Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:08:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818868.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_SRR1818868 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818868.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:08:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818868.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,377,369
Mapped reads	2,192,454 / 92.22%
Unmapped reads	184,915 / 7.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,932 / 1.43%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	788,455 / 33.17%
Duplication rate	30.66%
Clipped reads	2,205,212 / 92.76%

2.2. ACGT Content

Number/percentage of A's	58,311,242 / 28.77%
Number/percentage of C's	43,030,988 / 21.23%
Number/percentage of T's	58,353,154 / 28.79%
Number/percentage of G's	42,994,183 / 21.21%
Number/percentage of N's	2,831 / 0%
GC Percentage	42.44%

2.3. Coverage

Mean	0.0655

Standard Deviation	0.8643

2.4. Mapping Quality

Mean Mapping Quality	49.16

2.5. Mismatches and indels

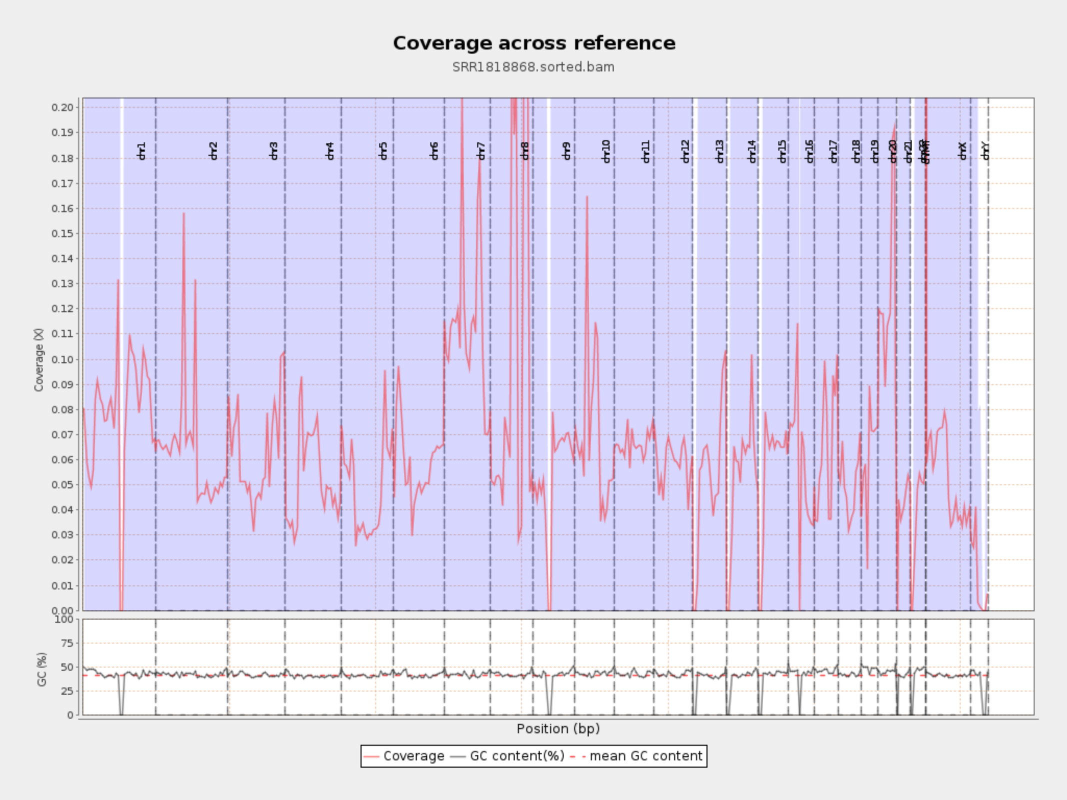
General error rate	0.67%
Mismatches	1,276,472
Insertions	29,859
Mapped reads with at least one insertion	1.31%
Deletions	68,755
Mapped reads with at least one deletion	3.06%
Homopolymer indels	41.76%

2.6. Chromosome stats

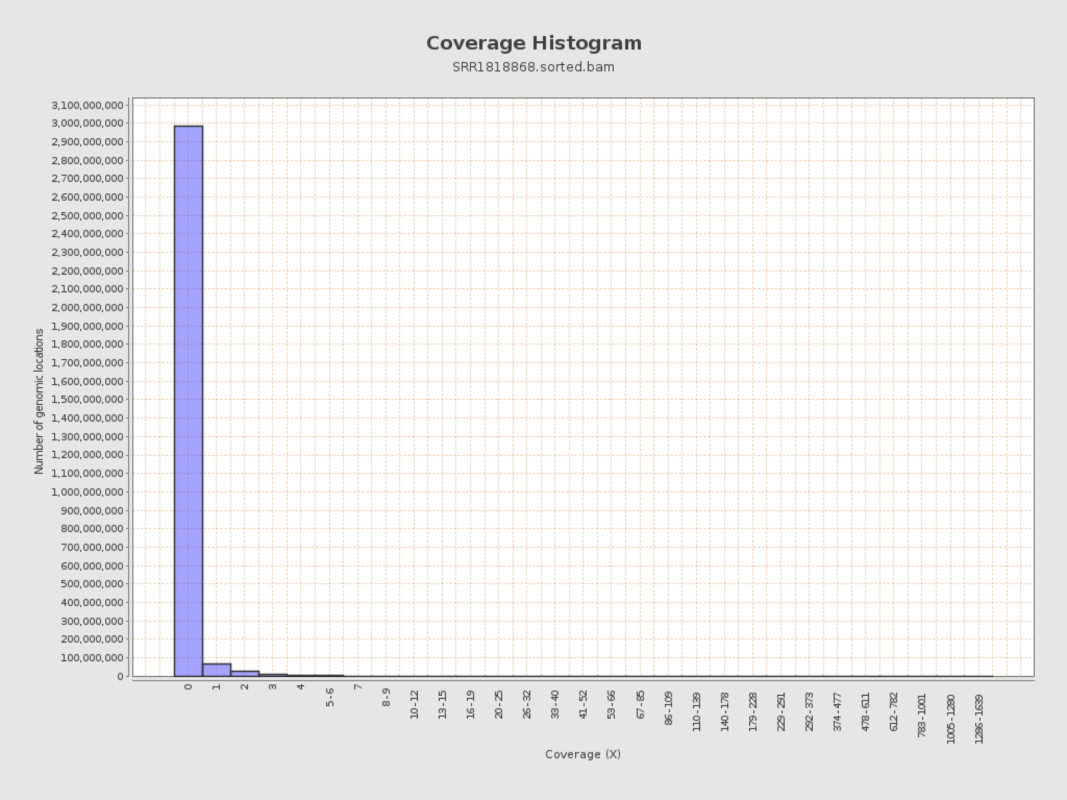
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19504363	0.0783	1.3212
chr2	243199373	15523737	0.0638	1.3065
chr3	198022430	12503900	0.0631	0.408
chr4	191154276	10158108	0.0531	0.4851
chr5	180915260	8799775	0.0486	0.3819
chr6	171115067	10035683	0.0586	0.4421
chr7	159138663	18252853	0.1147	1.8678

chr8	146364022	17436413	0.1191	0.7117
chr9	141213431	7531630	0.0533	0.7227
chr10	135534747	9451098	0.0697	1.0893
chr11	135006516	8934473	0.0662	0.5215
chr12	133851895	7888897	0.0589	0.4063
chr13	115169878	6136077	0.0533	0.3703
chr14	107349540	5846388	0.0545	0.4194
chr15	102531392	5675445	0.0554	0.3831
chr16	90354753	5160564	0.0571	0.8955
chr17	81195210	5160236	0.0636	0.529
chr18	78077248	3915849	0.0502	0.807
chr19	59128983	3617033	0.0612	1.0755
chr20	63025520	8187570	0.1299	0.6335
chr21	48129895	1976532	0.0411	0.383
chr22	51304566	1844226	0.0359	0.3535
chrMT	16571	339012	20.4581	12.3411
chrX	155270560	8202167	0.0528	0.4433
chrY	59373566	743191	0.0125	0.9837

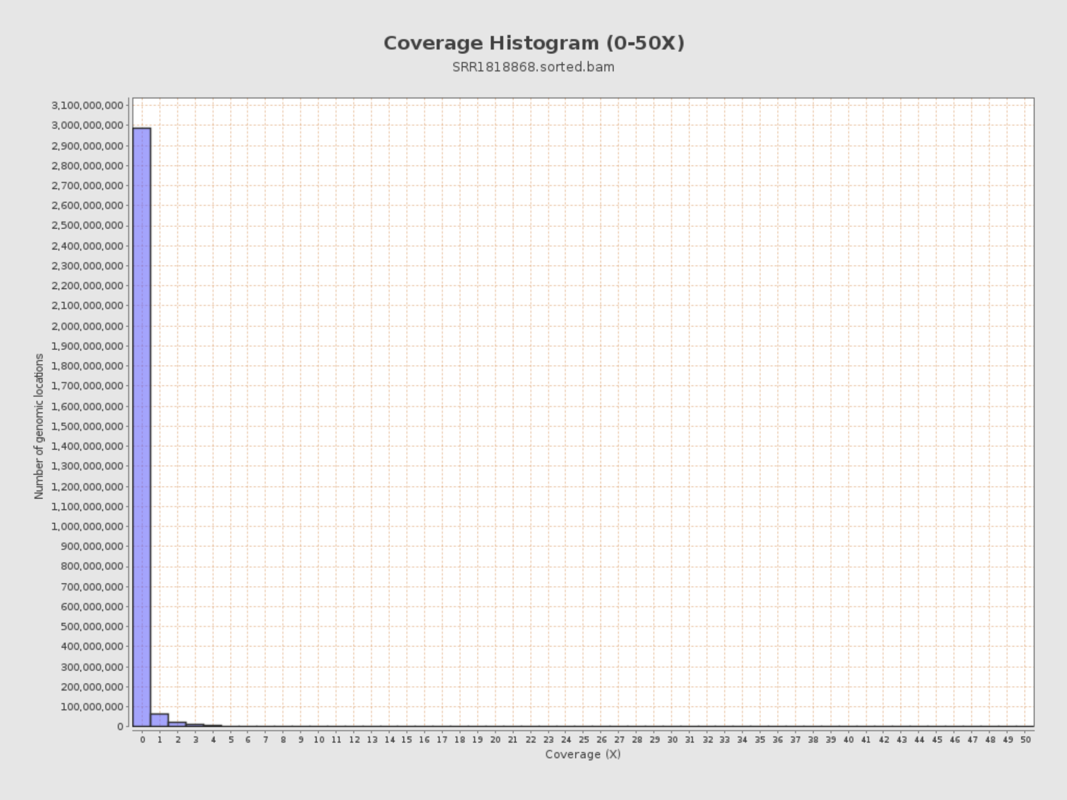
3. Results : Coverage across reference



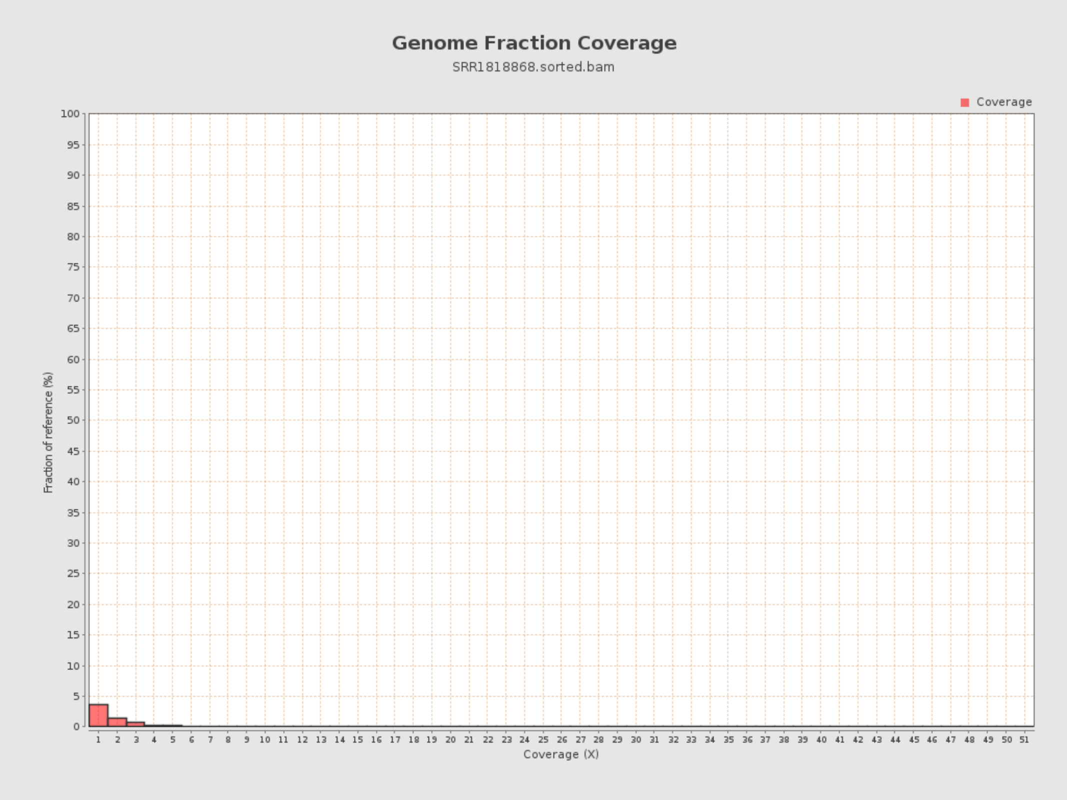
4. Results : Coverage Histogram



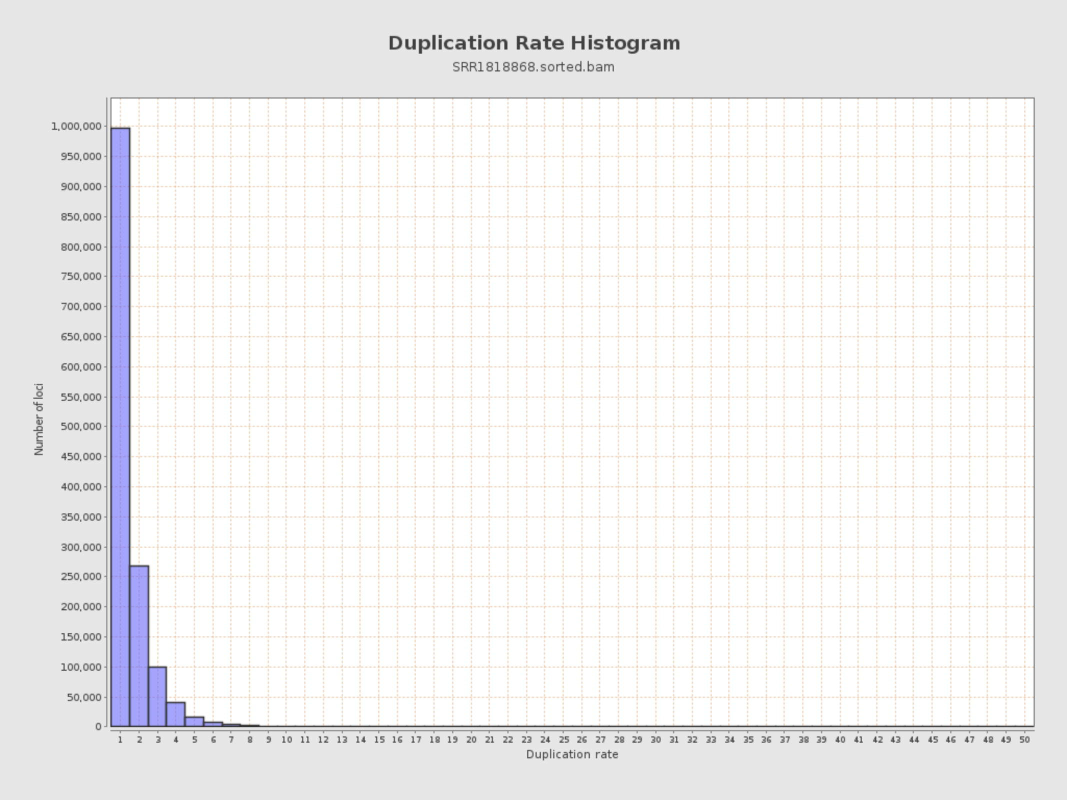
5. Results : Coverage Histogram (0-50X)



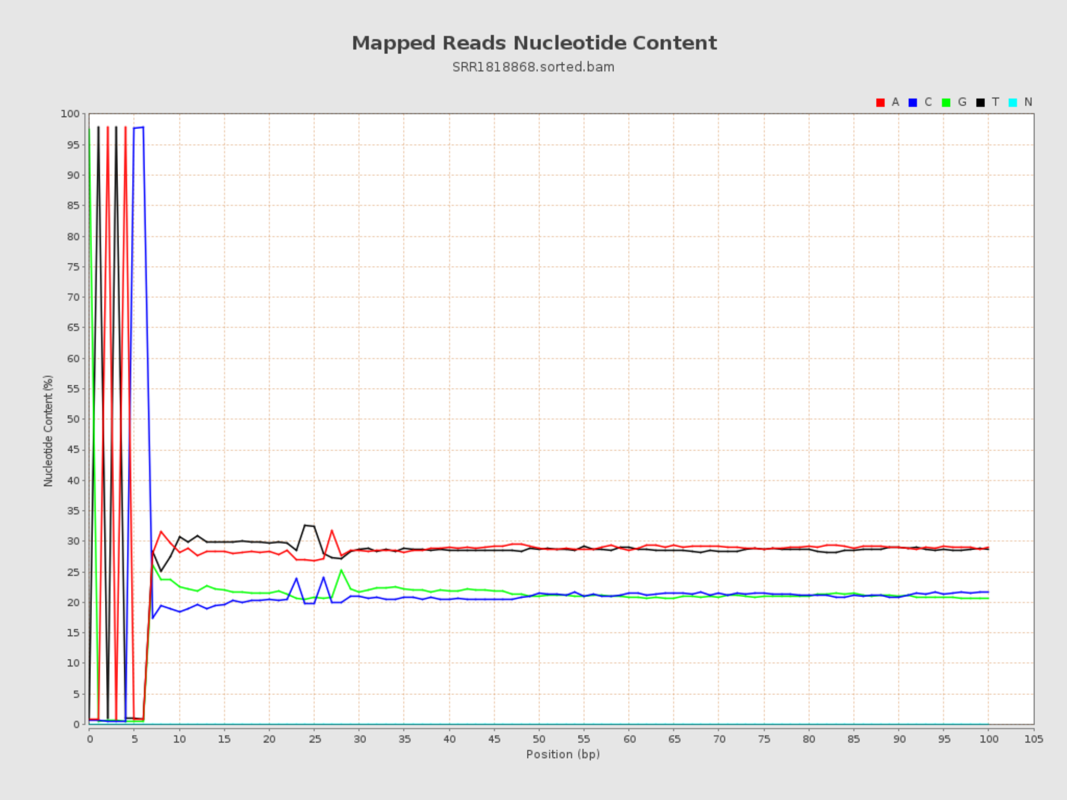
6. Results : Genome Fraction Coverage



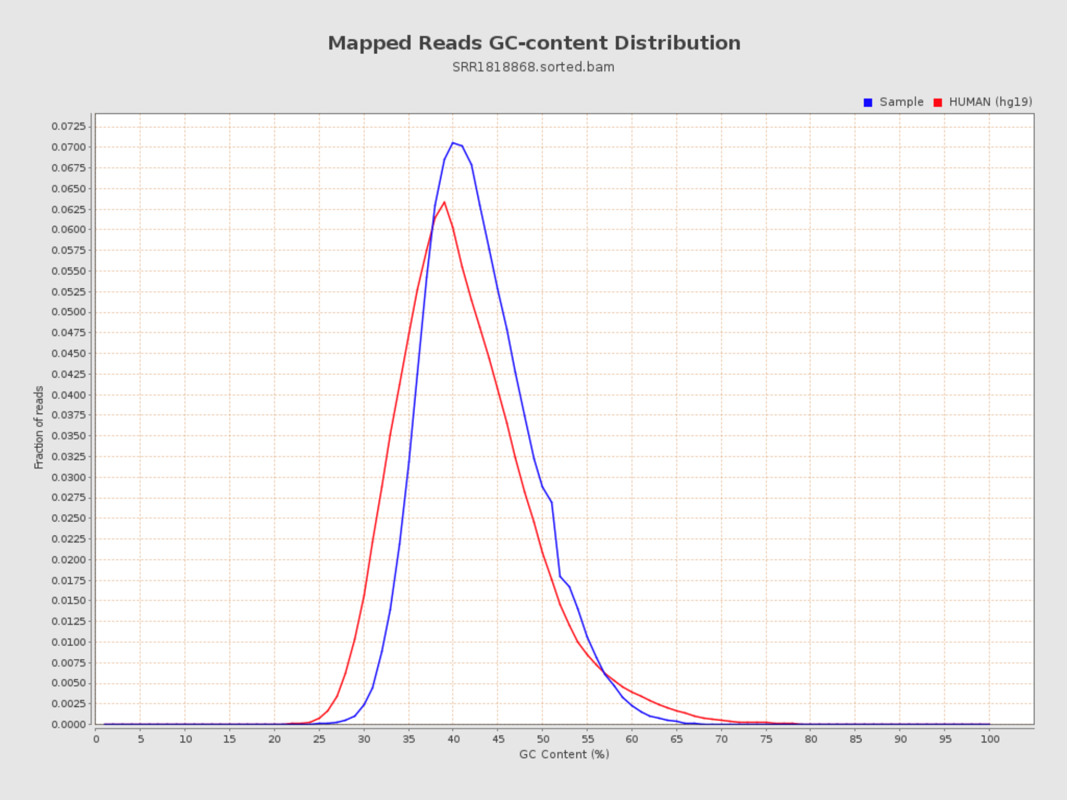
7. Results : Duplication Rate Histogram



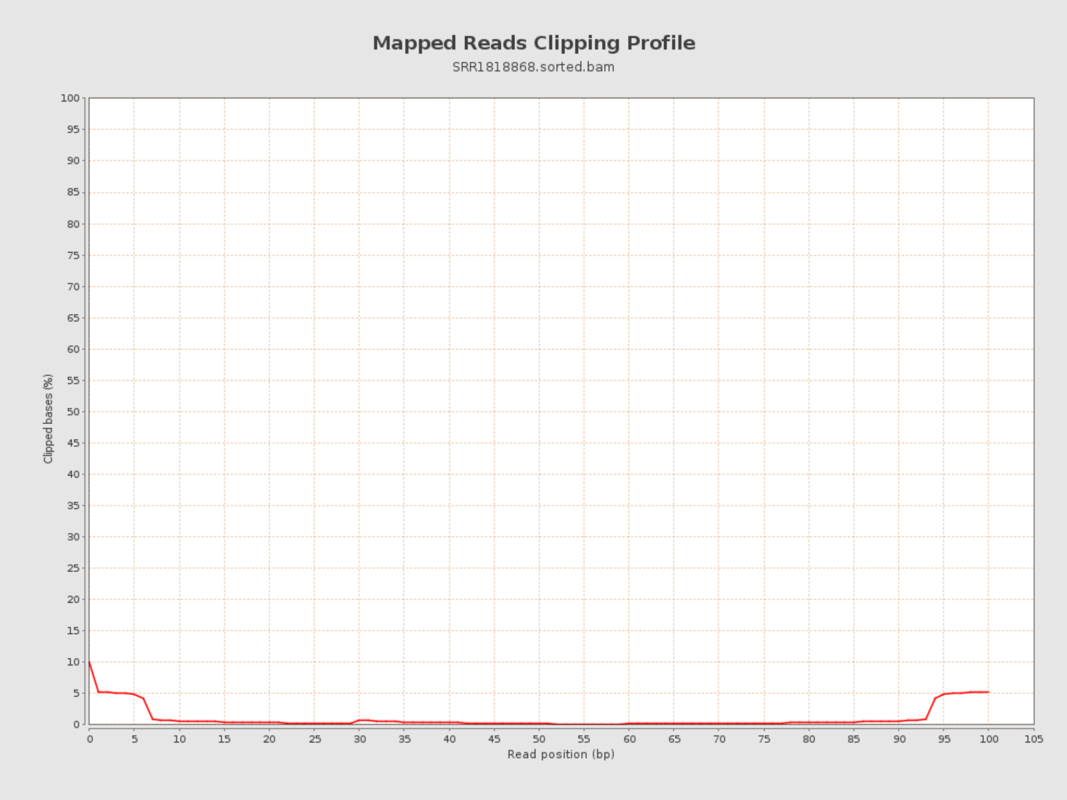
8. Results : Mapped Reads Nucleotide Content



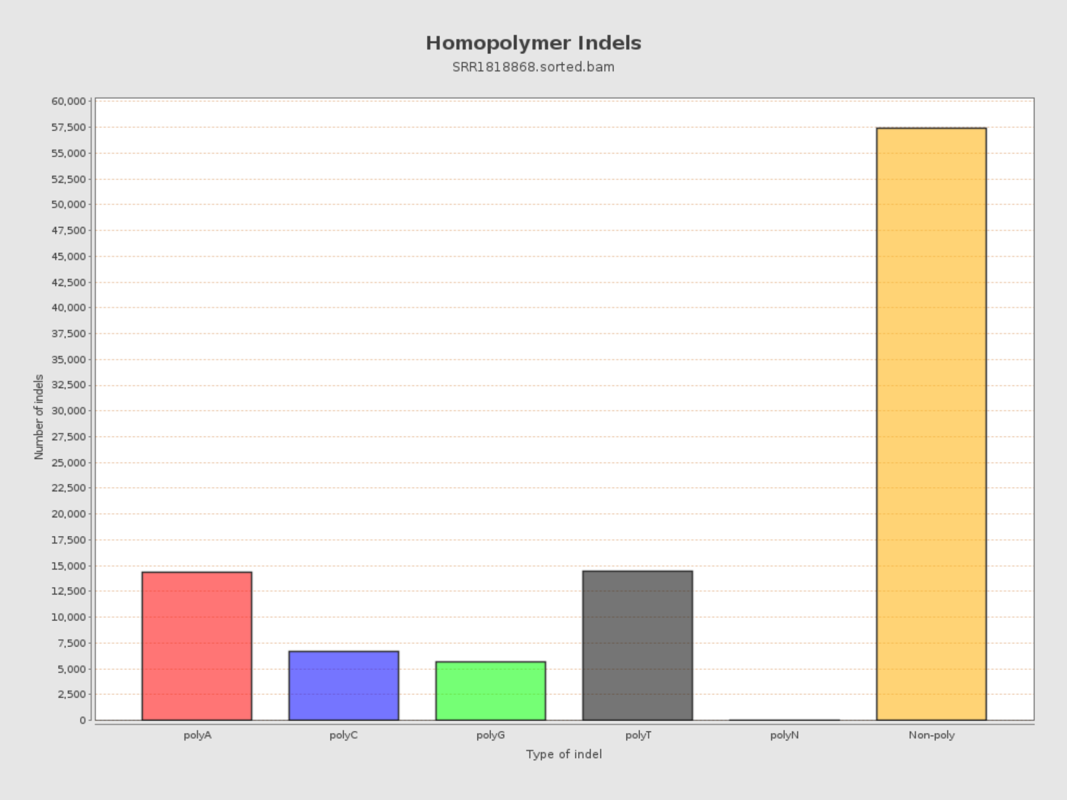
9. Results : Mapped Reads GC-content Distribution



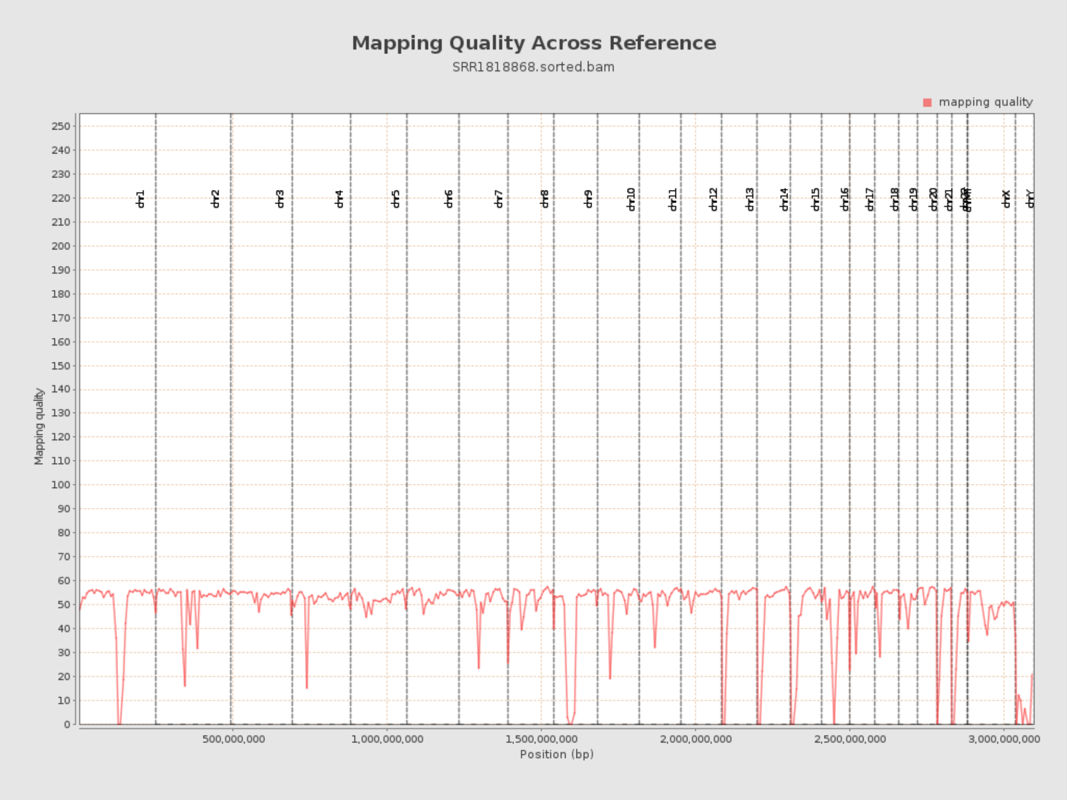
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram