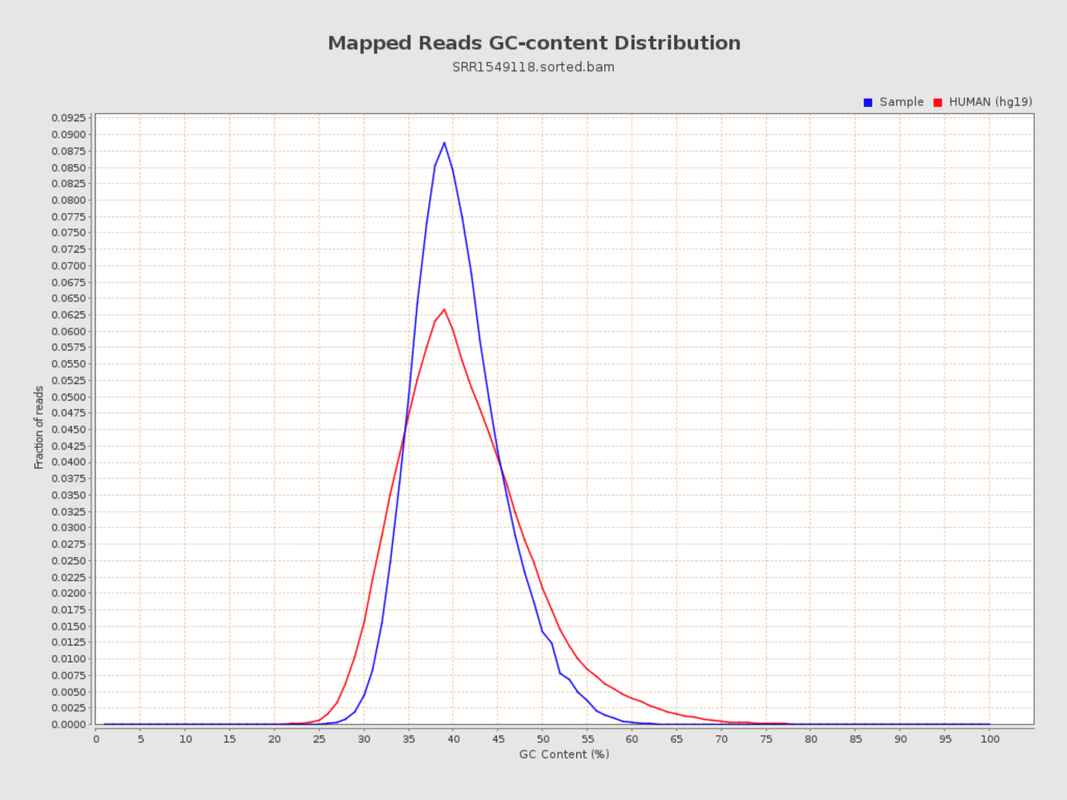
7. Results : Duplication Rate Histogram



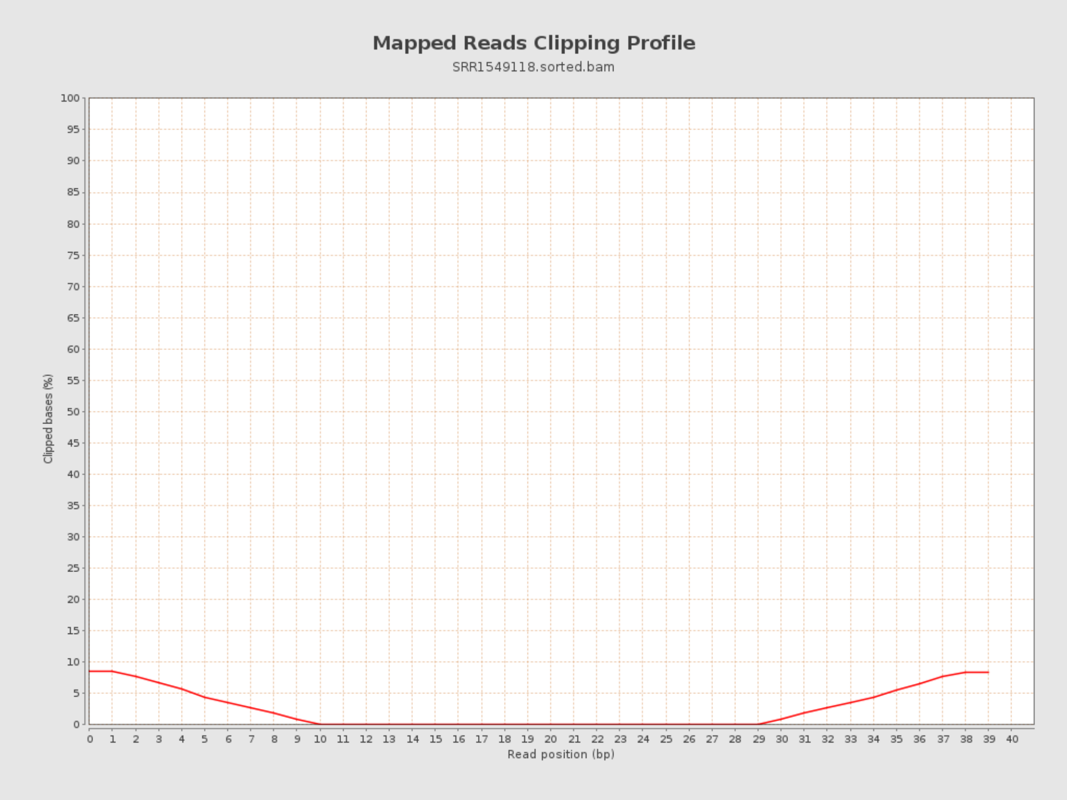
8. Results : Mapped Reads Nucleotide Content



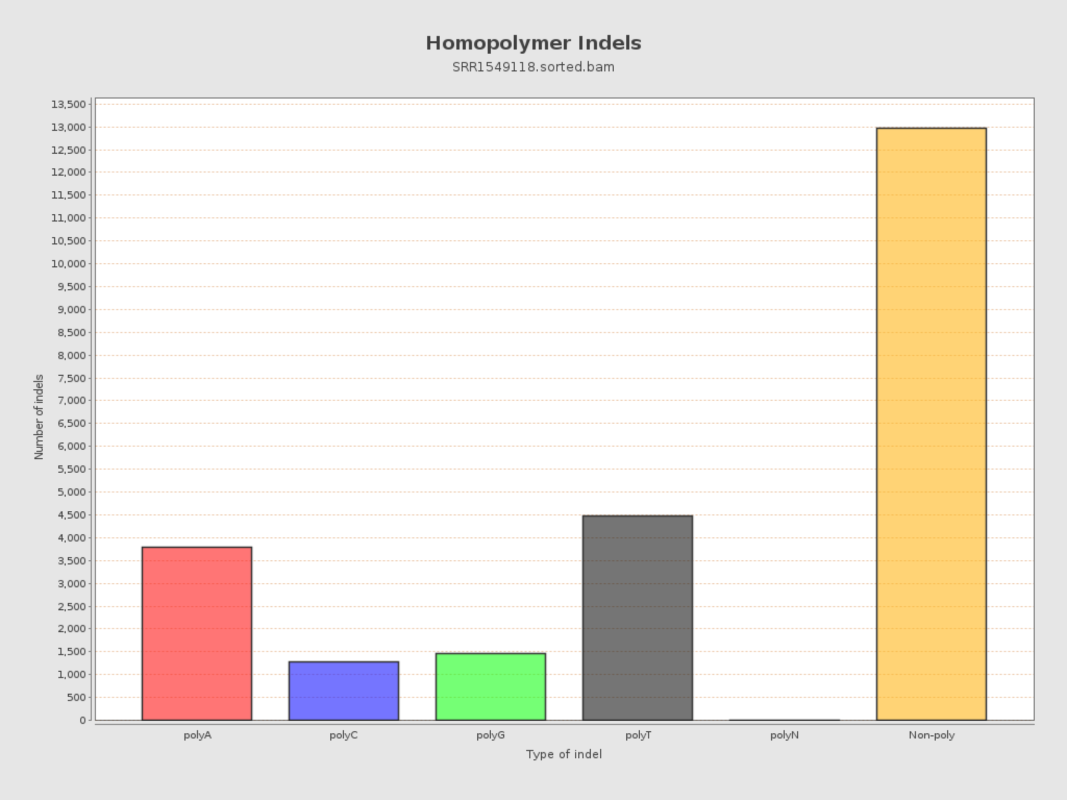
9. Results : Mapped Reads GC-content Distribution



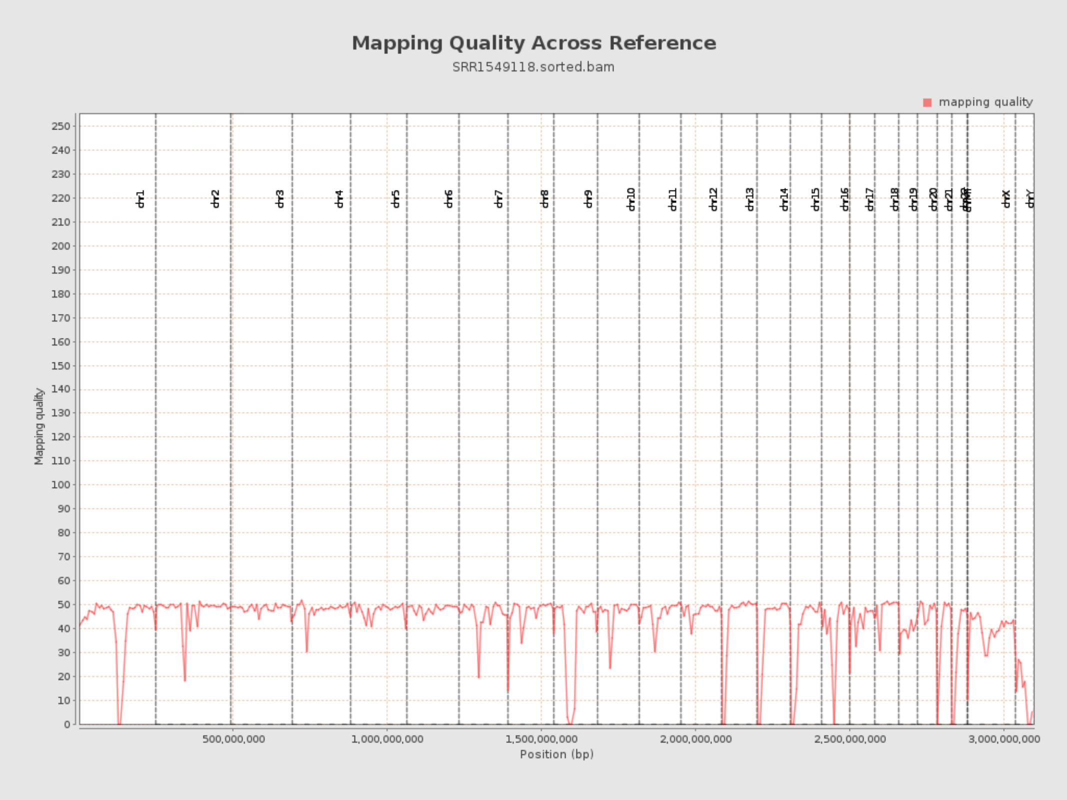
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram