Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 13:09:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818800.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_SRR1818800 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818800.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 13:09:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818800.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,359,749
Mapped reads	1,322,186 / 97.24%
Unmapped reads	37,563 / 2.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,397 / 0.84%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	539,859 / 39.7%
Duplication rate	34.61%
Clipped reads	1,329,145 / 97.75%

2.2. ACGT Content

Number/percentage of A's	26,083,944 / 29.09%
Number/percentage of C's	20,464,246 / 22.82%
Number/percentage of T's	24,635,713 / 27.48%
Number/percentage of G's	18,475,275 / 20.6%
Number/percentage of N's	5,553 / 0.01%
GC Percentage	43.43%

2.3. Coverage

Mean	0.029

Standard Deviation	0.3817

2.4. Mapping Quality

Mean Mapping Quality	47.89

2.5. Mismatches and indels

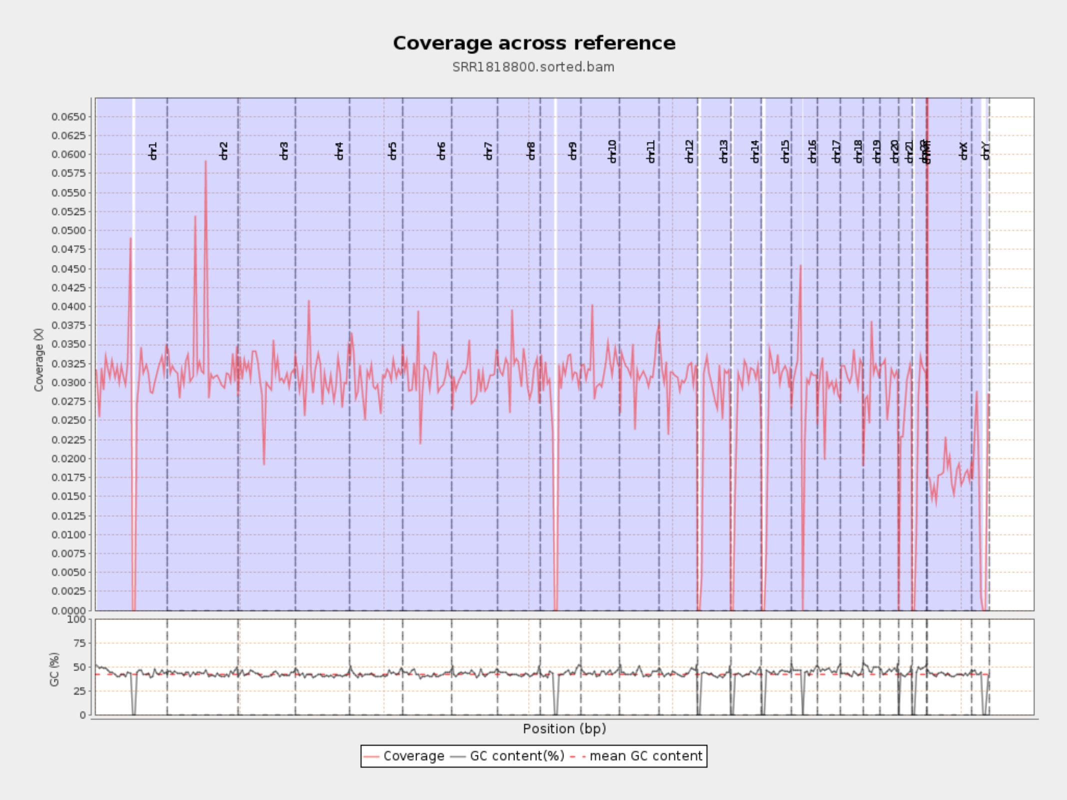
General error rate	0.54%
Mismatches	465,218
Insertions	8,151
Mapped reads with at least one insertion	0.61%
Deletions	22,392
Mapped reads with at least one deletion	1.68%
Homopolymer indels	44.44%

2.6. Chromosome stats

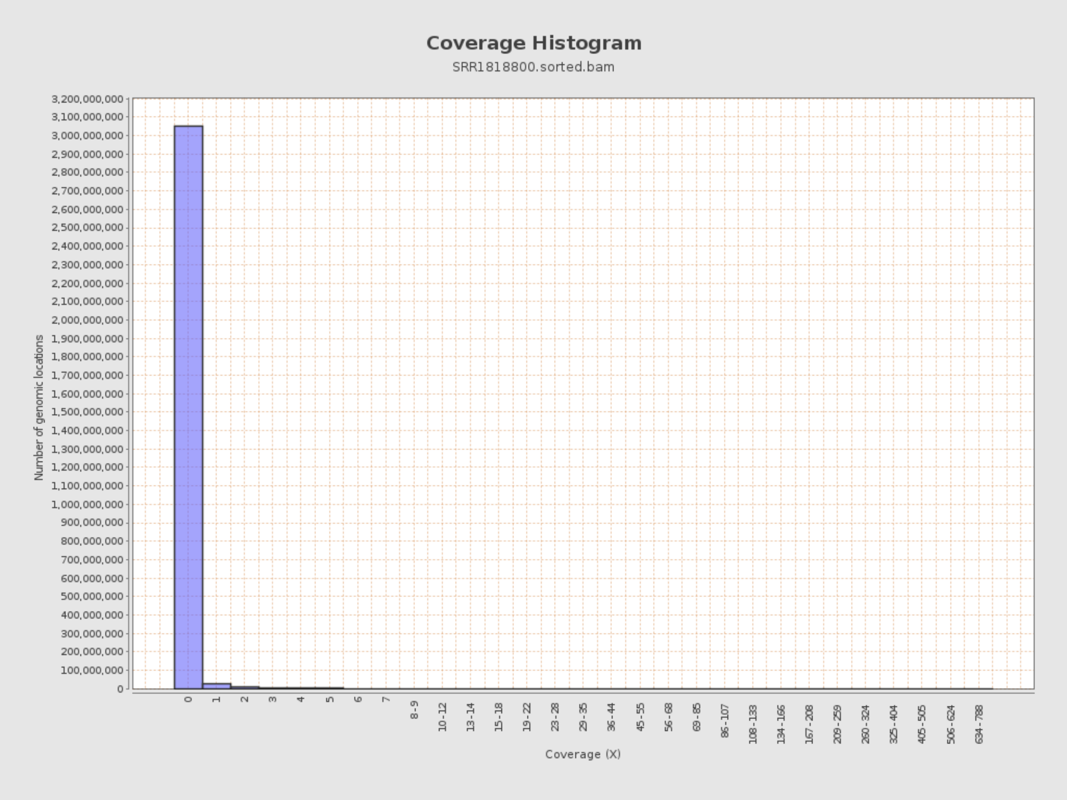
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7413725	0.0297	0.5281
chr2	243199373	7954333	0.0327	0.5993
chr3	198022430	6122781	0.0309	0.3028
chr4	191154276	5888423	0.0308	0.333
chr5	180915260	5543602	0.0306	0.3056
chr6	171115067	5305379	0.031	0.3231
chr7	159138663	4851434	0.0305	0.3494

chr8	146364022	4620356	0.0316	0.3335
chr9	141213431	3884707	0.0275	0.3285
chr10	135534747	4347383	0.0321	0.3964
chr11	135006516	4247567	0.0315	0.3336
chr12	133851895	4123639	0.0308	0.3351
chr13	115169878	2880754	0.025	0.2707
chr14	107349540	2778234	0.0259	0.3162
chr15	102531392	2614447	0.0255	0.2765
chr16	90354753	2584949	0.0286	0.4002
chr17	81195210	2361601	0.0291	0.3066
chr18	78077248	2471285	0.0317	0.4033
chr19	59128983	1769743	0.0299	0.4511
chr20	63025520	1925111	0.0305	0.319
chr21	48129895	1196946	0.0249	0.2836
chr22	51304566	1099584	0.0214	0.2825
chrMT	16571	91092	5.4971	5.8537
chrX	155270560	2751702	0.0177	0.2402
chrY	59373566	871878	0.0147	0.5744

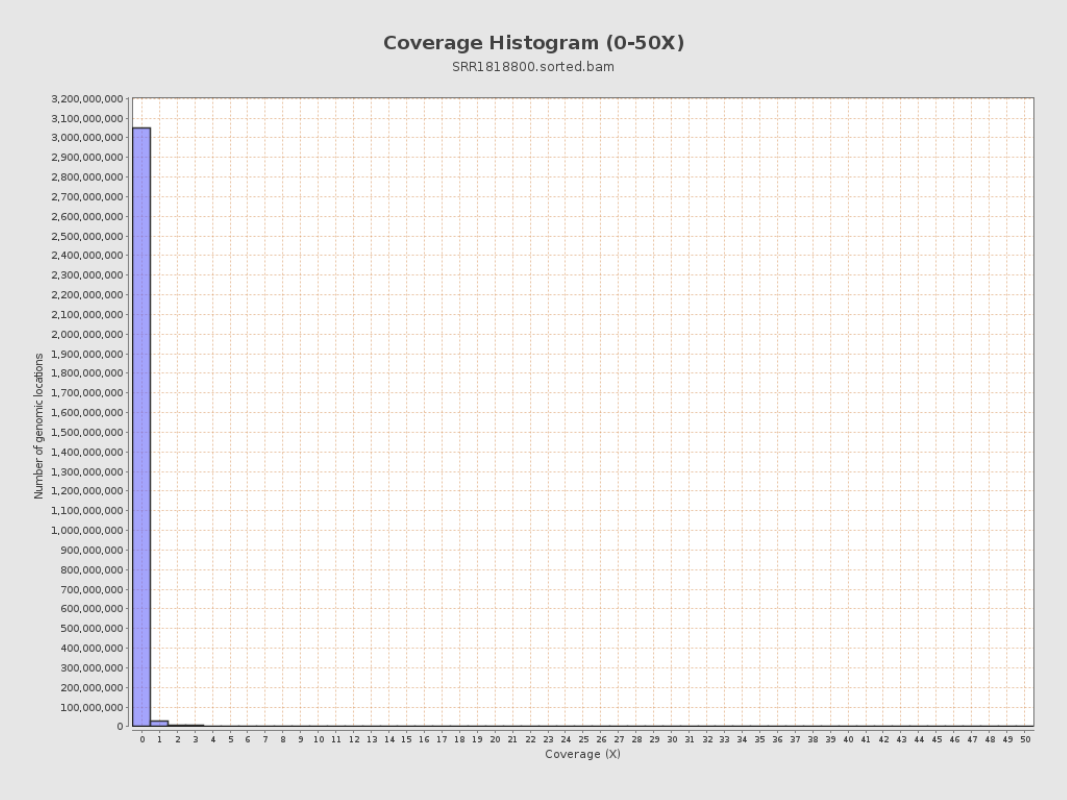
3. Results : Coverage across reference



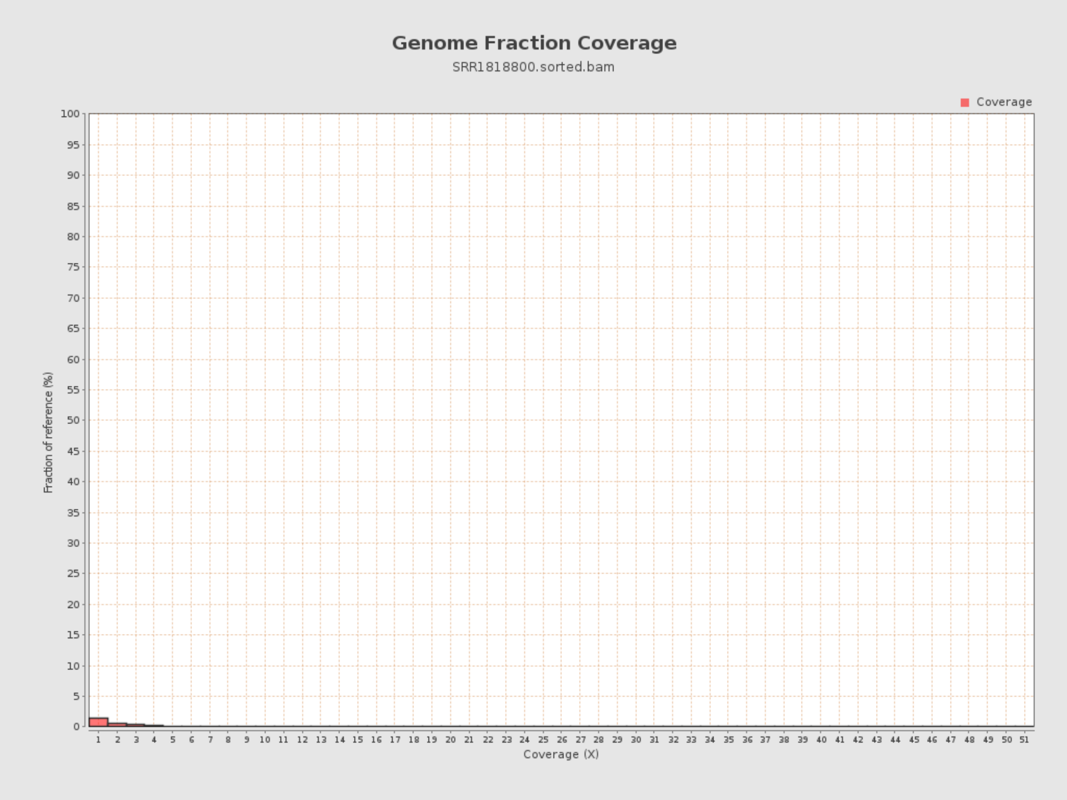
4. Results : Coverage Histogram



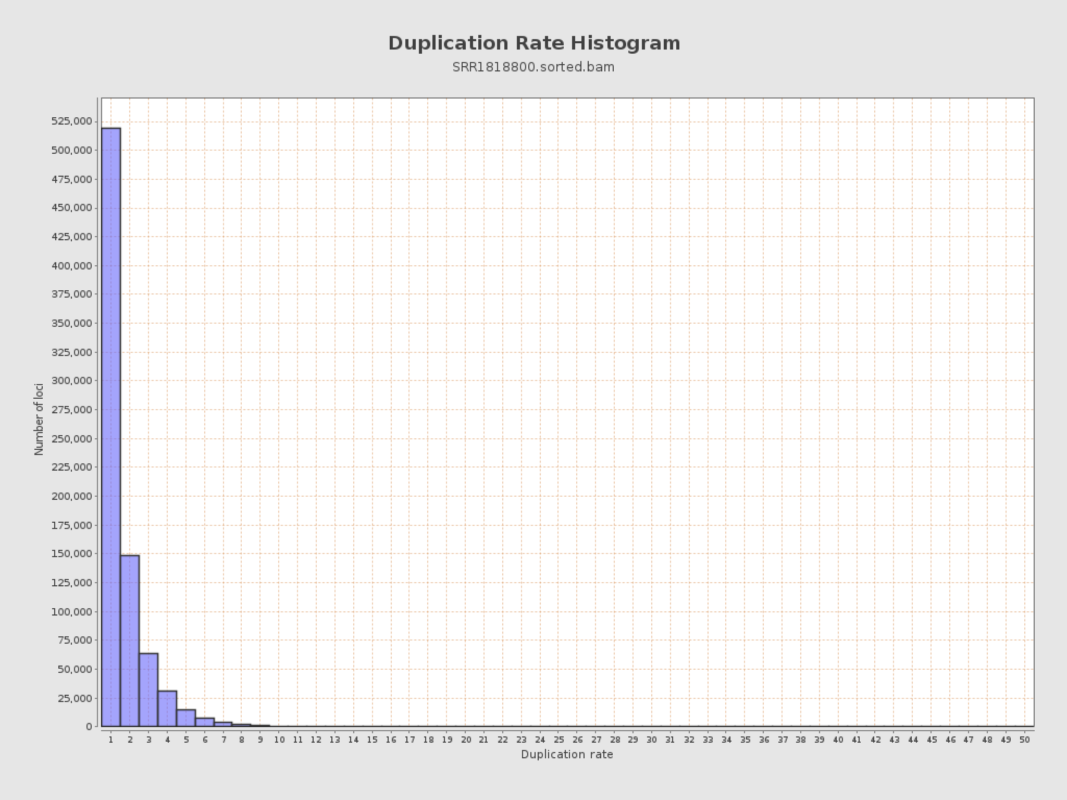
5. Results : Coverage Histogram (0-50X)



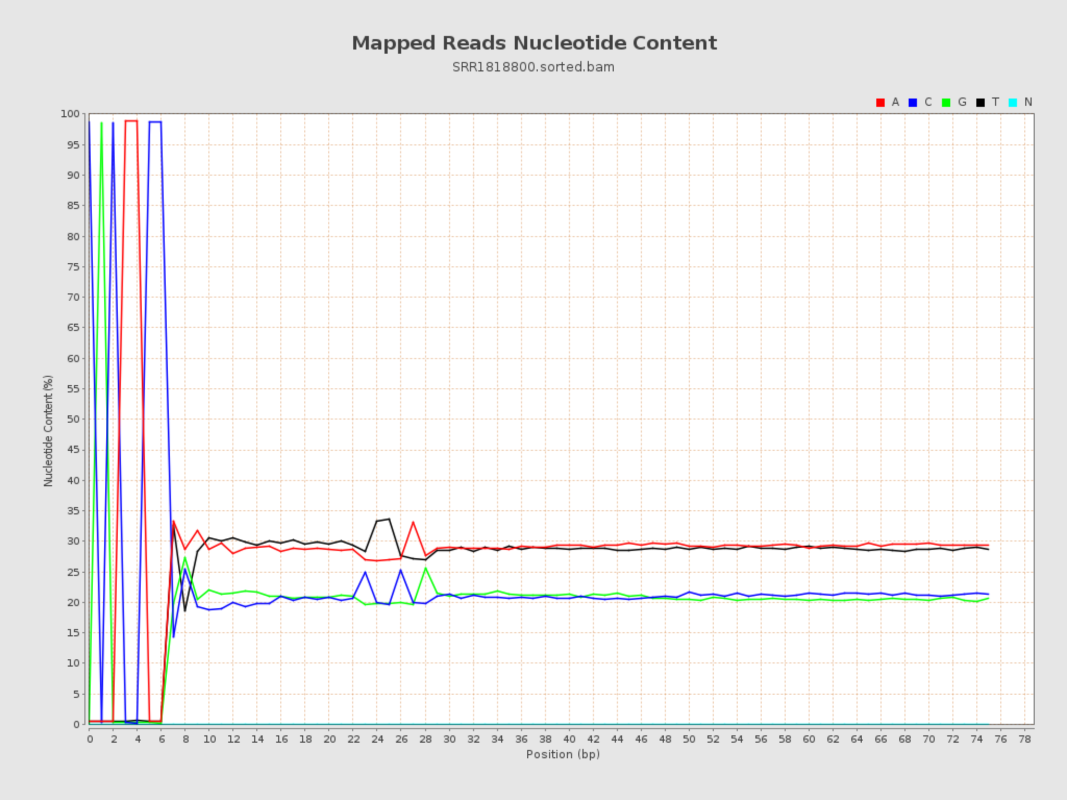
6. Results : Genome Fraction Coverage



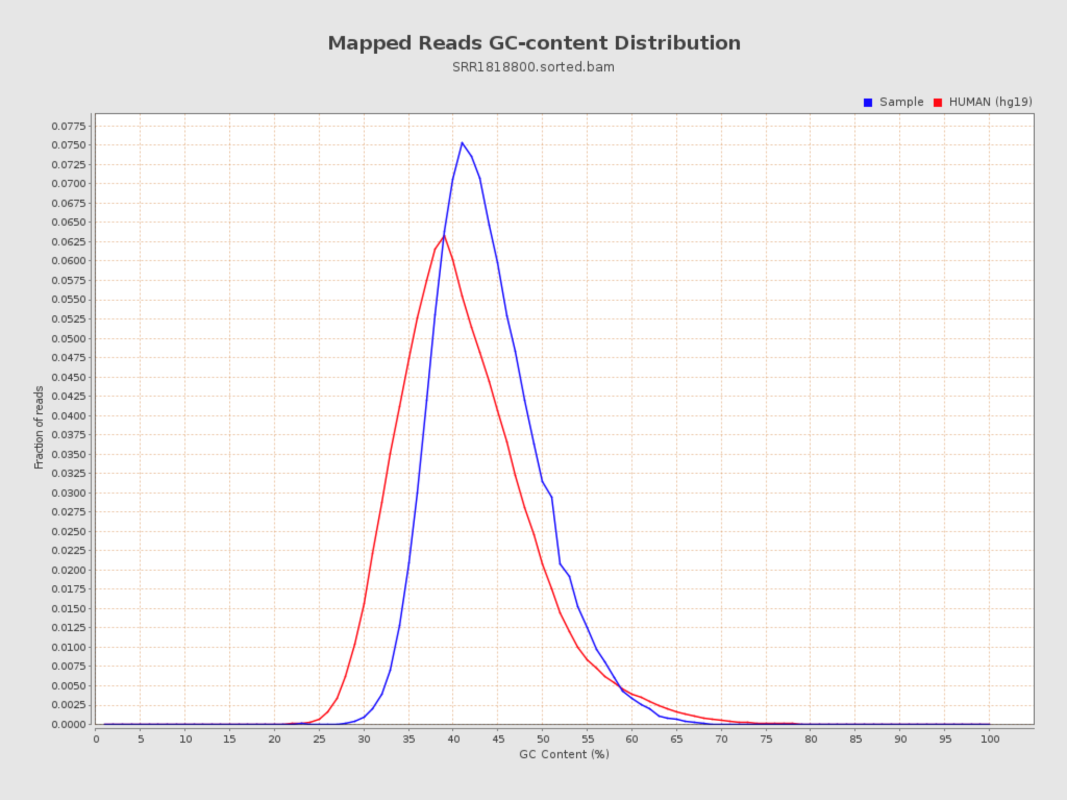
7. Results : Duplication Rate Histogram



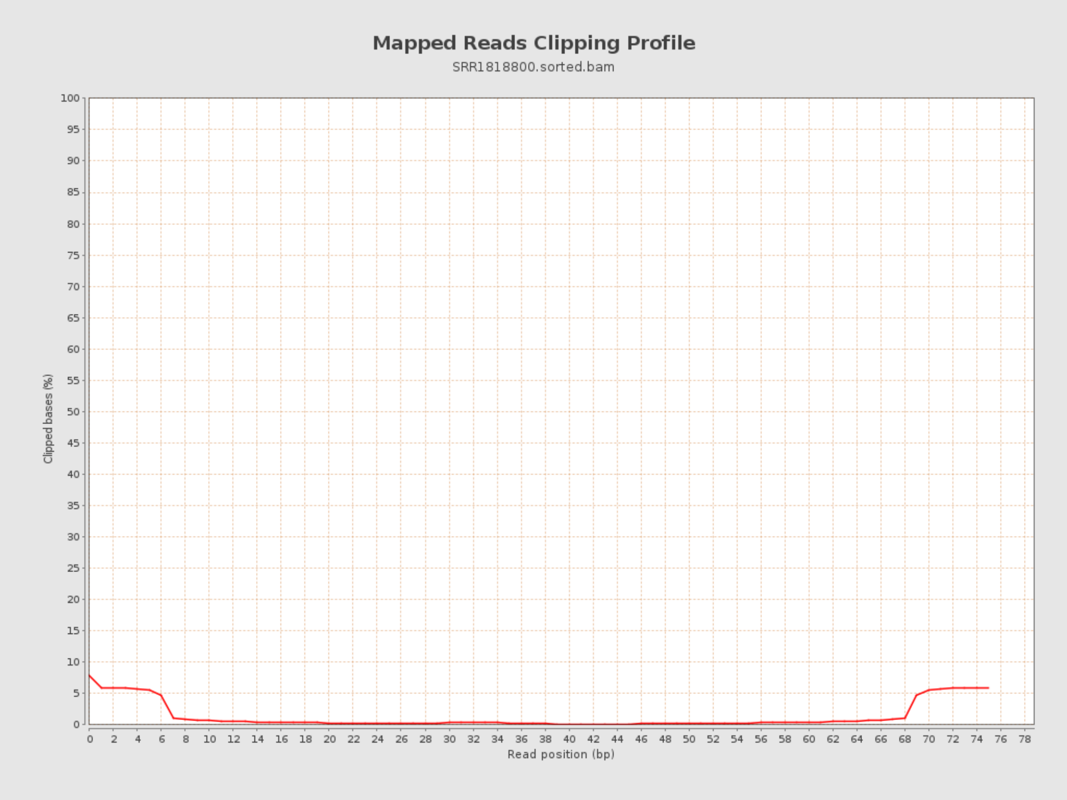
8. Results : Mapped Reads Nucleotide Content



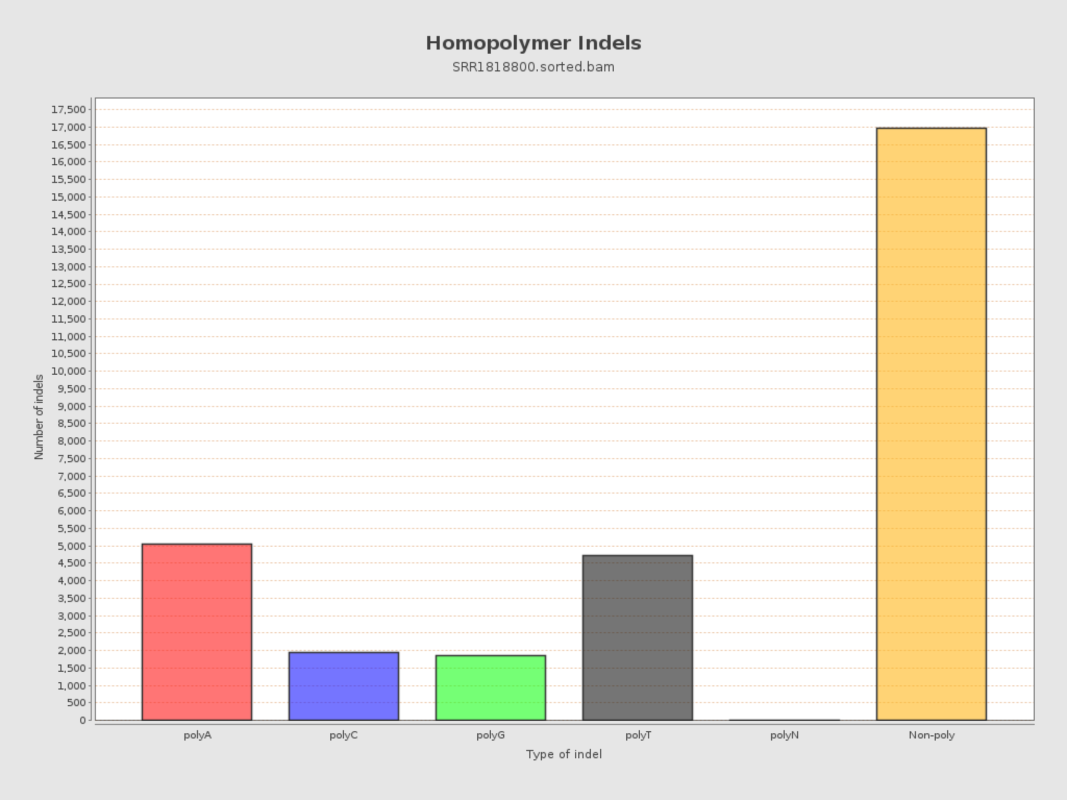
9. Results : Mapped Reads GC-content Distribution



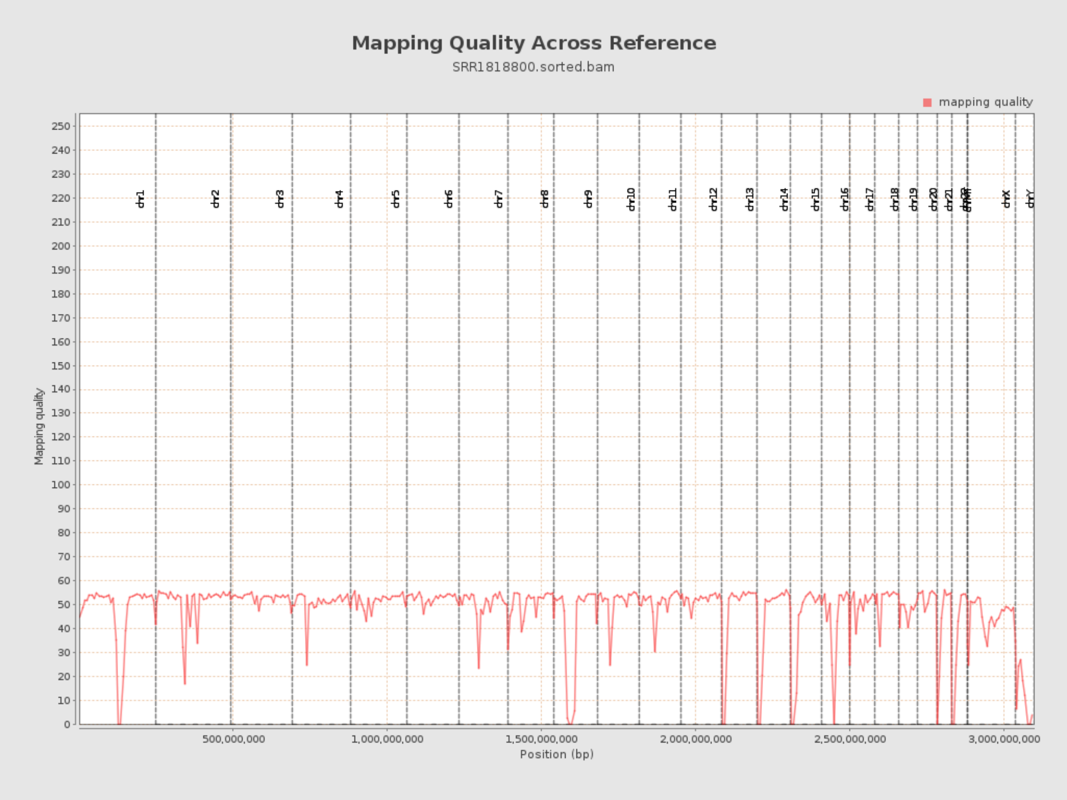
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram