Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:27:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525134.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_SRR10525134 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525134.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:27:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525134.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,951,374
Mapped reads	1,782,937 / 91.37%
Unmapped reads	168,437 / 8.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	50,550 / 2.59%
Read min/max/mean length	30 / 101 / 101.97
Duplicated reads (estimated)	62,500 / 3.2%
Duplication rate	2.04%
Clipped reads	1,832,948 / 93.93%

2.2. ACGT Content

Number/percentage of A's	35,866,258 / 26.06%
Number/percentage of C's	27,015,347 / 19.63%
Number/percentage of T's	42,398,808 / 30.8%
Number/percentage of G's	32,368,523 / 23.51%
Number/percentage of N's	4,887 / 0%
GC Percentage	43.14%

2.3. Coverage

Mean	0.0445

Standard Deviation	0.4775

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

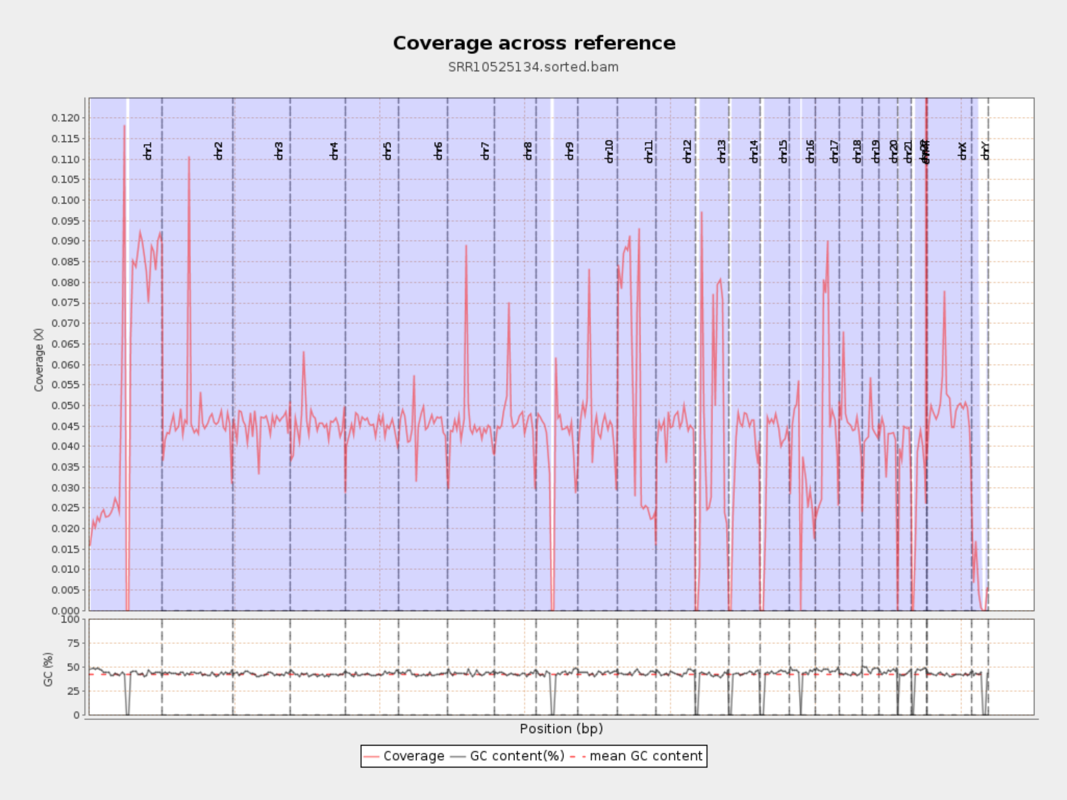
General error rate	0.76%
Mismatches	1,024,398
Insertions	11,542
Mapped reads with at least one insertion	0.64%
Deletions	31,631
Mapped reads with at least one deletion	1.75%
Homopolymer indels	43.12%

2.6. Chromosome stats

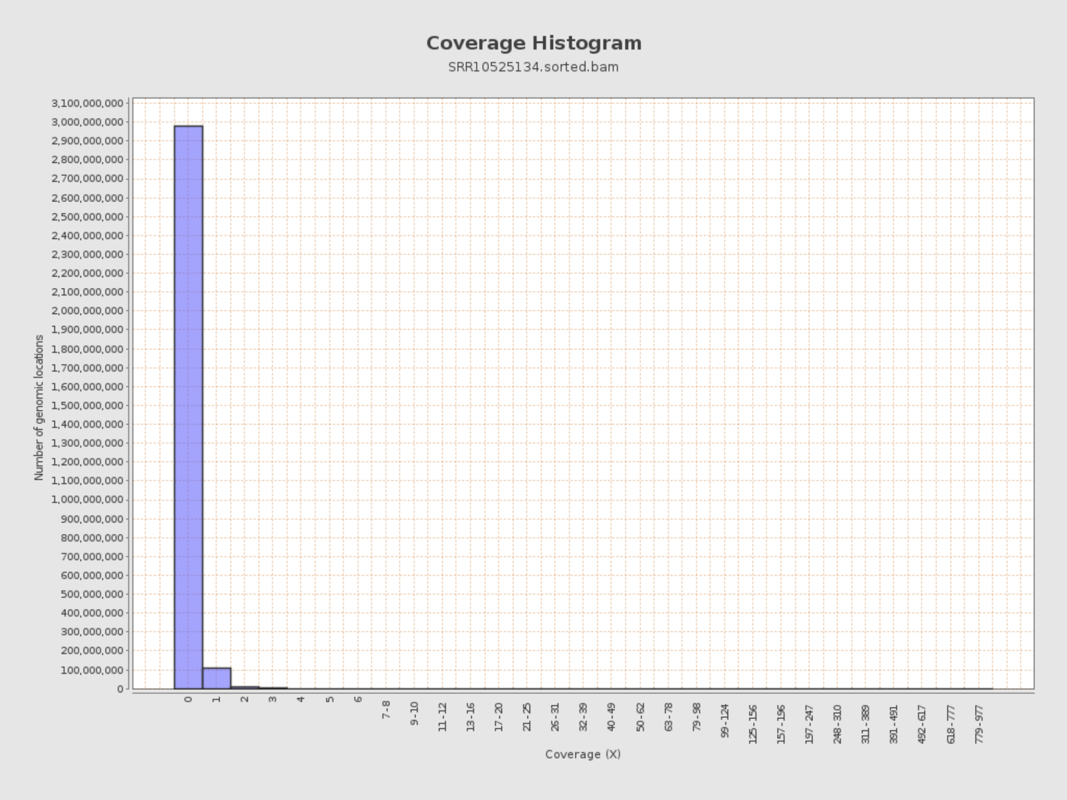
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13303056	0.0534	0.8481
chr2	243199373	11474540	0.0472	0.6845
chr3	198022430	9003365	0.0455	0.2415
chr4	191154276	8702567	0.0455	0.255
chr5	180915260	8131673	0.0449	0.2413
chr6	171115067	7736854	0.0452	0.2819
chr7	159138663	7334775	0.0461	0.6788

chr8	146364022	6848688	0.0468	0.5881
chr9	141213431	5568133	0.0394	0.4252
chr10	135534747	6309685	0.0466	0.487
chr11	135006516	7460738	0.0553	0.5465
chr12	133851895	5998674	0.0448	0.2398
chr13	115169878	4996815	0.0434	0.2337
chr14	107349540	4014408	0.0374	0.2576
chr15	102531392	3700118	0.0361	0.2108
chr16	90354753	2992899	0.0331	0.2408
chr17	81195210	3978713	0.049	0.3023
chr18	78077248	3708024	0.0475	0.8205
chr19	59128983	2580946	0.0436	0.5945
chr20	63025520	2600457	0.0413	0.2434
chr21	48129895	1774769	0.0369	0.2428
chr22	51304566	1388735	0.0271	0.1812
chrMT	16571	12875	0.777	1.4323
chrX	155270560	7741267	0.0499	0.3694
chrY	59373566	345128	0.0058	0.1292

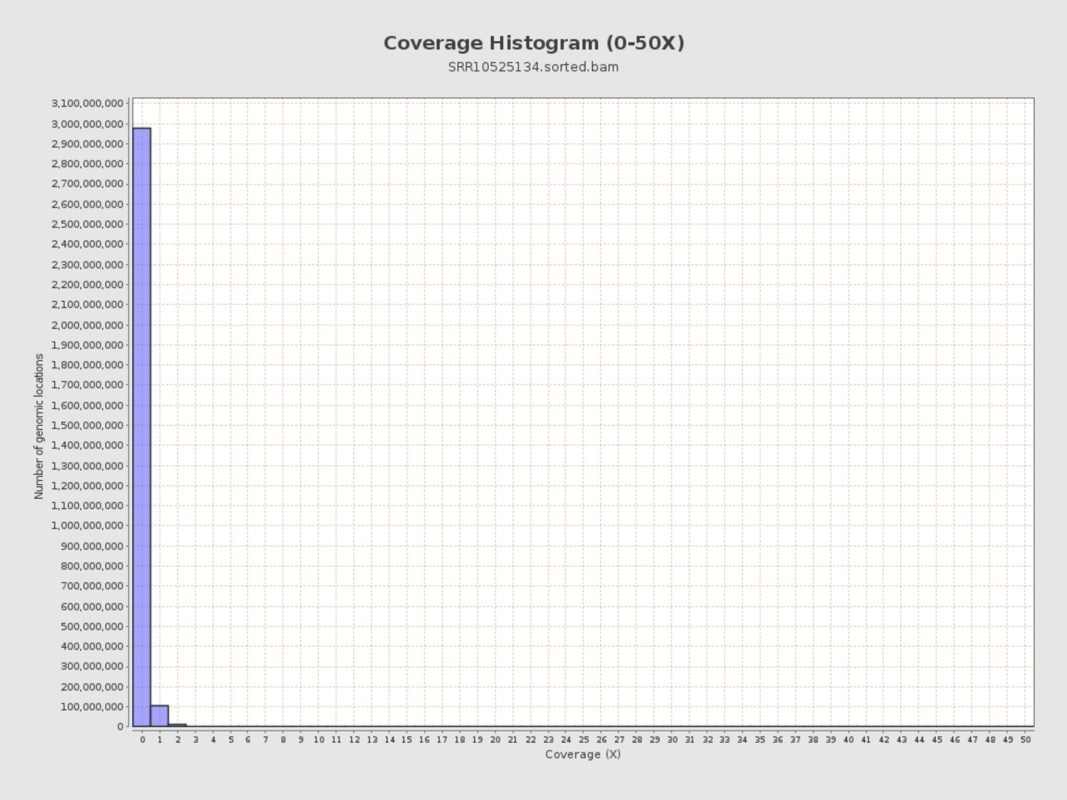
3. Results : Coverage across reference



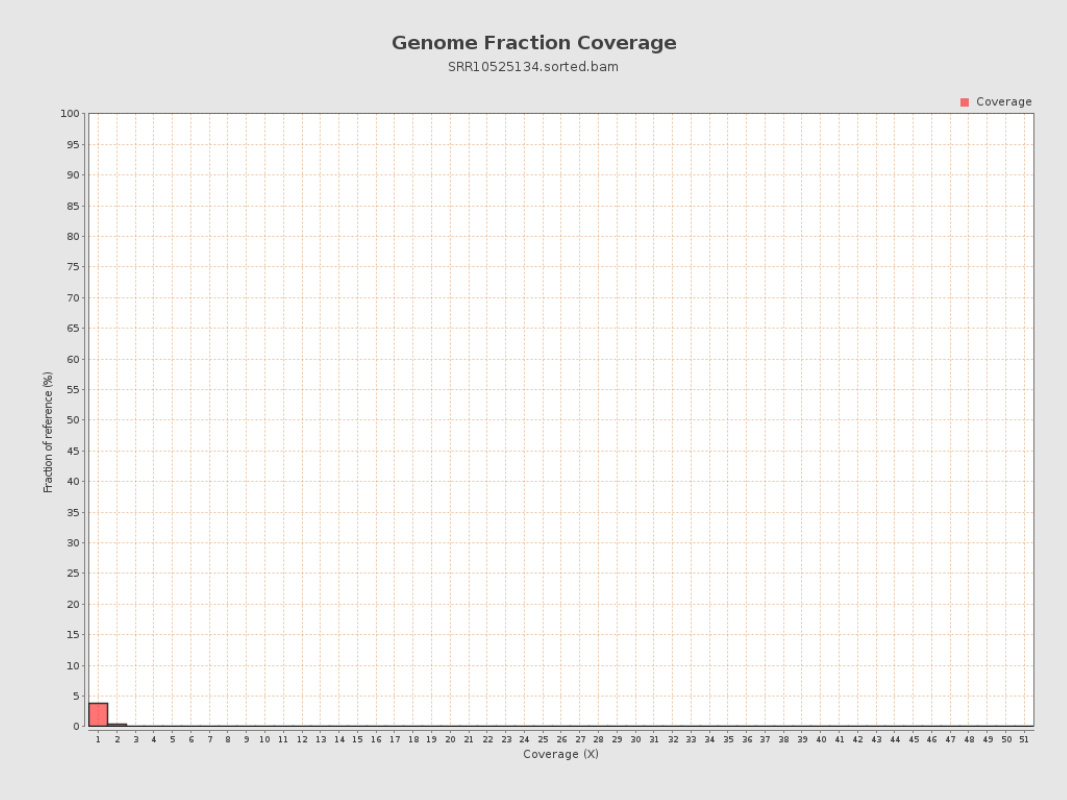
4. Results : Coverage Histogram



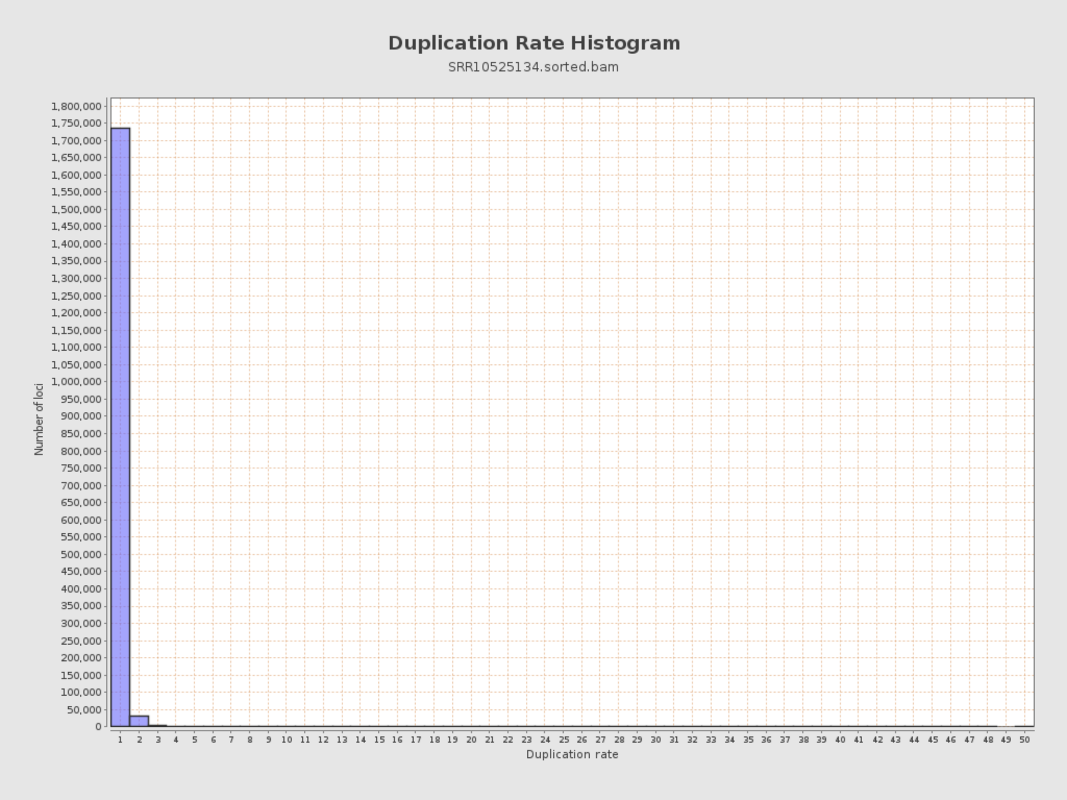
5. Results : Coverage Histogram (0-50X)



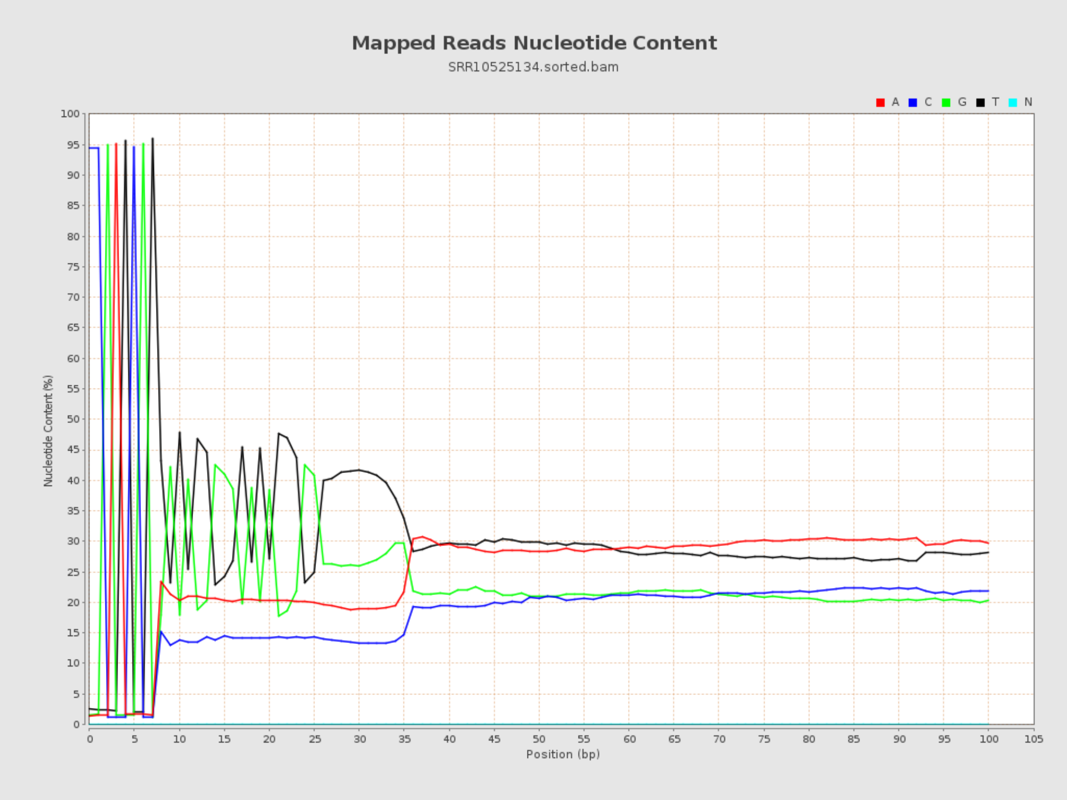
6. Results : Genome Fraction Coverage



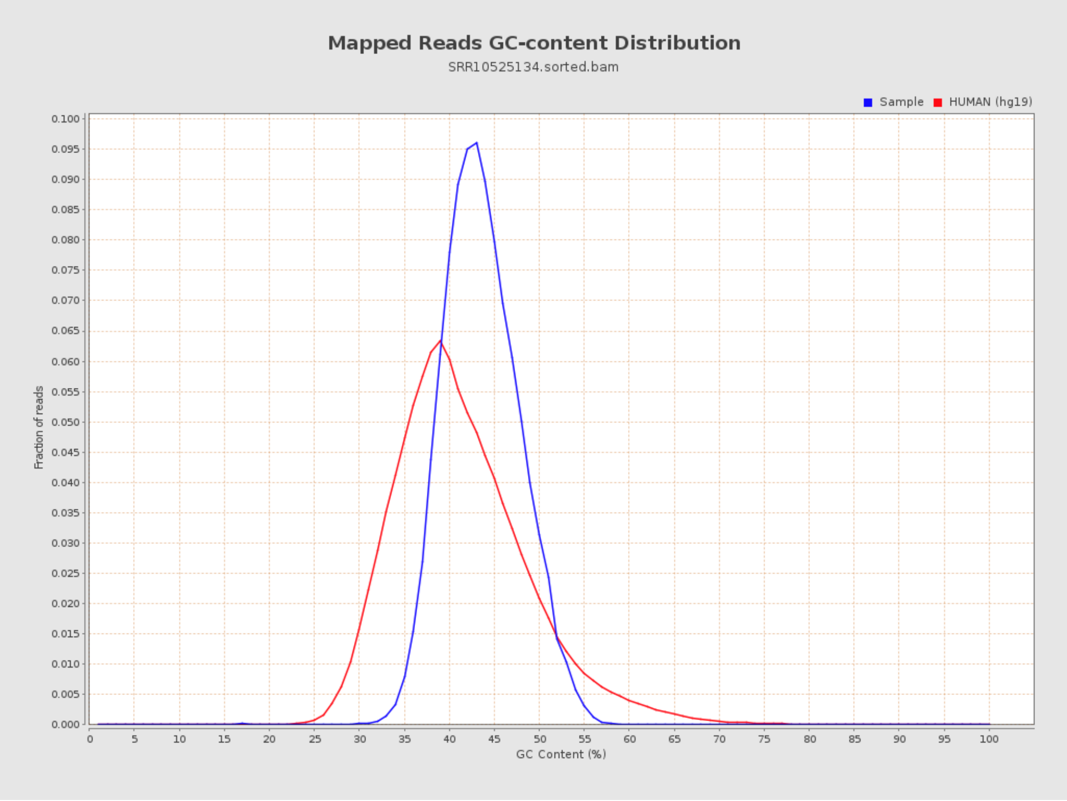
7. Results : Duplication Rate Histogram



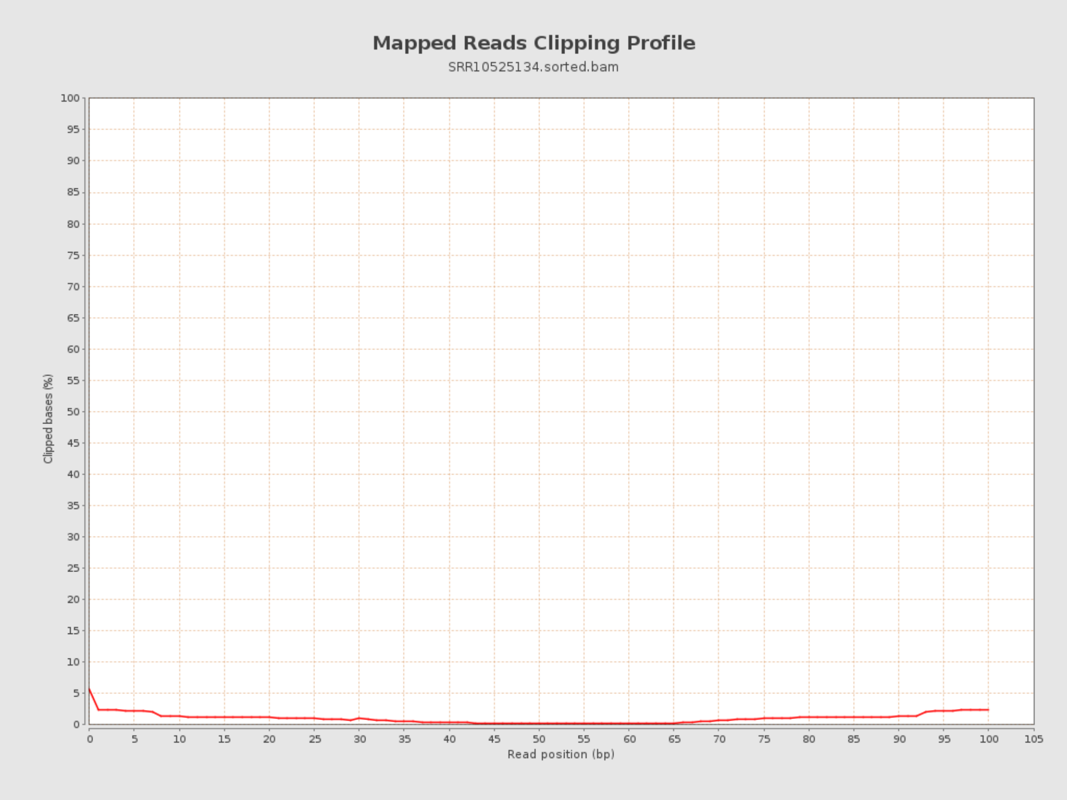
8. Results : Mapped Reads Nucleotide Content



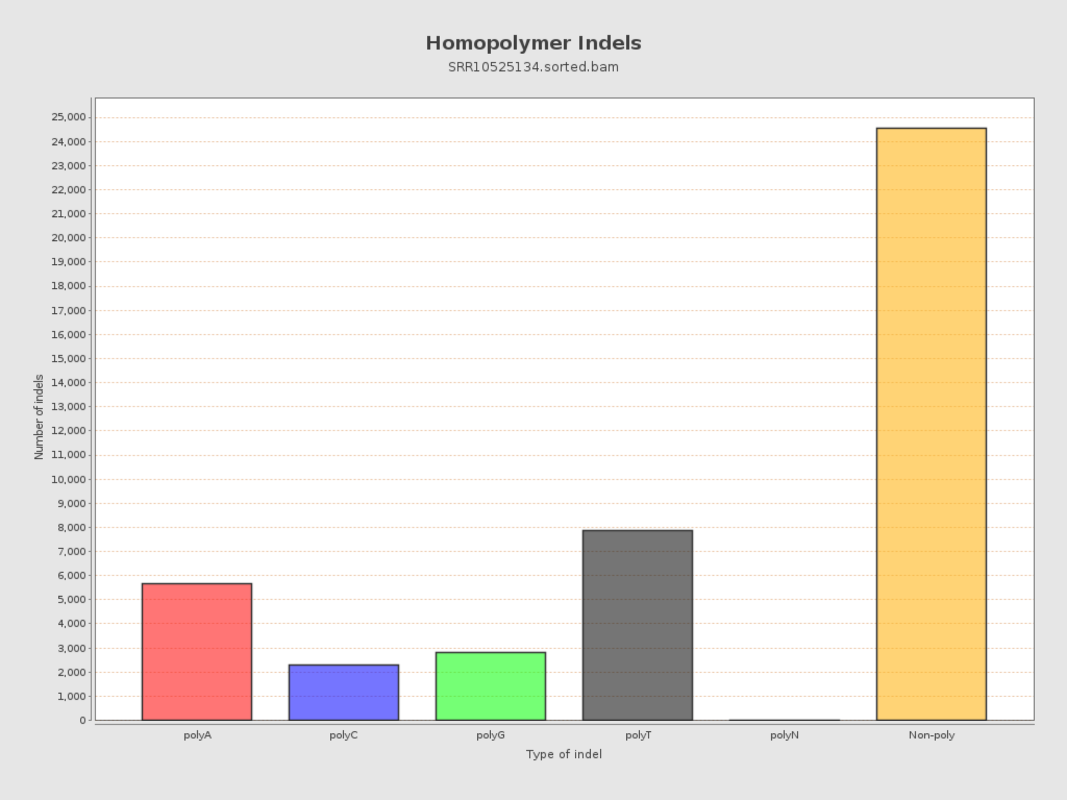
9. Results : Mapped Reads GC-content Distribution



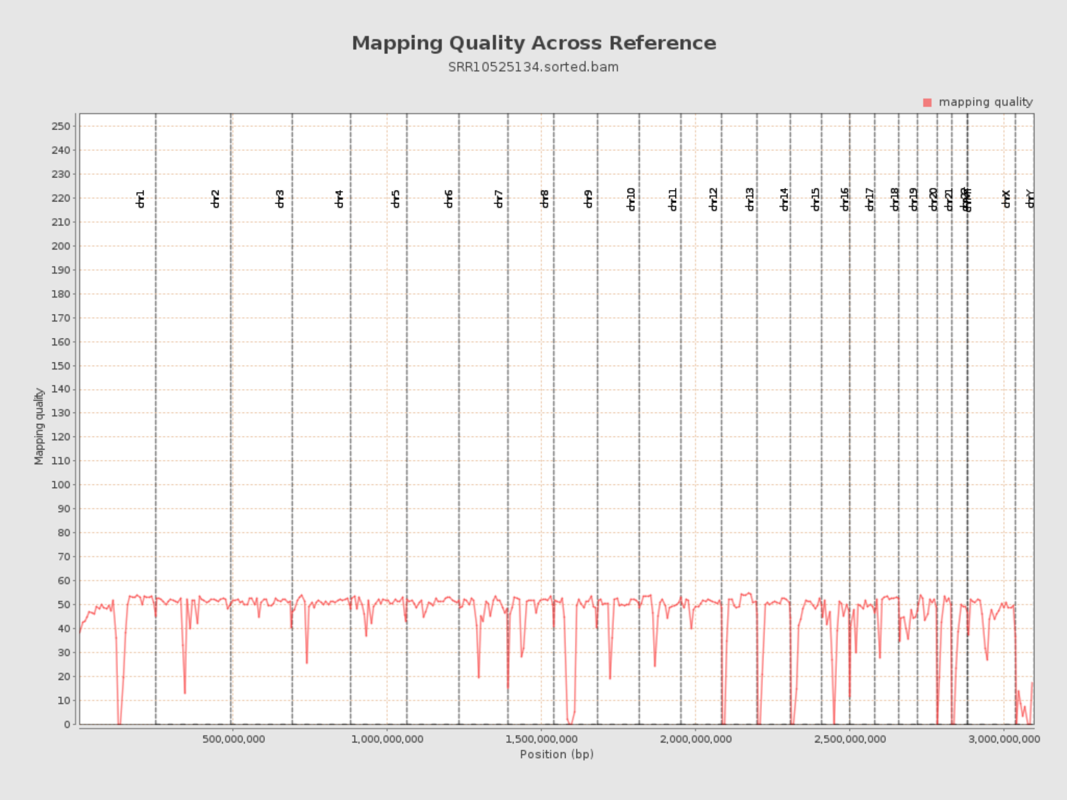
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram