Whole-genome Sequence Quality Report using Chinese Quartet Reference Samples

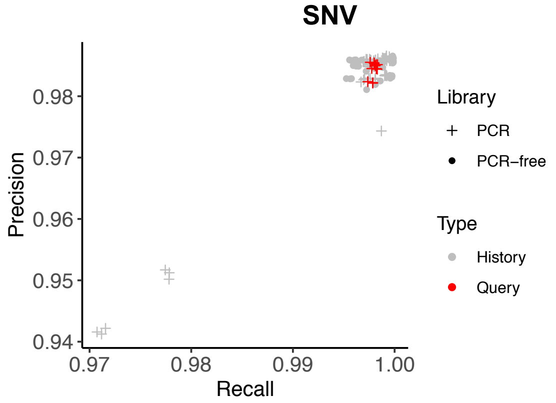
Data Generation Information

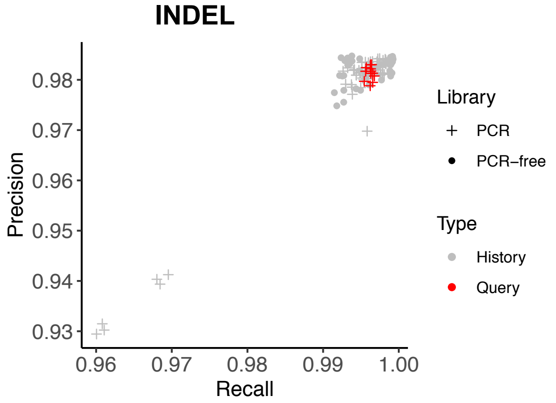
Sequence Site	**ShenZhen**
Sequence Platform	**DNBSEQ-T5**
Library Protocol	**PCR**
Sequencing Chemistry	**MGIEasy Universal DNA Library Prep Set**
Read Length	**PE100bp**
Coverage	**50x ~ 60x**
Date	**2020/7/16**

Performance assessment

Depend on reference datasets (v202007)

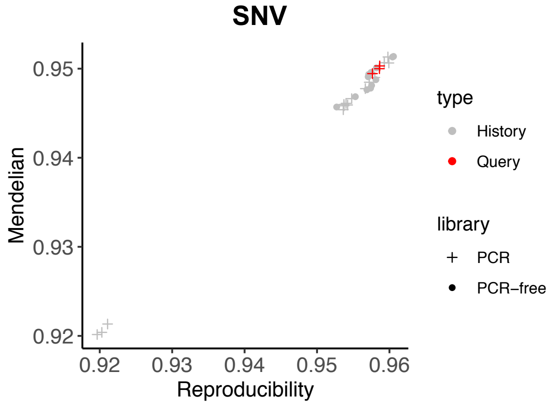
	Precision	Recall
SNV	0.9843 ± 0.0013	0.9980 ± 0.0002
INDEL	0.9813 ± 0.0014	0.9962 ± 0.0004

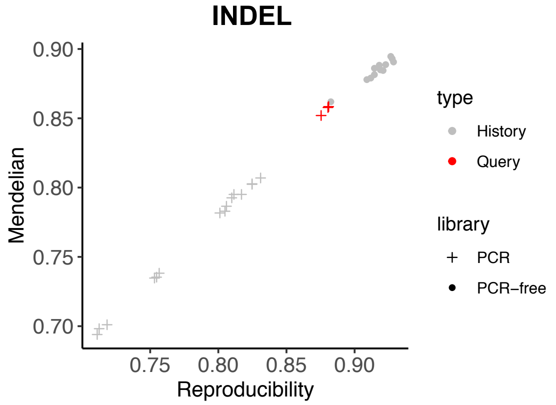




Depend on Quartet family genetic built-in truth

		Family1	Family2	Family3
Reproducibility of monozygotic twin daughters	SNV	0.958	0.959	0.959
	INDEL	0.875	0.880	0.881
Mendelian concordant ratio	SNV	0.949	0.950	0.950
	INDEL	0.852	0.858	0.858





No obvious failures observed in raw fastq files and bam files quality control. More information is available in the online version of the report.

Disclaimer

This quality control report is only for this specific test data and doesn’t represent an evaluation of the business level of the sequencing company. This report is only used for scientific research, not for clinical or commercial use. We don’t bear any economic and legal liabilities for any benefit or losses (including direct and indirect losses) from using the results of this report.

Supplementary

Raw Fastq Files Quality Control

Sample	percent duplicates	percent gc	avg sequence length	total sequences	per base sequence quality	per sequence quality scores	per base sequence content	per sequence gc content	per base n content	sequence length distribution	sequence duplication levels	overrepresented sequences	adapter content	kmer content
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL5_1_20200716.R1	11.92943621	40	100	722552158	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL5_1_20200716.R2	13.42780641	40	100	722552158	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL5_2_20200716.R1	13.90774657	40	100	931127216	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL5_2_20200716.R2	15.63215585	40	100	931127216	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL5_3_20200716.R1	12.61287738	40	100	906191425	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL5_3_20200716.R2	15.04170285	40	100	906191425	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL6_1_20200716.R1	12.21509058	40	100	791033092	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL6_1_20200716.R2	14.00065334	40	100	791033092	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL6_2_20200716.R1	12.47842187	40	100	833792292	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL6_2_20200716.R2	14.413627	40	100	833792292	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL6_3_20200716.R1	12.55351651	40	100	879648578	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL6_3_20200716.R2	14.91356513	40	100	879648578	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL7_1_20200716.R1	11.55191544	40	100	710799197	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL7_1_20200716.R2	13.35526206	40	100	710799197	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL7_2_20200716.R1	13.28934296	40	100	858725915	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL7_2_20200716.R2	14.98229621	40	100	858725915	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL7_3_20200716.R1	13.31807264	40	100	899248584	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL7_3_20200716.R2	15.2540613	40	100	899248584	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL8_1_20200716.R1	11.03042938	40	100	674235185	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL8_1_20200716.R2	12.71002251	40	100	674235185	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL8_2_20200716.R1	12.89353208	40	100	860500410	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL8_2_20200716.R2	14.56531917	40	100	860500410	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL8_3_20200716.R1	12.45879228	40	100	884993536	pass	pass	warn	warn	pass	pass	pass	pass	pass	pass
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL8_3_20200716.R2	14.52340576	40	100	884993536	pass	pass	warn	warn	pass	pass	pass	pass	pass	fail

Bam Files Quality Control

Sample	avg_gc	median insert size	30_x_pc	median coverage	percentage aligned	mapping ratio	general error rate
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL5_1_20200716	41.08562	366	89.83363	46	99.97632	0.999763	0.36
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL5_2_20200716	41.01698	366	91.79826	59	99.97761	0.999776	0.37
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL5_3_20200716	41.02434	363	91.78129	58	99.97374	0.999737	0.41
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL6_1_20200716	41.15124	347	90.99881	51	99.97662	0.999766	0.36
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL6_2_20200716	41.10148	359	91.25942	53	99.97794	0.999779	0.36
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL6_3_20200716	41.0934	345	91.6955	56	99.97172	0.999717	0.39
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL7_1_20200716	41.11506	350	85.94824	46	99.97428	0.999743	0.37
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL7_2_20200716	40.97801	350	88.92505	55	99.97555	0.999756	0.36
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL7_3_20200716	41.00224	363	89.61747	58	99.97456	0.999746	0.42
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL8_1_20200716	41.28913	342	88.43124	43	99.97499	0.99975	0.35
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL8_2_20200716	41.1651	341	91.55062	55	99.97586	0.999759	0.36
Quartet_DNA_BGI_DNBSEQT5_SZ_LCL8_3_20200716	41.15626	350	91.77517	57	99.97372	0.999737	0.39