nature portfolio

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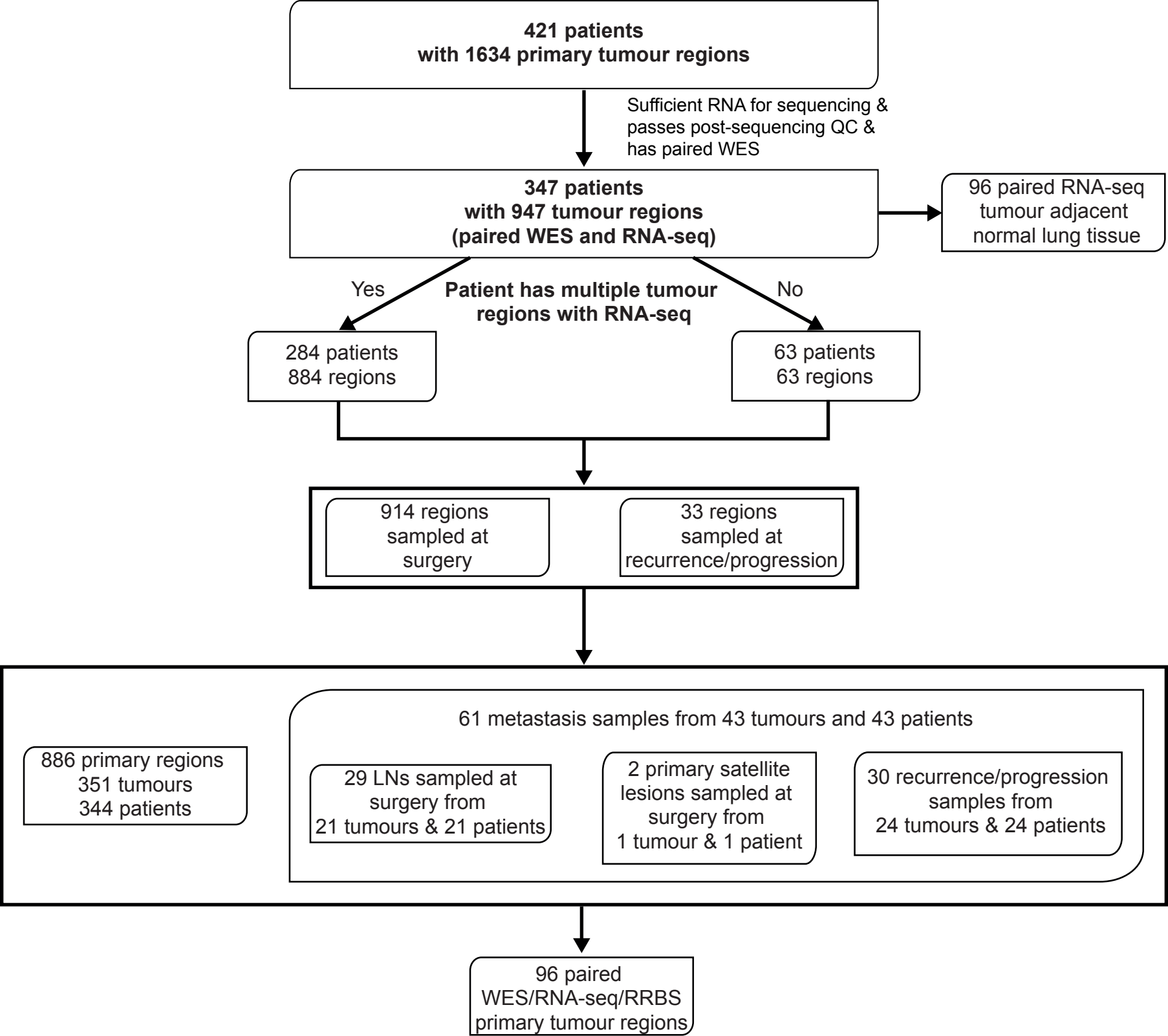
Supplementary information

Genomic–transcriptomic evolution in lung cancer and metastasis

In the format provided by the authors and unedited


421 patients
with 1634 primary tumour regions
Sufficient RNA for sequencing &
passes post-sequencing QC &
has paired WES
347 patients
with 947 tumour regions
(paired WES and RNA-seq)
96 paired RNA-seq
tumour adjacent
normal lung tissue
Yes
Patient has multiple tumour
regions with RNA-seq
No
284 patients
884 regions
63 patients
63 regions
914 regions
sampled at
surgery
33 regions
sampled at
recurrence/progression
886 primary regions
351 tumours
344 patients
61 metastasis samples from 43 tumours and 43 patients
29 LNs sampled at
surgery from
21 tumours & 21 patients
2 primary satellite
lesions sampled at
surgery from
1 tumour & 1 patient
30 recurrence/progression
samples from
24 tumours & 24 patients
96 paired
WES/RNA-seq/RRBS
primary tumour regions