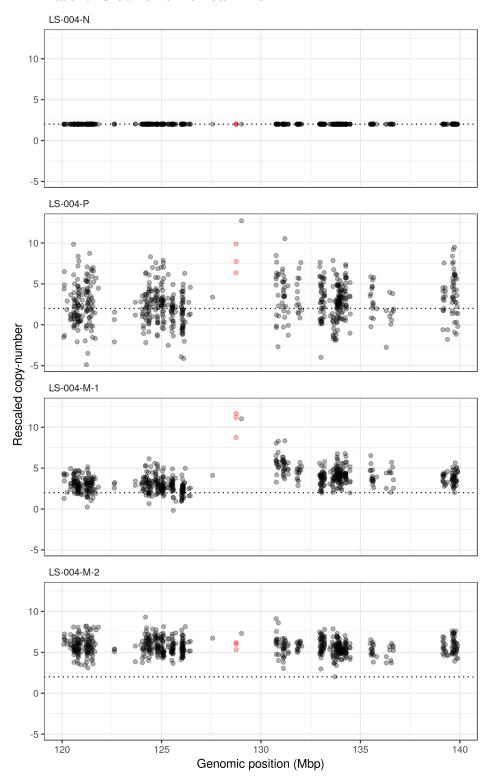
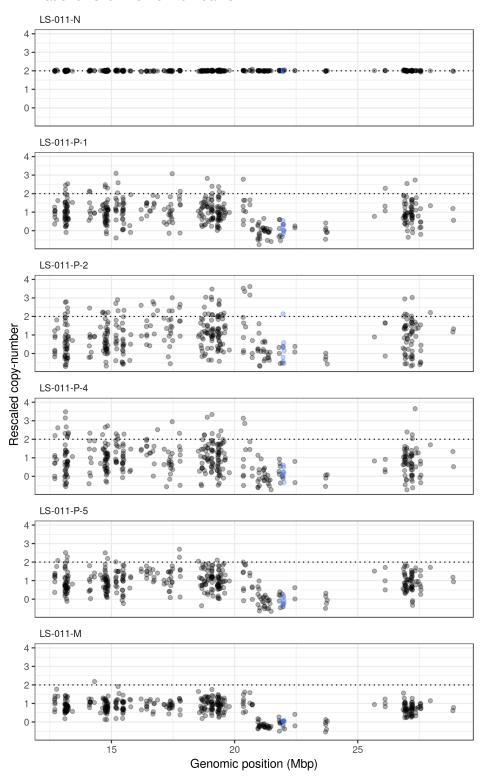
Patient LS-004 on chr 8 near MYC



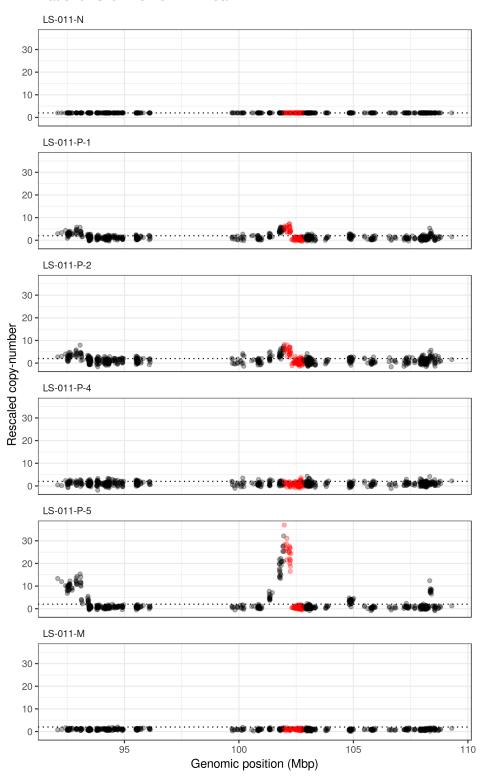
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient LS-011 on chr 9 near CDKN2A



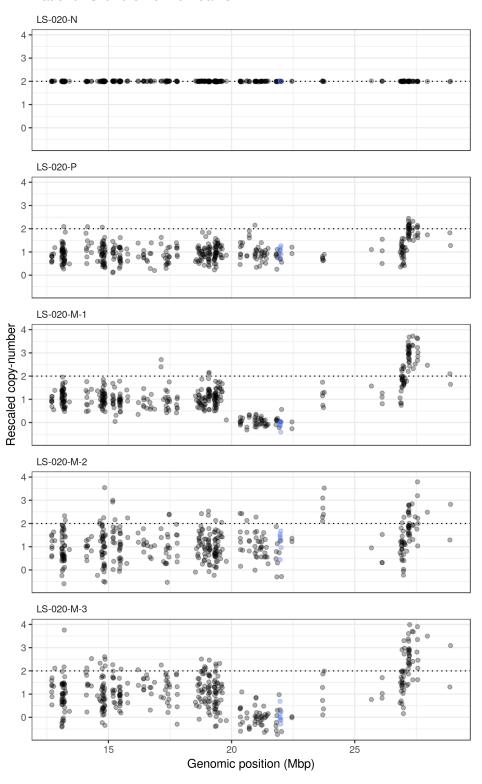
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient LS-011 on chr 11 near YAP1



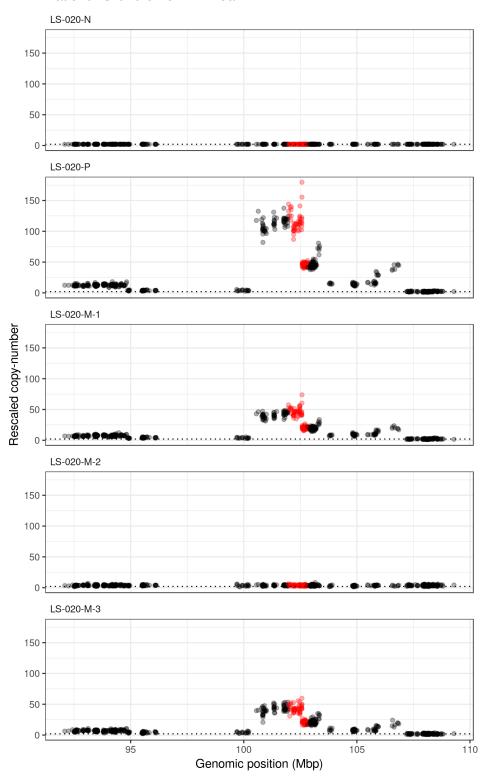
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient LS-020 on chr 9 near CDKN2A



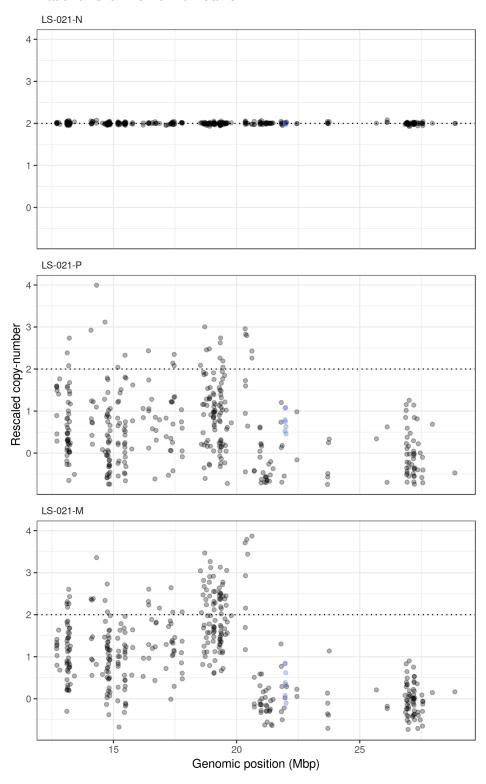
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient LS-020 on chr 11 near YAP1



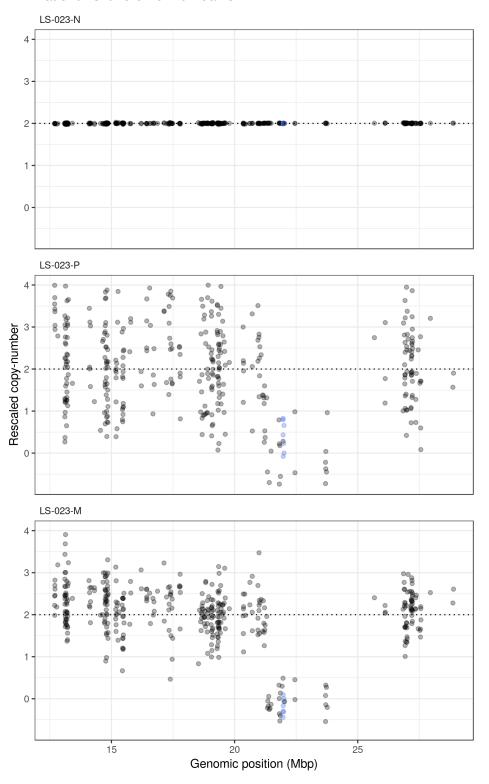
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient LS-021 on chr 9 near CDKN2A



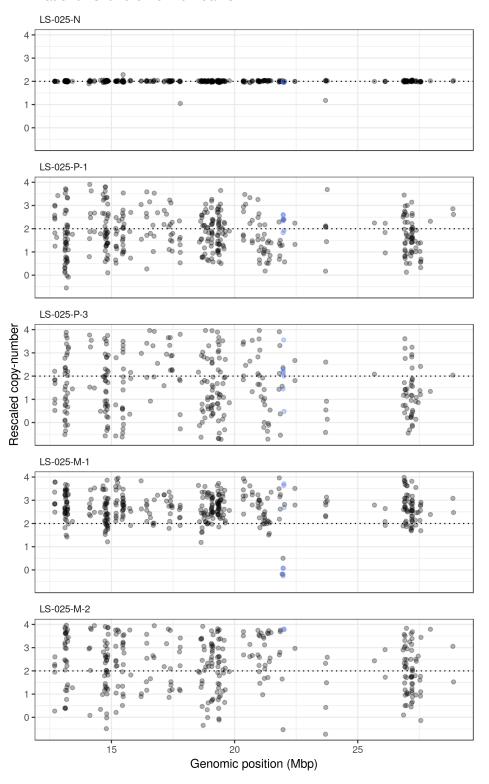
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient LS-023 on chr 9 near CDKN2A



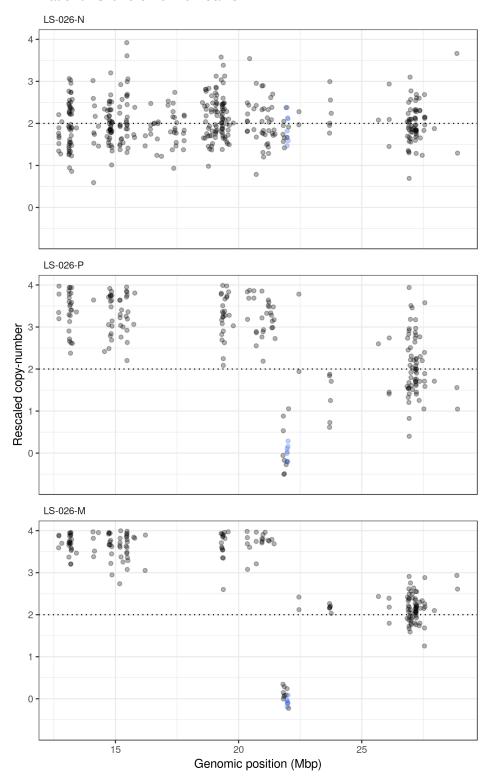
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient LS-025 on chr 9 near CDKN2A



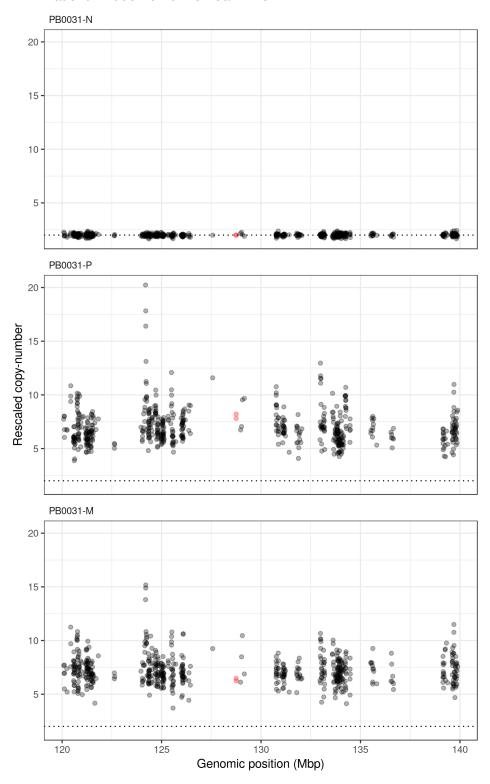
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient LS-026 on chr 9 near CDKN2A



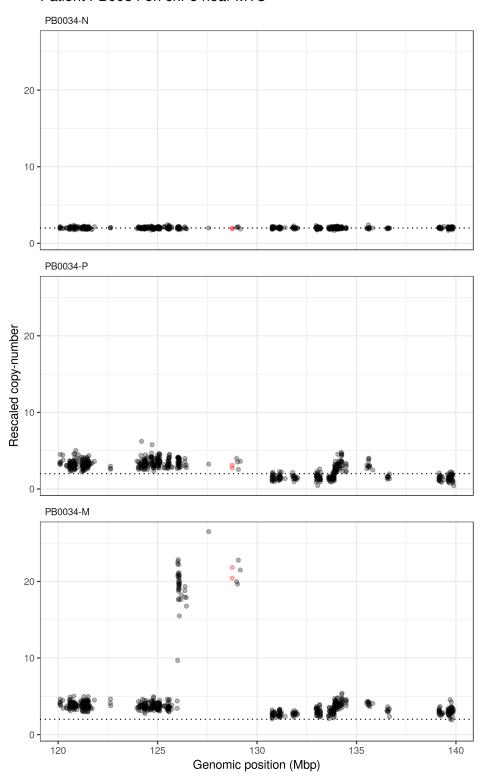
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0031 on chr 8 near MYC



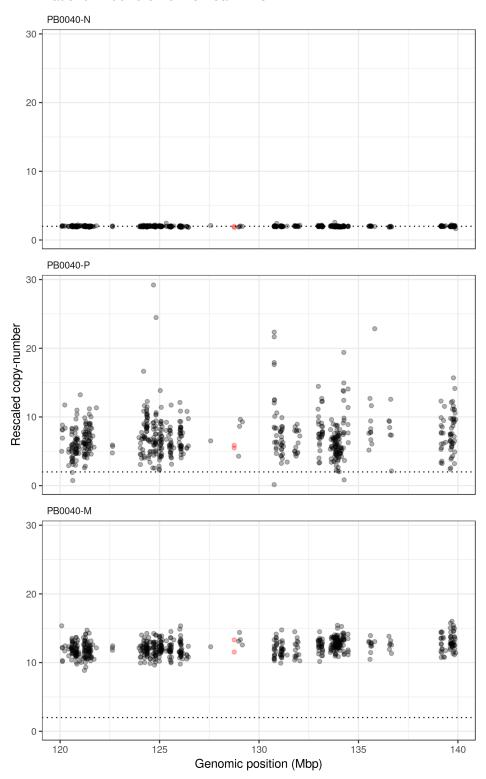
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0034 on chr 8 near MYC



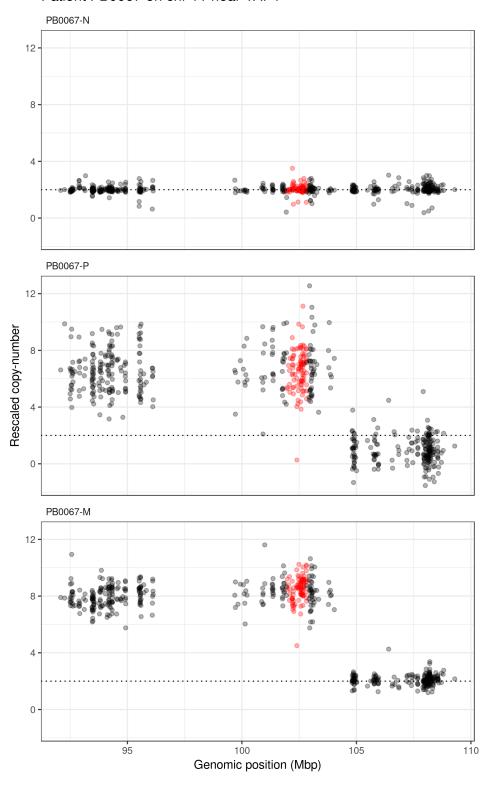
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0040 on chr 8 near MYC



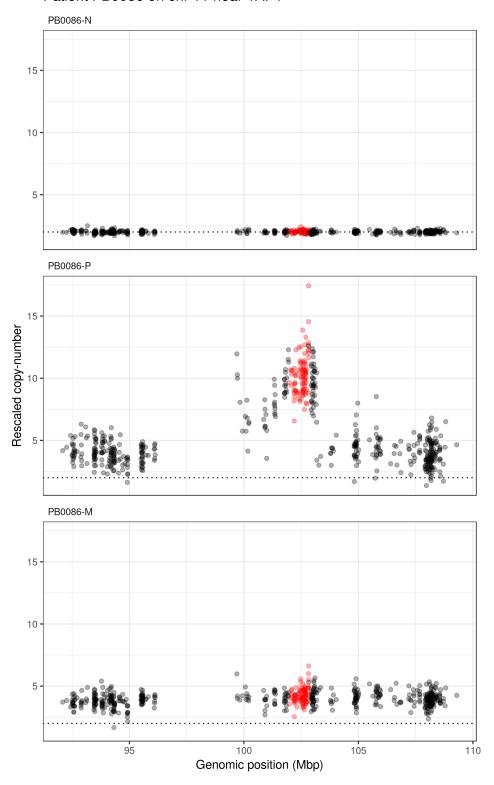
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0067 on chr 11 near YAP1



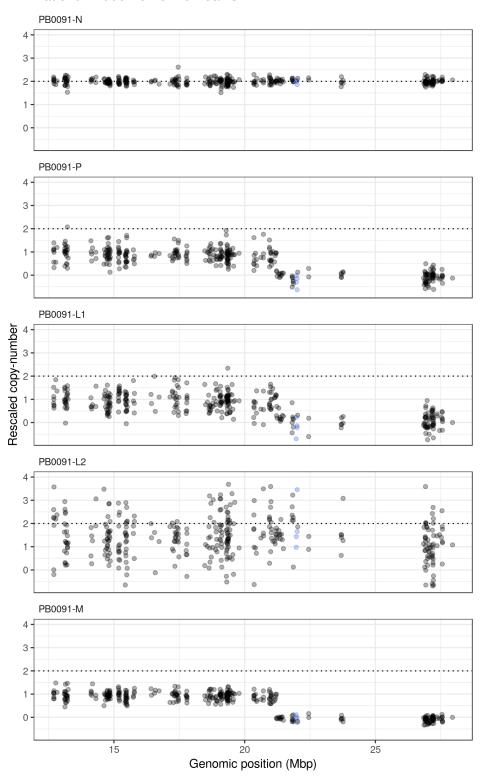
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0086 on chr 11 near YAP1



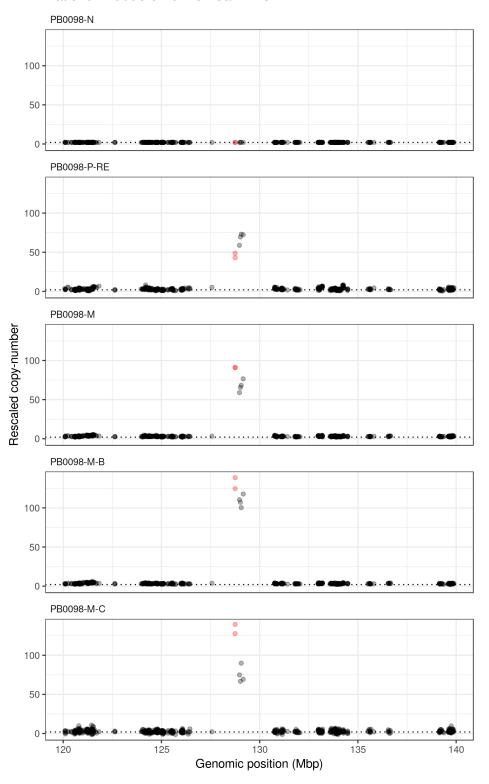
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0091 on chr 9 near CDKN2A



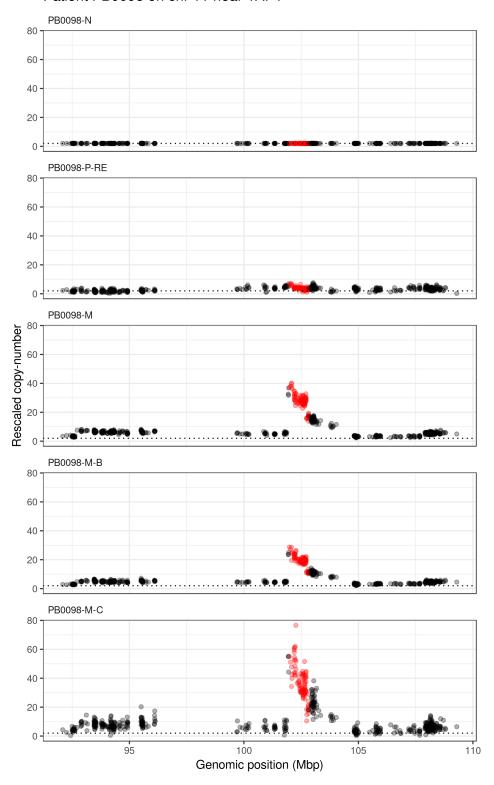
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0098 on chr 8 near MYC



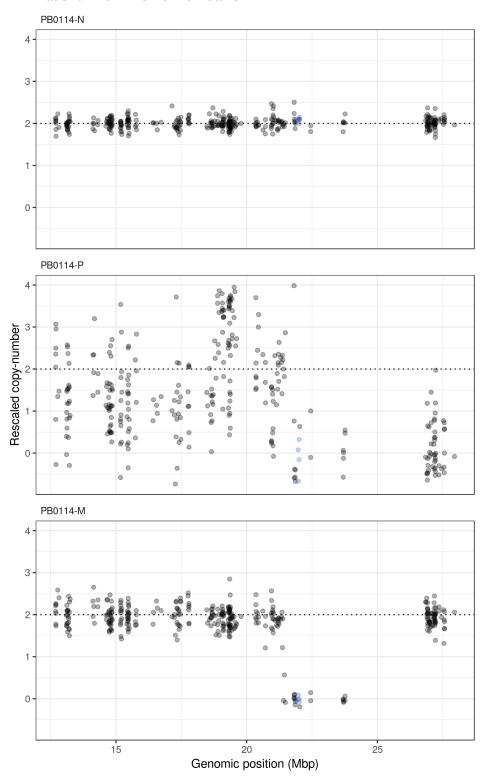
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0098 on chr 11 near YAP1



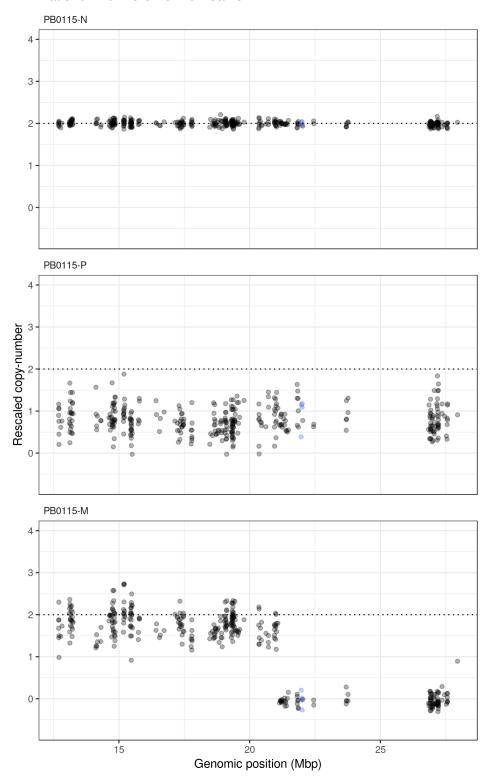
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0114 on chr 9 near CDKN2A



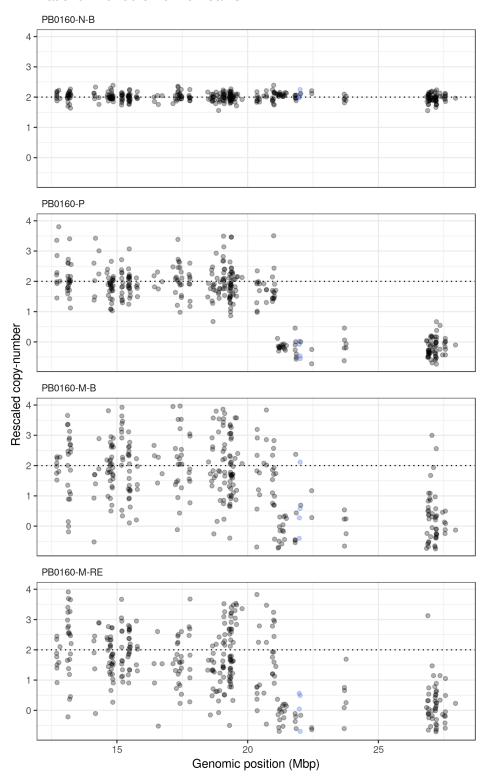
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0115 on chr 9 near CDKN2A



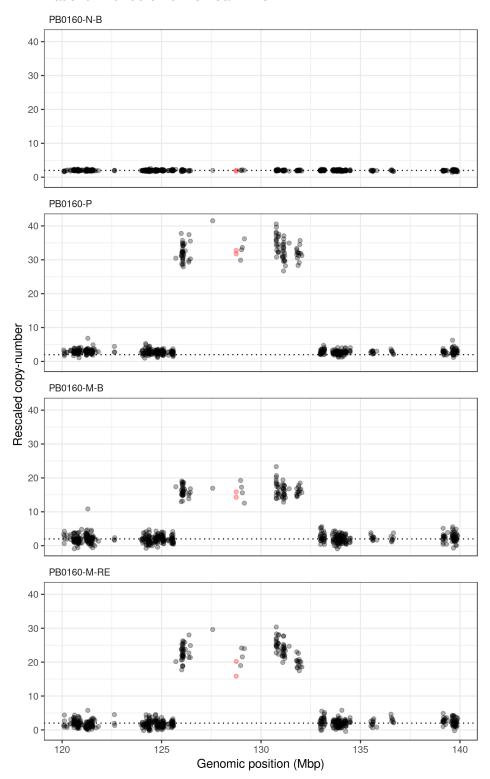
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0160 on chr 9 near CDKN2A



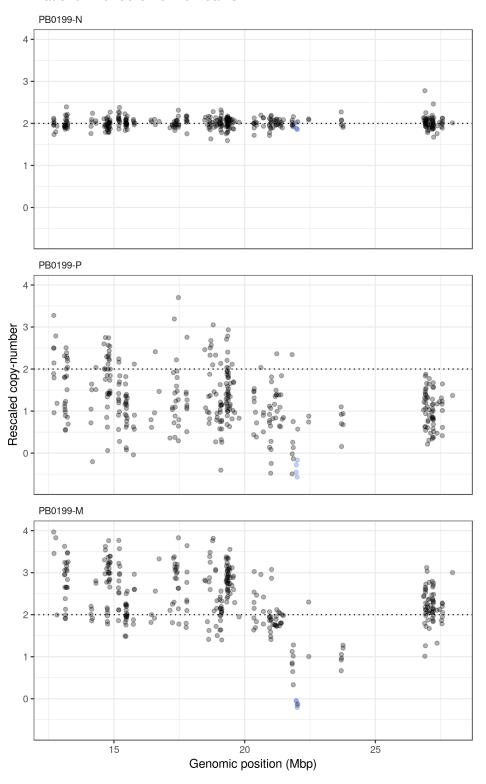
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0160 on chr 8 near MYC



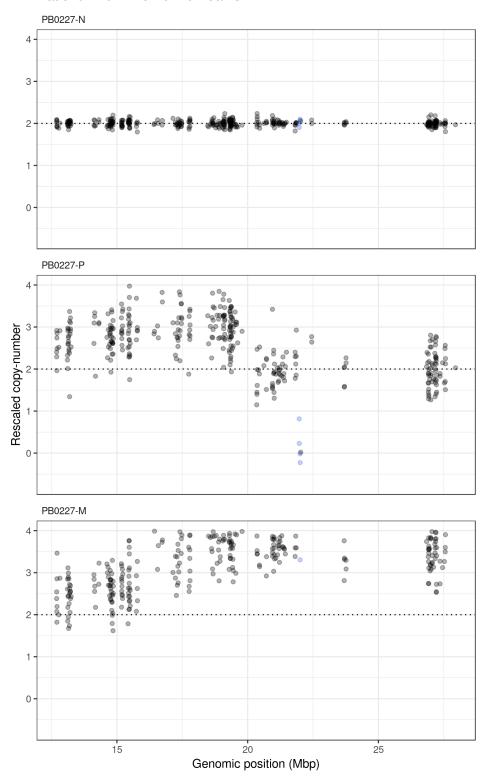
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0199 on chr 9 near CDKN2A



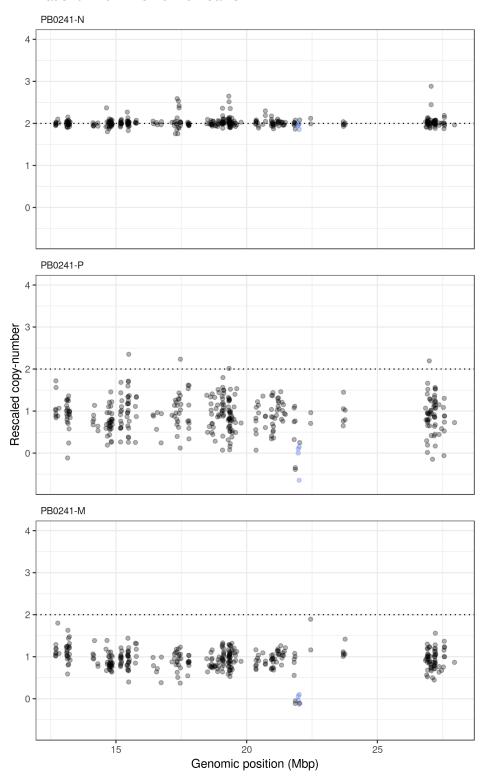
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0227 on chr 9 near CDKN2A



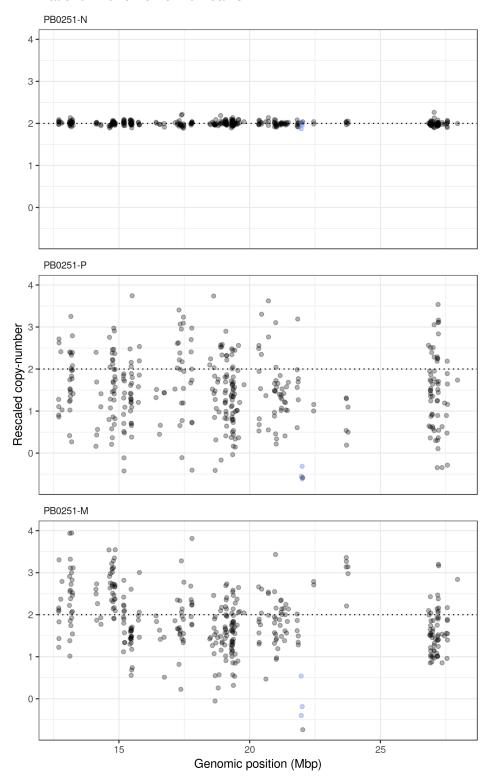
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0241 on chr 9 near CDKN2A



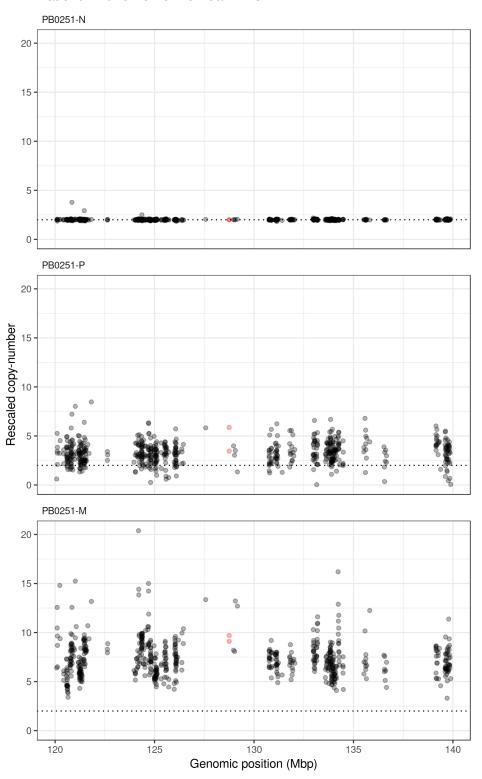
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0251 on chr 9 near CDKN2A



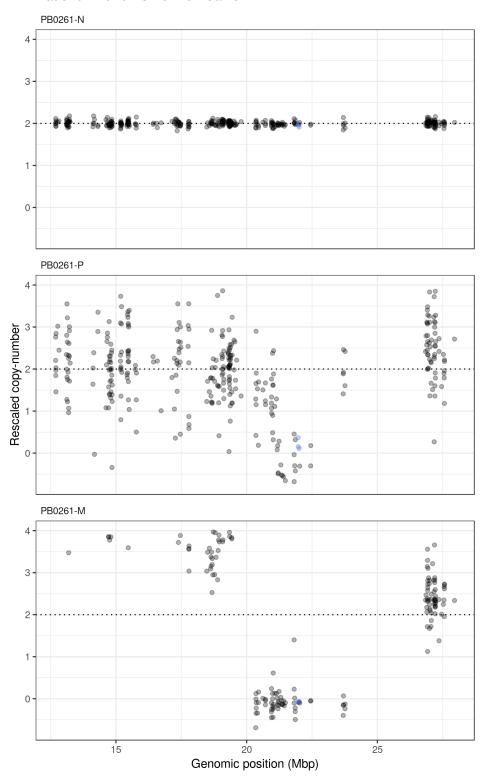
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0251 on chr 8 near MYC



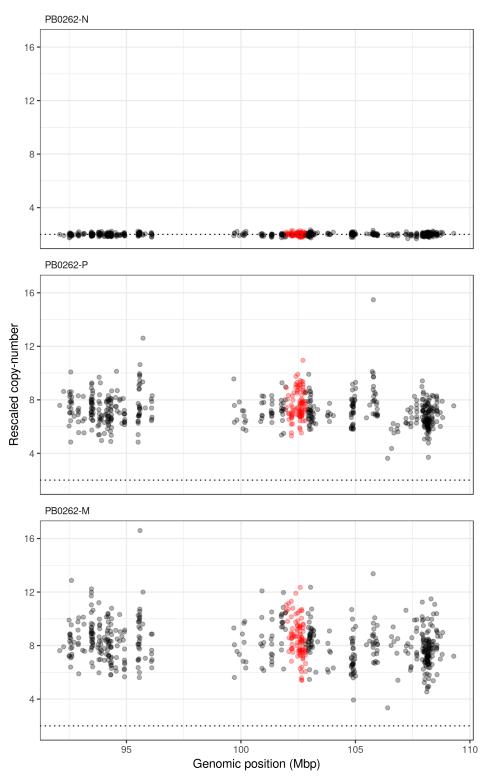
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0261 on chr 9 near CDKN2A



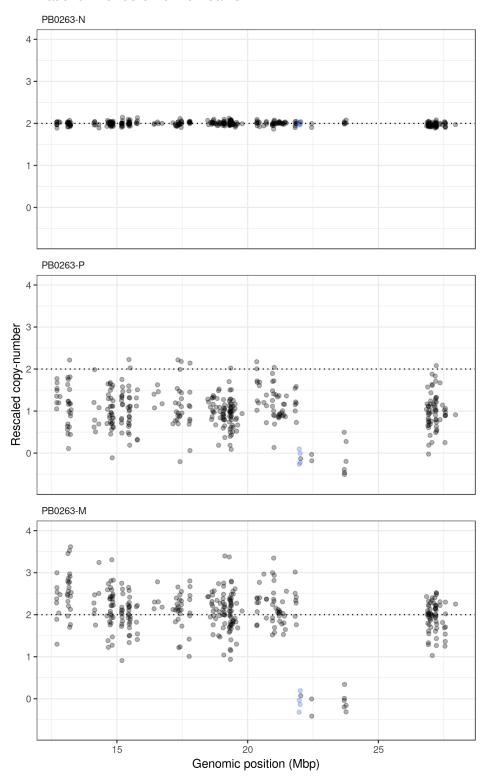
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0262 on chr 11 near YAP1



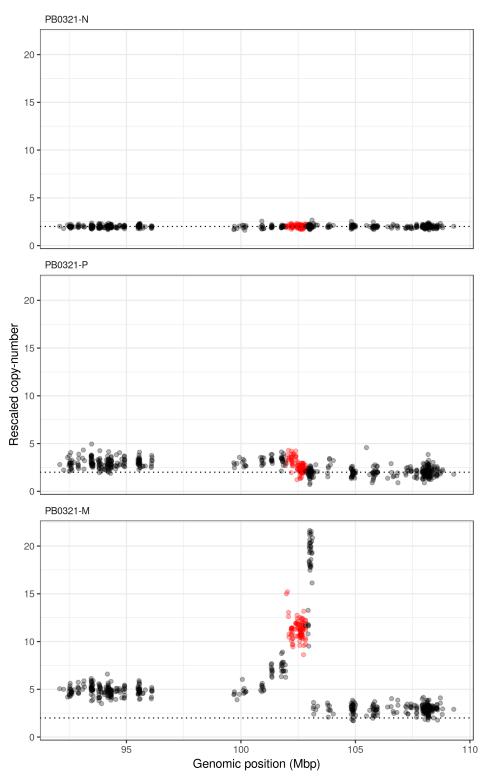
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0263 on chr 9 near CDKN2A



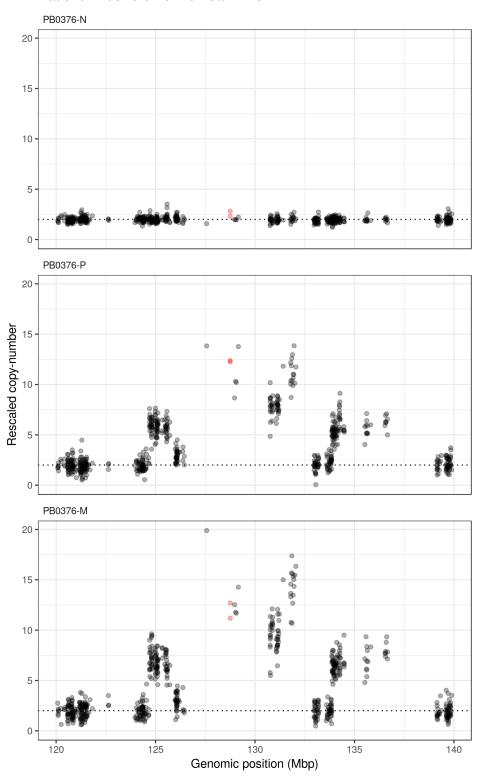
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0321 on chr 11 near YAP1

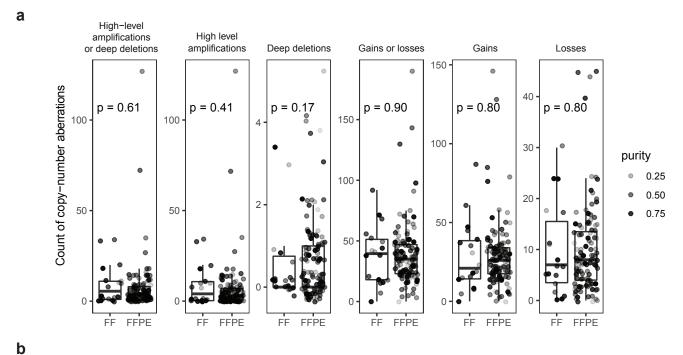


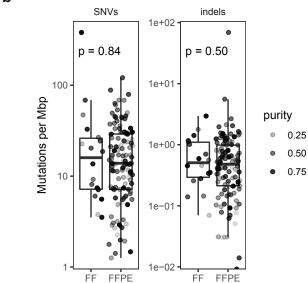
Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.

Patient PB0376 on chr 8 near MYC



Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the locus of interest is shown in red or blue. See Supplementary Table 3 for event calls.





Supplementary Fig. 2 | Comparable detections of CNAs on fresh frozen vs. formalin-fixed tissues.

- **a**, Frequencies of copy-number aberrations detected in fresh frozen vs. formalin-fixed tissues. Box represents interquartile range; middle line represents median. Each point represents the frequency of copy-number event in a tumor sample, shaded according to tumor purity.
- **b**, Mutation rates per megabase pair for SNVs and indels detected in fresh frozen vs. formalin-fixed tissues.

FF, fresh frozen. FFPE, formalin-fixed paraffin-embedded.

High-level amplification, > 8 total copy-number; Deep deletion, < 0.5 total copy-number; Gain, > 3/2 normalized copy-ratio; Loss, < 1/2 normalized copy-ratio. Normalized copy-ratio is total copy-number scaled to tumor ploidy.