Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:36:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819112.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_SRR1819112 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819112.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:36:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819112.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,007,309
Mapped reads	1,840,106 / 91.67%
Unmapped reads	167,203 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,734 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	103,538 / 5.16%
Duplication rate	4.29%
Clipped reads	1,842,672 / 91.8%

2.2. ACGT Content

Number/percentage of A's	27,413,933 / 25.48%
Number/percentage of C's	20,262,654 / 18.84%
Number/percentage of T's	34,492,577 / 32.06%
Number/percentage of G's	25,408,365 / 23.62%
Number/percentage of N's	1,655 / 0%
GC Percentage	42.45%

2.3. Coverage

Mean	0.0348

Standard Deviation	0.3251

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

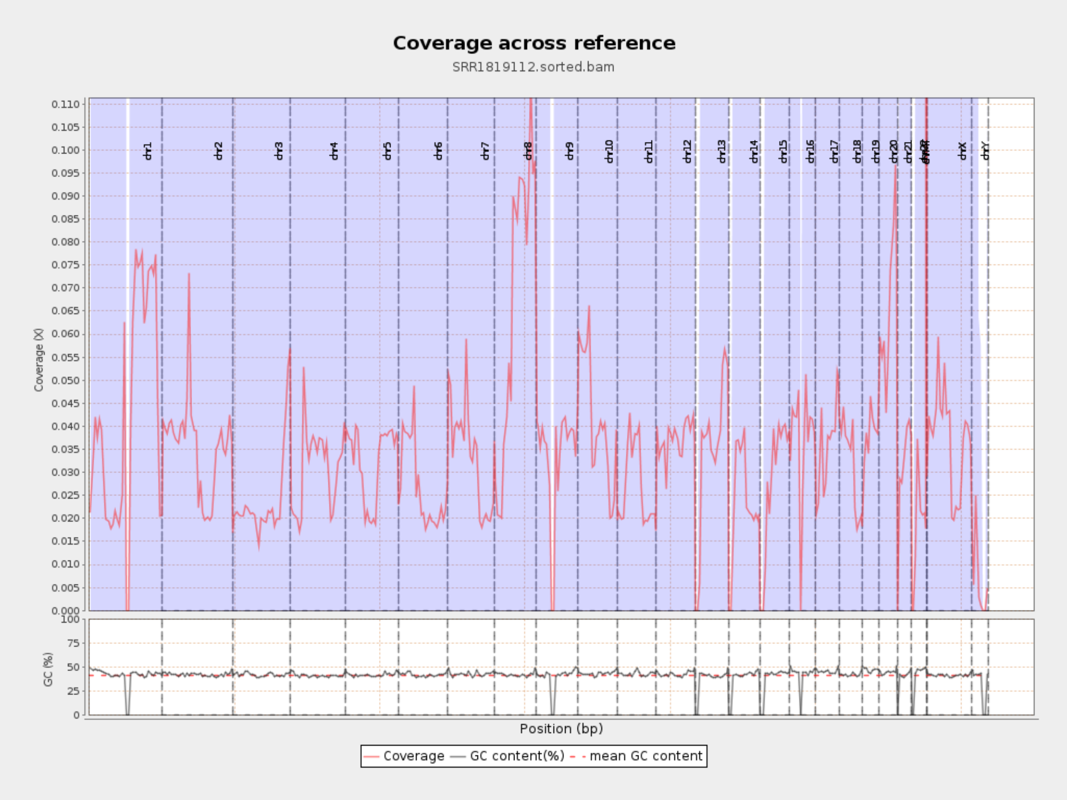
General error rate	0.53%
Mismatches	553,675
Insertions	8,152
Mapped reads with at least one insertion	0.44%
Deletions	20,497
Mapped reads with at least one deletion	1.11%
Homopolymer indels	42.6%

2.6. Chromosome stats

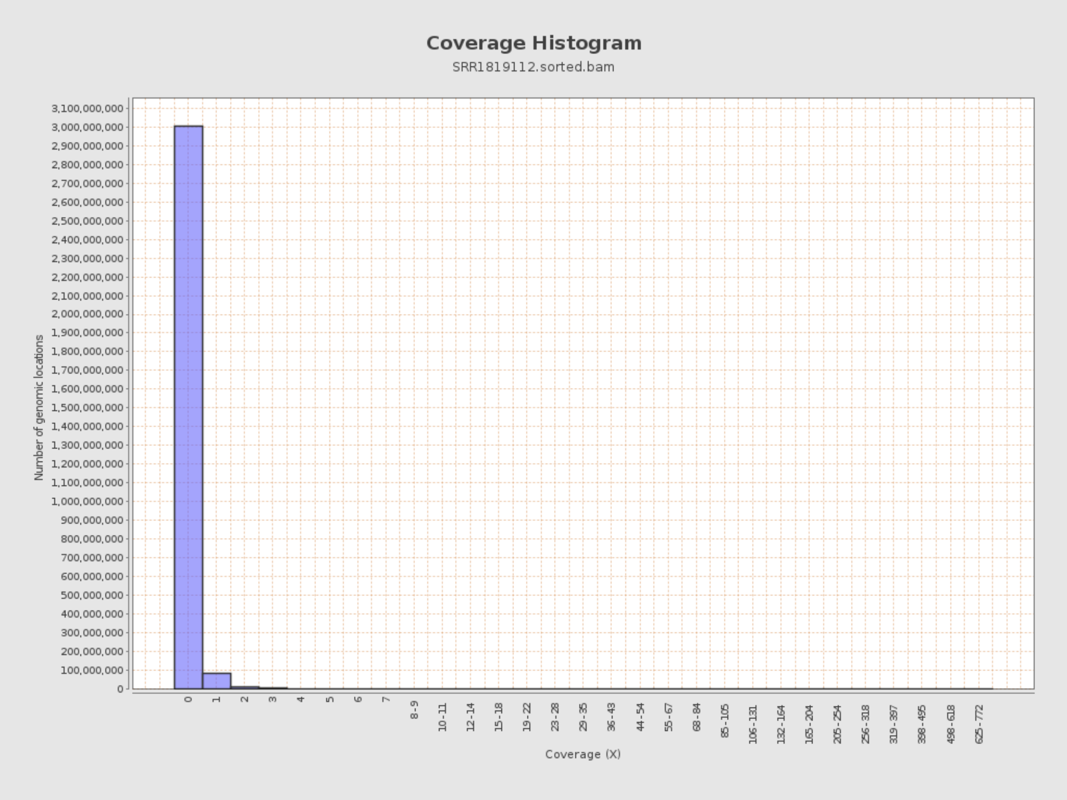
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10622501	0.0426	0.6035
chr2	243199373	8702507	0.0358	0.4177
chr3	198022430	4686860	0.0237	0.1745
chr4	191154276	5887427	0.0308	0.2441
chr5	180915260	5851656	0.0323	0.204
chr6	171115067	4569928	0.0267	0.2366
chr7	159138663	5338340	0.0335	0.3804

chr8	146364022	9881918	0.0675	0.38
chr9	141213431	4625200	0.0328	0.2916
chr10	135534747	5633634	0.0416	0.3329
chr11	135006516	3676889	0.0272	0.2788
chr12	133851895	4998886	0.0373	0.2205
chr13	115169878	3979042	0.0345	0.2111
chr14	107349540	2526869	0.0235	0.1762
chr15	102531392	2853751	0.0278	0.1909
chr16	90354753	3365382	0.0372	0.2305
chr17	81195210	2880613	0.0355	0.2297
chr18	78077248	2521652	0.0323	0.4921
chr19	59128983	2247935	0.038	0.3853
chr20	63025520	4186929	0.0664	0.2966
chr21	48129895	1506829	0.0313	0.2344
chr22	51304566	905724	0.0177	0.1492
chrMT	16571	18711	1.1291	1.3315
chrX	155270560	5772443	0.0372	0.2493
chrY	59373566	371831	0.0063	0.2224

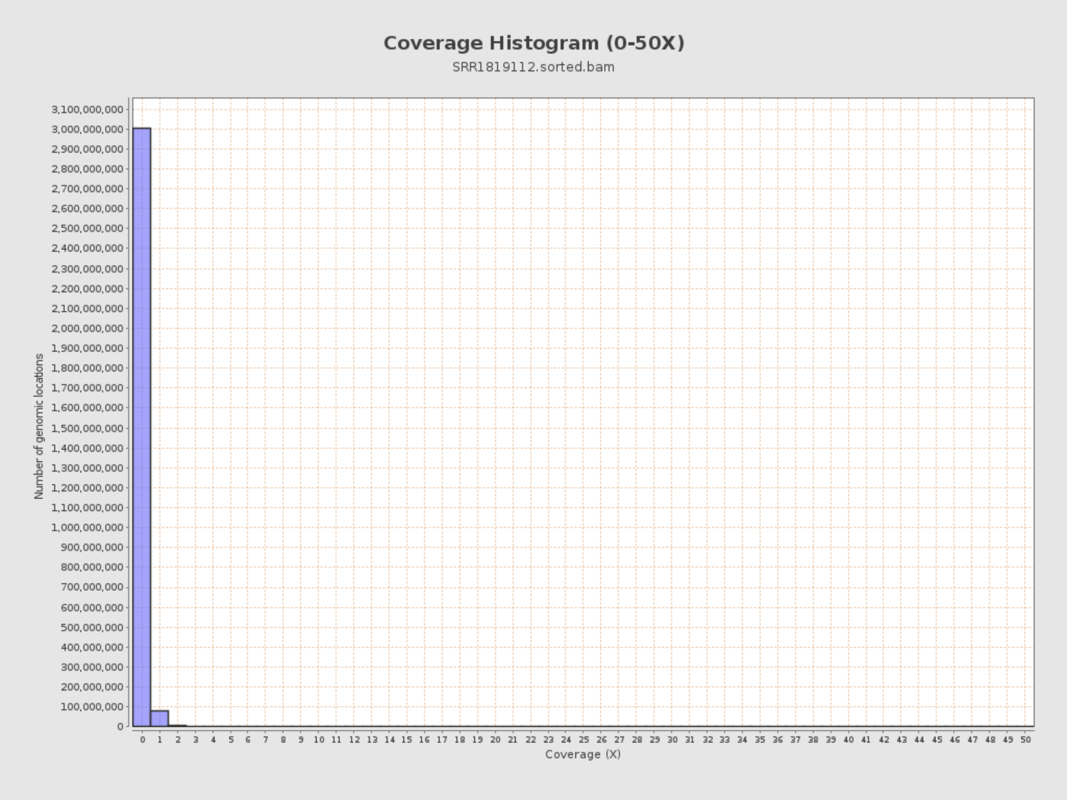
3. Results : Coverage across reference



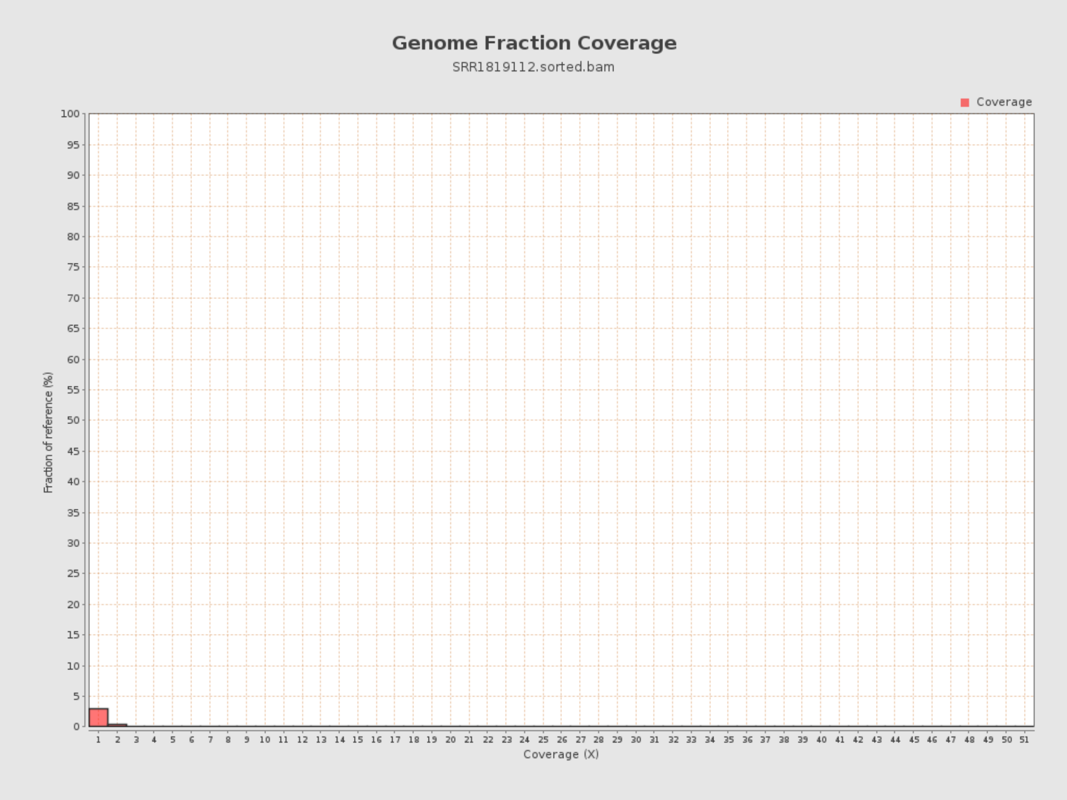
4. Results : Coverage Histogram



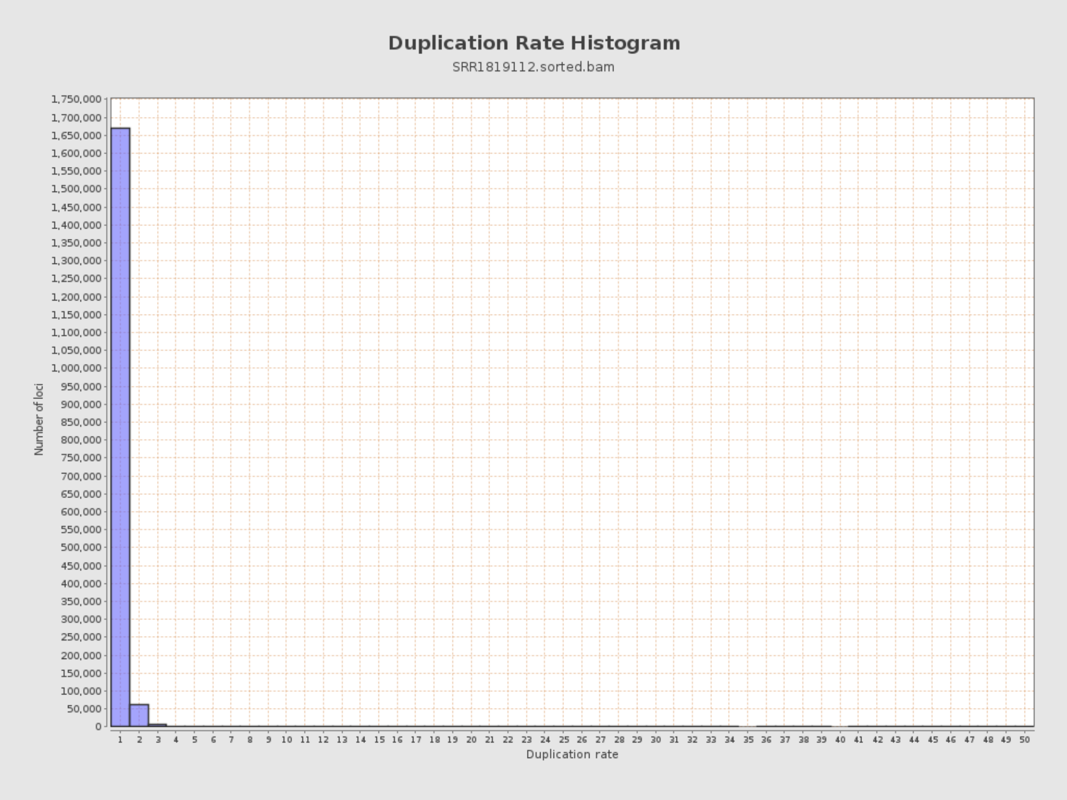
5. Results : Coverage Histogram (0-50X)



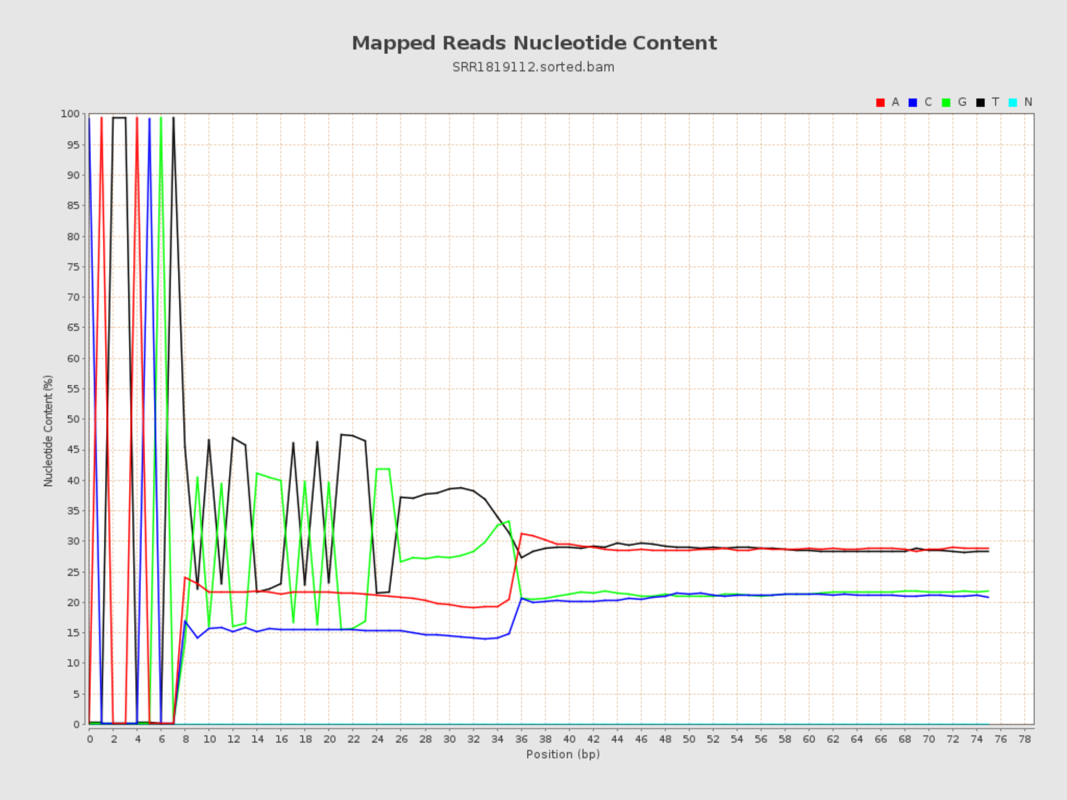
6. Results : Genome Fraction Coverage



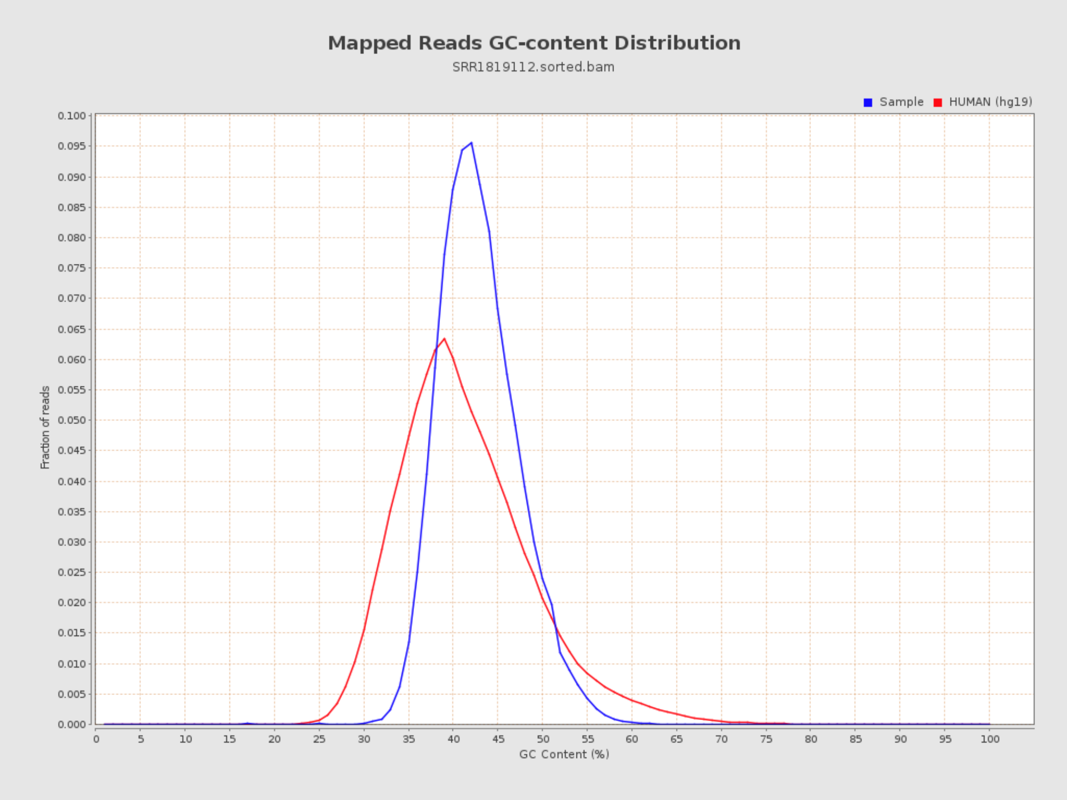
7. Results : Duplication Rate Histogram



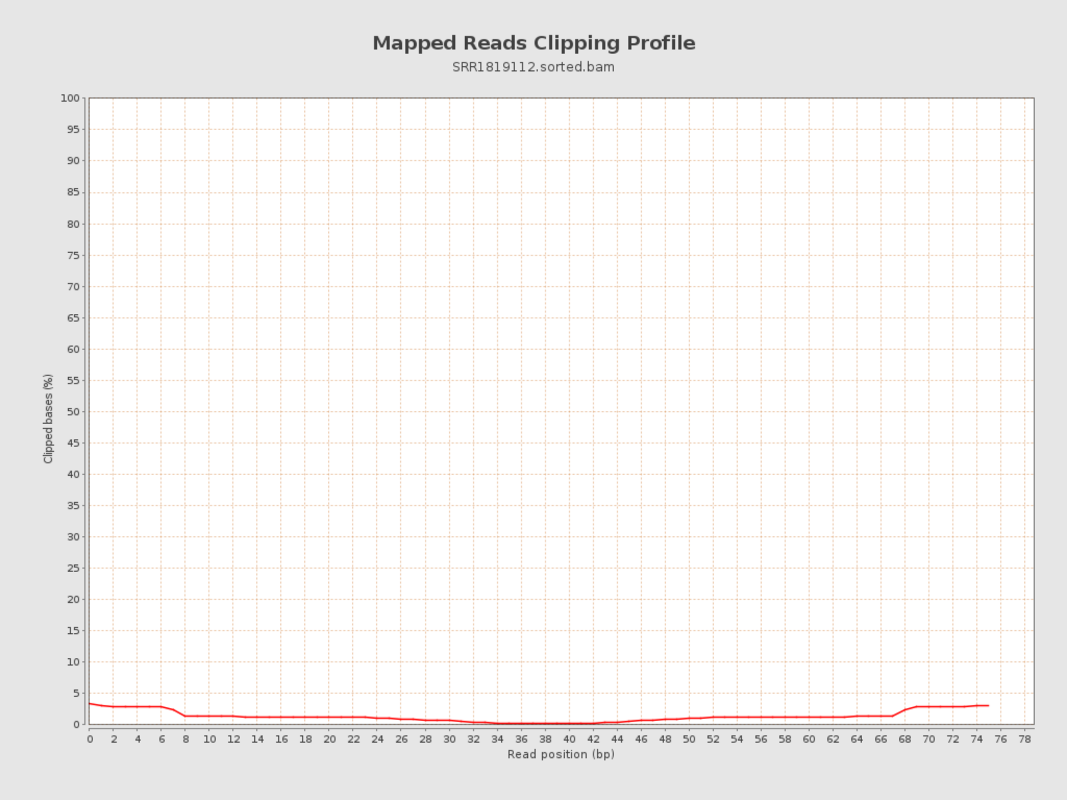
8. Results : Mapped Reads Nucleotide Content



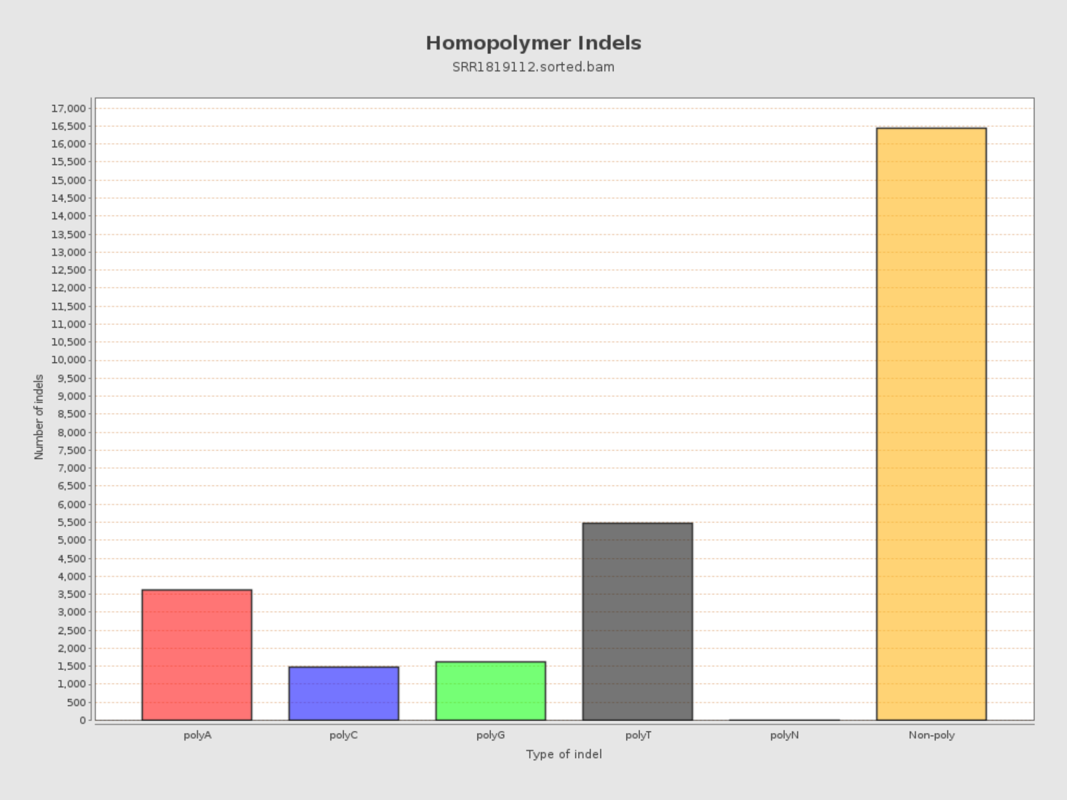
9. Results : Mapped Reads GC-content Distribution



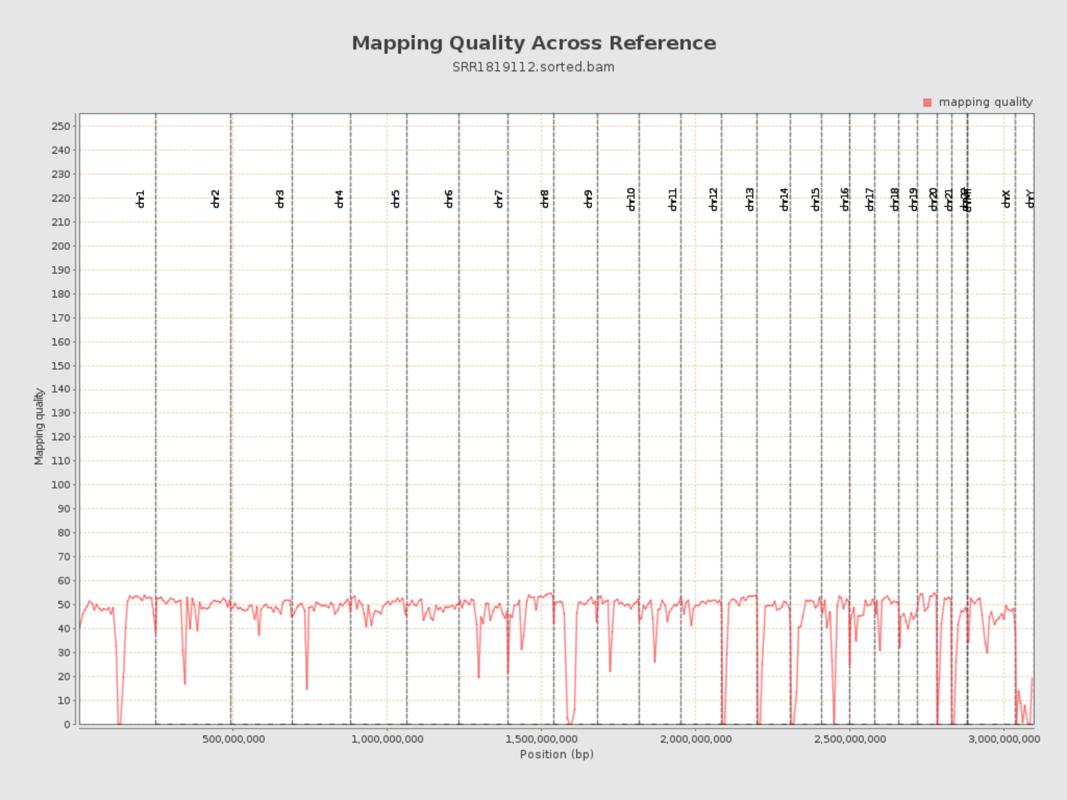
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram