

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2021/01/12 16:14:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /opt/tsinghua/zhangwei/Pipeline_test/o_WGS-
PE/intermediate_result/step_05_bamsort/H1186-Pre_sorted.bam -nw 400 -
hm 3
```

1.2. Alignment

Command line:	"/home/zhangwei/software/miniconda3/envs/cfDNApipe/bin/bowtie2-align-s --wrapper basic-0 -x /home/zhangwei/Genome/hg19_bowtie2/hg19 -q -N 1 --time -p 60 --passthrough -1 /opt/tsinghua/zhangwei/Pipeline_test/o_WGS-PE/intermediate_result/step_03_adapterremoval/H1186-Pre.pair1.truncated.gz -2 /opt/tsinghua/zhangwei/Pipeline_test/o_WGS-PE/intermediate_result/step_03_adapterremoval/H1186-Pre.pair2.truncated.gz"
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bowtie2 (2.4.2)
Analysis date:	Tue Jan 12 16:14:45 CST 2021
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400

BAM file:

/opt/tsinghua/zhangwei/Pipeline_test/
o_WGS-
PE/intermediate_result/step_05_bam
sort/H1186-Pre_sorted.bam

2. Summary

2.1. Globals

Reference size	3,137,161,264
Number of reads	1,995,032
Mapped reads	1,889,403 / 94.71%
Unmapped reads	105,629 / 5.29%
Mapped paired reads	1,889,403 / 94.71%
Mapped reads, first in pair	946,927 / 47.46%
Mapped reads, second in pair	942,476 / 47.24%
Mapped reads, both in pair	1,879,196 / 94.19%
Mapped reads, singletons	10,207 / 0.51%
Secondary alignments	0
Read min/max/mean length	20 / 150 / 145.86
Duplicated reads (estimated)	267,732 / 13.42%
Duplication rate	15.8%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	79,116,677 / 28.73%
Number/percentage of C's	58,538,946 / 21.26%
Number/percentage of T's	79,119,879 / 28.74%
Number/percentage of G's	58,564,914 / 21.27%
Number/percentage of N's	5,114 / 0%
GC Percentage	42.53%

2.3. Coverage

Mean	0.0878
Standard Deviation	0.6432

2.4. Mapping Quality

Mean Mapping Quality	32.33
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2.5. Insert size

Mean	13,183.53
Standard Deviation	1,151,967.42
P25/Median/P75	149 / 164 / 175

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	1,400,636
Insertions	32,694
Mapped reads with at least one insertion	1.6%
Deletions	30,564
Mapped reads with at least one deletion	1.55%
Homopolymer indels	60.52%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

chr1	249250621	25272613	0.1014	1.1331
chr2	243199373	23962544	0.0985	0.5396
chr3	198022430	17410365	0.0879	0.4207
chr4	191154276	15975146	0.0836	0.4038
chr5	180915260	17382792	0.0961	0.4244
chr6	171115067	15796692	0.0923	0.5444
chr7	159138663	15132073	0.0951	0.7693
chr8	146364022	13781875	0.0942	0.4439
chr9	141213431	10368403	0.0734	0.386
chr10	135534747	14416678	0.1064	1.4037
chr11	135006516	13204339	0.0978	0.5112
chr12	133851895	11868393	0.0887	0.405
chr13	115169878	8055711	0.0699	0.3616
chr14	107349540	9091017	0.0847	0.3984
chr15	102531392	8126963	0.0793	0.3852
chr16	90354753	8564124	0.0948	0.7481
chr17	81195210	8038496	0.099	0.4765
chr18	78077248	7269362	0.0931	0.5745
chr19	59128983	5997717	0.1014	0.9719
chr20	63025520	6299500	0.1	0.4305
chr21	48129895	3343037	0.0695	0.374
chr22	51304566	3779989	0.0737	0.3742
chrX	155270560	7421686	0.0478	0.3195
chrY	59373566	1447361	0.0244	0.3273

chrM	16571	3034	0.1831	0.5871
chr1_gl000191_random	106433	3712	0.0349	0.2472
chr1_gl000192_random	547496	62334	0.1139	0.4629
chr4_ctg9_hap1	590426	23177	0.0393	0.2677
chr4_gl000193_random	189789	56772	0.2991	0.8802
chr4_gl000194_random	191469	41875	0.2187	0.6309
chr6_apd_hap1	4622290	28114	0.0061	0.1048
chr6_cox_hap2	4795371	86269	0.018	0.1812
chr6_dbb_hap3	4610396	54105	0.0117	0.1467
chr6_mann_hap4	4683263	46124	0.0098	0.1344
chr6_mcf_hap5	4833398	57868	0.012	0.1493
chr6_qbl_hap6	4611984	58201	0.0126	0.1534
chr6_ssto_hap7	4928567	61875	0.0126	0.1533
chr7_gl000195_random	182896	61693	0.3373	0.8079
chr8_gl000196_random	38914	1484	0.0381	0.2703

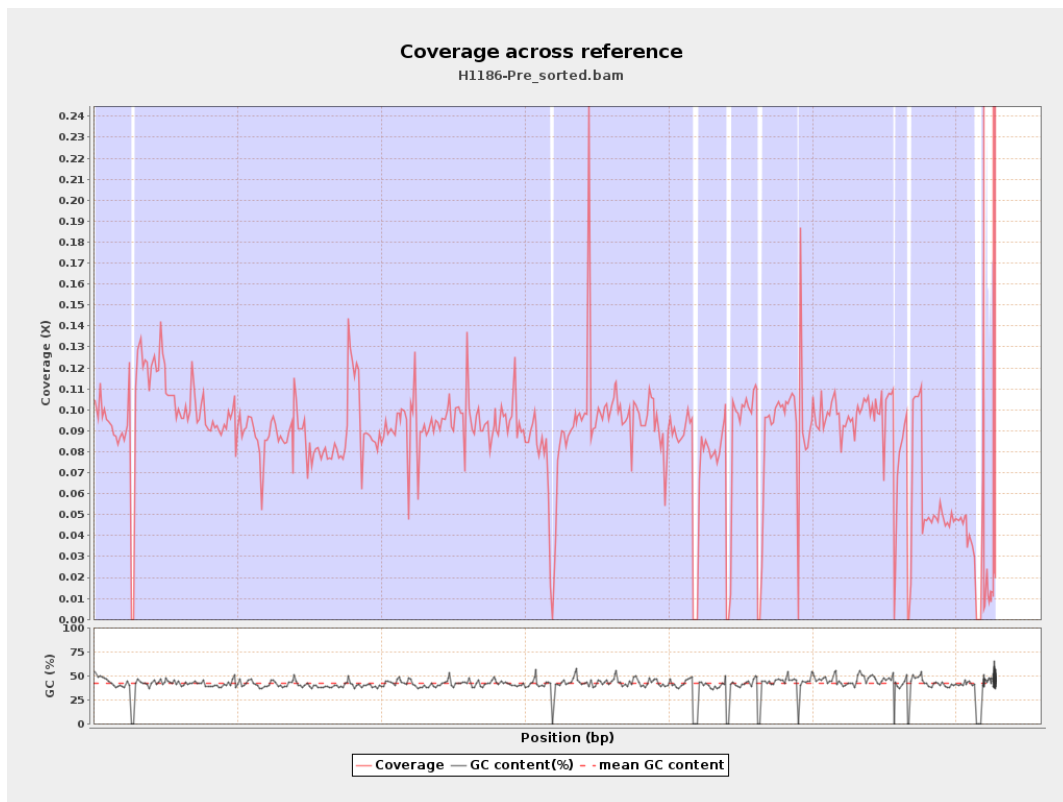
chr8_gl000197_random	37175	2206	0.0593	0.317
chr9_gl000198_random	90085	24898	0.2764	0.784
chr9_gl000199_random	169874	365724	2.1529	5.046
chr9_gl000200_random	187035	4058	0.0217	0.1938
chr9_gl000201_random	36148	3194	0.0884	0.4185
chr11_gl000202_random	40103	4356	0.1086	0.4341
chr17_ctg5_hap1	1680828	42479	0.0253	0.2187
chr17_gl000203_random	37498	2218	0.0591	0.3252
chr17_gl000204_random	81310	7836	0.0964	0.4269
chr17_gl000205_random	174588	52432	0.3003	0.7598
chr17_gl000206_random	41001	1794	0.0438	0.2825
chr18_gl000207_random	4262	899	0.2109	0.5718
chr19_gl000208_random	92689	46224	0.4987	1.6413
chr19_gl000209_random	159169	4294	0.027	0.2262
chr21_gl000210_random	27682	1486	0.0537	0.2832

chrUn_gl0002 11	166566	15644	0.0939	0.4298
chrUn_gl0002 12	186858	62249	0.3331	3.5834
chrUn_gl0002 13	164239	6391	0.0389	0.2579
chrUn_gl0002 14	137718	115918	0.8417	1.8736
chrUn_gl0002 15	172545	6444	0.0373	0.2571
chrUn_gl0002 16	172294	69365	0.4026	1.7551
chrUn_gl0002 17	172149	24437	0.142	0.5192
chrUn_gl0002 18	161147	22445	0.1393	0.5069
chrUn_gl0002 19	179198	46182	0.2577	0.7143
chrUn_gl0002 20	161802	894378	5.5276	8.8933
chrUn_gl0002 21	155397	33314	0.2144	0.6314
chrUn_gl0002 22	186861	20527	0.1099	0.7451
chrUn_gl0002 23	180455	4686	0.026	0.2161
chrUn_gl0002 24	179693	140435	0.7815	2.3972
chrUn_gl0002 25	211173	254138	1.2035	2.6798

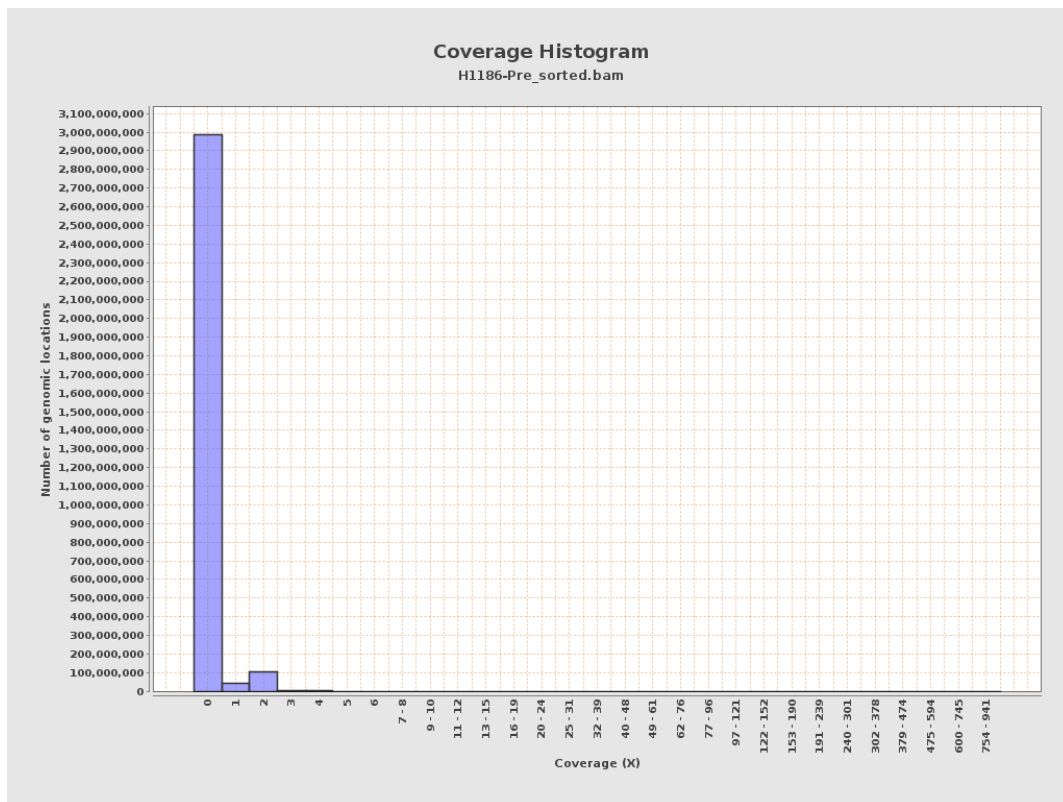
chrUn_gl0002 26	15008	298573	19.8943	16.5113
chrUn_gl0002 27	128374	7312	0.057	0.3636
chrUn_gl0002 28	129120	48552	0.376	2.81
chrUn_gl0002 29	19913	6846	0.3438	0.7664
chrUn_gl0002 30	43691	854	0.0195	0.1935
chrUn_gl0002 31	27386	9675	0.3533	0.815
chrUn_gl0002 32	40652	14487	0.3564	0.8553
chrUn_gl0002 33	45941	3152	0.0686	0.3374
chrUn_gl0002 34	40531	12909	0.3185	0.7691
chrUn_gl0002 35	34474	7816	0.2267	0.7033
chrUn_gl0002 36	41934	2715	0.0647	0.3447
chrUn_gl0002 37	45867	9735	0.2122	0.682
chrUn_gl0002 38	39939	1142	0.0286	0.2308
chrUn_gl0002 39	33824	5945	0.1758	0.5717
chrUn_gl0002 40	41933	1900	0.0453	0.3166

chrUn_gl0002 41	42152	18287	0.4338	0.9513
chrUn_gl0002 42	43523	2524	0.058	0.3244
chrUn_gl0002 43	43341	8030	0.1853	0.6168
chrUn_gl0002 44	39929	3560	0.0892	0.3913
chrUn_gl0002 45	36651	8138	0.222	0.66
chrUn_gl0002 46	38154	2846	0.0746	0.3562
chrUn_gl0002 47	36422	3808	0.1046	0.4856
chrUn_gl0002 48	39786	1178	0.0296	0.2392
chrUn_gl0002 49	38502	2382	0.0619	0.3159

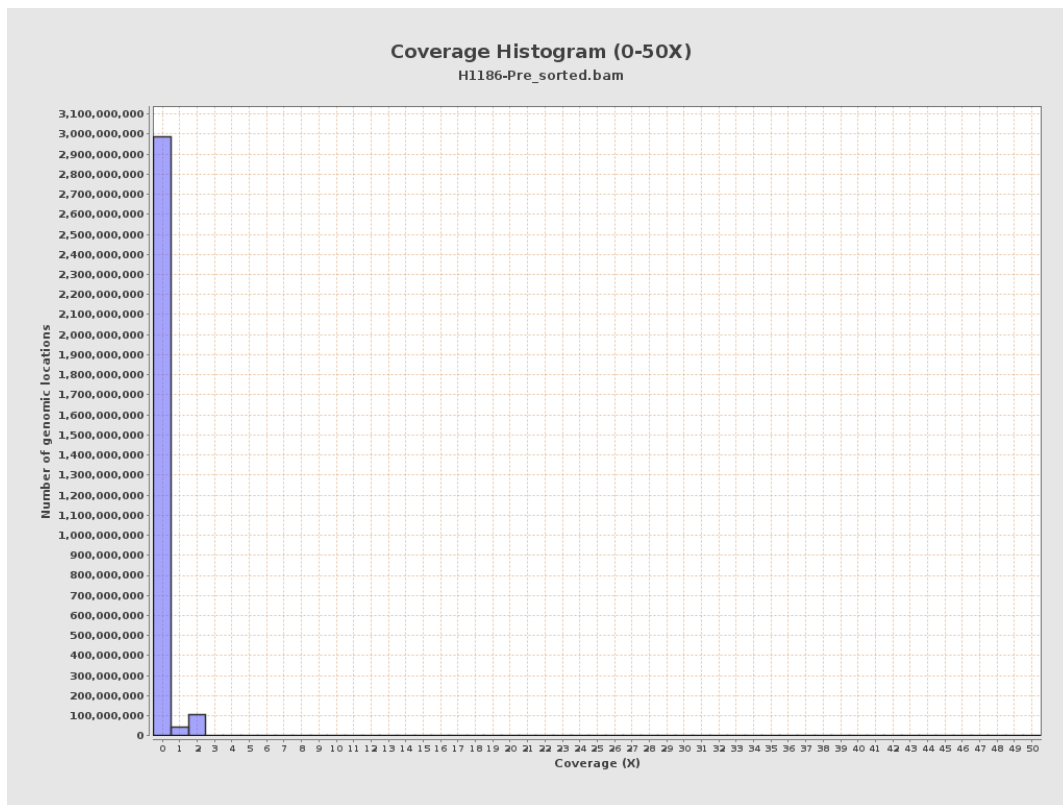
3. Results : Coverage across reference



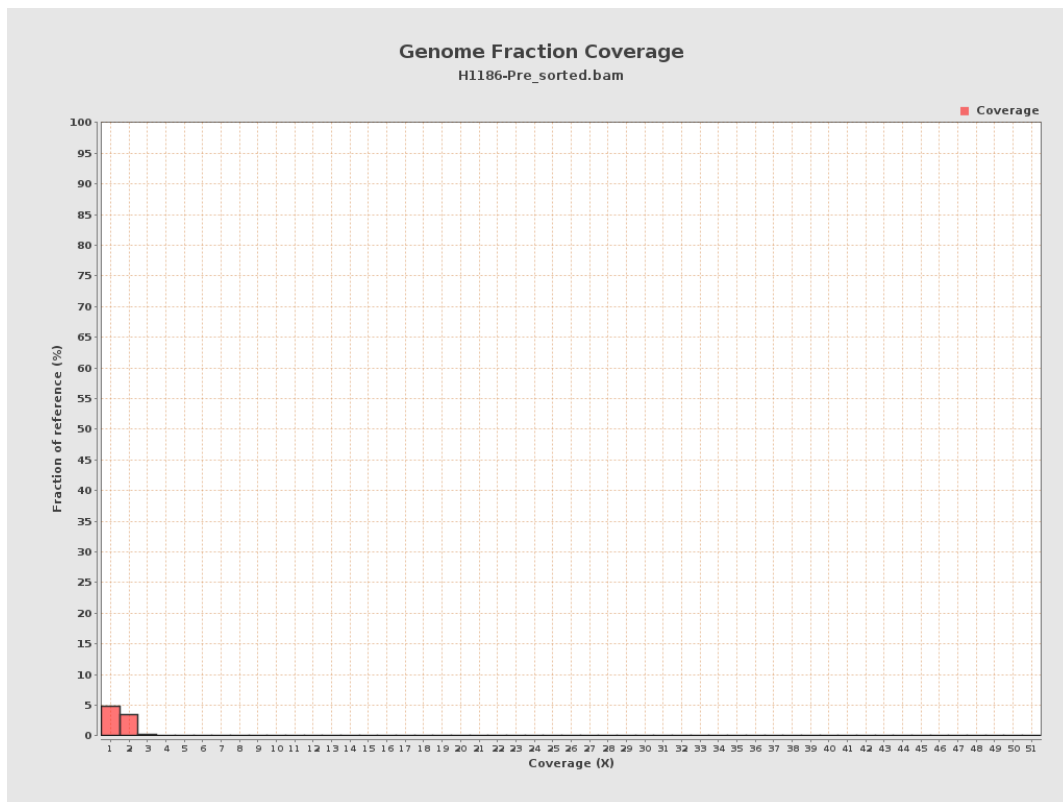
4. Results : Coverage Histogram



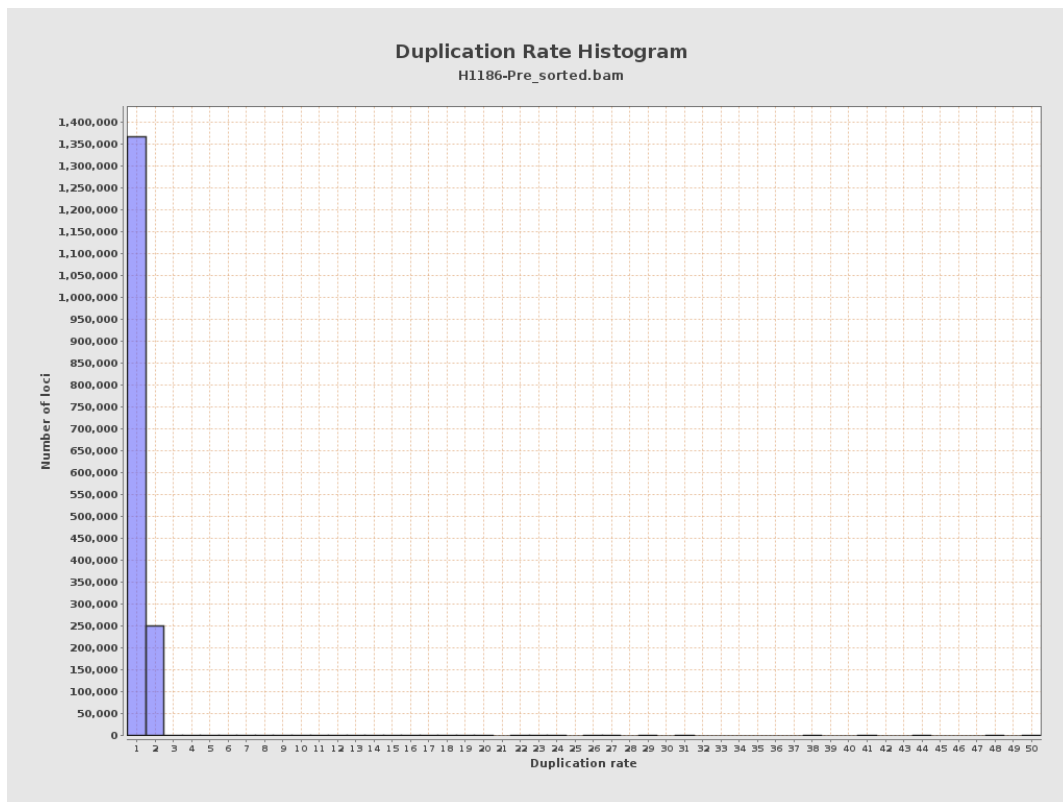
5. Results : Coverage Histogram (0-50X)



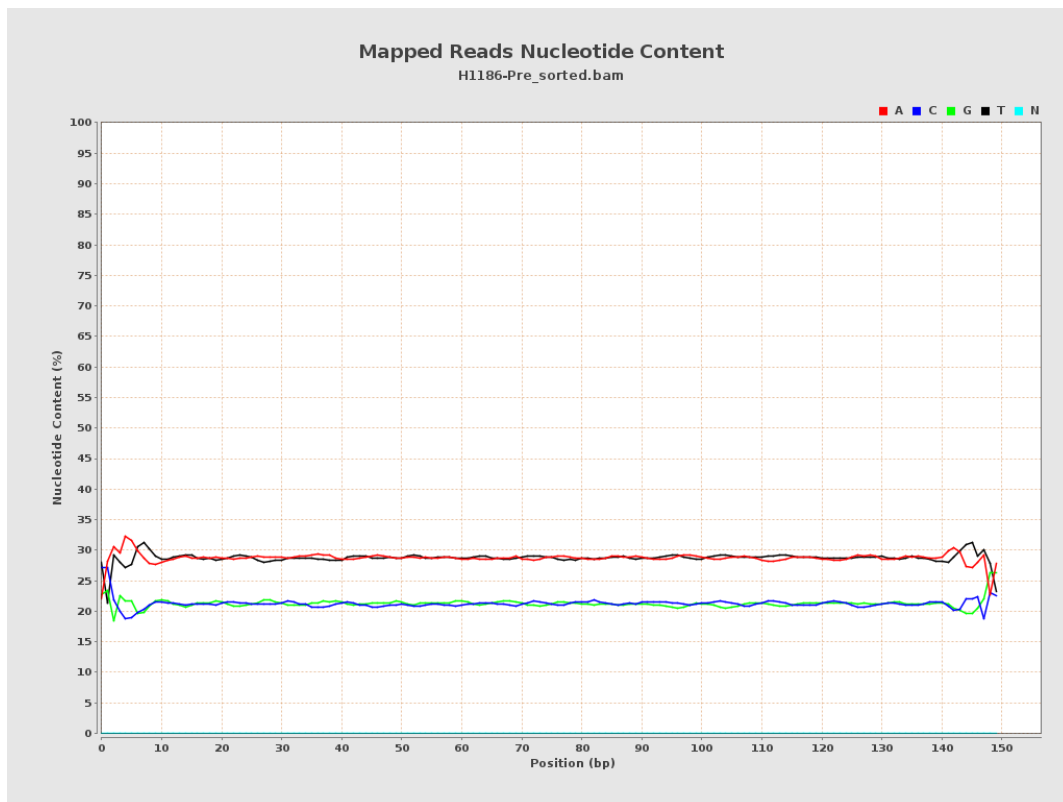
6. Results : Genome Fraction Coverage



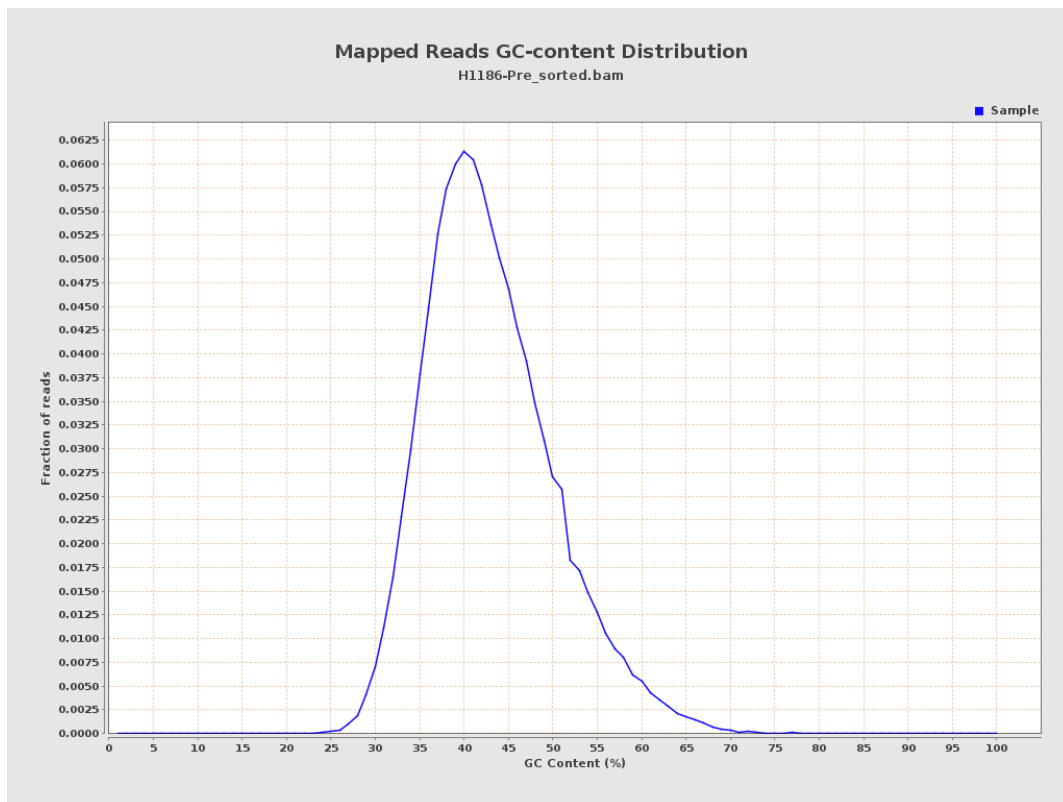
7. Results : Duplication Rate Histogram



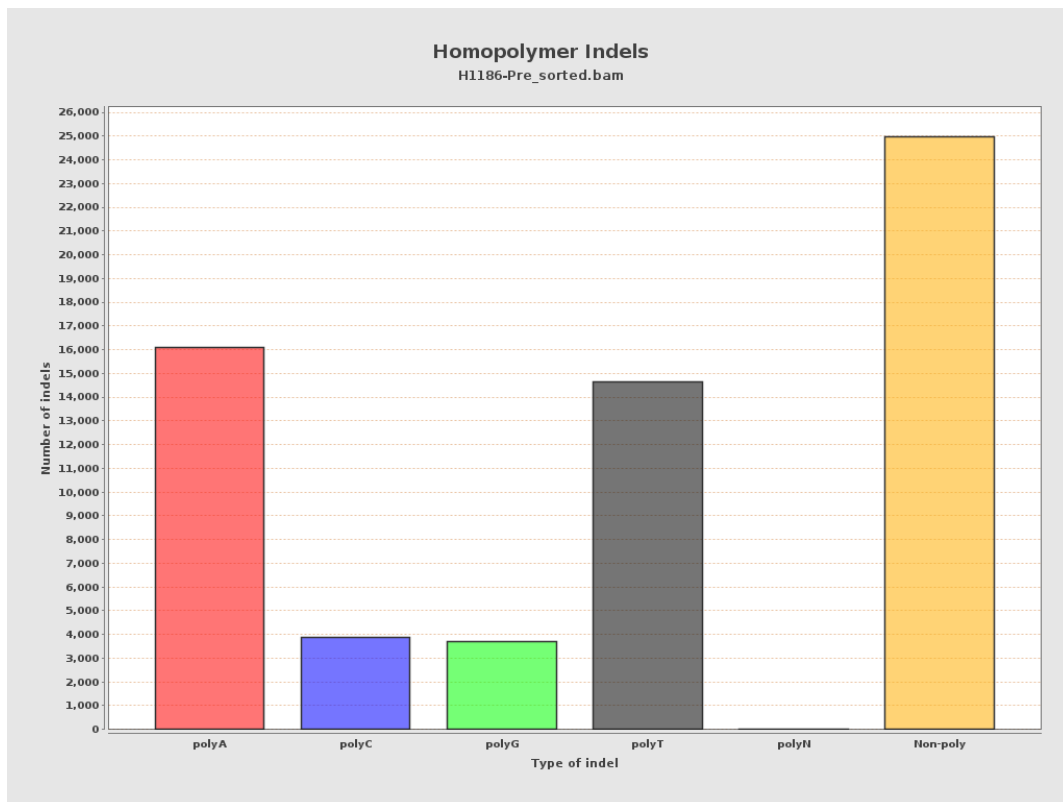
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



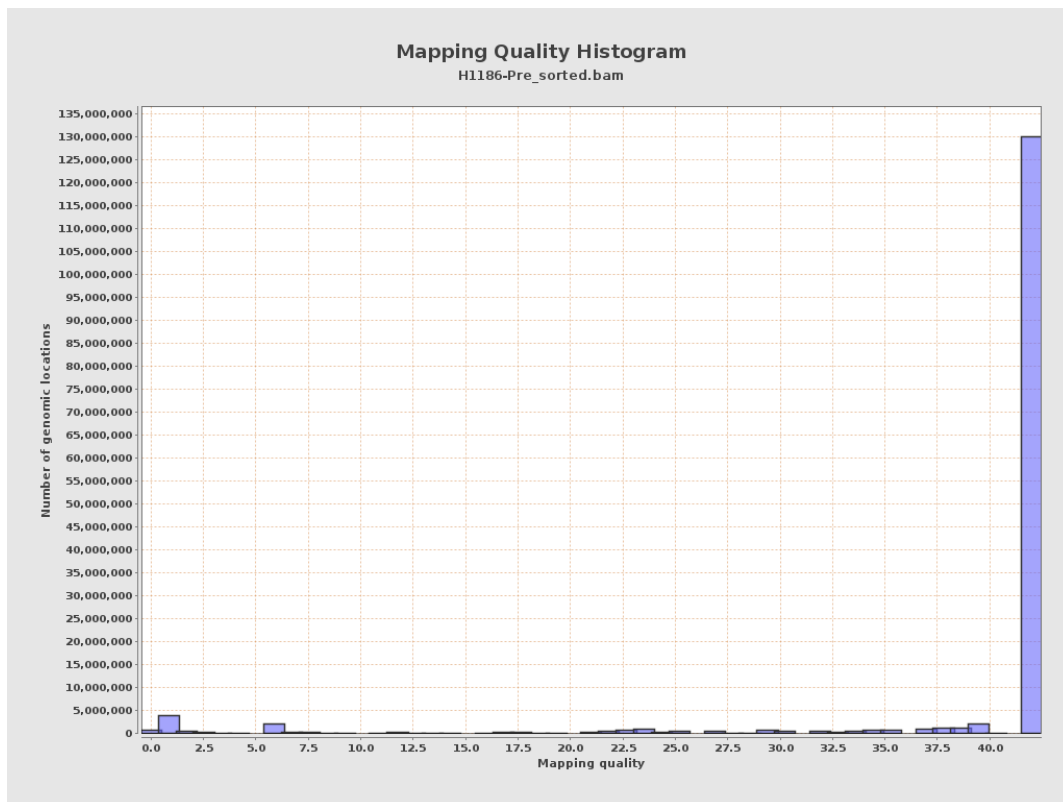
10. Results : Homopolymer Indels



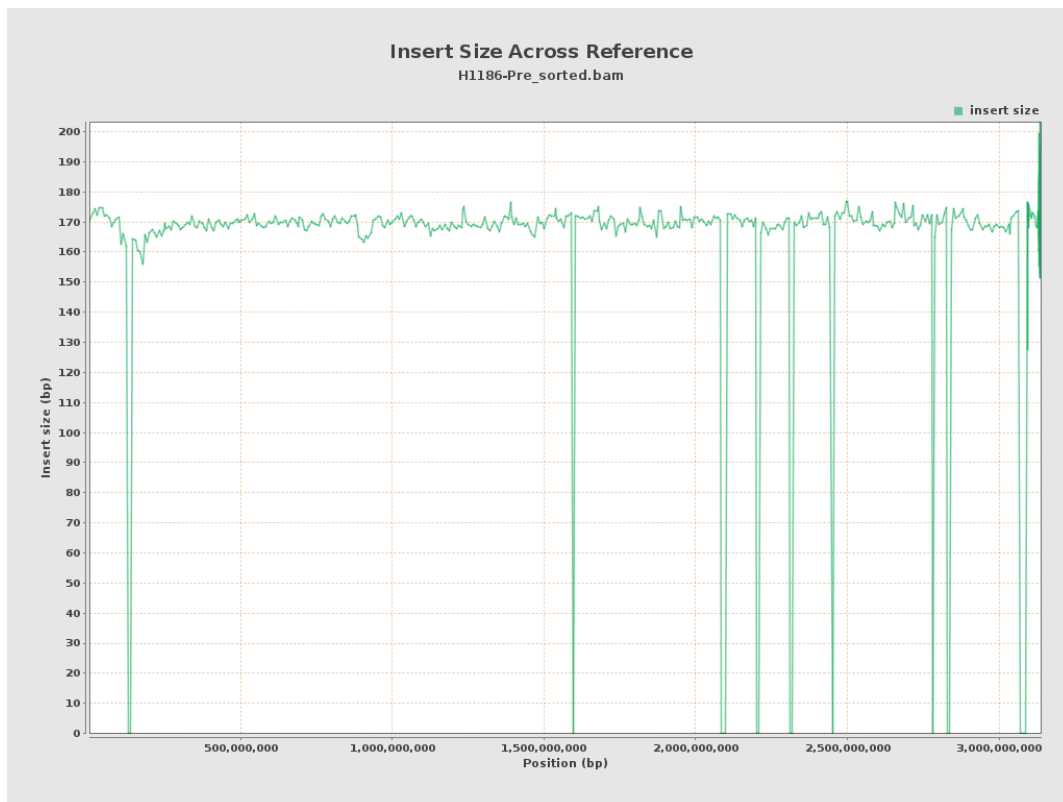
11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram



13. Results : Insert Size Across Reference



14. Results : Insert Size Histogram

