Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:33:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525177.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_SRR10525177 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525177.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:33:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525177.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,328,290
Mapped reads	3,859,448 / 89.17%
Unmapped reads	468,842 / 10.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,260 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	257,686 / 5.95%
Duplication rate	4.97%
Clipped reads	3,864,973 / 89.3%

2.2. ACGT Content

Number/percentage of A's	55,331,784 / 25.04%
Number/percentage of C's	39,824,096 / 18.02%
Number/percentage of T's	72,446,455 / 32.79%
Number/percentage of G's	53,365,583 / 24.15%
Number/percentage of N's	5,184 / 0%
GC Percentage	42.17%

2.3. Coverage

Mean	0.0714

Standard Deviation	0.6113

2.4. Mapping Quality

Mean Mapping Quality	44.33

2.5. Mismatches and indels

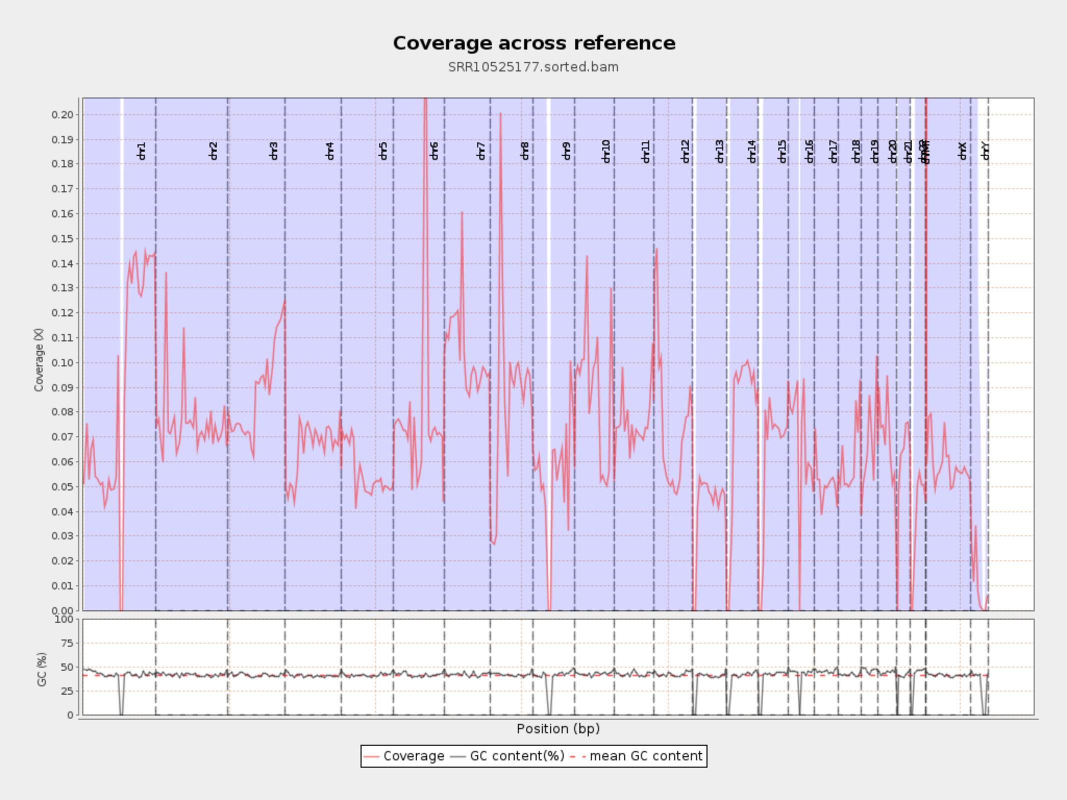
General error rate	0.53%
Mismatches	1,131,656
Insertions	15,400
Mapped reads with at least one insertion	0.4%
Deletions	41,763
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.81%

2.6. Chromosome stats

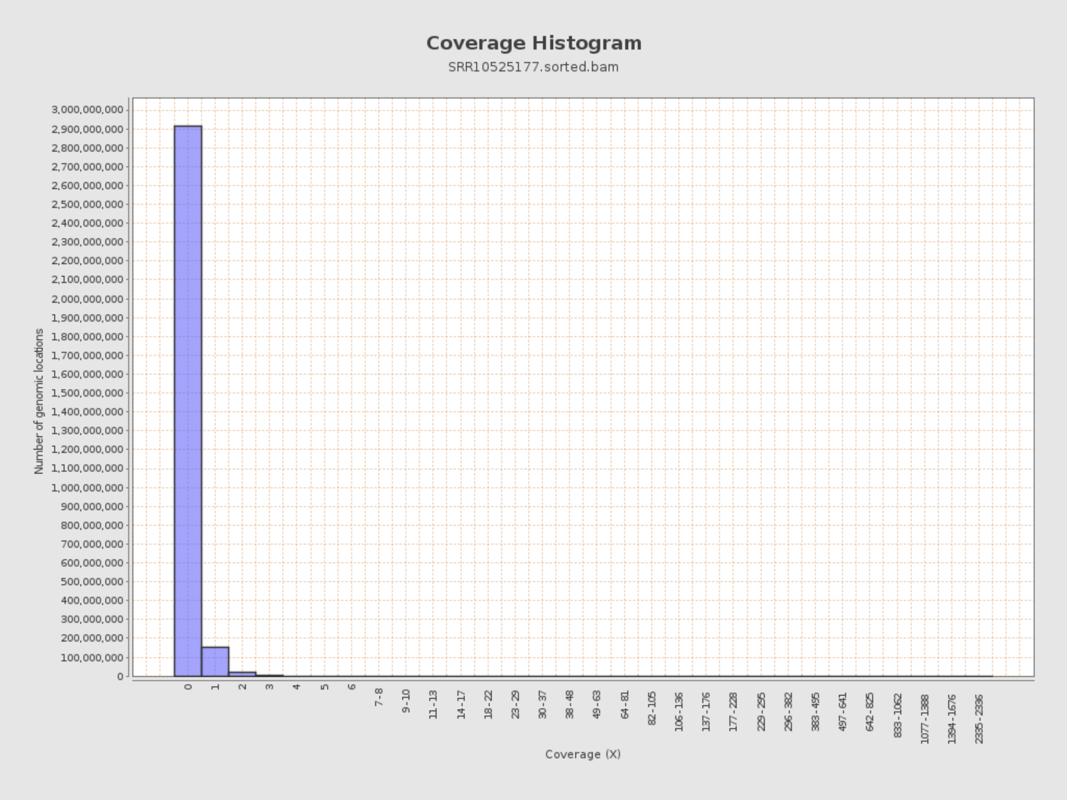
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21789632	0.0874	1.0507
chr2	243199373	18503243	0.0761	0.9984
chr3	198022430	17382640	0.0878	0.3652
chr4	191154276	12588213	0.0659	0.3388
chr5	180915260	9997763	0.0553	0.2871
chr6	171115067	13897976	0.0812	0.4201
chr7	159138663	16664974	0.1047	1.1587

chr8	146364022	12814200	0.0876	0.5338
chr9	141213431	7494297	0.0531	0.4296
chr10	135534747	11964781	0.0883	0.5893
chr11	135006516	10234810	0.0758	0.463
chr12	133851895	10113045	0.0756	0.3397
chr13	115169878	4863990	0.0422	0.2579
chr14	107349540	8437718	0.0786	0.3544
chr15	102531392	6132515	0.0598	0.3131
chr16	90354753	6082104	0.0673	0.3565
chr17	81195210	4210850	0.0519	0.298
chr18	78077248	4764156	0.061	0.7724
chr19	59128983	4004616	0.0677	0.7217
chr20	63025520	4335338	0.0688	0.327
chr21	48129895	2857458	0.0594	0.3225
chr22	51304566	1846085	0.036	0.224
chrMT	16571	282305	17.0361	10.1285
chrX	155270560	9165552	0.059	0.3567
chrY	59373566	611314	0.0103	0.2653

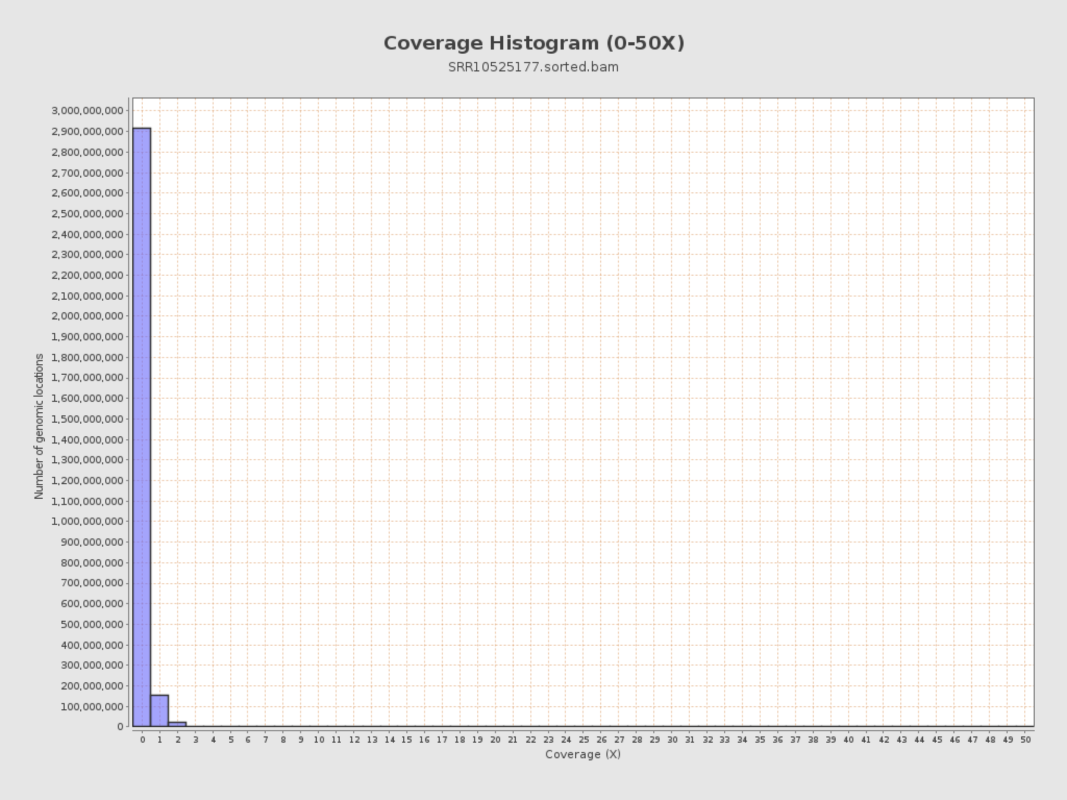
3. Results : Coverage across reference



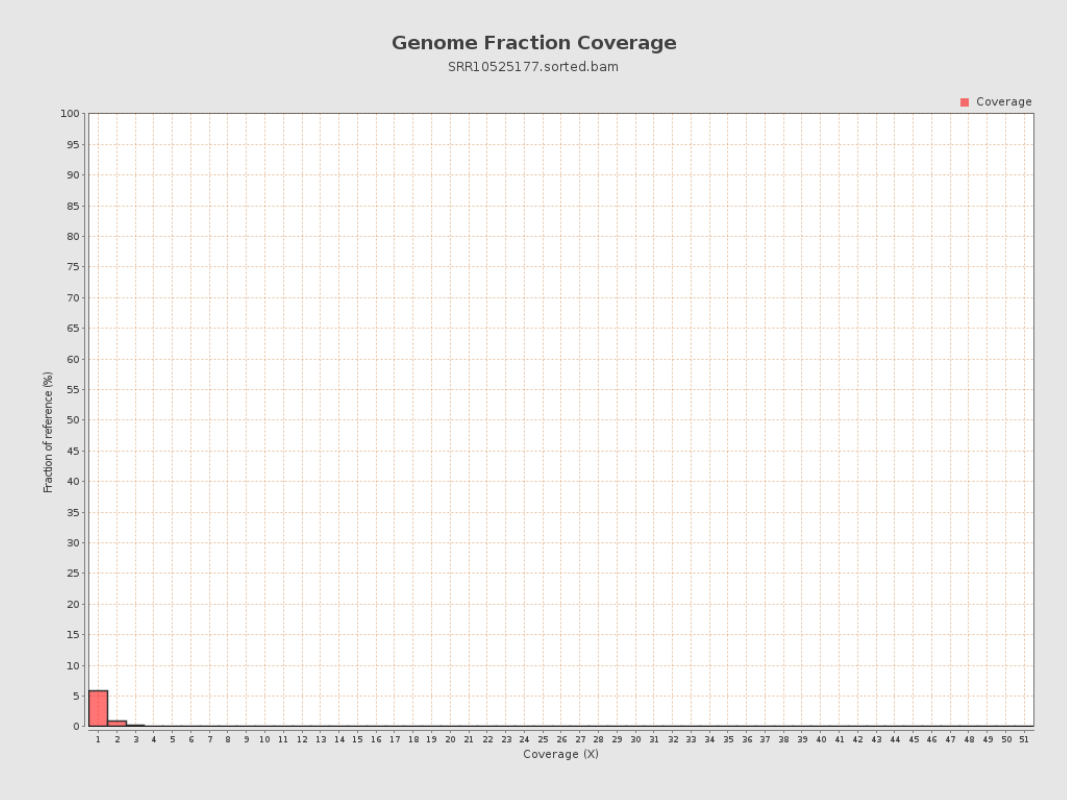
4. Results : Coverage Histogram



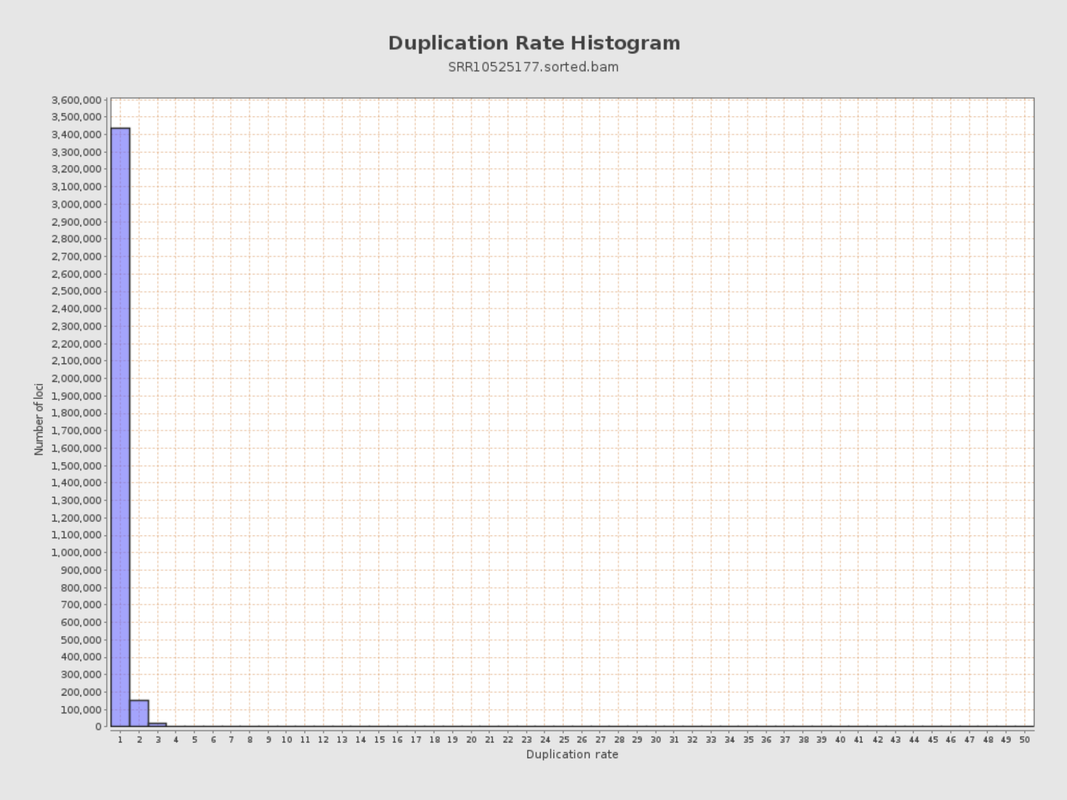
5. Results : Coverage Histogram (0-50X)



