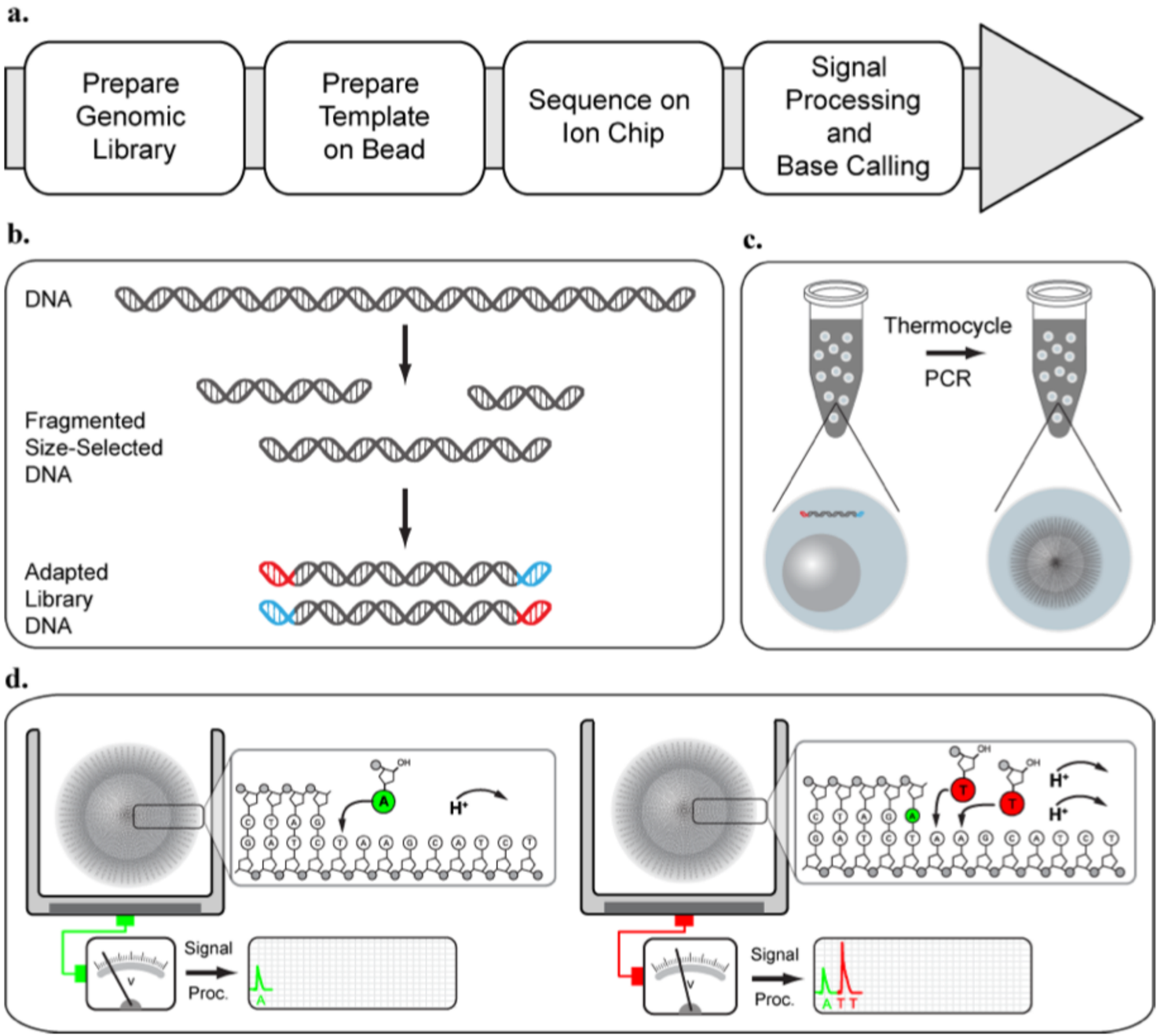
IonTorrent



Rothberg et al. 2011

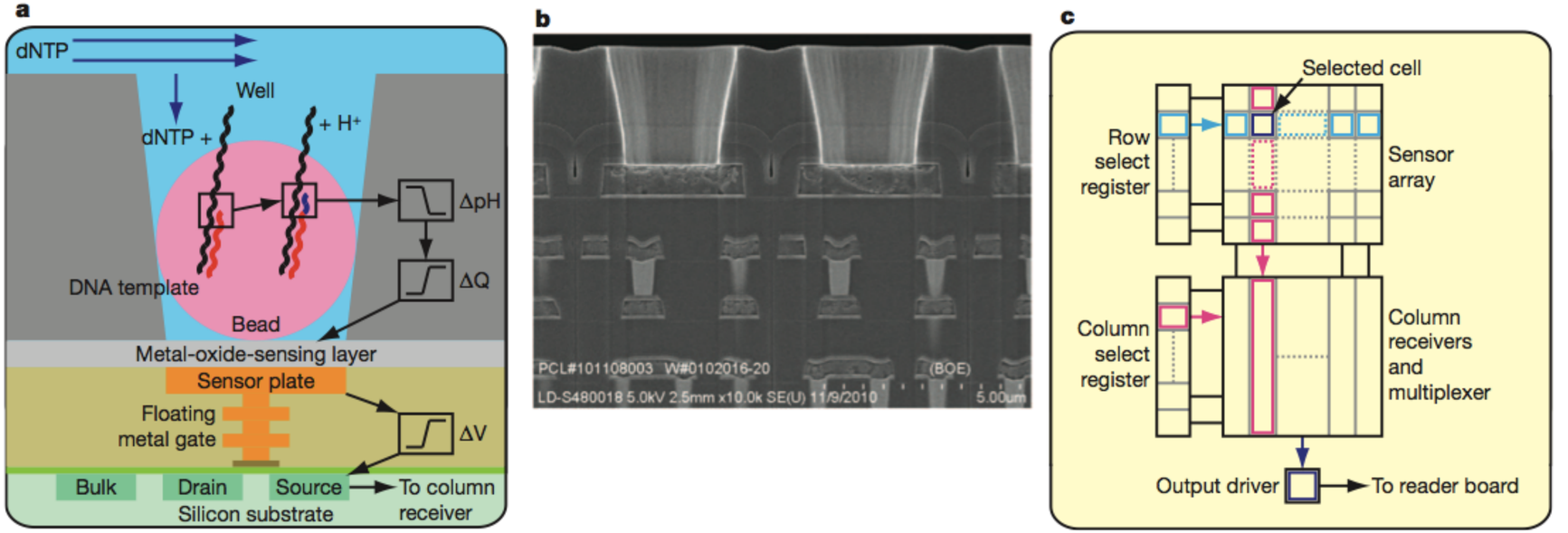


Figure 1 | Sensor, well and chip architecture. **a**, A simplified drawing of a well, a bead containing DNA template, and the underlying sensor and electronics. Protons (H^+) are released when nucleotides (dNTP) are incorporated on the growing DNA strands, changing the pH of the well (ΔpH). This induces a change in surface potential of the metal-oxide-sensing layer, and a change in potential (ΔV) of the source terminal of the underlying field-effect transistor. **b**, Electron micrograph showing alignment of the wells over the ISFET metal sensor plate and the underlying electronic layers. **c**, Sensors are arranged in a two-dimensional array. A row select register enables one row of sensors at a time, causing each sensor to drive its source voltage onto a column. A column select register selects one of the columns for output to external electronics.

Rothberg et al. 2011

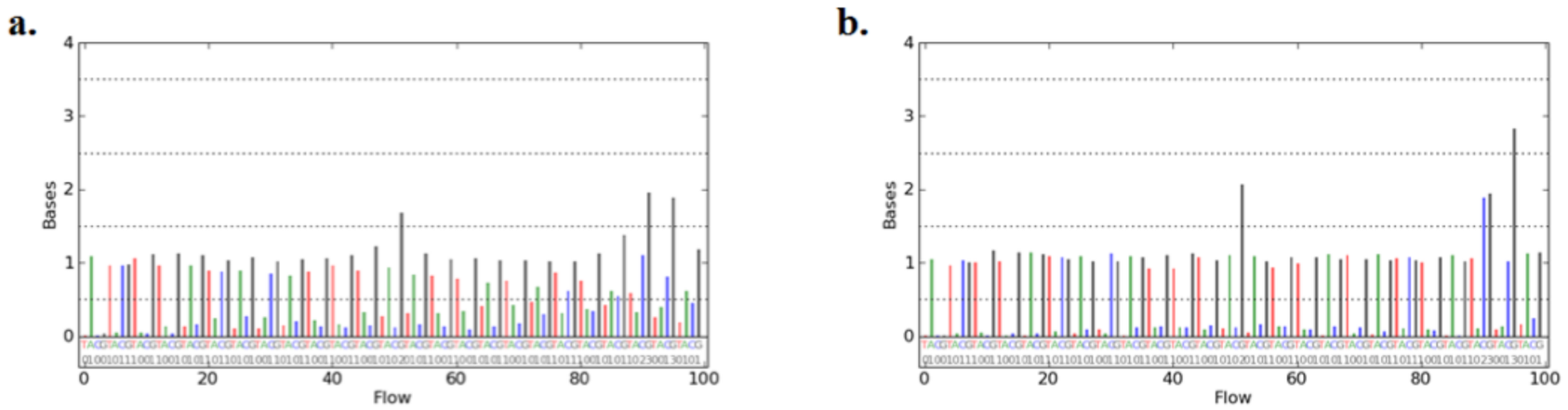
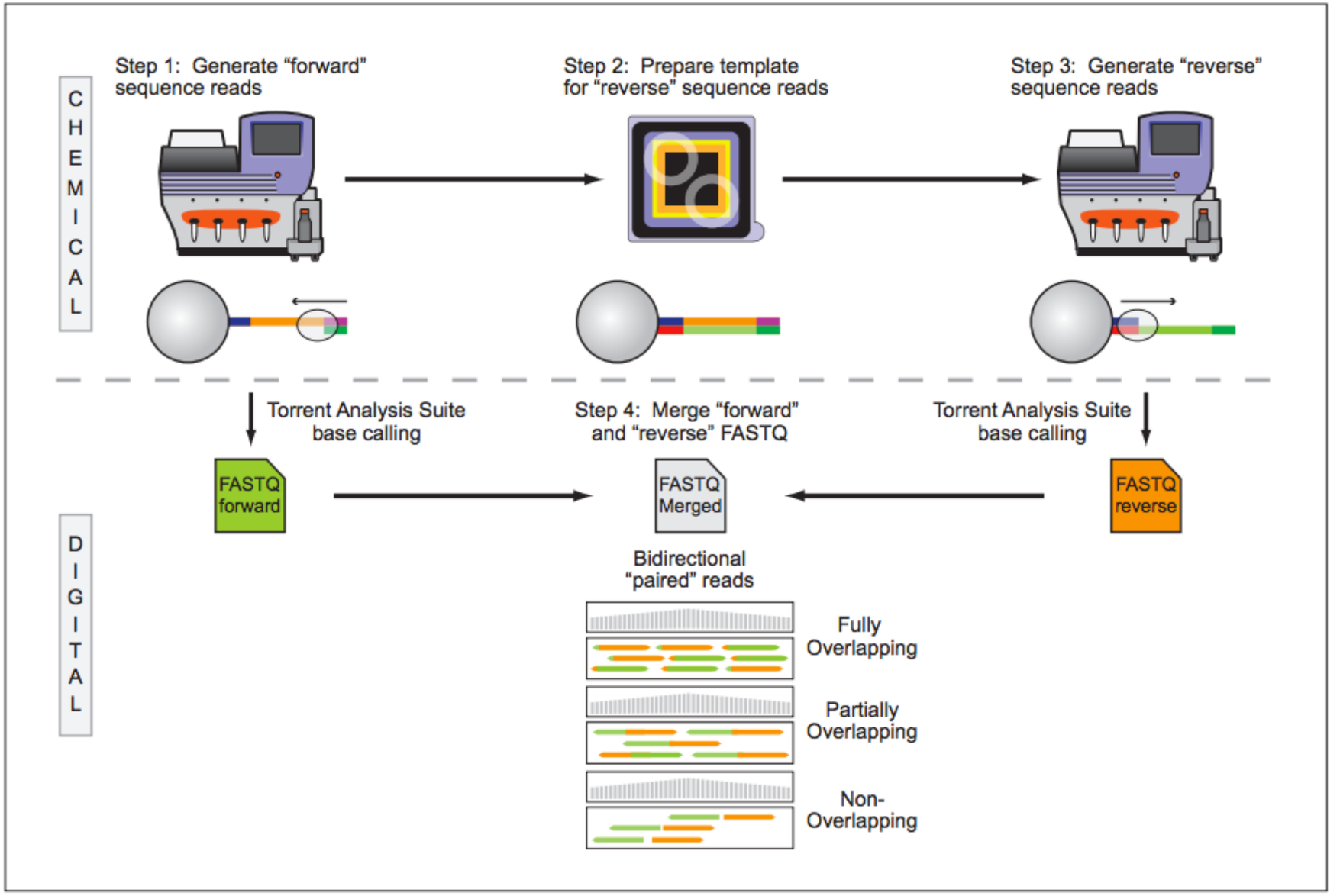


Figure S12 Phase correction

a, Raw measures of incorporation from the first 100 nucleotide flows are shown. These measures are the output of the physical model, prior to correcting for phase and signal loss. Phase errors are evident, especially in the expected 0-mer flows. We estimate the phase and signal loss parameters using these raw measurements and expected incorporations. **b**, The estimates of the magnitude of signal loss and de-phasing are then used in an algorithm that reconstructs the in-phase signal and simultaneously estimates the associated base calls. Bases are called from the corrected measurements simply by rounding each measurement to the nearest integer.

Rothberg et al. 2011

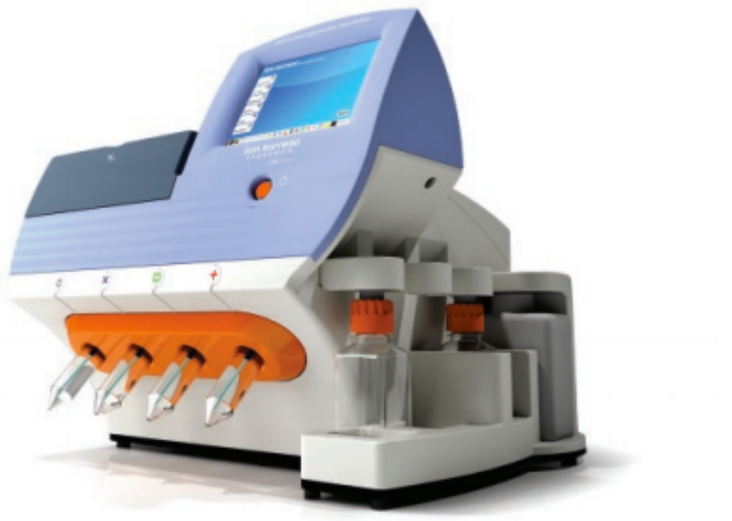

CHEMICAL
Step 1: Generate "forward" sequence reads
Step 2: Prepare template for "reverse" sequence reads
Step 3: Generate "reverse" sequence reads
Torrent Analysis Suite base calling
Step 4: Merge "forward" and "reverse" FASTQ
Torrent Analysis Suite base calling
FASTQ forward
FASTQ Merged
FASTQ reverse
DIGITAL
Bidirectional "paired" reads
Fully Overlapping
Partially Overlapping
Non-Overlapping

The Ion PGM™ Sequencer

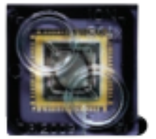
The fastest and most affordable benchtop sequencer

The Ion PGM™ Sequencer:

- Delivers the fastest run times of any next-generation sequencer, enabling a single-day workflow
- Supports three semiconductor chips with a range of prices and outputs for flexible and scalable projects
- Supports read lengths of up to 400 bases
- Requires the lowest capital investment of any next-generation sequencer
- Is supported by a global community of users and developers—the Ion Community



The Ion PGM™ Sequencer performs real-time measurements of hydrogen ions produced during DNA replication. Ion semiconductor chips employ a massively parallel array of semiconductor sensors to directly translate genetic information (DNA) to digital information (DNA sequence). This groundbreaking technology enables rapid and scalable sequencing across a range of applications.

Chip	Expected sequencing run time			Expected output*		
	35-base reads	200-base reads	400-base reads	35-base reads	200-base reads	400-base reads
 Ion 314™ Chip	0.5 hr	2.3 hr	3.7 hr	3 Mb	20 Mb	40 Mb
 Ion 316™ Chip	0.7 hr	3.0 hr	4.9 hr	30 Mb	200 Mb	400 Mb
 Ion 318™ Chip	0.9 hr	4.4 hr	7.3 hr	300 Mb	500 Mb–1 Gb	1–2 Gb

*Expected output with >99% aligned/measured accuracy. Output is dependent on read length and application.

The Ion Proton™ System

Rapid genome-scale benchtop sequencing

The Ion Proton™ System is a benchtop sequencing system that delivers exome and transcritpome sequencing in a few hours on the Ion PI™ Chip. With the release of the Ion PII™ Chip*, the Ion Proton™ System will deliver human-scale genome sequencing—with DNA to variants in a single day.

Table 1 Technical specifications of Next Generation Sequencing platforms utilised in this study

Platform	Illumina MiSeq	Ion Torrent PGM	PacBio RS	Illumina GAIIx	Illumina HiSeq 2000
Instrument Cost*	$128 K	$80 K**	$695 K	$256 K	$654 K
Sequence yield per run	1.5-2Gb	20-50 Mb on 314 chip, 100-200 Mb on 316 chip, 1Gb on 318 chip	100 Mb	30Gb	600Gb
Sequencing cost per Gb*	$502	$1000 (318 chip)	$2000	$148	$41
Run Time	27 hours***	2 hours	2 hours	10 days	11 days
Reported Accuracy	Mostly > Q30	Mostly Q20	<Q10	Mostly > Q30	Mostly > Q30
Observed Raw Error Rate	0.80 %	1.71 %	12.86 %	0.76 %	0.26 %
Read length	up to 150 bases	~200 bases	Average 1500 bases**** (C1 chemistry)	up to 150 bases	up to 150 bases
Paired reads	Yes	Yes	No	Yes	Yes
Insert size	up to 700 bases	up to 250 bases	up to 10 kb	up to 700 bases	up to 700 bases
Typical DNA requirements	50-1000 ng	100-1000 ng	~1 μg	50-1000 ng	50-1000 ng

* All cost calculations are based on list price quotations obtained from the manufacturer and assume expected sequence yield stated.
** System price including PGM, server, OneTouch and OneTouch ES.
*** Includes two hours of cluster generation.
**** Mean mapped read length includes adapter and reverse strand sequences. Subread lengths, i.e. the individual stretches of sequence originating from the sequenced fragment, are significantly shorter.