Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:06:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013356.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_SRR6013356 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013356.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:06:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013356.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,534,910
Mapped reads	970,489 / 63.23%
Unmapped reads	564,421 / 36.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,577 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	33,578 / 2.19%
Duplication rate	2.75%
Clipped reads	676,503 / 44.07%

2.2. ACGT Content

Number/percentage of A's	16,805,235 / 29.2%
Number/percentage of C's	11,123,360 / 19.33%
Number/percentage of T's	17,137,179 / 29.78%
Number/percentage of G's	12,479,685 / 21.69%
Number/percentage of N's	696 / 0%
GC Percentage	41.02%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.2016

2.4. Mapping Quality

Mean Mapping Quality	44.13

2.5. Mismatches and indels

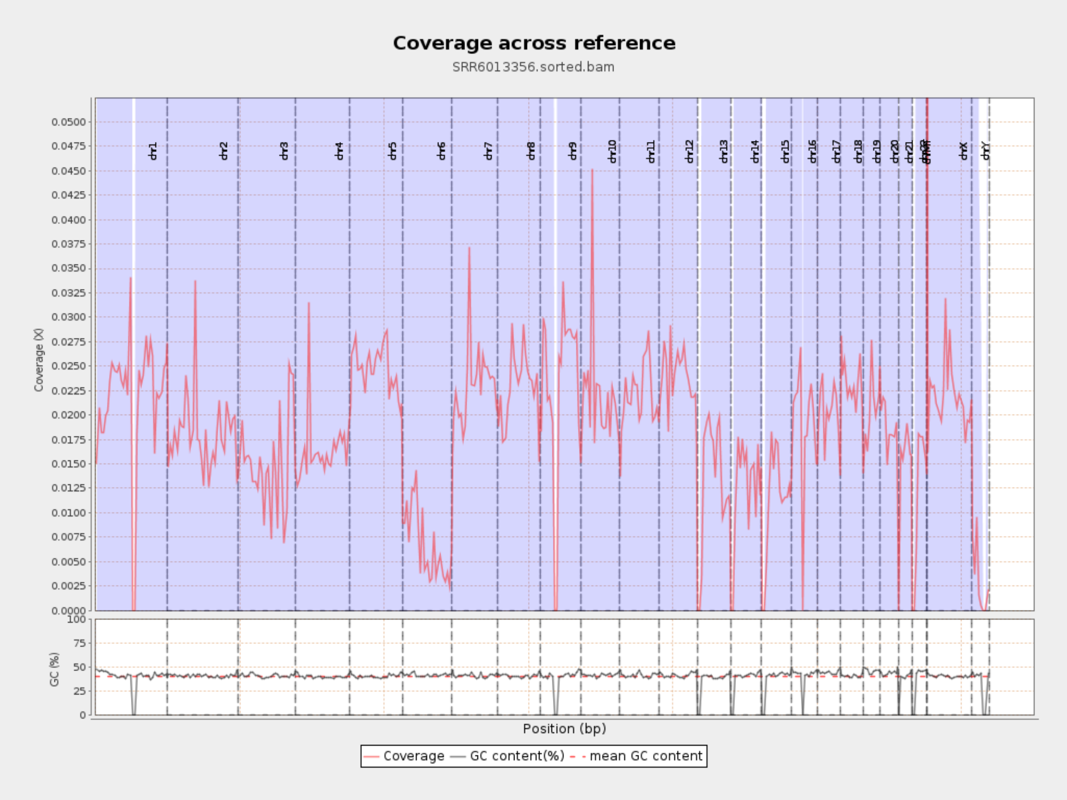
General error rate	0.79%
Mismatches	447,332
Insertions	4,129
Mapped reads with at least one insertion	0.42%
Deletions	15,118
Mapped reads with at least one deletion	1.54%
Homopolymer indels	43.77%

2.6. Chromosome stats

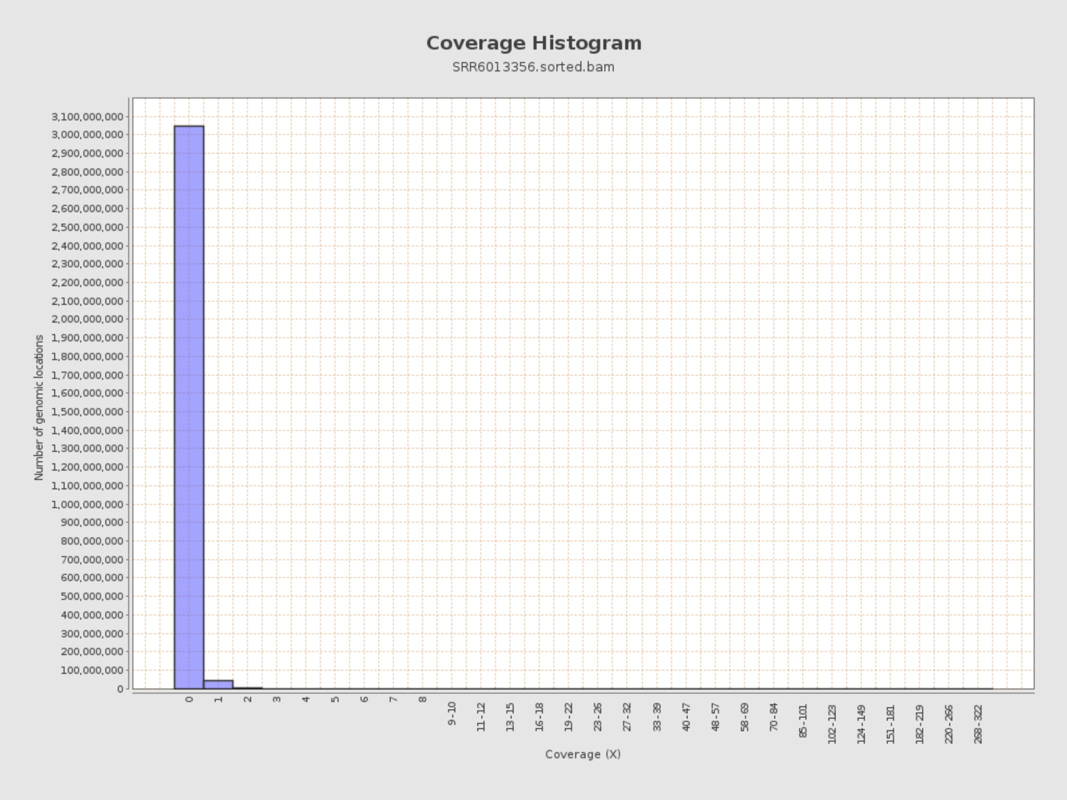
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5400899	0.0217	0.3152
chr2	243199373	4435387	0.0182	0.2368
chr3	198022430	2996076	0.0151	0.1377
chr4	191154276	3136273	0.0164	0.1566
chr5	180915260	4506999	0.0249	0.1748
chr6	171115067	1145547	0.0067	0.1009
chr7	159138663	3696824	0.0232	0.2729

chr8	146364022	3359980	0.023	0.2458
chr9	141213431	3236241	0.0229	0.198
chr10	135534747	2987312	0.022	0.2471
chr11	135006516	2993464	0.0222	0.1809
chr12	133851895	3221941	0.0241	0.1739
chr13	115169878	1499251	0.013	0.1273
chr14	107349540	1305490	0.0122	0.1302
chr15	102531392	1149498	0.0112	0.1178
chr16	90354753	1686066	0.0187	0.1622
chr17	81195210	1649743	0.0203	0.1701
chr18	78077248	1821246	0.0233	0.2917
chr19	59128983	1215221	0.0206	0.2395
chr20	63025520	1167333	0.0185	0.1521
chr21	48129895	729928	0.0152	0.1494
chr22	51304566	610538	0.0119	0.1204
chrMT	16571	18275	1.1028	1.4112
chrX	155270560	3428948	0.0221	0.1787
chrY	59373566	173677	0.0029	0.091

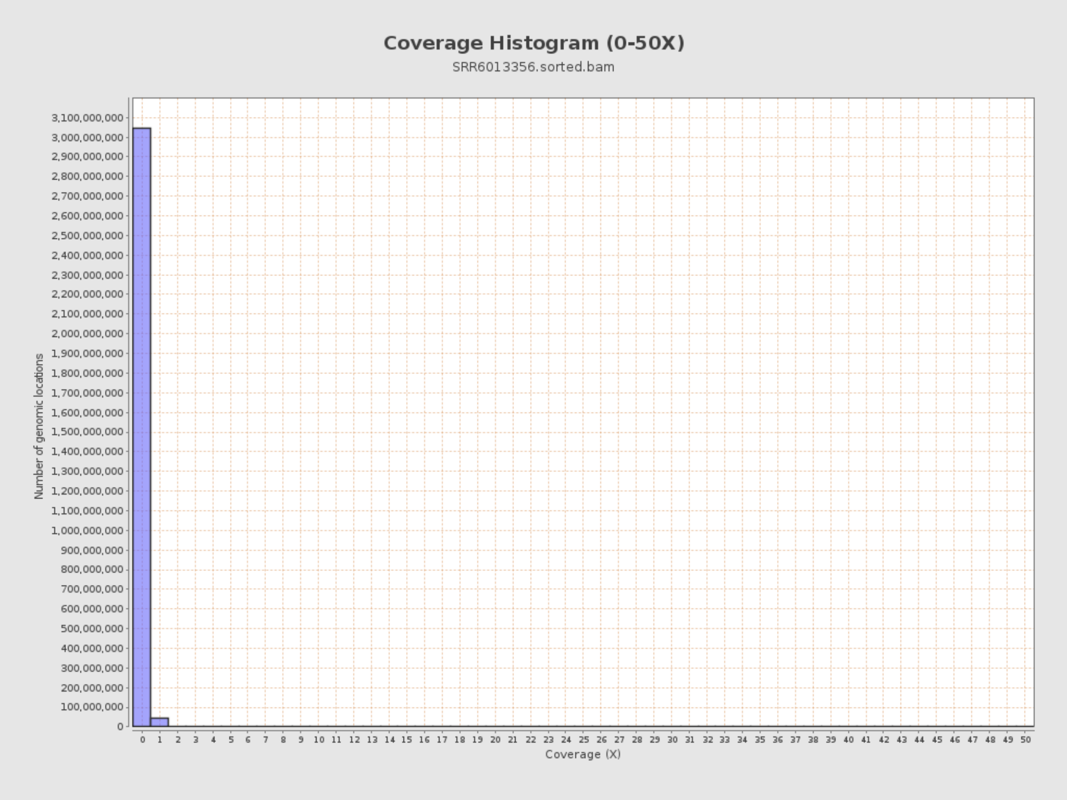
3. Results : Coverage across reference



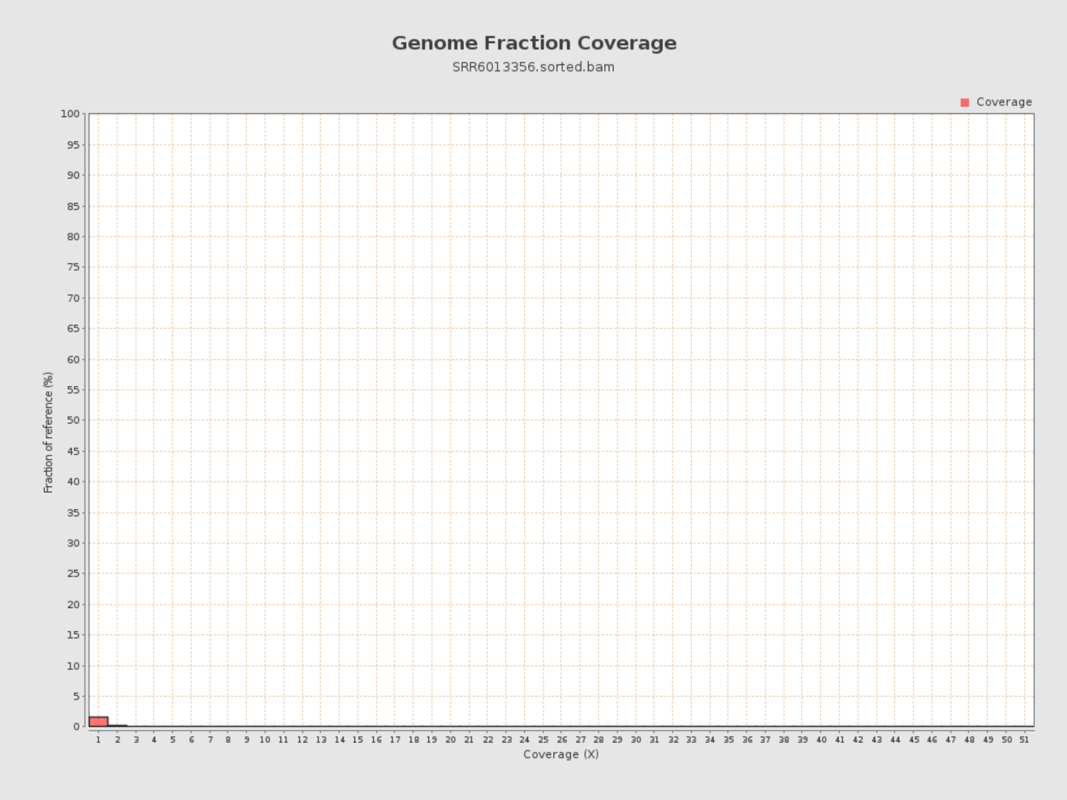
4. Results : Coverage Histogram



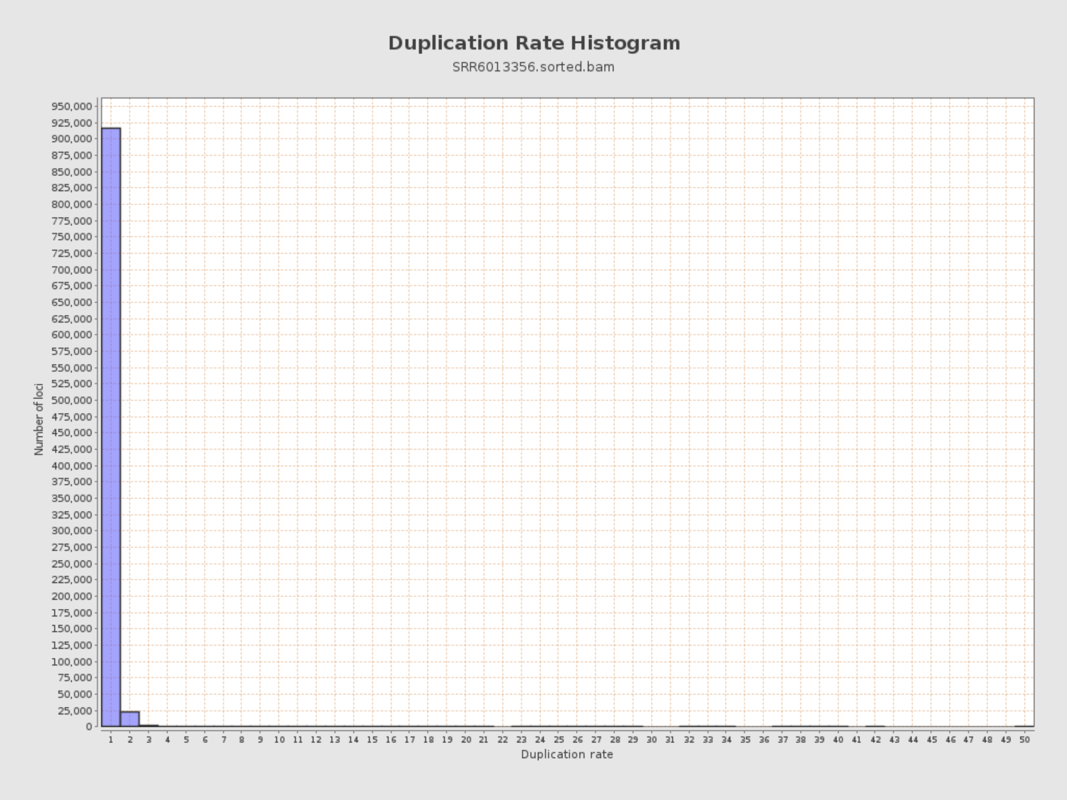
5. Results : Coverage Histogram (0-50X)



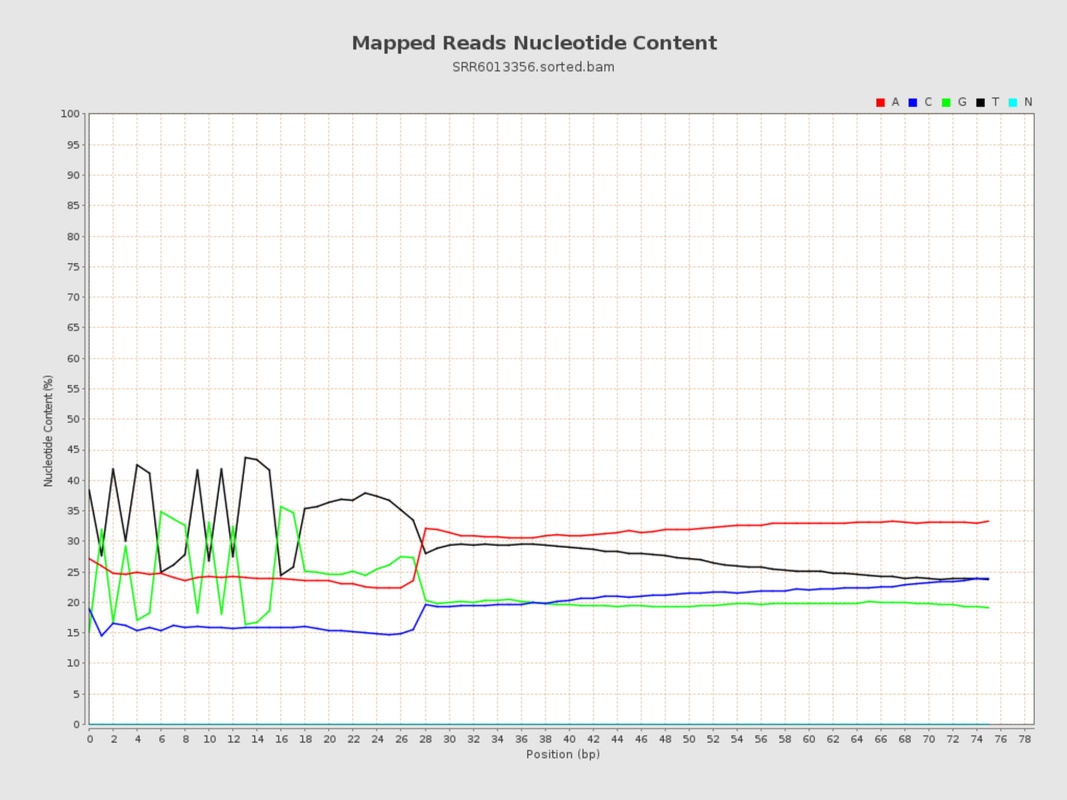
6. Results : Genome Fraction Coverage



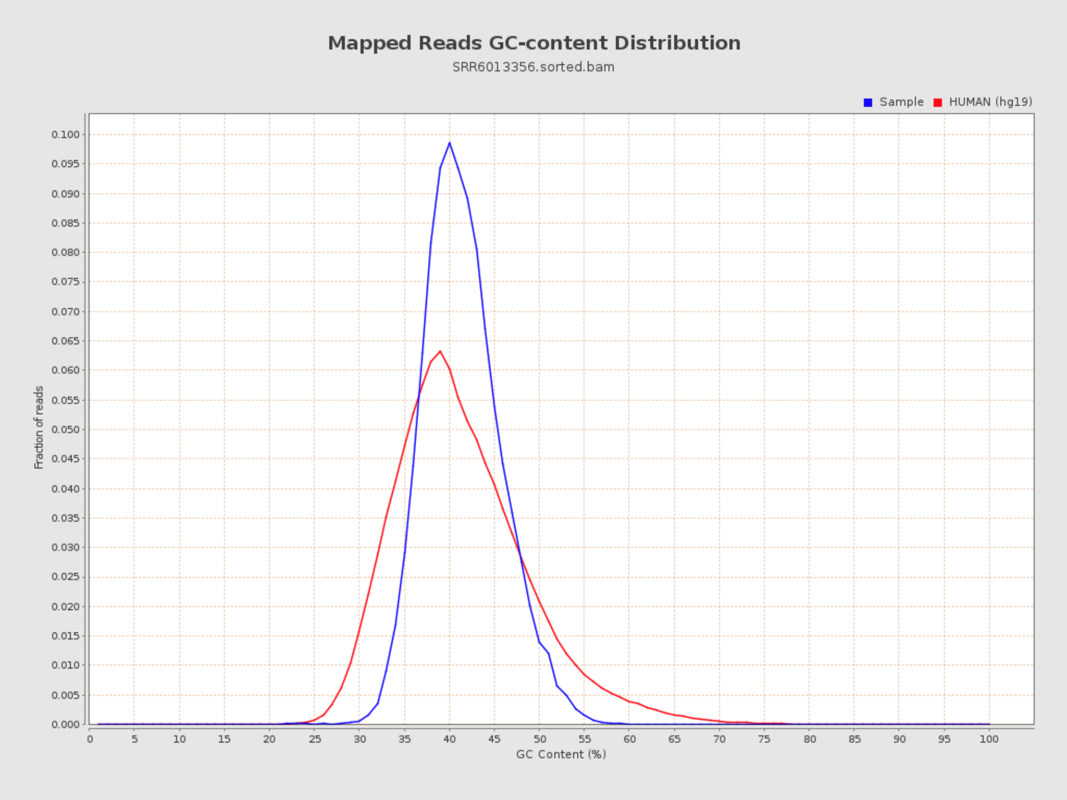
7. Results : Duplication Rate Histogram



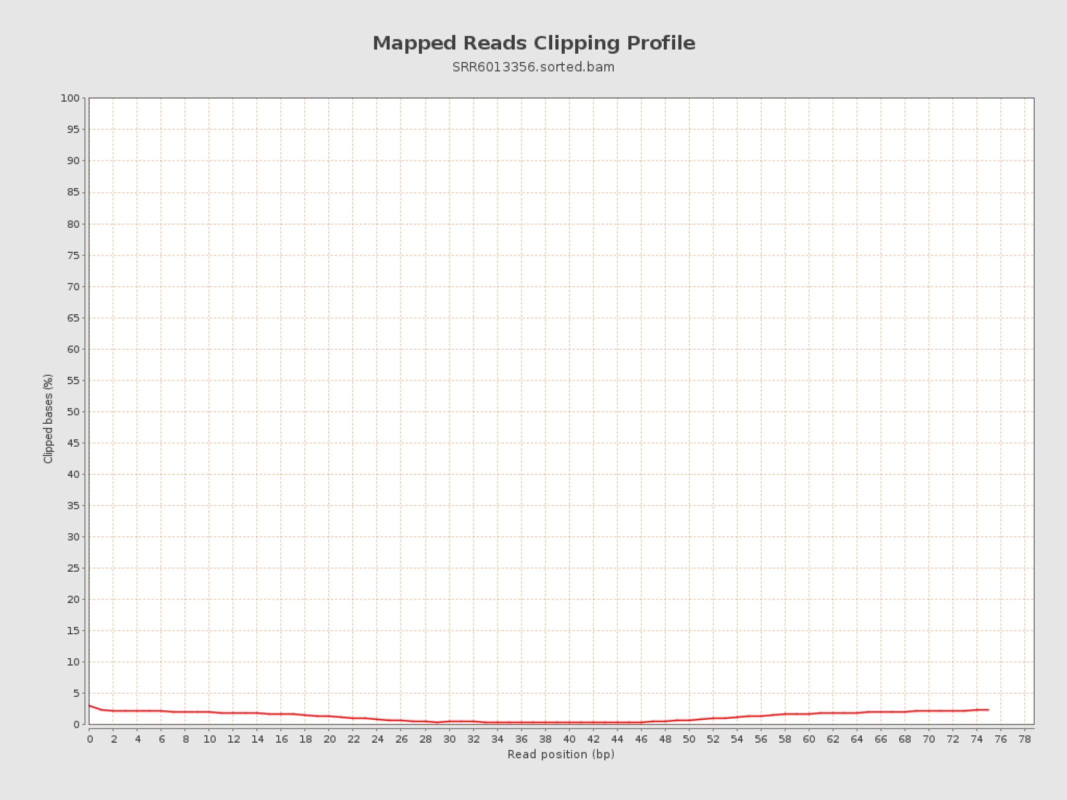
8. Results : Mapped Reads Nucleotide Content



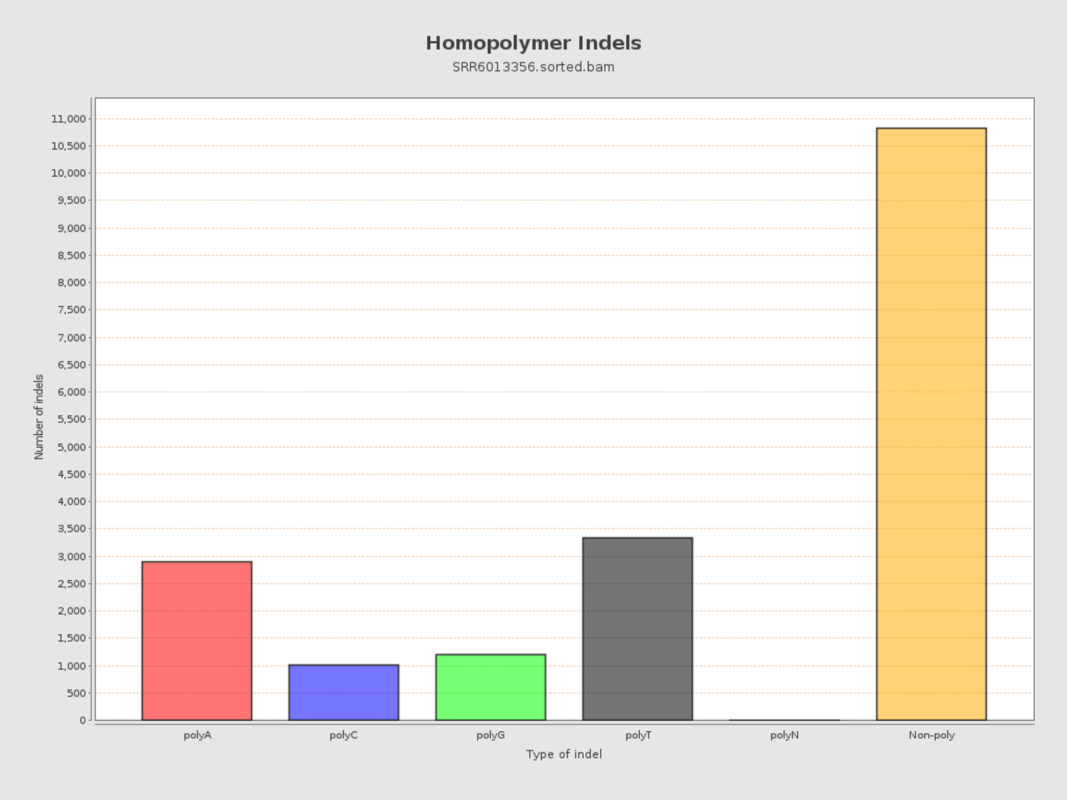
9. Results : Mapped Reads GC-content Distribution



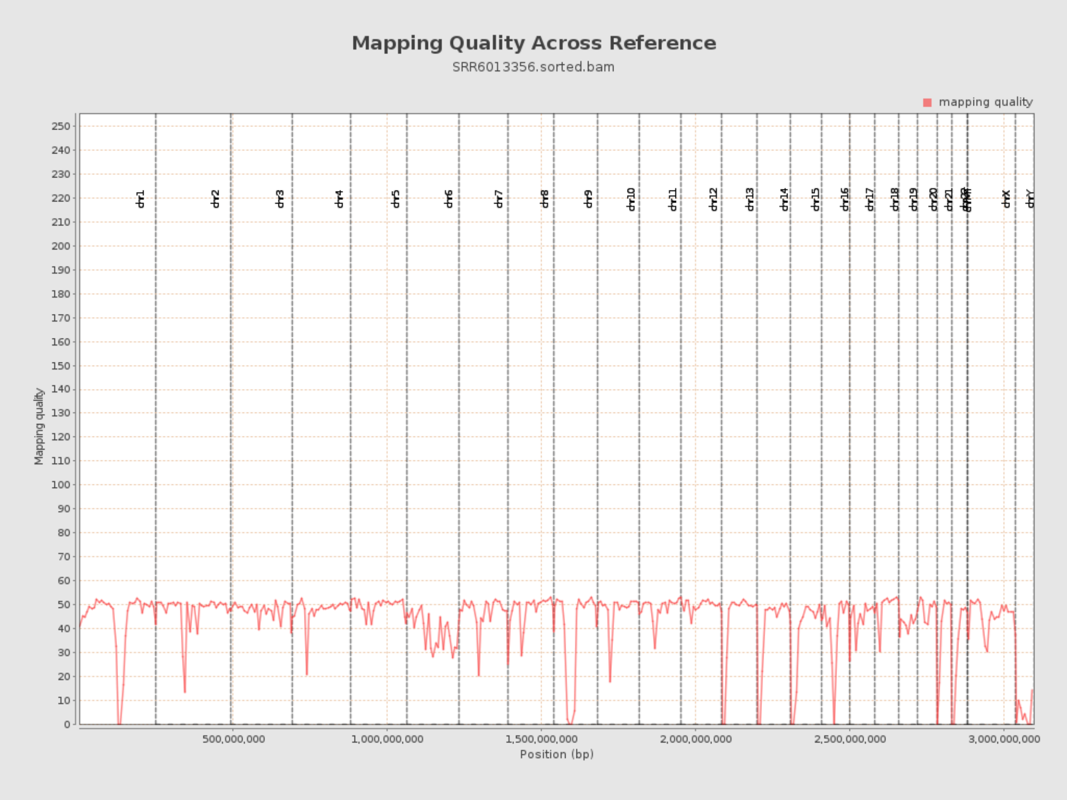
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram