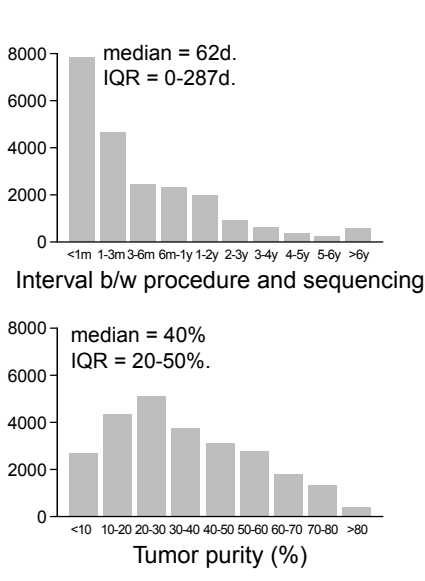
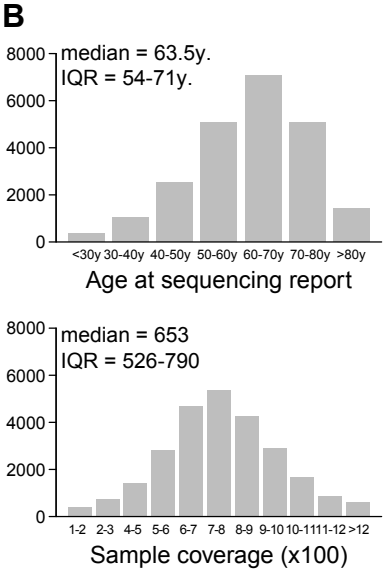


- 1,601 samples excluded based on:
 - Unavailable matched normal
 - Low sequencing coverage (<100x)
 - Low tumor purity (absence of somatic alterations including silent)
- 2,474 samples excluded based on:
 - Pediatric status of patients (<18y)
 - Presence of >1 sequenced tumor type
- 11,227 samples excluded based on:
 - Cancer of unknown primary
 - Tumor types in which distant metastases are rare (Gliomas)
 - Unavailable breast cancer subtypes
 - Tumor type with small n (n < 80 and either primary n < 30 or metastasis n < 30)
- 2,323 samples excluded based on:
 - >1 sample per patient*



*priority rules: the presence of a FACETS fit that passed qc > highest purity > highest sample coverage > most recent gene panel

