Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:05:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525148.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_SRR10525148 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:05:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,091,651
Mapped reads	1,906,519 / 91.15%
Unmapped reads	185,132 / 8.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,266 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	66,295 / 3.17%
Duplication rate	2.58%
Clipped reads	1,911,044 / 91.37%

2.2. ACGT Content

Number/percentage of A's	29,490,805 / 26.52%
Number/percentage of C's	22,130,417 / 19.9%
Number/percentage of T's	34,178,268 / 30.73%
Number/percentage of G's	25,407,717 / 22.85%
Number/percentage of N's	3,407 / 0%
GC Percentage	42.75%

2.3. Coverage

Mean	0.0359

Standard Deviation	0.3116

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

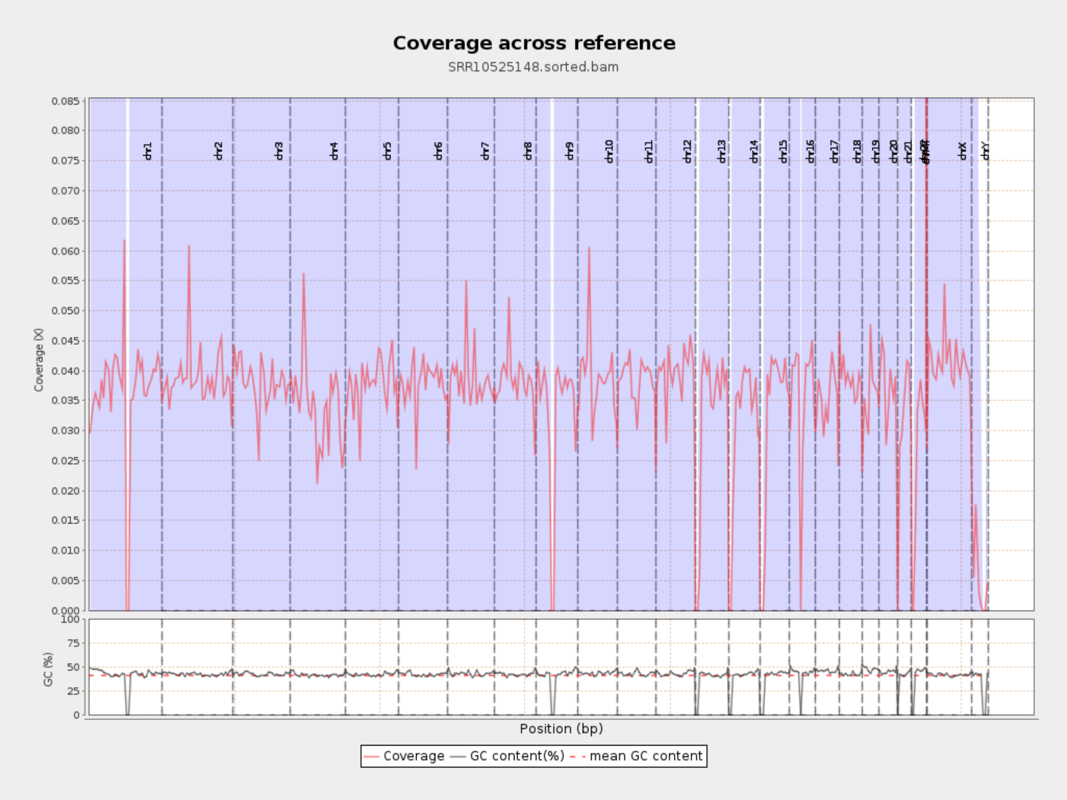
General error rate	0.48%
Mismatches	516,910
Insertions	7,606
Mapped reads with at least one insertion	0.4%
Deletions	17,498
Mapped reads with at least one deletion	0.91%
Homopolymer indels	42.4%

2.6. Chromosome stats

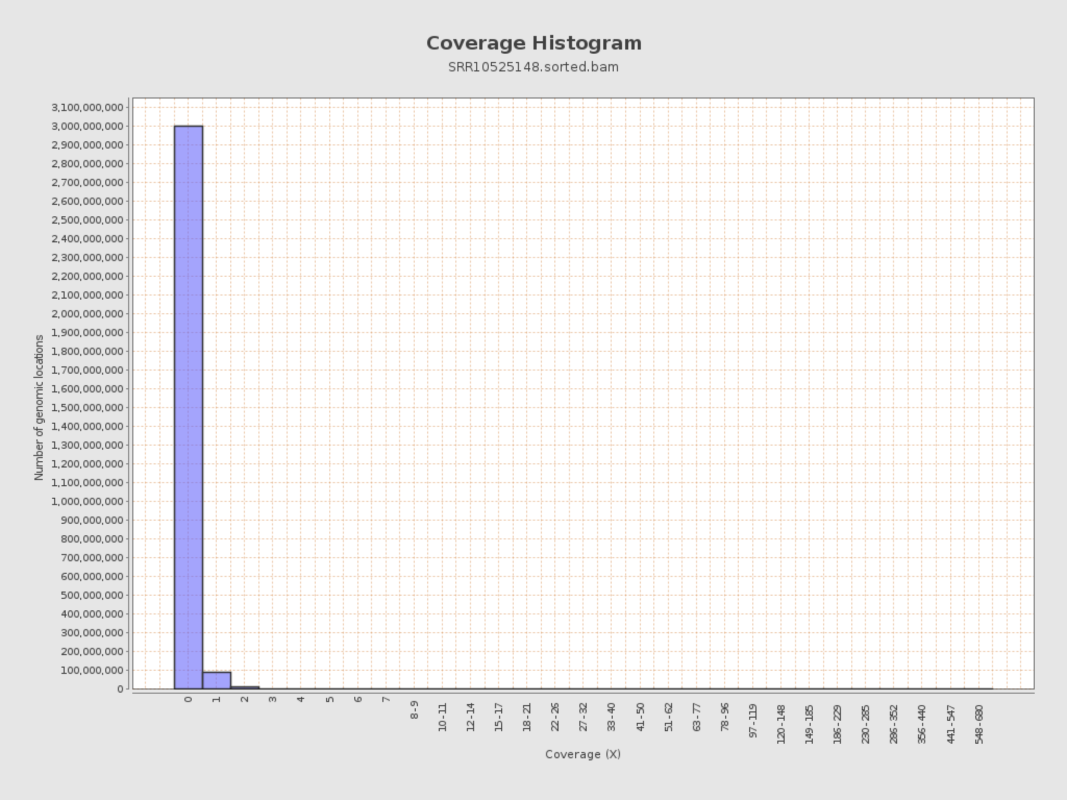
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9094207	0.0365	0.585
chr2	243199373	9458850	0.0389	0.3274
chr3	198022430	7512379	0.0379	0.2146
chr4	191154276	6491427	0.034	0.2288
chr5	180915260	6829911	0.0378	0.2156
chr6	171115067	6500445	0.038	0.2431
chr7	159138663	6138693	0.0386	0.3365

chr8	146364022	5590625	0.0382	0.3874
chr9	141213431	4635686	0.0328	0.2865
chr10	135534747	5285017	0.039	0.2976
chr11	135006516	5181145	0.0384	0.2849
chr12	133851895	5317362	0.0397	0.2271
chr13	115169878	3700026	0.0321	0.1971
chr14	107349540	3269835	0.0305	0.2145
chr15	102531392	3246154	0.0317	0.1963
chr16	90354753	3225745	0.0357	0.2232
chr17	81195210	2841292	0.035	0.2216
chr18	78077248	3018405	0.0387	0.5079
chr19	59128983	2122591	0.0359	0.417
chr20	63025520	2334797	0.037	0.2213
chr21	48129895	1487026	0.0309	0.2192
chr22	51304566	1236278	0.0241	0.1709
chrMT	16571	5181	0.3127	0.6304
chrX	155270560	6402792	0.0412	0.2513
chrY	59373566	313754	0.0053	0.1344

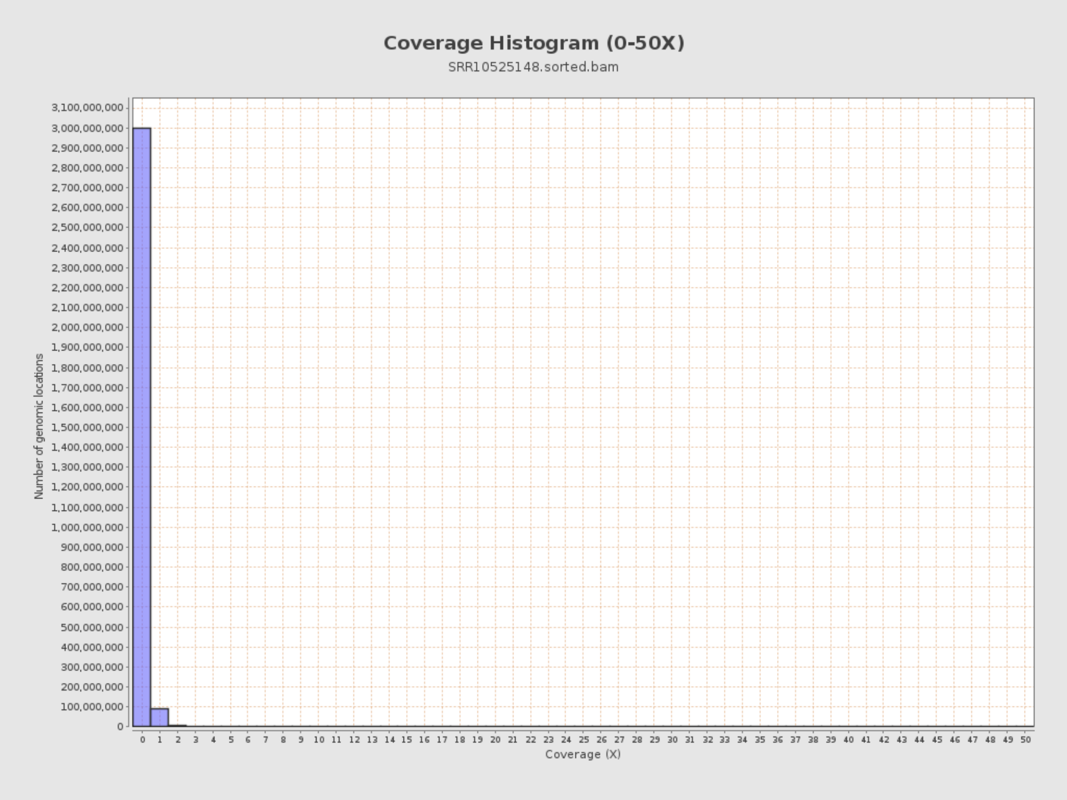
3. Results : Coverage across reference



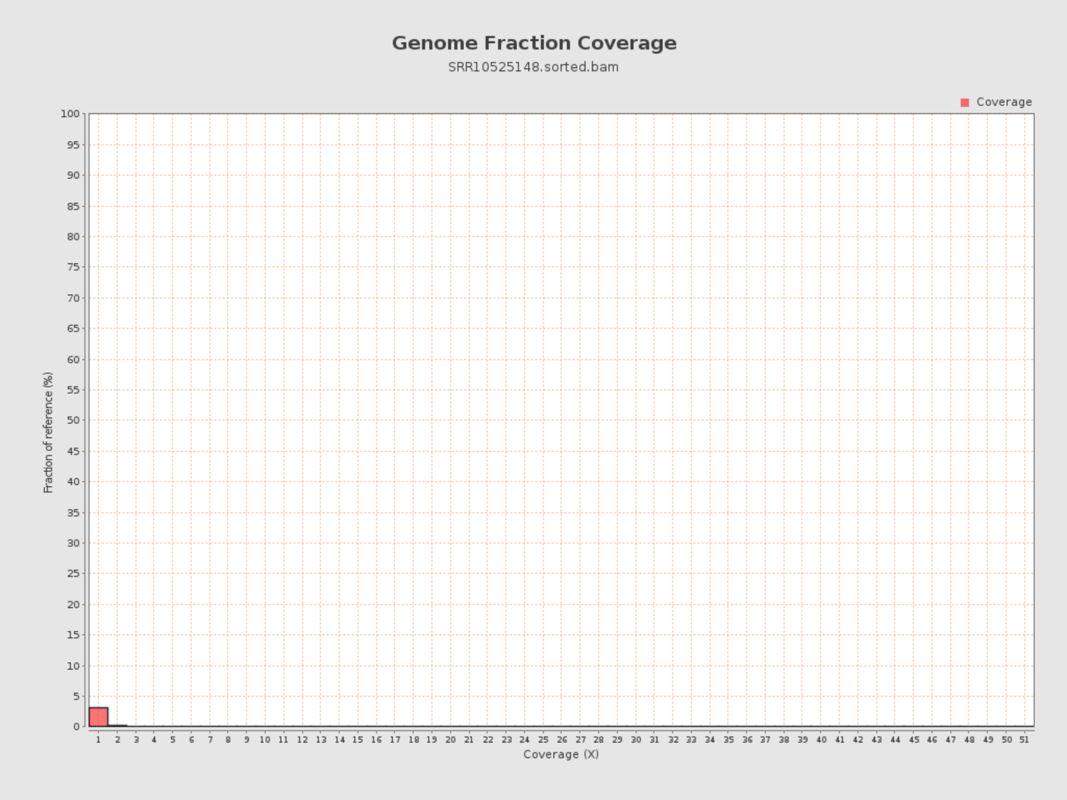
4. Results : Coverage Histogram



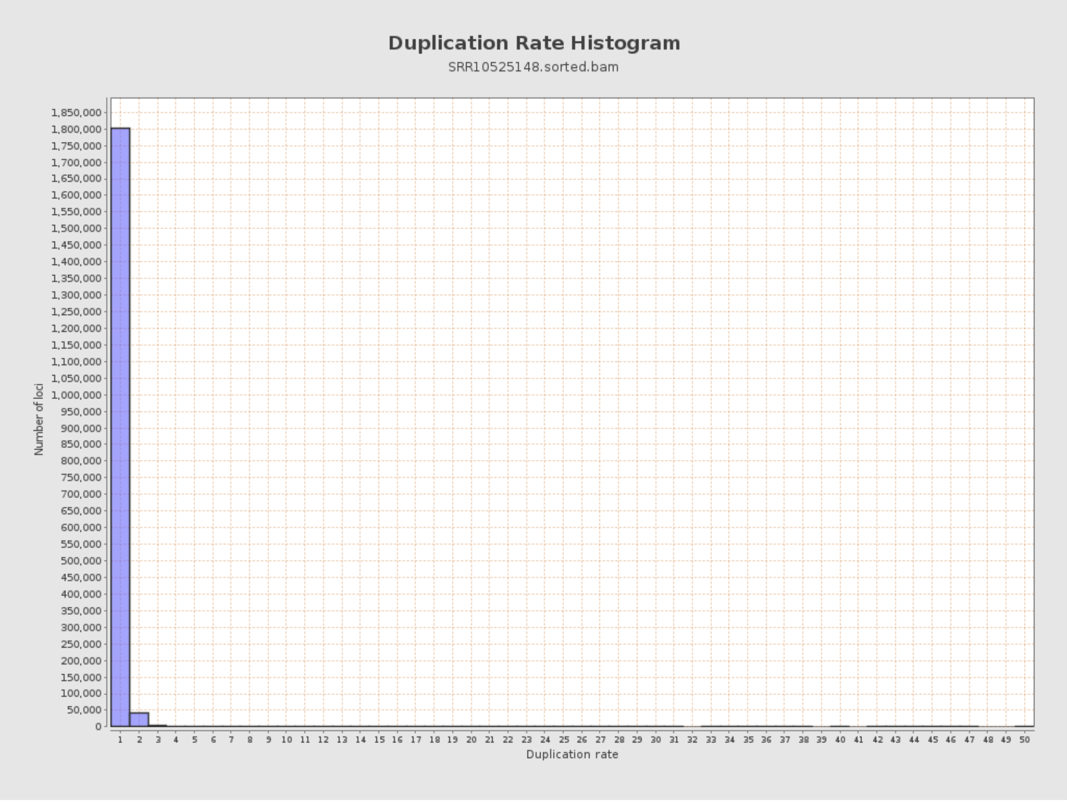
5. Results : Coverage Histogram (0-50X)



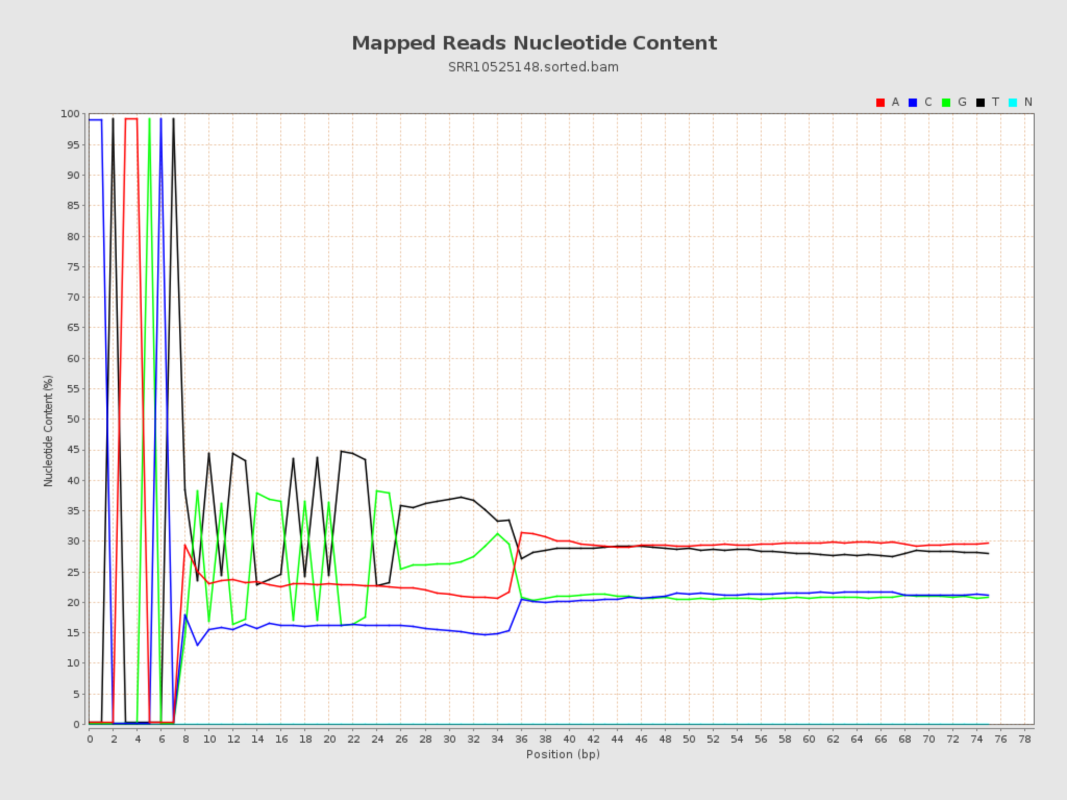
6. Results : Genome Fraction Coverage



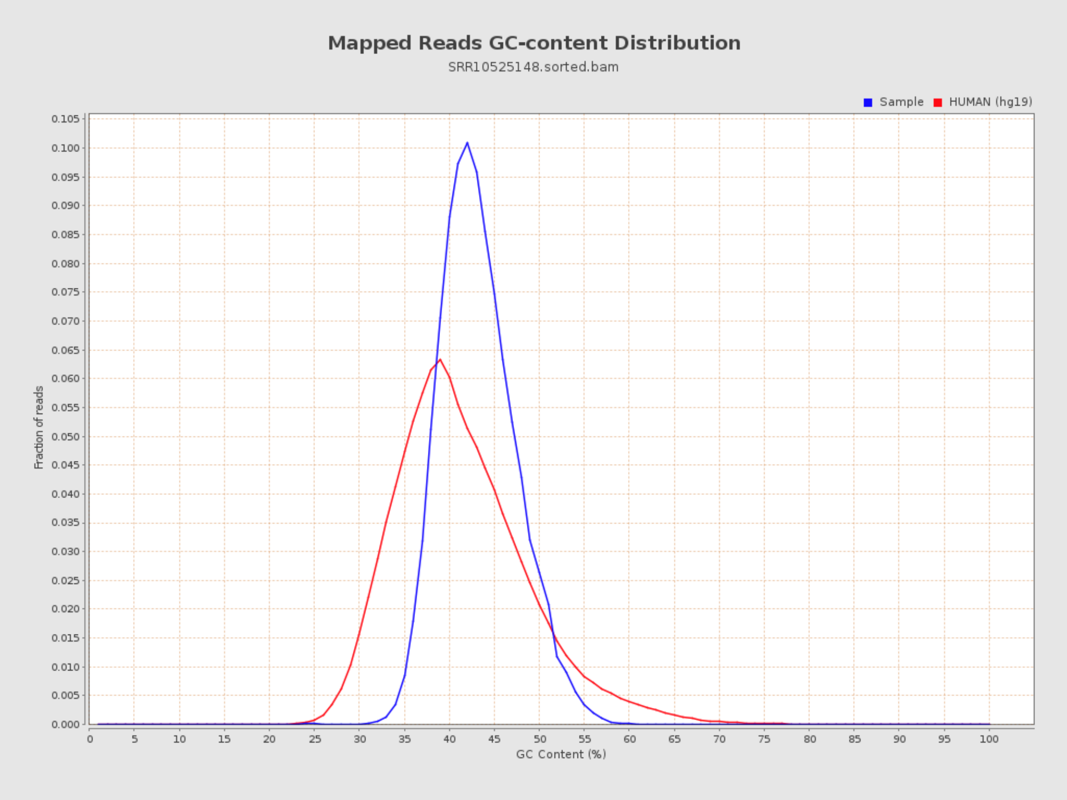
7. Results : Duplication Rate Histogram



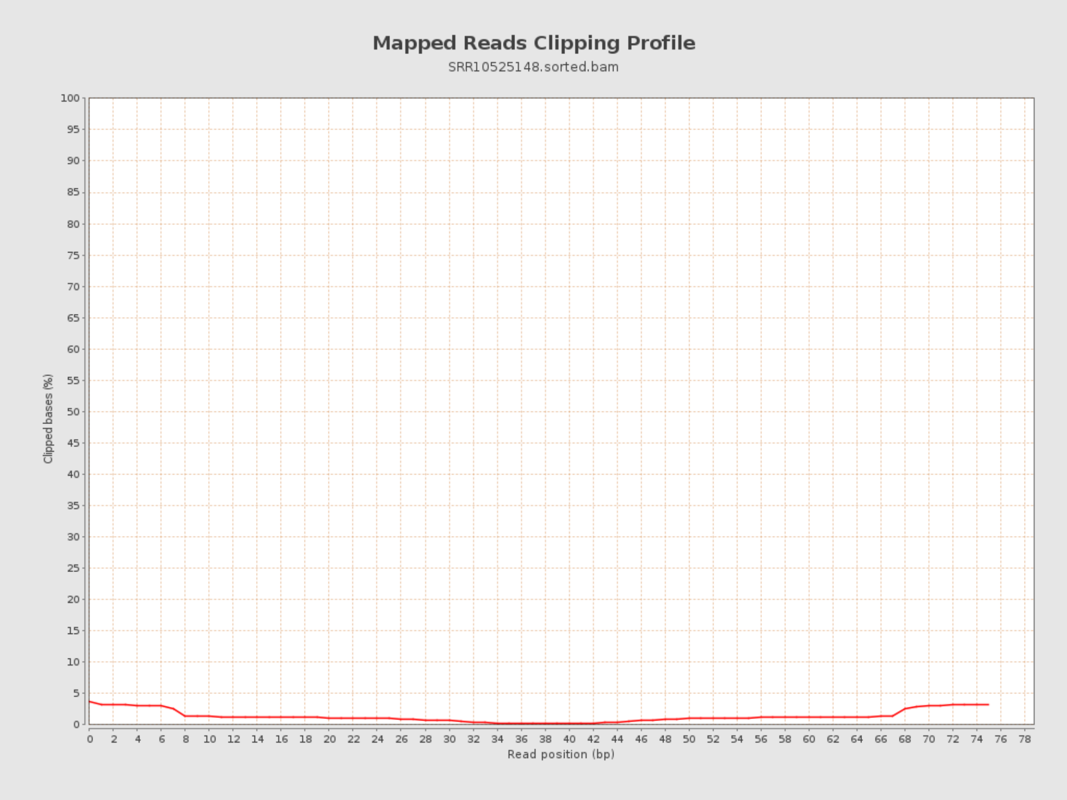
8. Results : Mapped Reads Nucleotide Content



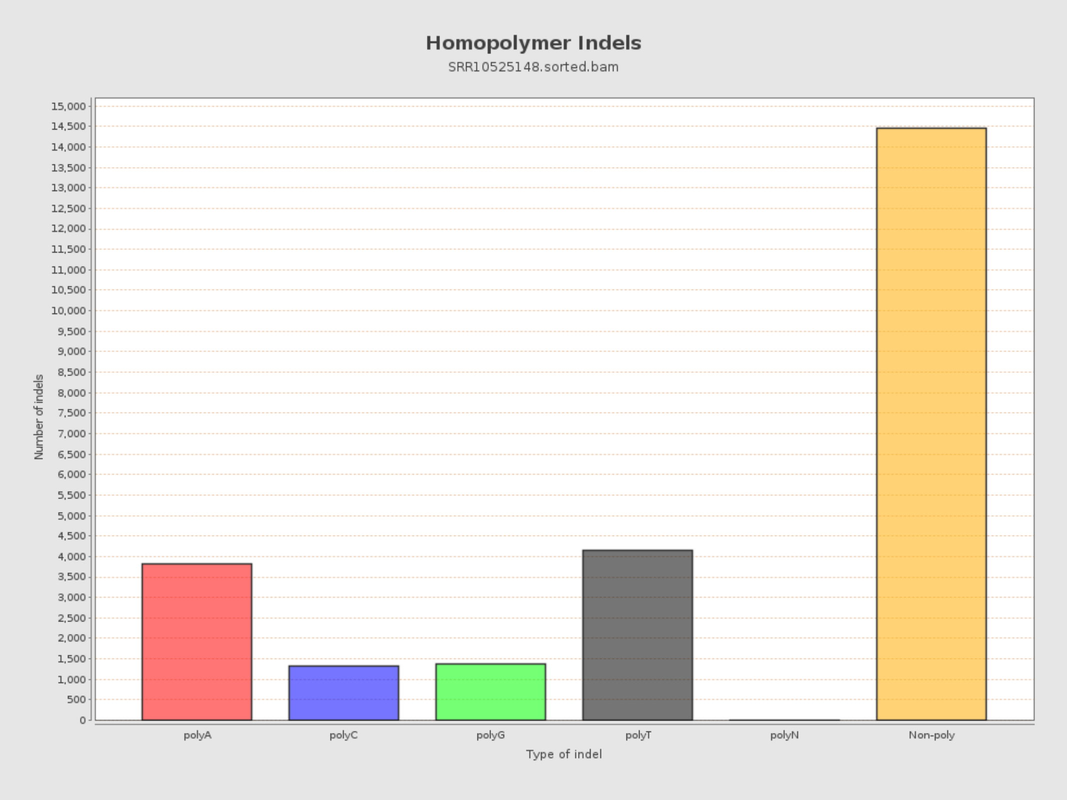
9. Results : Mapped Reads GC-content Distribution



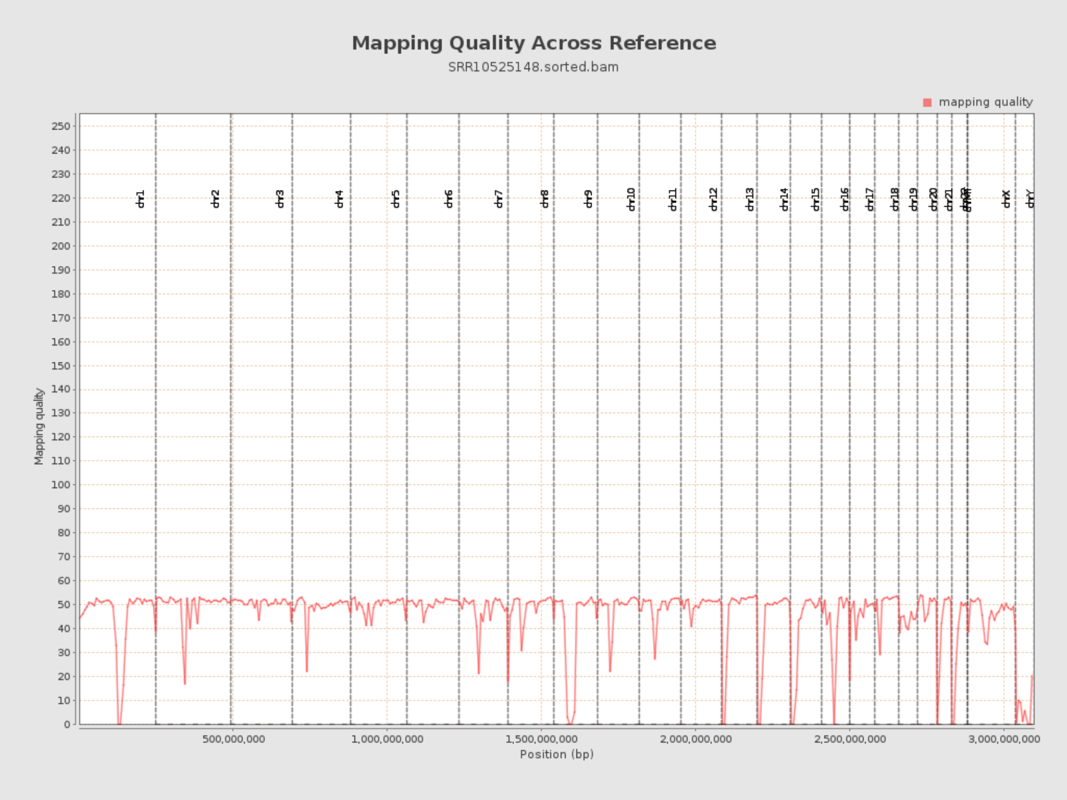
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram