Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 15:48:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818815.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_SRR1818815 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818815.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 15:48:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818815.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	583,459
Mapped reads	540,545 / 92.64%
Unmapped reads	42,914 / 7.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,704 / 0.81%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	142,850 / 24.48%
Duplication rate	23.66%
Clipped reads	541,929 / 92.88%

2.2. ACGT Content

Number/percentage of A's	10,417,855 / 28.42%
Number/percentage of C's	7,833,542 / 21.37%
Number/percentage of T's	10,589,144 / 28.89%
Number/percentage of G's	7,816,326 / 21.32%
Number/percentage of N's	2,288 / 0.01%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0118

Standard Deviation	0.189

2.4. Mapping Quality

Mean Mapping Quality	47.84

2.5. Mismatches and indels

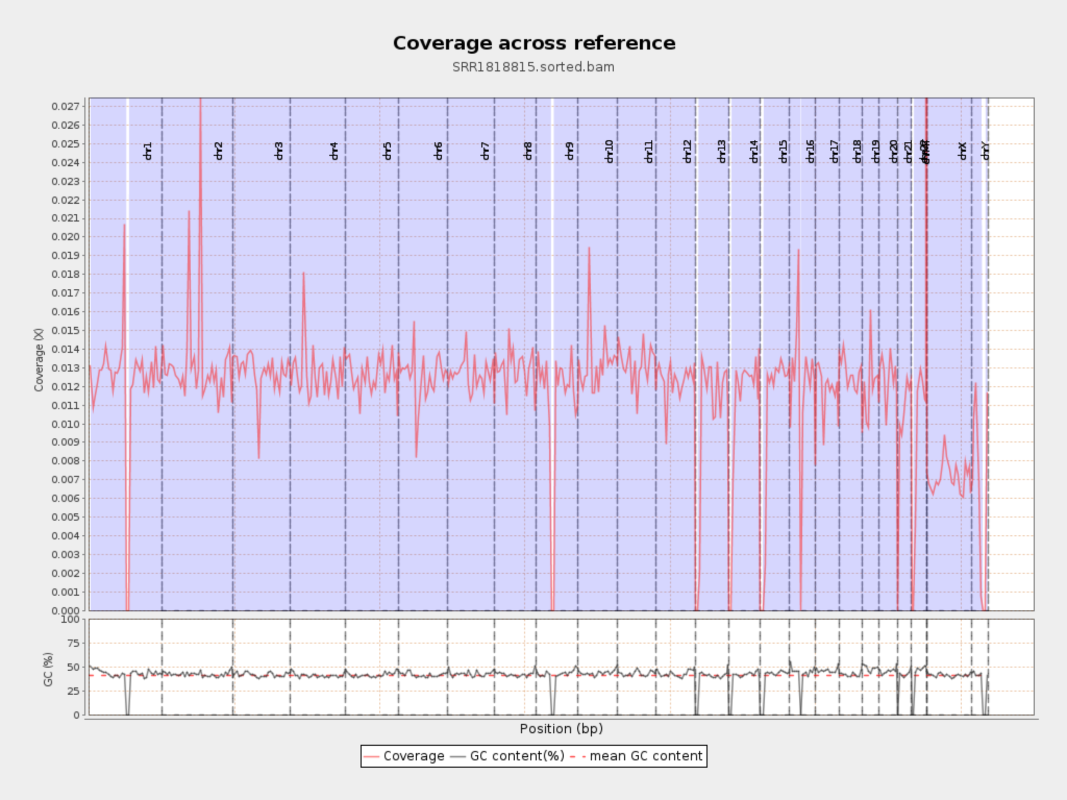
General error rate	0.54%
Mismatches	185,221
Insertions	5,161
Mapped reads with at least one insertion	0.94%
Deletions	9,446
Mapped reads with at least one deletion	1.73%
Homopolymer indels	41.37%

2.6. Chromosome stats

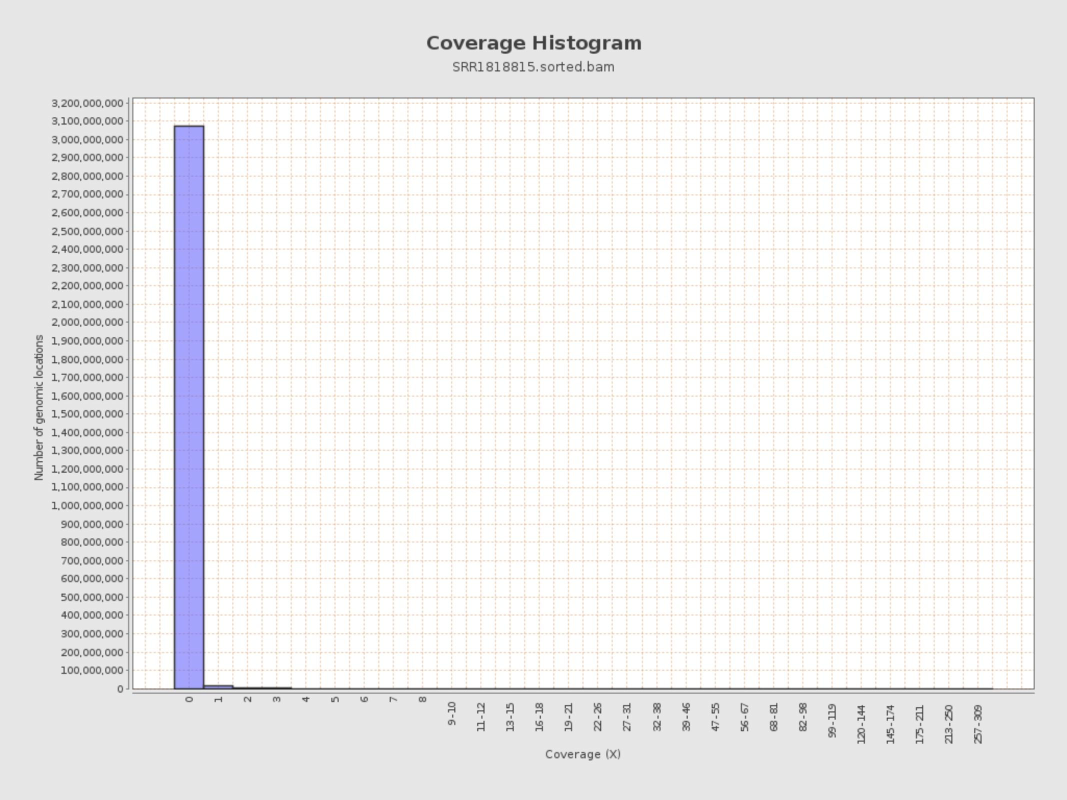
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3025652	0.0121	0.244
chr2	243199373	3253364	0.0134	0.2881
chr3	198022430	2525812	0.0128	0.1572
chr4	191154276	2430588	0.0127	0.1679
chr5	180915260	2283420	0.0126	0.1575
chr6	171115067	2143635	0.0125	0.1638
chr7	159138663	2019052	0.0127	0.1756

chr8	146364022	1896502	0.013	0.1711
chr9	141213431	1553704	0.011	0.1563
chr10	135534747	1797843	0.0133	0.2093
chr11	135006516	1783526	0.0132	0.1716
chr12	133851895	1644444	0.0123	0.1631
chr13	115169878	1173762	0.0102	0.1398
chr14	107349540	1125437	0.0105	0.1509
chr15	102531392	1040857	0.0102	0.1403
chr16	90354753	1094971	0.0121	0.2141
chr17	81195210	965028	0.0119	0.1587
chr18	78077248	995605	0.0128	0.1929
chr19	59128983	709527	0.012	0.2113
chr20	63025520	792371	0.0126	0.1611
chr21	48129895	479979	0.01	0.1431
chr22	51304566	430823	0.0084	0.1359
chrMT	16571	26333	1.5891	2.3579
chrX	155270560	1120942	0.0072	0.1222
chrY	59373566	361030	0.0061	0.3081

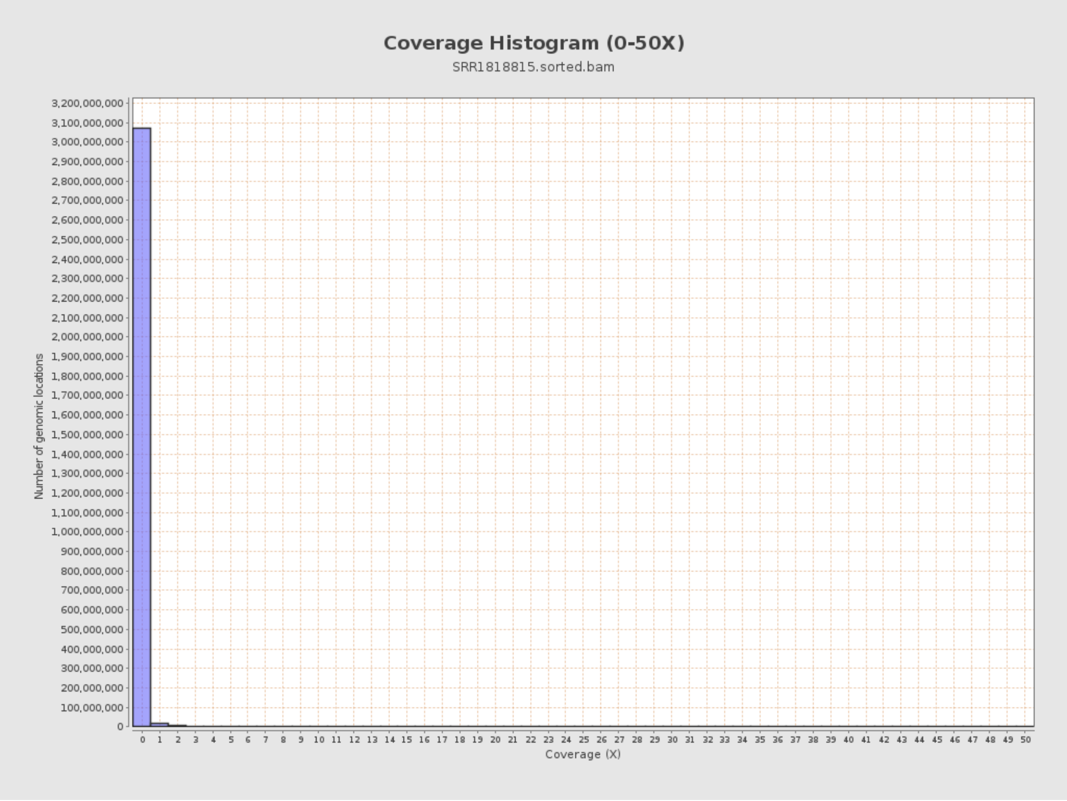
3. Results : Coverage across reference



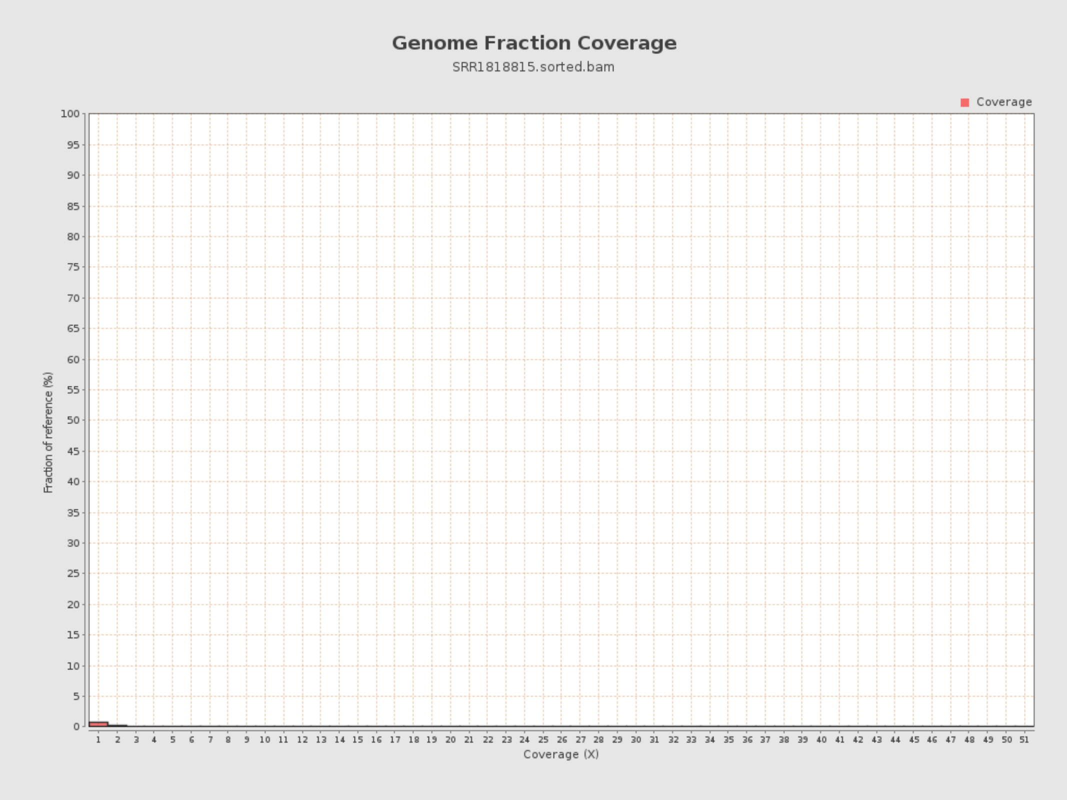
4. Results : Coverage Histogram



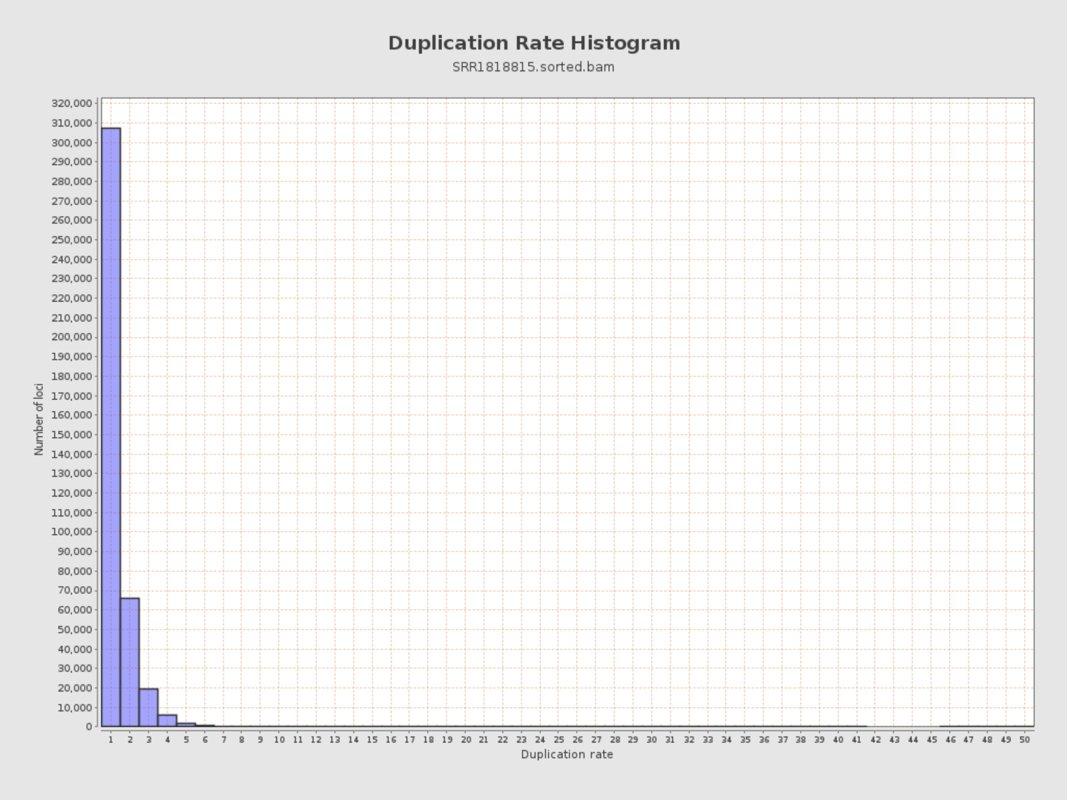
5. Results : Coverage Histogram (0-50X)



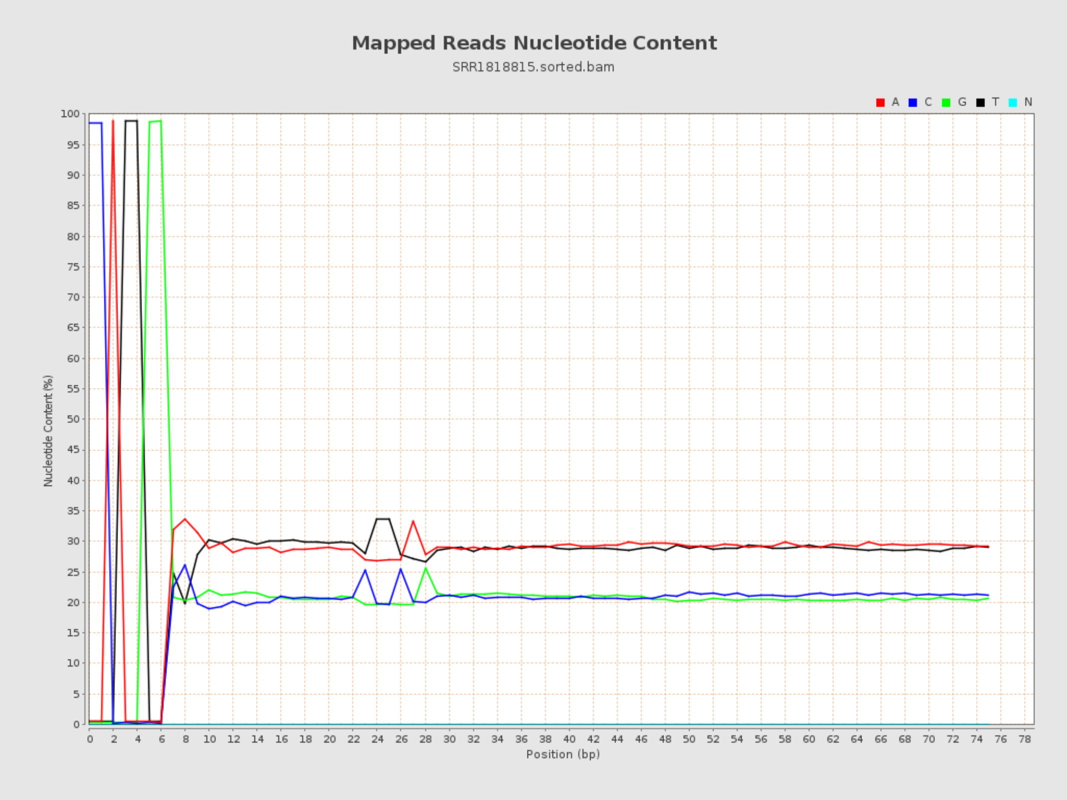
6. Results : Genome Fraction Coverage



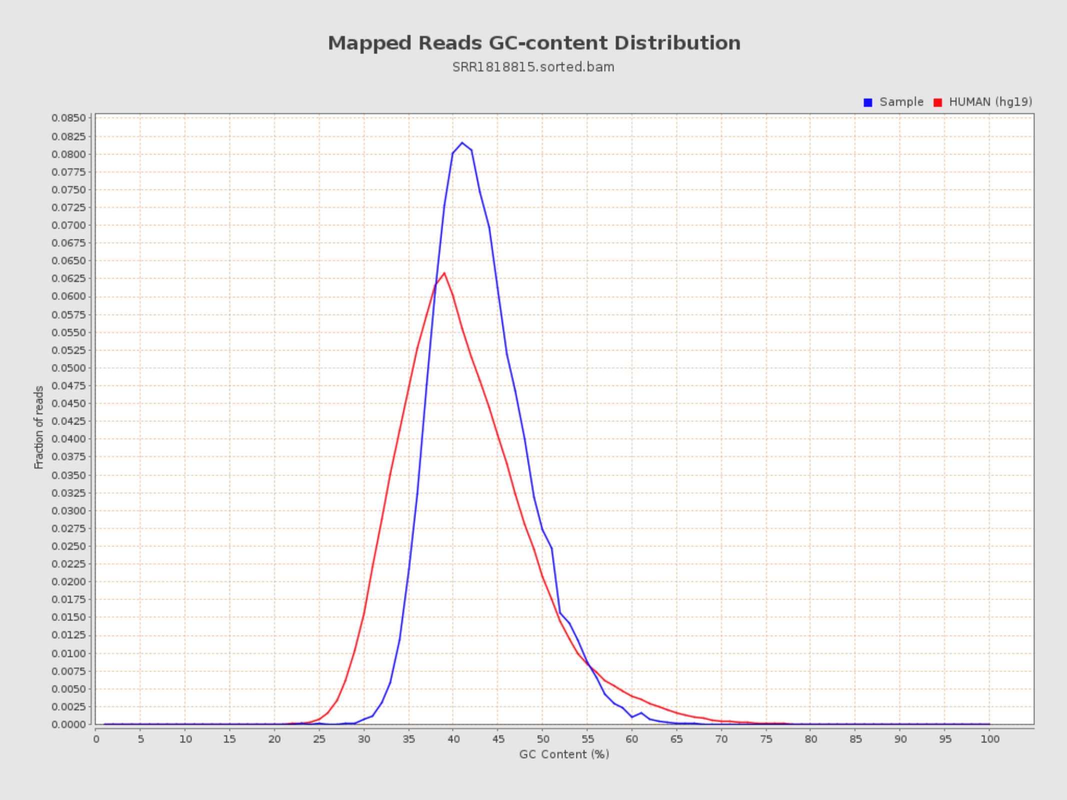
7. Results : Duplication Rate Histogram



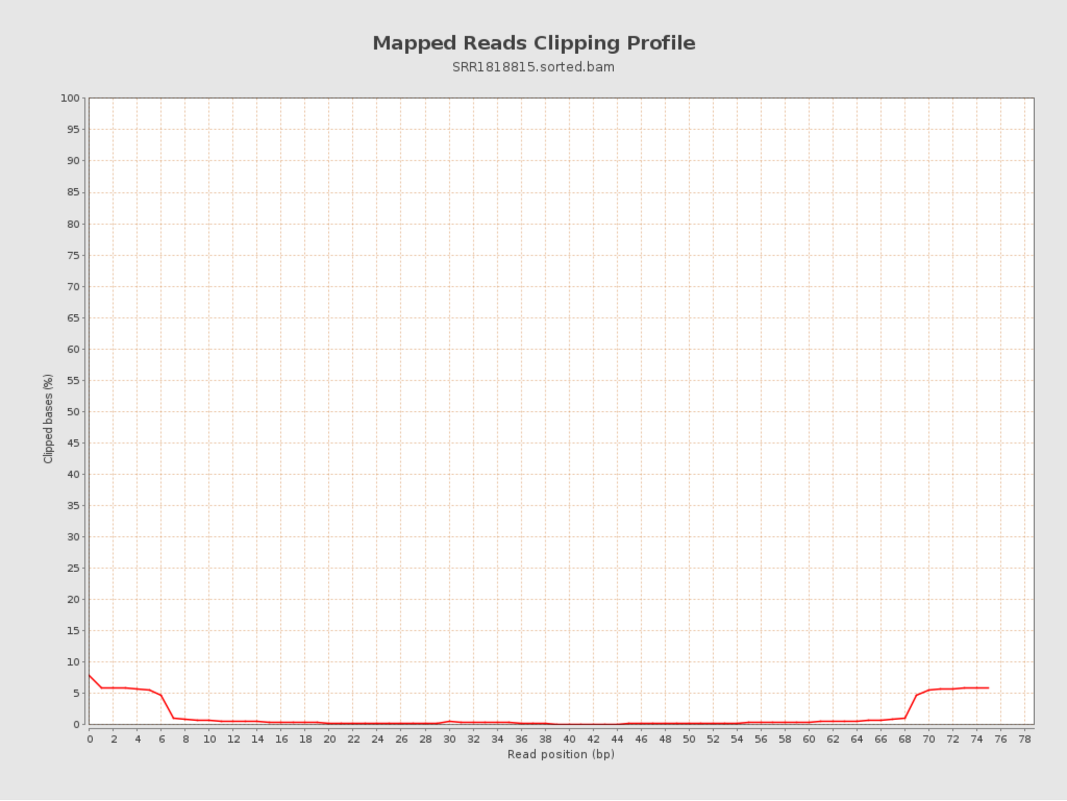
8. Results : Mapped Reads Nucleotide Content



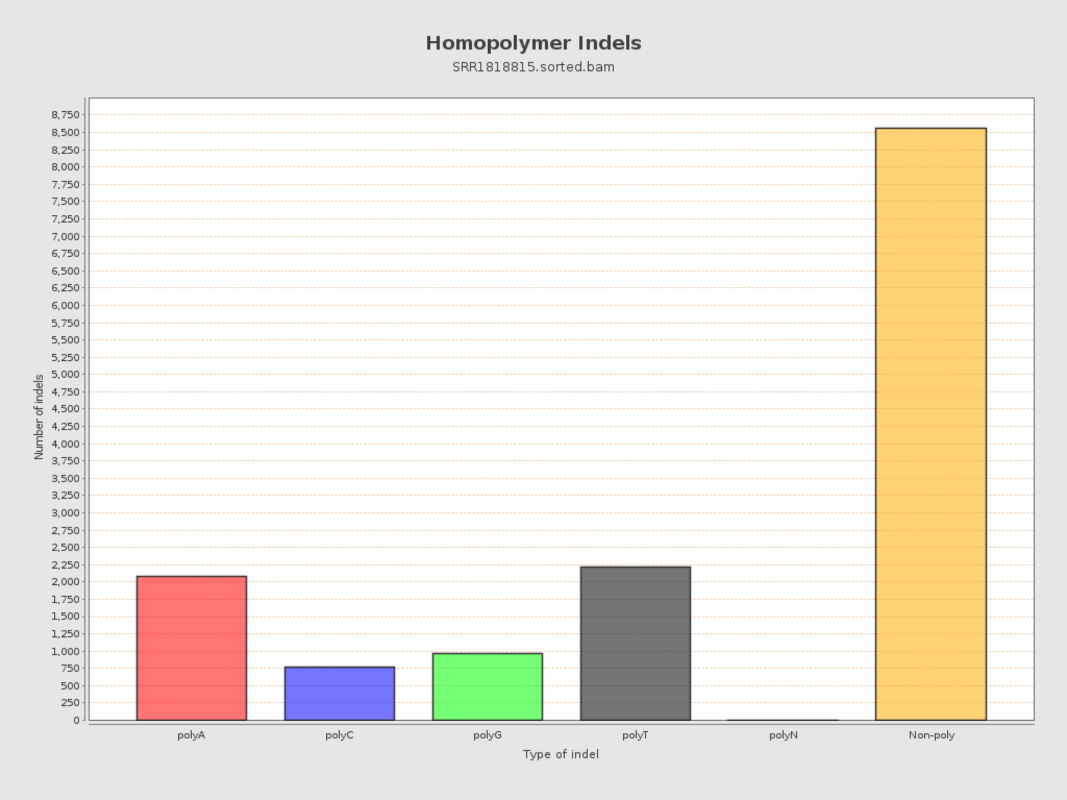
9. Results : Mapped Reads GC-content Distribution



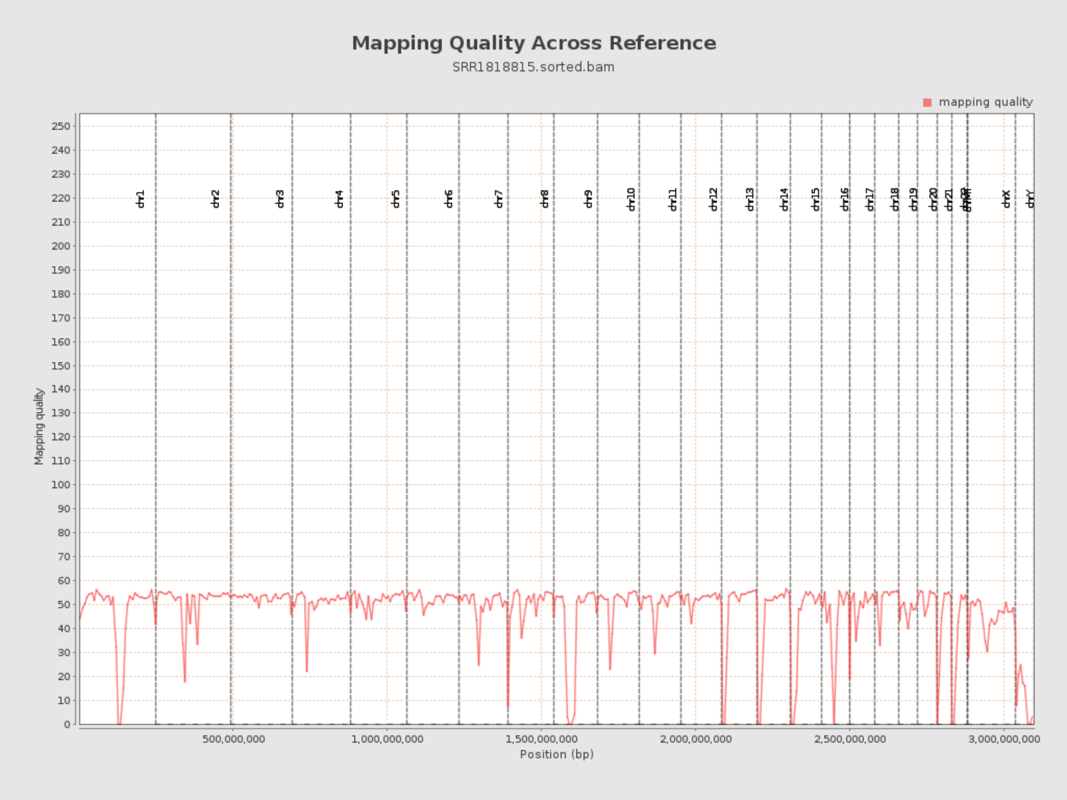
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram