Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:57:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505954.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_SRR1505954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505954.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:57:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,400,331
Mapped reads	9,436,771 / 76.1%
Unmapped reads	2,963,560 / 23.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	317 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	395,397 / 3.19%
Duplication rate	2.64%
Clipped reads	1,294,934 / 10.44%

2.2. ACGT Content

Number/percentage of A's	131,079,351 / 29.76%
Number/percentage of C's	89,579,043 / 20.34%
Number/percentage of T's	128,648,853 / 29.21%
Number/percentage of G's	91,109,712 / 20.69%
Number/percentage of N's	1,334 / 0%
GC Percentage	41.03%

2.3. Coverage

Mean	0.1423

Standard Deviation	1.2333

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

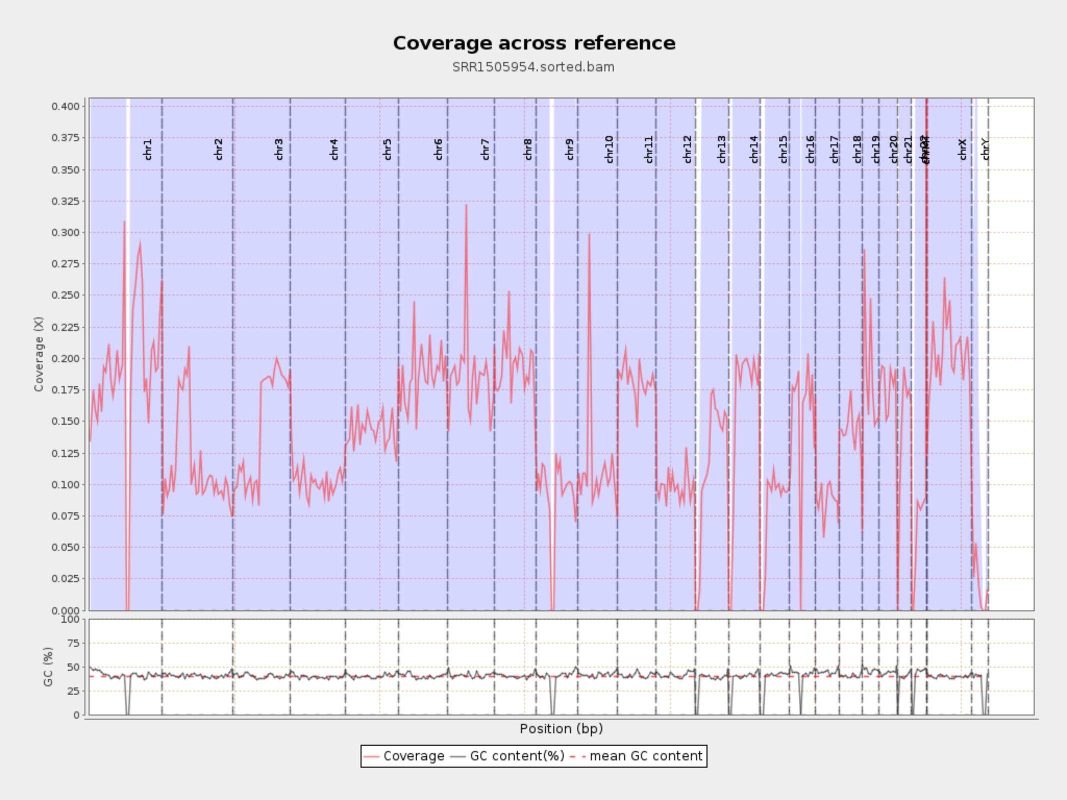
General error rate	0.46%
Mismatches	2,015,766
Insertions	17,683
Mapped reads with at least one insertion	0.19%
Deletions	64,643
Mapped reads with at least one deletion	0.68%
Homopolymer indels	47.3%

2.6. Chromosome stats

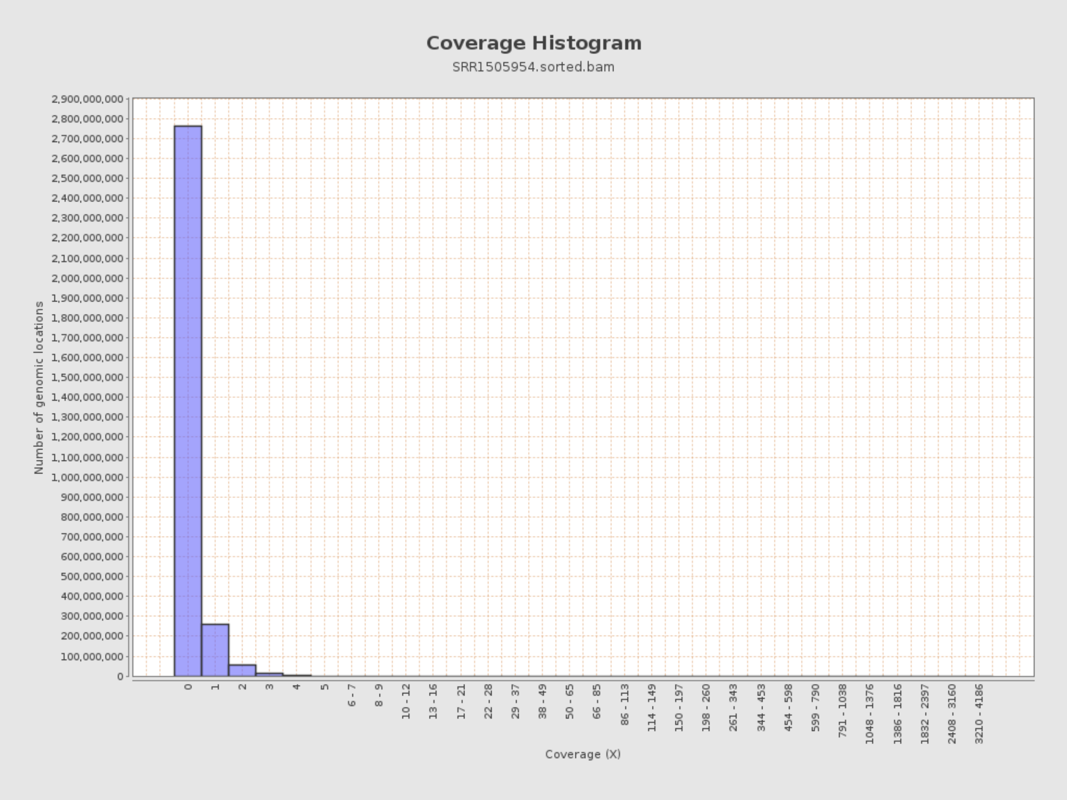
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	47106577	0.189	2.9711
chr2	243199373	28152020	0.1158	0.8145
chr3	198022430	28579830	0.1443	0.5095
chr4	191154276	19697647	0.103	0.4049
chr5	180915260	25857488	0.1429	0.4854
chr6	171115067	32084062	0.1875	0.7933
chr7	159138663	29775957	0.1871	1.9358

chr8	146364022	28210684	0.1927	1.4108
chr9	141213431	12739261	0.0902	0.6694
chr10	135534747	15389716	0.1135	1.6209
chr11	135006516	24354036	0.1804	1.0304
chr12	133851895	13143266	0.0982	0.4511
chr13	115169878	13375834	0.1161	0.4117
chr14	107349540	17023607	0.1586	0.5837
chr15	102531392	8097623	0.079	0.3444
chr16	90354753	14047577	0.1555	0.7157
chr17	81195210	7032985	0.0866	0.4807
chr18	78077248	11301256	0.1447	1.4044
chr19	59128983	10960812	0.1854	1.924
chr20	63025520	11079338	0.1758	0.5359
chr21	48129895	6886578	0.1431	0.5379
chr22	51304566	3074499	0.0599	0.3272
chrMT	16571	29845	1.801	1.7081
chrX	155270560	31266636	0.2014	0.7319
chrY	59373566	1241054	0.0209	0.2525

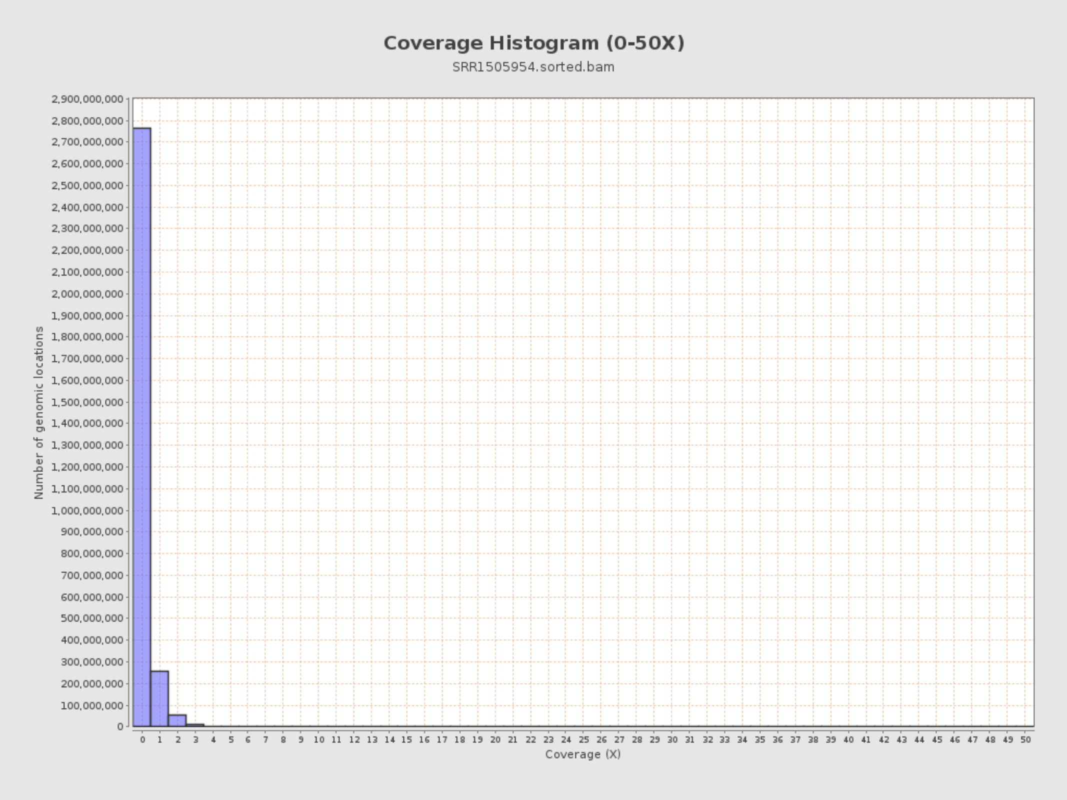
3. Results : Coverage across reference



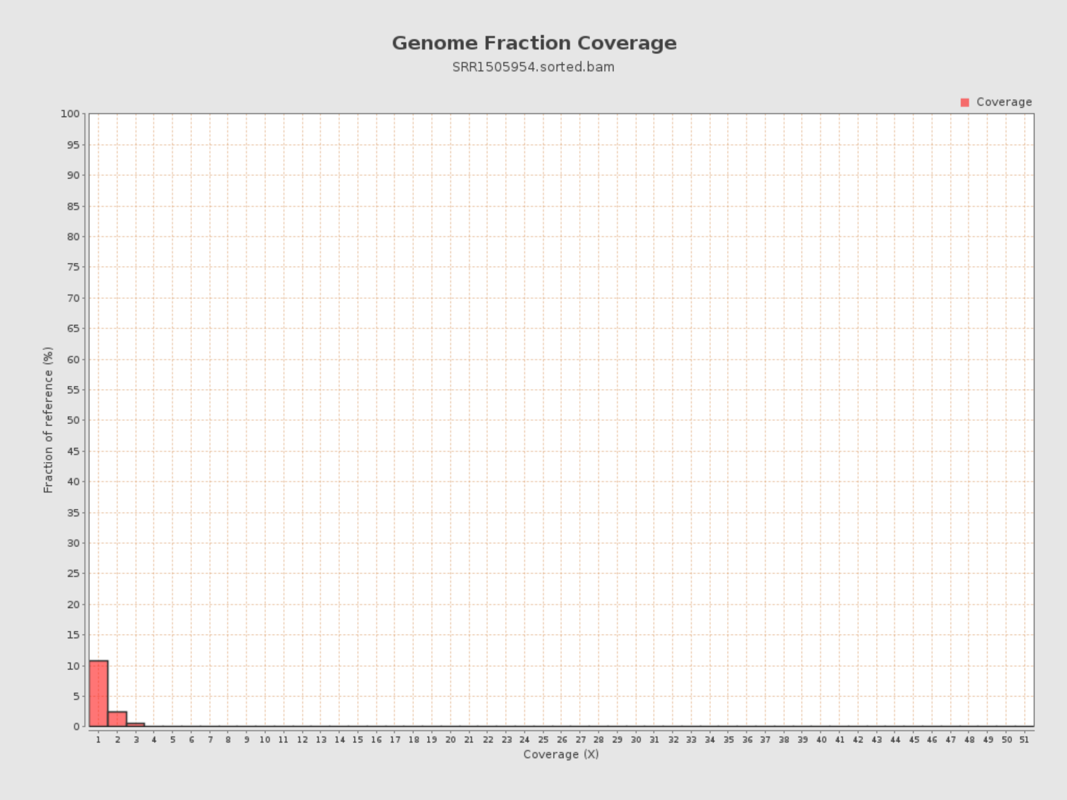
4. Results : Coverage Histogram



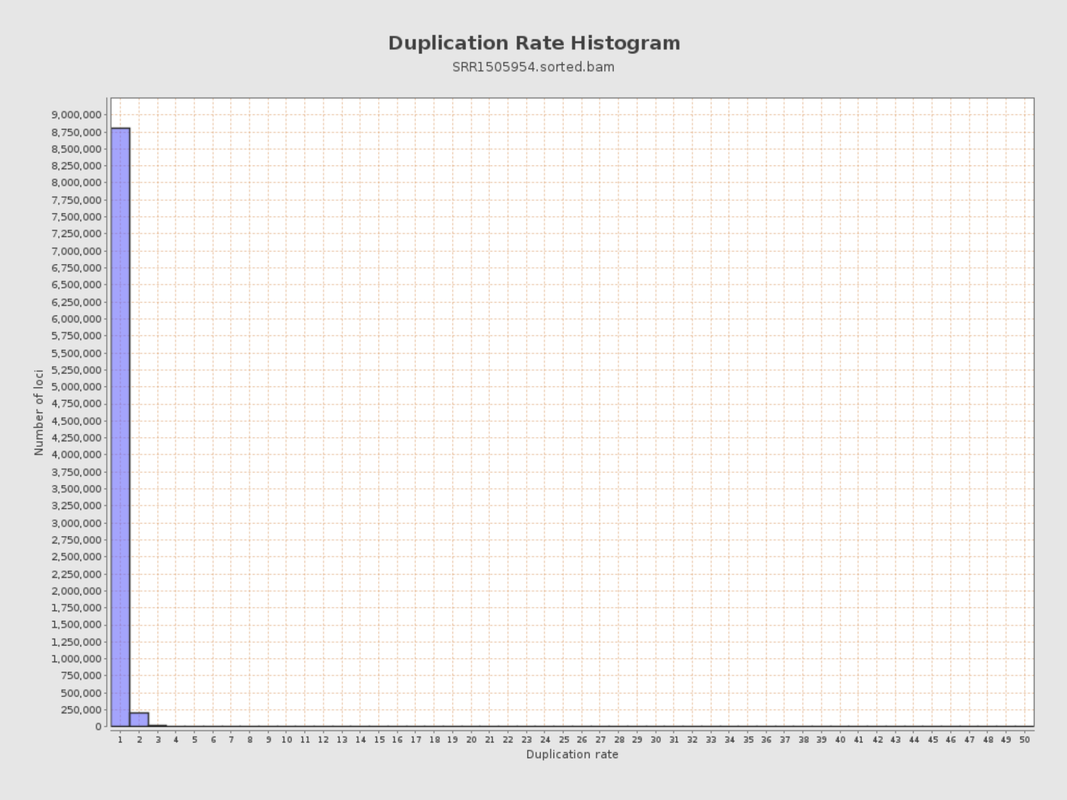
5. Results : Coverage Histogram (0-50X)



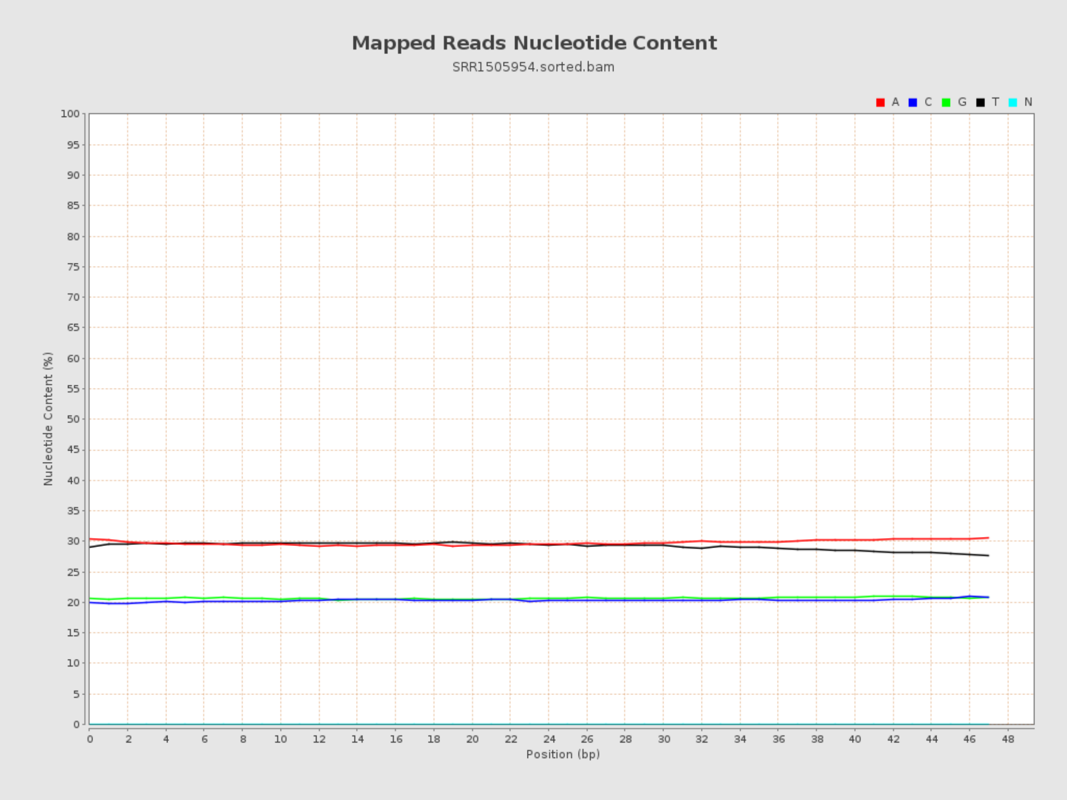
6. Results : Genome Fraction Coverage



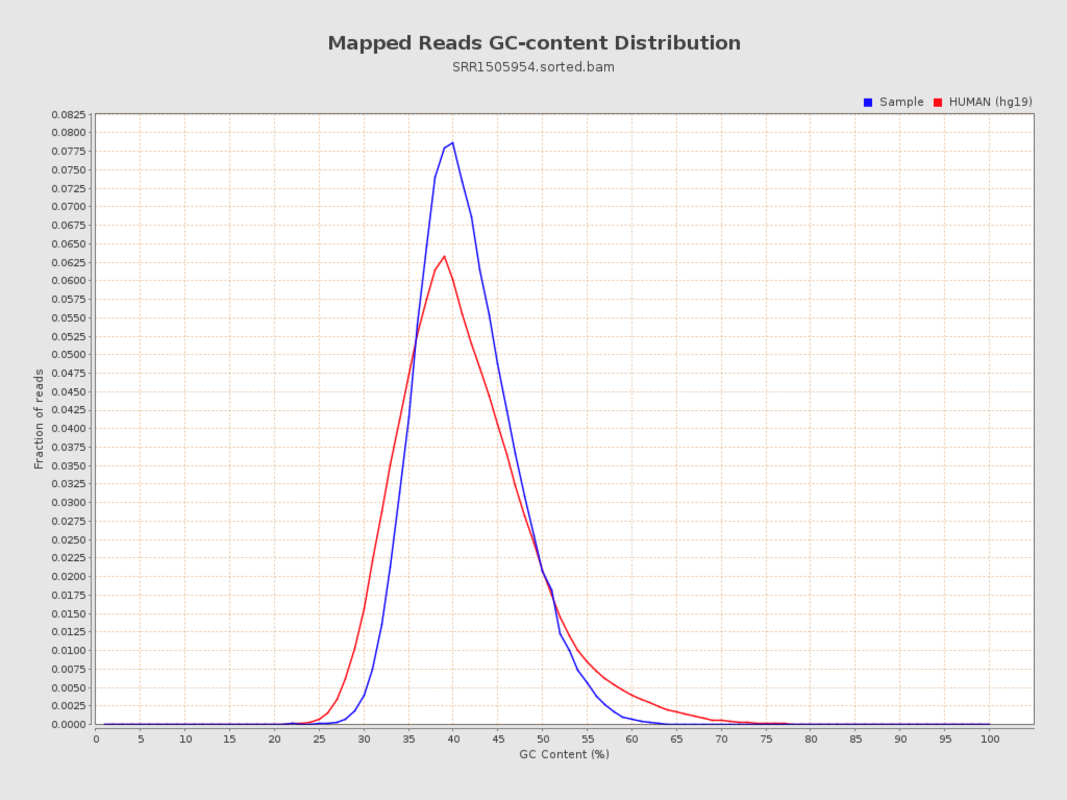
7. Results : Duplication Rate Histogram



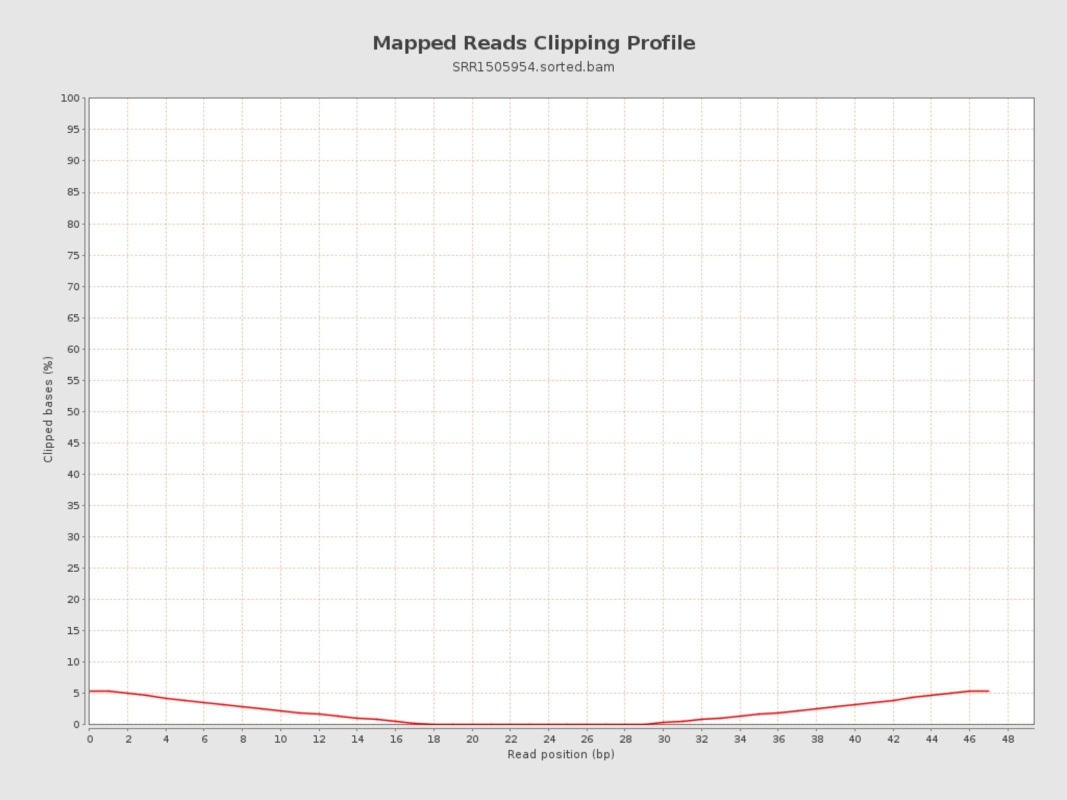
8. Results : Mapped Reads Nucleotide Content



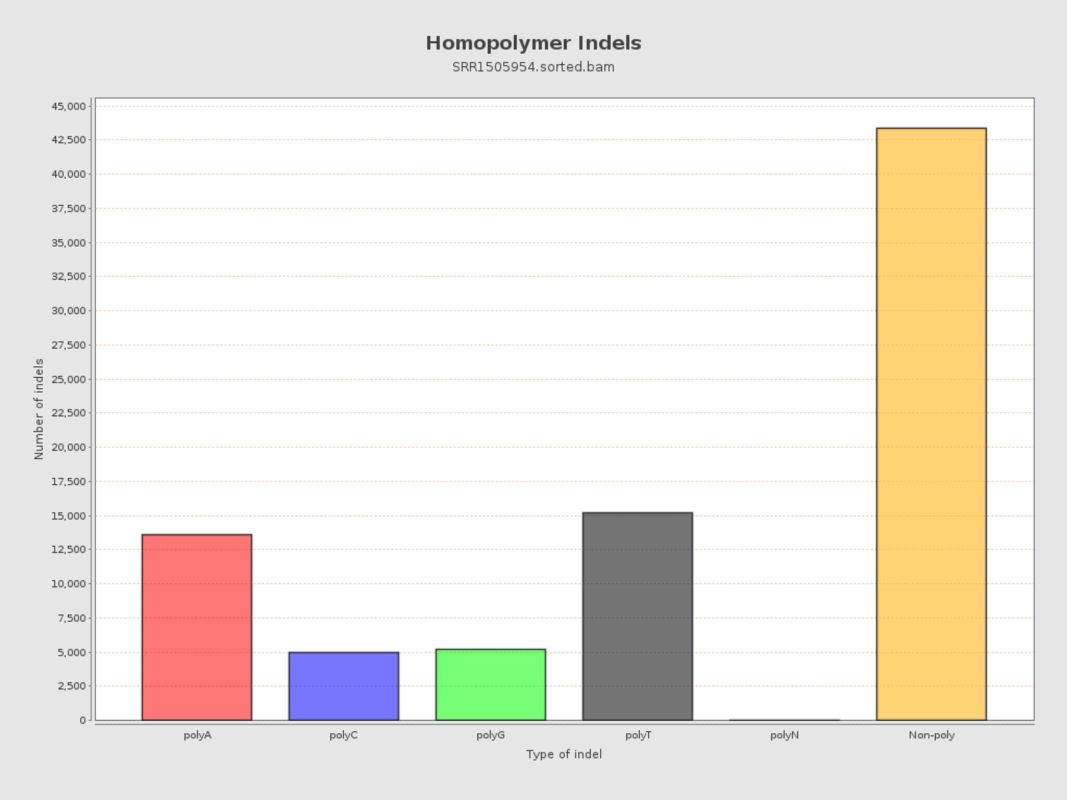
9. Results : Mapped Reads GC-content Distribution



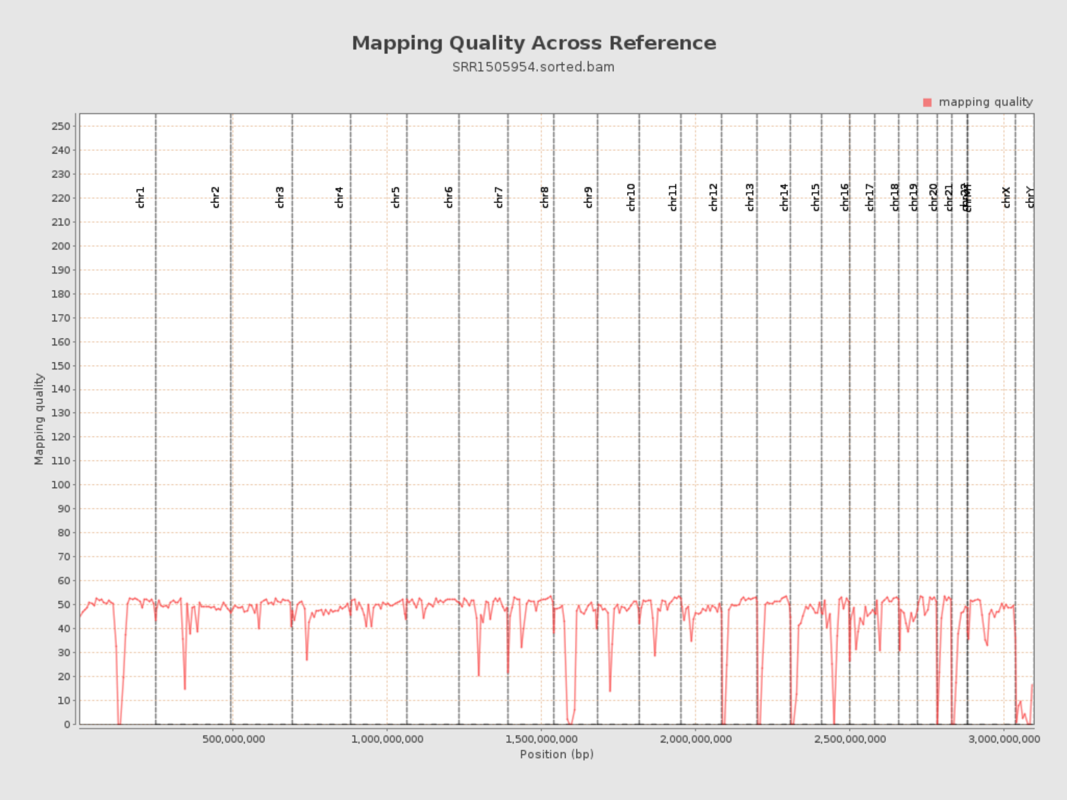
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram