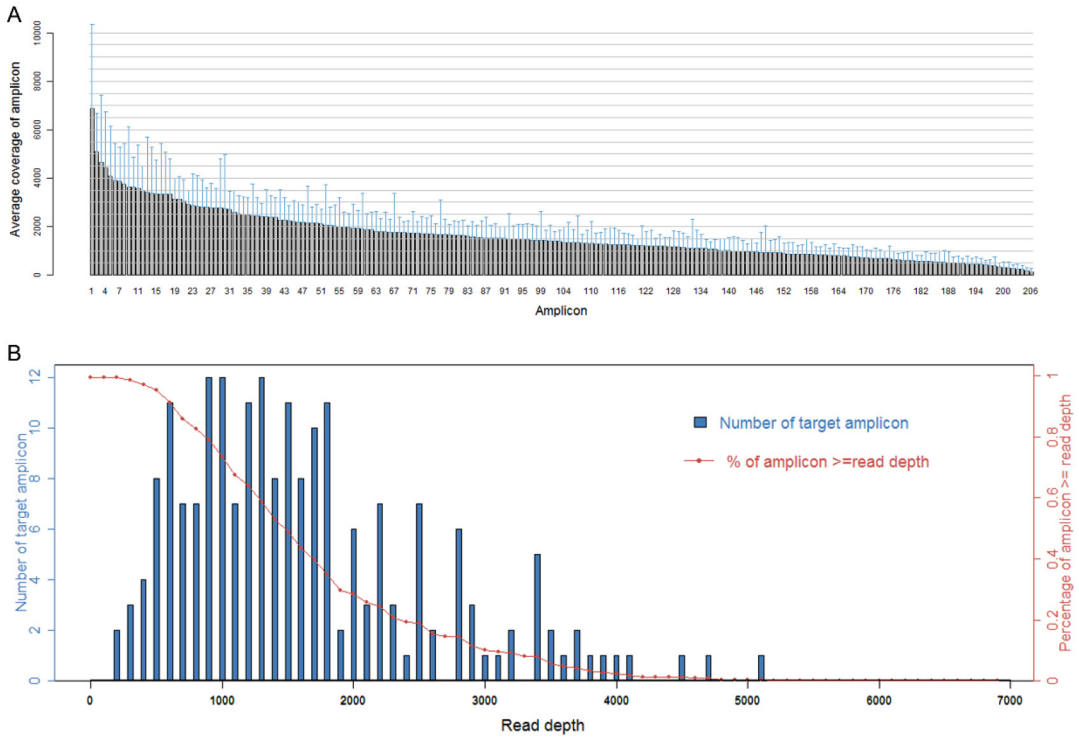
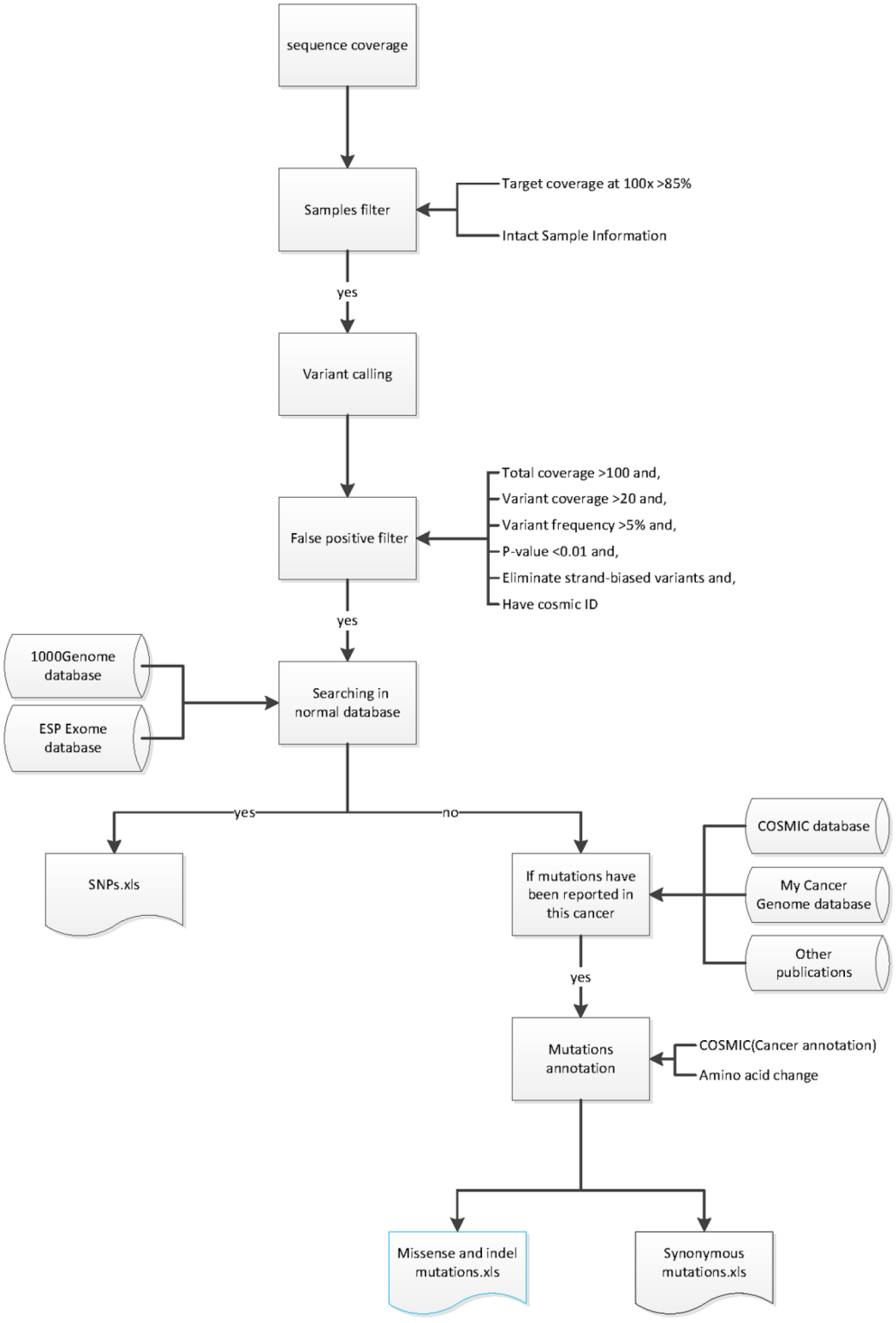
SUPPLEMENTARY FIGURES AND TABLES



Supplementary Figure S1: Sequence read distribution across 207 amplicons generated from 157 FFPE specimens. A. Distribution of average coverage of each amplicon; data are shown as mean ± SD. **B.** Number of amplicons with a given read depth, sorted in bins of 100 reads. Blue bars represent number of target amplicons within read depth; red line represents percent of target amplicons ≥ read depth.



Supplementary Figure S2: Workflow of bioinformatical analysis for Ion Torrent PGM sequencing data.

Supplementary Table S1: Summary of mutations identified by Ion Torrent targeted sequencing in SqCLC.

See Supplementary File 1

Supplementary Table S2: The Association between clinicopathologic characteristics and mutational status of *EGFR*, *KRAS*, *PIK3CA*, *CDKN2A* and *TP53* in 157 SqCLC.

See Supplementary File 2

Supplementary Table S3: Univariate and multivariate analyses of prognostic factors for DFS and OS.

See Supplementary File 3

Supplementary Table S4: The Association between clinicopathologic characteristics and copy number alterations in 157 SqCLC.

See Supplementary File 4

Supplementary Table S5: The Association between clinicopathologic characteristics and expression of PTEN, PD-L1 and VEGFR2 in 157 SqCLC.

See Supplementary File 5

Supplementary Table S6: Correlation between the various main molecular alterations.

See Supplementary File 6

SUPPLEMENTARY METHODS

Definitions of *FGFR1* amplification [1, 2]

Patients were considered as *FGFR1* amplification if satisfied one of the following conditions:

(1) FGFR1/CEN8 ratio ≥2.0;

(2) average number of *FGFR1* signals per tumor cell ≥6;

(3) percentage of tumor cells containing ≥15 *FGFR1* signals or large clusters ≥10%;

(4) percentage of tumor cells containing ≥5 *FGFR1* signals ≥50%.

Cases with condition (1–3) represent a high-level *FGFR1* amplification, and cases with condition (4) represent low-level *FGFR1* amplification.

Definitions of *EGFR* amplification [3]

(1) Low-level *EGFR* amplification defined as percentage of tumor cells containing ≥4 *EGFR* signals ≥40%;

(2) High-level *EGFR* amplification defined as EGFR/CEP7 ratio ≥2.0, or percentage of tumor cells containing ≥15 *EGFR* signals or large clusters ≥10%.

Definitions of *HER-2* amplification [3]

(1) Low-level *HER-2* amplification defined as percentage of tumor cells containing ≥4 *HER-2* signals ≥40%;

(2) High-level *HER-2* amplification defined as HER-2/CEP17 ratio ≥2.0, or percentage of tumor cells containing ≥15 *HER-2* signals or large clusters ≥10%.

Definitions of *PDGFRA* amplification [4]

(1) Low-level *PDGFRA* amplification defined as 4≤average number of *PDGFRA* signals per tumor cell<10;

(2) High-level *PDGFRA* amplification defined as average number of *PDGFRA* signals per tumor cell≥10.

Definitions of *CCND1* amplification [5]

(1) Low-level *CCND1* amplification defined as 2≤CCND1/CEP11 ratio<4, or 4≤average number of *CCND1* signals per tumor cell<8;

(2) High-level *CCND1* amplification defined as CCND1/CEP11 ratio≥4, or average number of *CCND1* signals per tumor cell≥8.

Definitions of *SOX2* amplification [6, 7]

(1) Low-level *SOX2* amplification were defined as samples with additional 2–9 *SOX2* signals exceeding the number of CEP3 signals in at least 30% of tumor cells;

(2) High-level *SOX2* amplification were defined as samples with additional ≥10 *SOX2* signals displaying a cluster-like formation in at least 30% of tumor cells.

Definitions of *CDKN2A* deletion [8]

Cases with ≥20% of nuclei lacking both signals of the *CDKN2A* probe and showing at least one signal for the *CEP 9* probe were defined as *CDKN2A* homozygous deletion.

Definitions of *PTEN* deletion [9]

Hemizygous deletion of *PTEN* gene was defined as one red *PTEN* signal and two green *CEP10* signals in a tumor cell. Homozygous deletion of *PTEN* gene was defined as none red *PTEN* signal but with at least one green *CEP10* signal in a tumor cell . *PTEN* deletion was defined as percentage of tumor cells with hemizygous deletion or homozygous deletion of *PTEN* ≥63%.

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