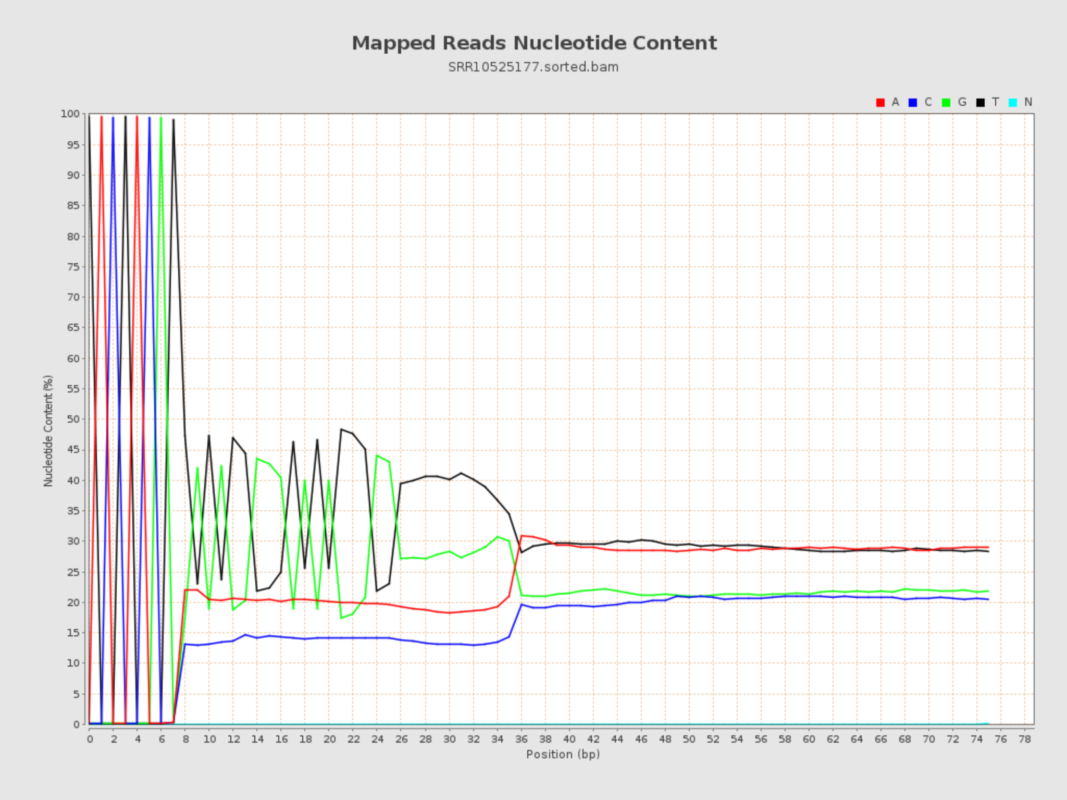
6. Results : Genome Fraction Coverage



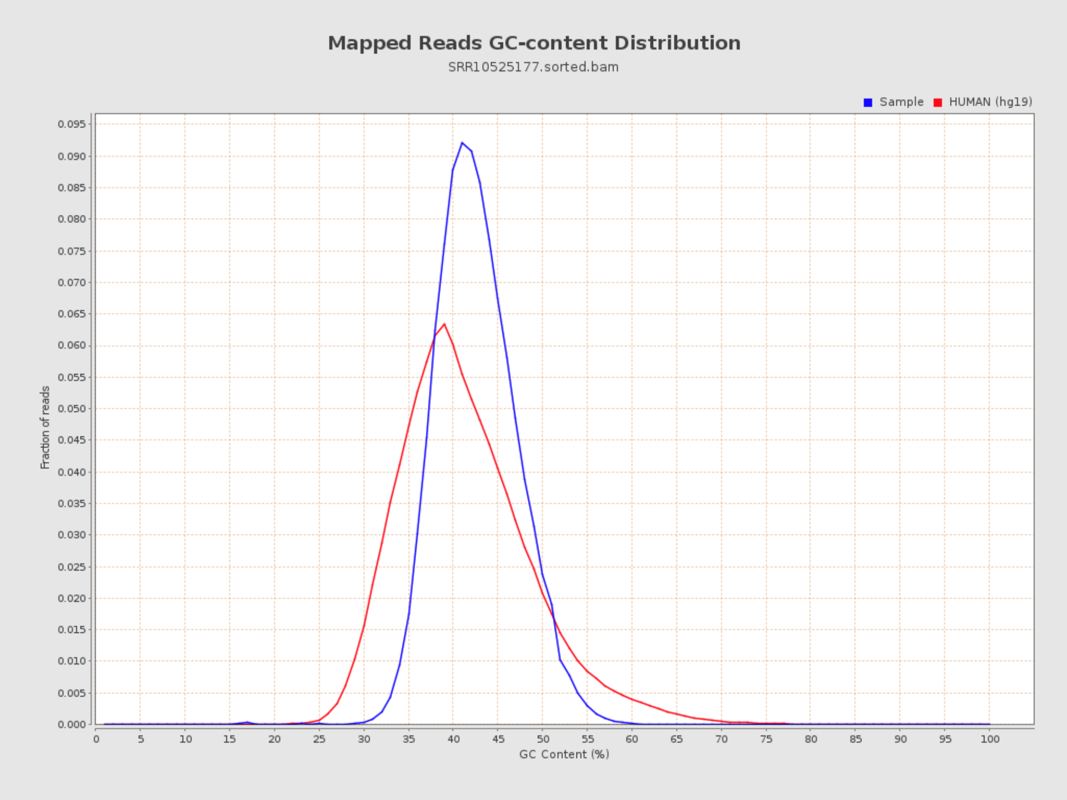
7. Results : Duplication Rate Histogram



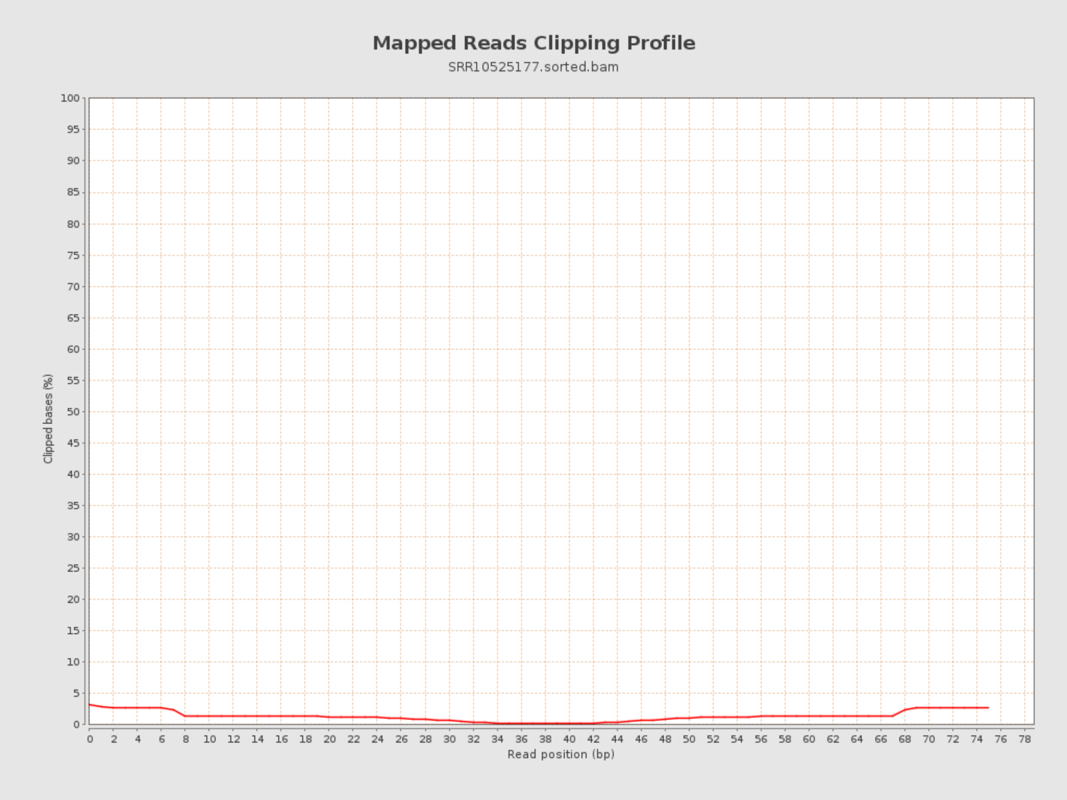
8. Results : Mapped Reads Nucleotide Content



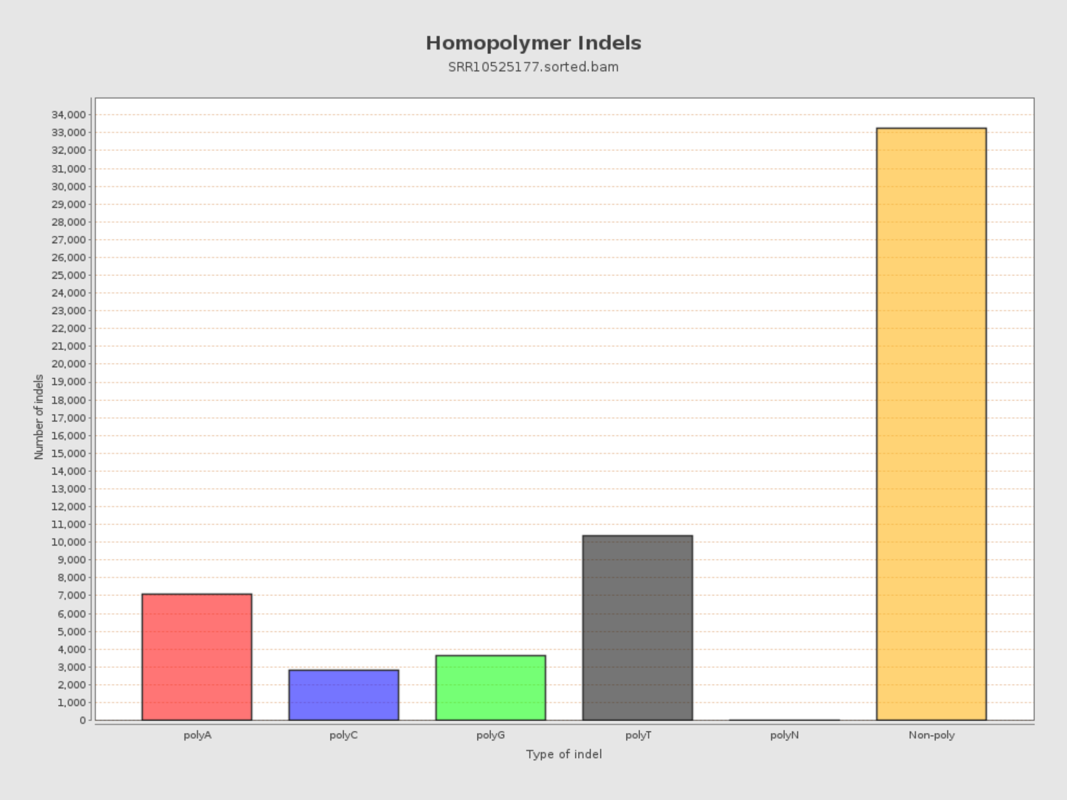
9. Results : Mapped Reads GC-content Distribution



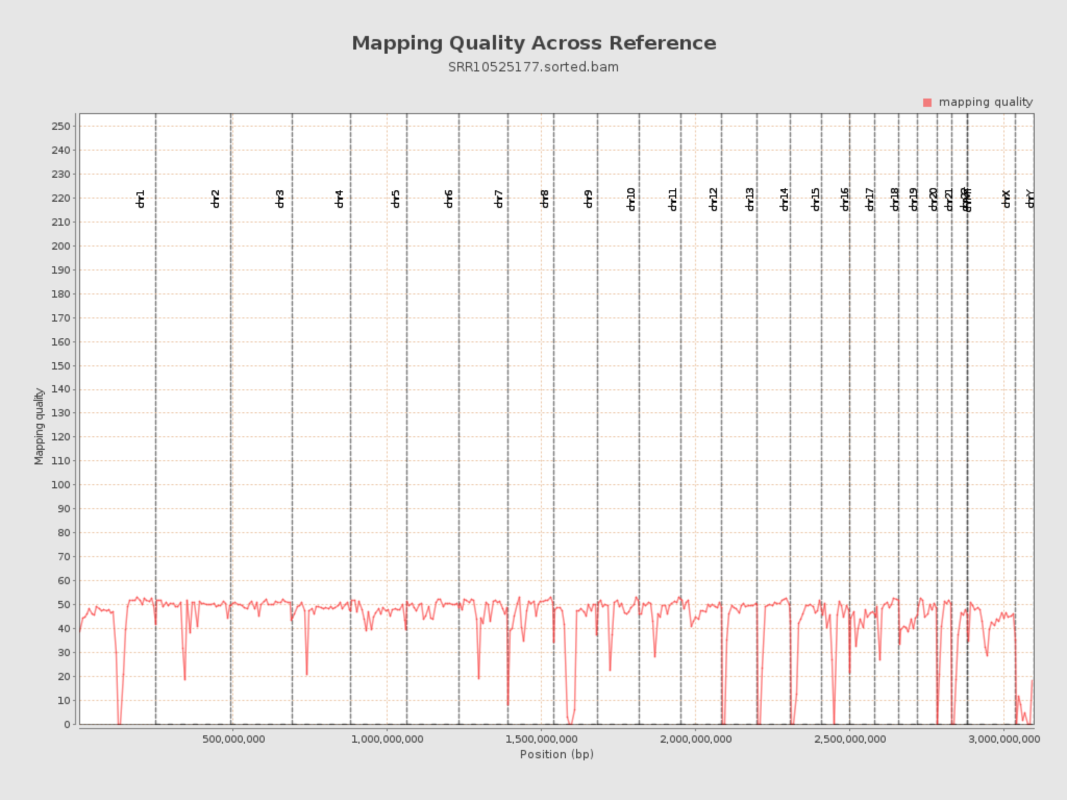
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram