

## Supplementary Tables

**Table S1. Key features of 3 generations of representative techniques for assaying genome sequence variants.**

Techniques	Range of variant detection	Number of detectable variants per run	Prior genomic information needed	Time consuming	Cost per run	Commercial platforms
Sanger	Less than 1 kb	Less than tens	Essential	Poor	A few US dollars	ABI 3730 Megabase 4000
Microarray	Genome-wide	100,000~ 1,000,000*	Essential	Efficient	Hundreds of US dollars	Affymetrix Genechip Illumina Beadchip
NGS	Genome	Unlimited	Non-necessary	Efficient	~ 1,000 US dollars	Illumina Solexa ABI SOLiD

\* NGS – the next generation sequencing

**Table S2. Basic features of 3 “reduced-representation” sequencing strategies for assaying the genome-wide polymorphisms.**

Platforms	Input resource	Reduced proportion	Prior genomic information	Time cost	Cost per sample	Reference
RNA-seq	Transcriptome	Fixed and rigid*	Non-necessary	Efficient	Hundreds of US dollars*	[1,2]
Capture-seq	Probes captured DNA fragments	tunable	Essential	Time-consuming to design capture probes	Hundreds of US dollars**	[3]
RAD-seq	Enzyme digested DNA fragments	tunable	Non-necessary	Efficient	Tens of US dollars	[4,5]

\* Depend on the transcribed proportion of genomic regions

\*\* Depend on the cost of custom capture probes design and the size of extracted genomic regions

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