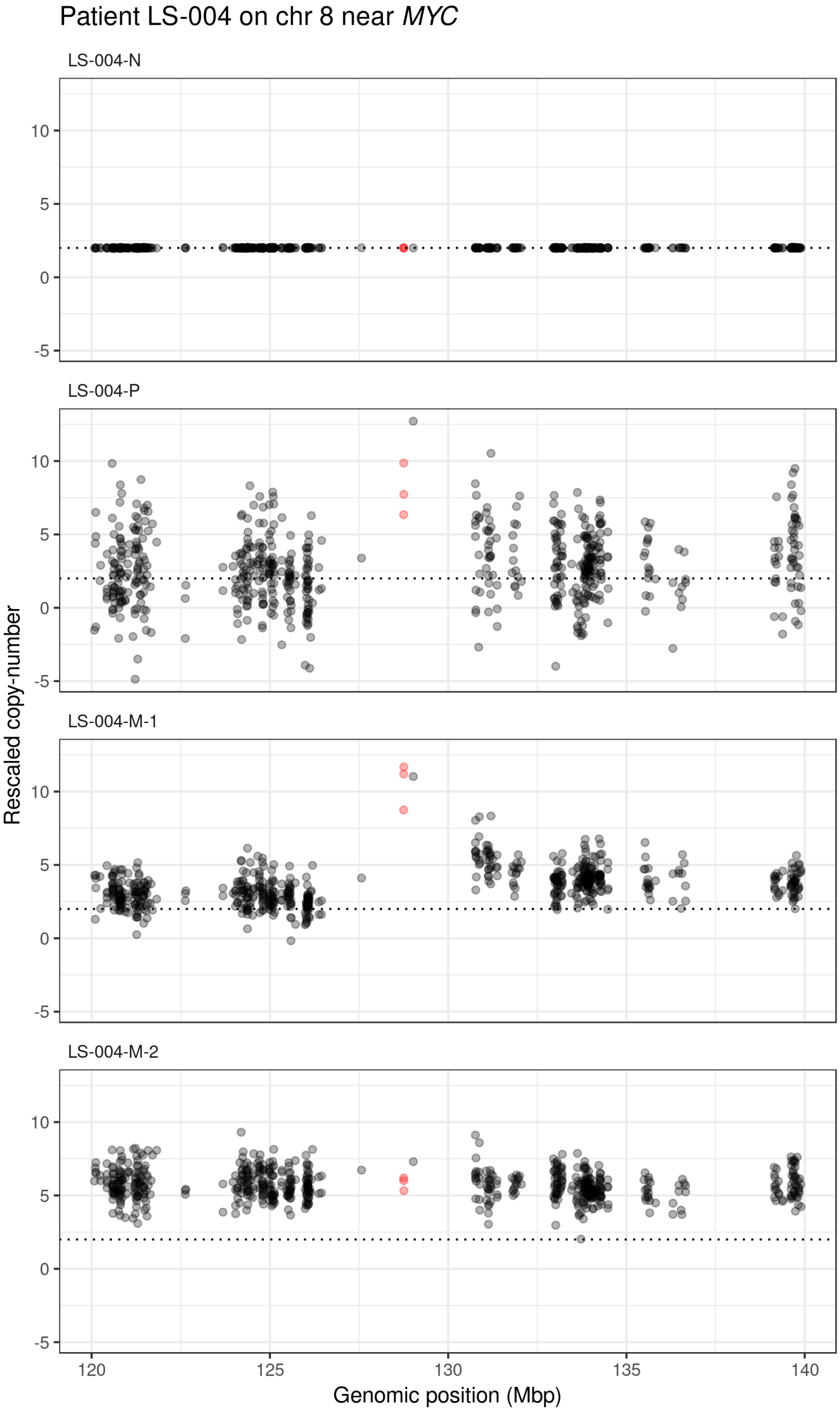
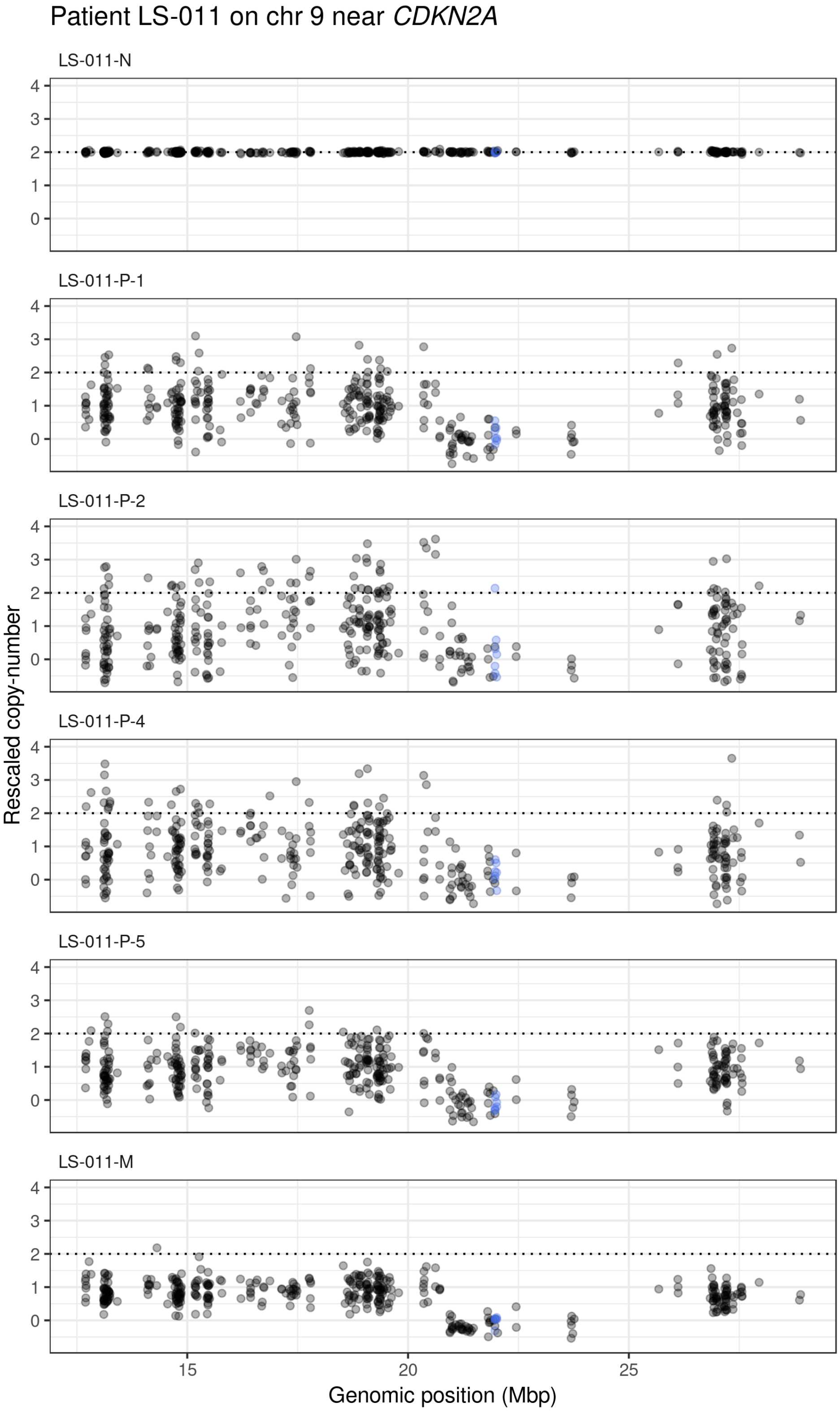


Supplementary Fig. 1 | Copy-number analyses of drivers in matched primary tumors and brain metastases. Each dot denotes the rescaled total copy-number (corrected for tumor purity and ploidy) in a target exome region for normal (N), primary tumor (P), or brain metastasis sample (M). Targets within the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



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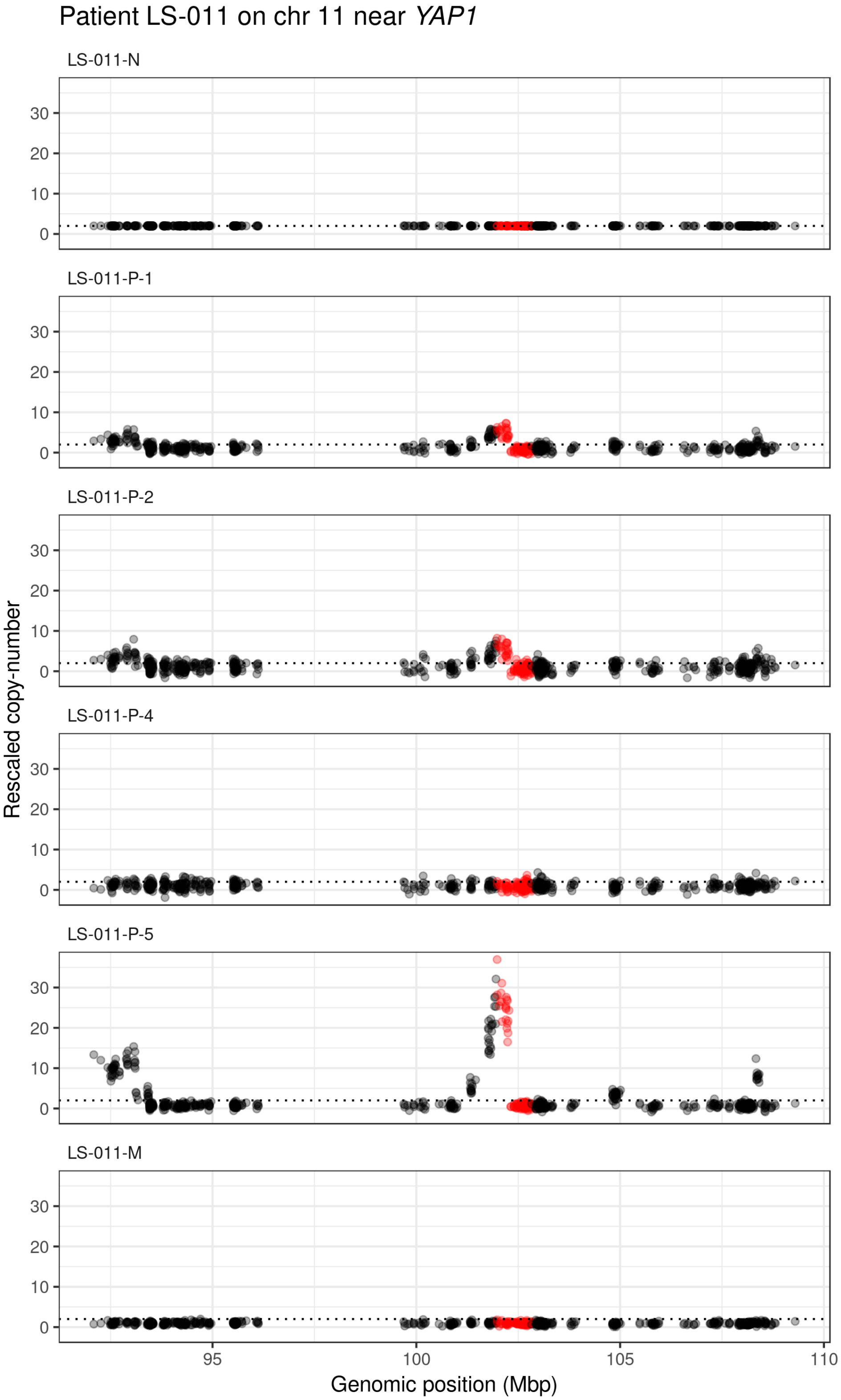

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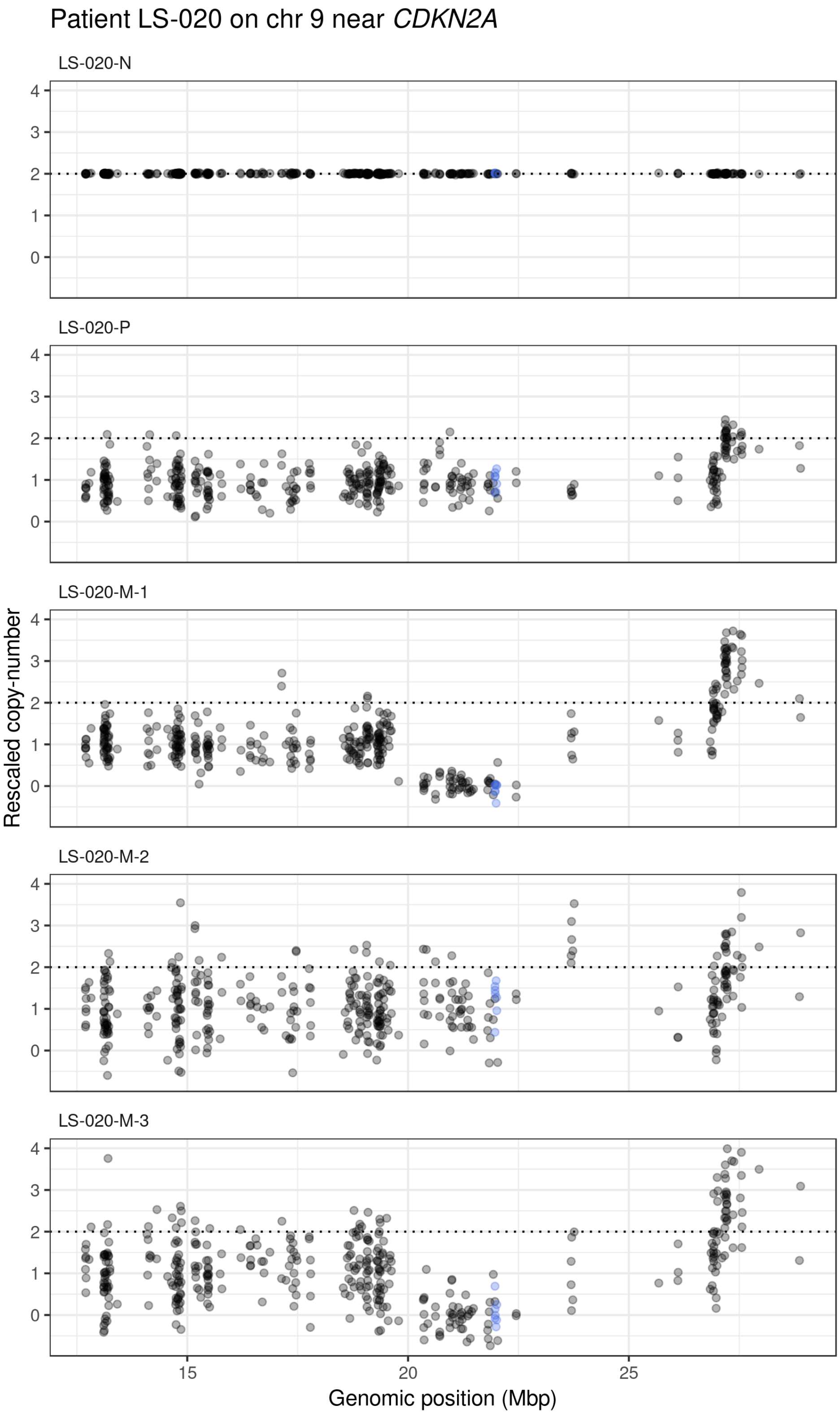

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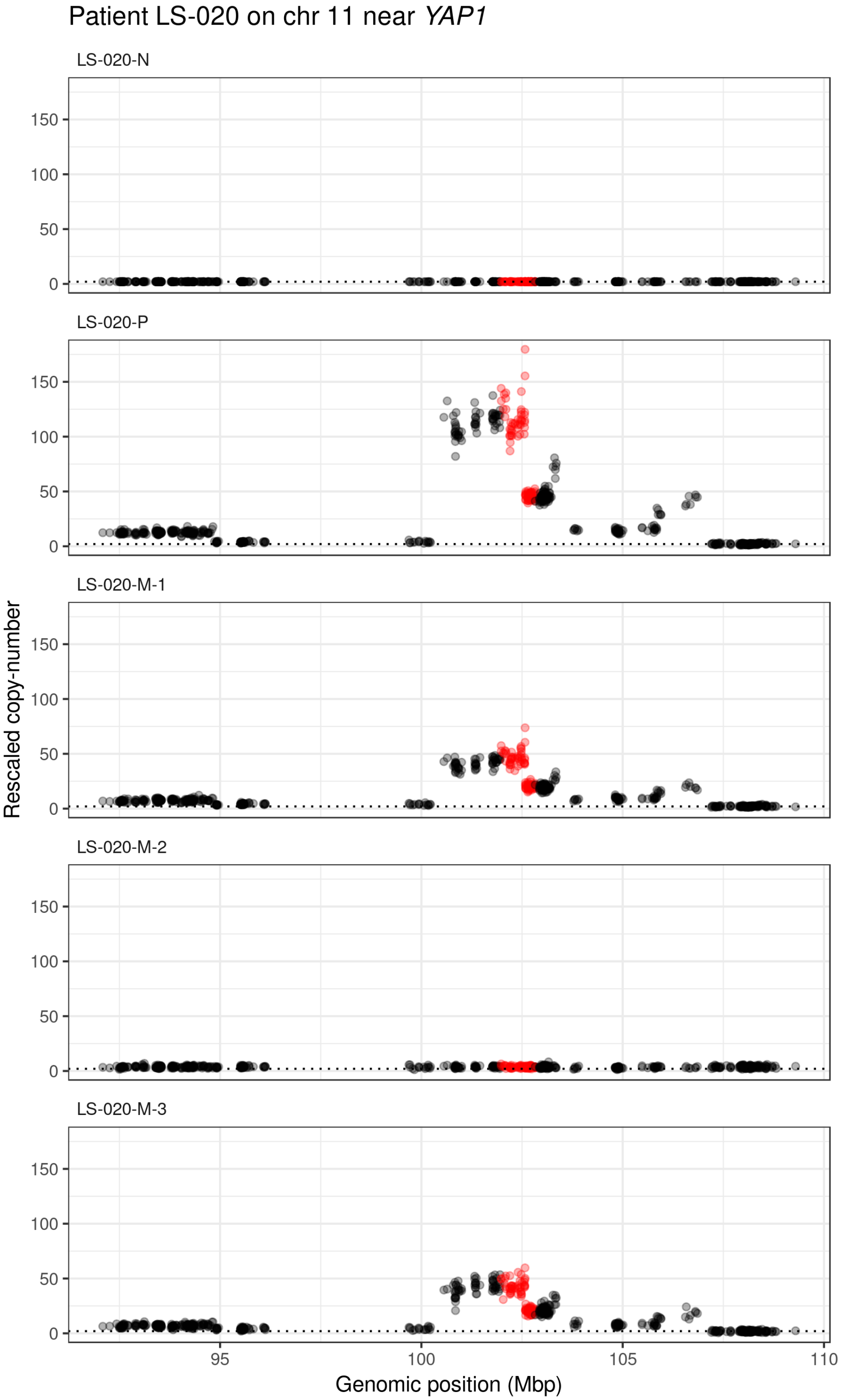

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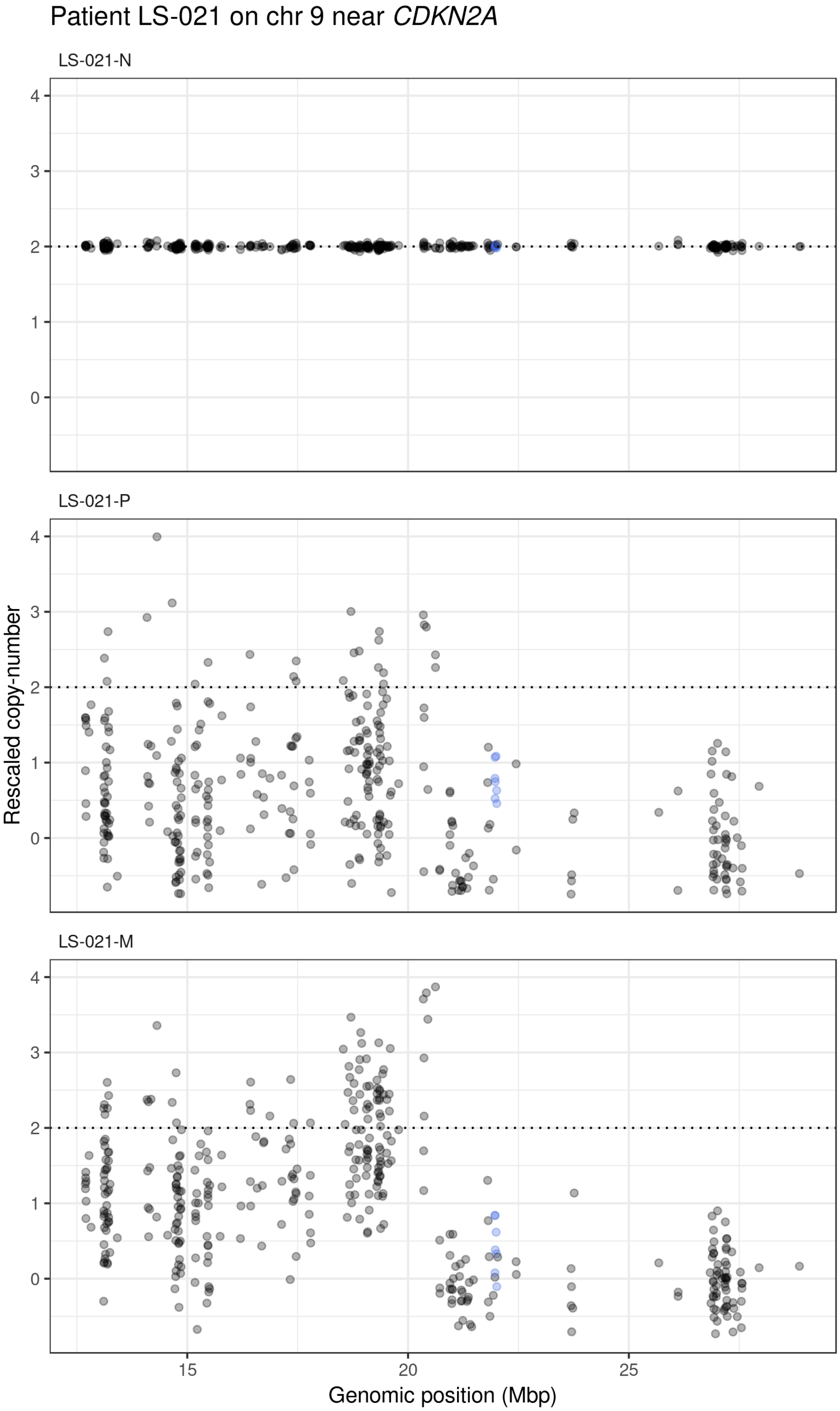

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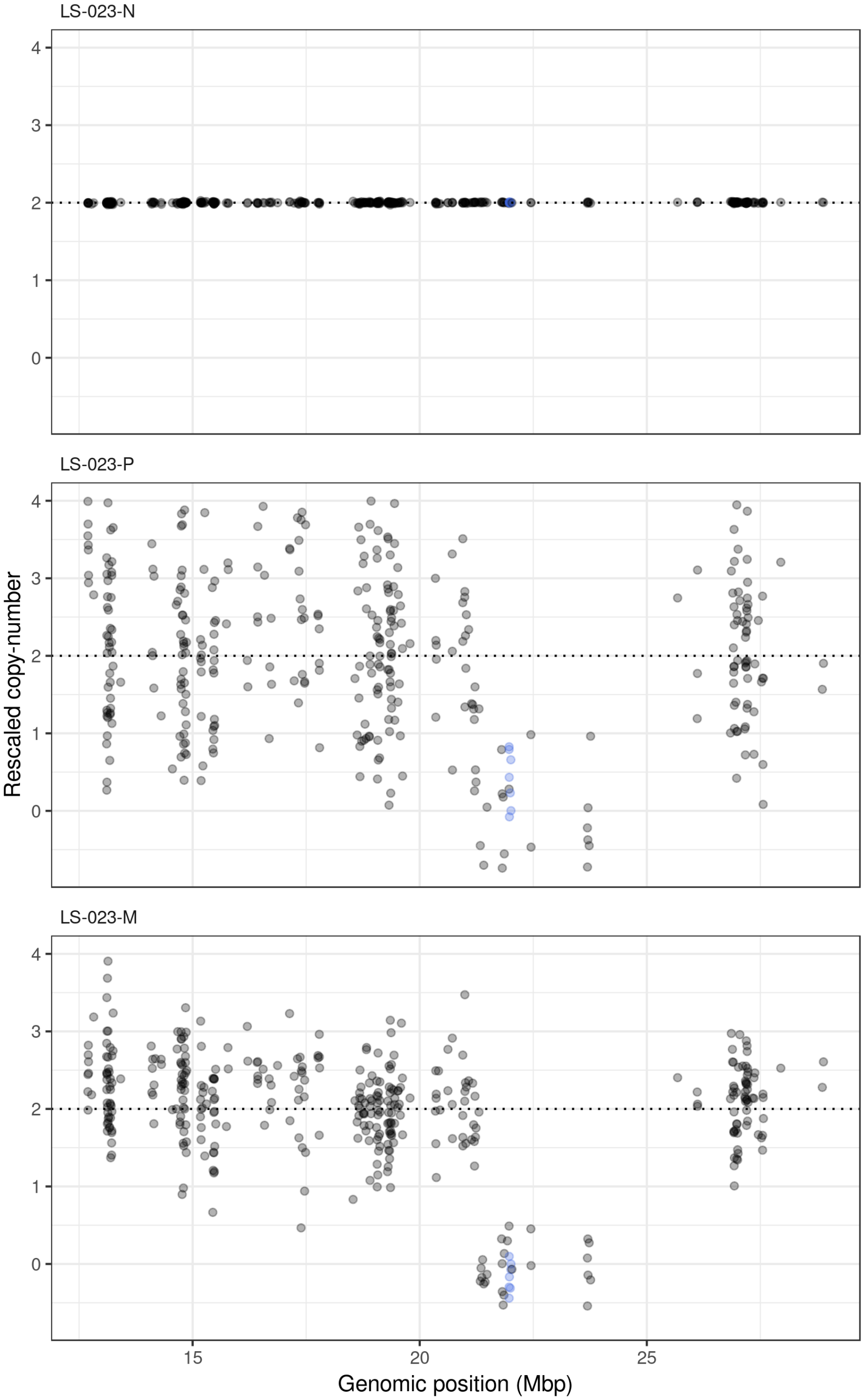
Patient LS-023 on chr 9 near *CDKN2A*



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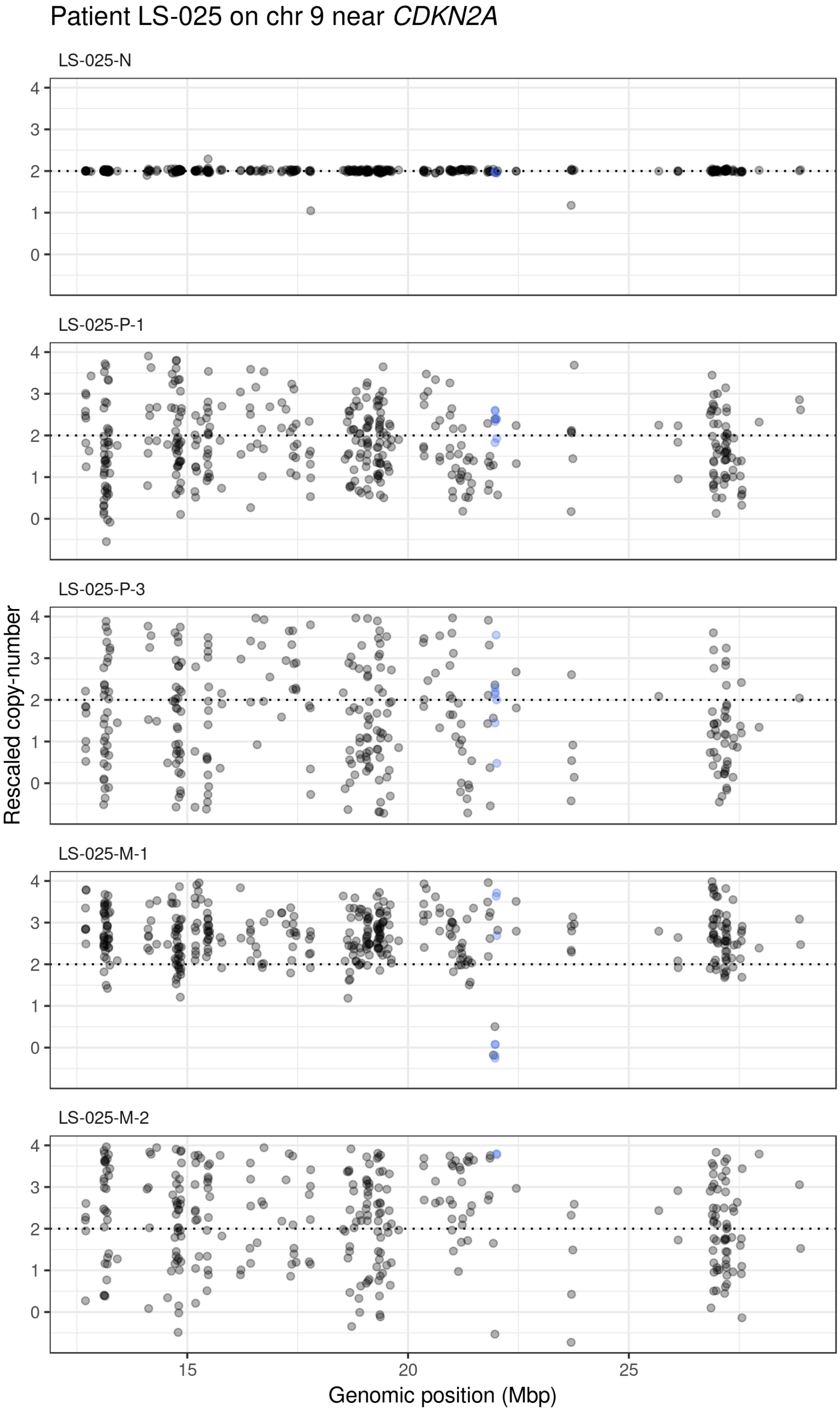

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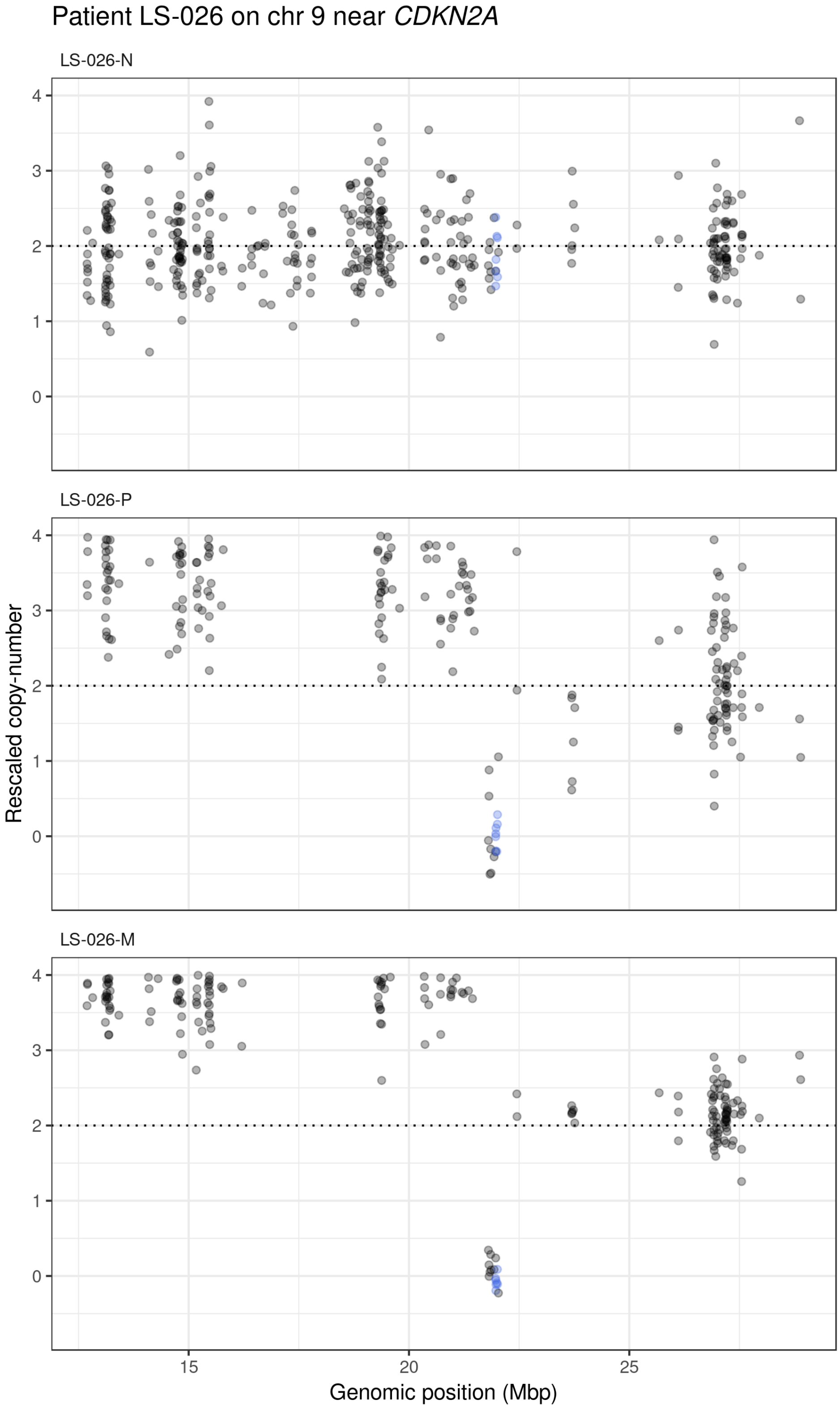

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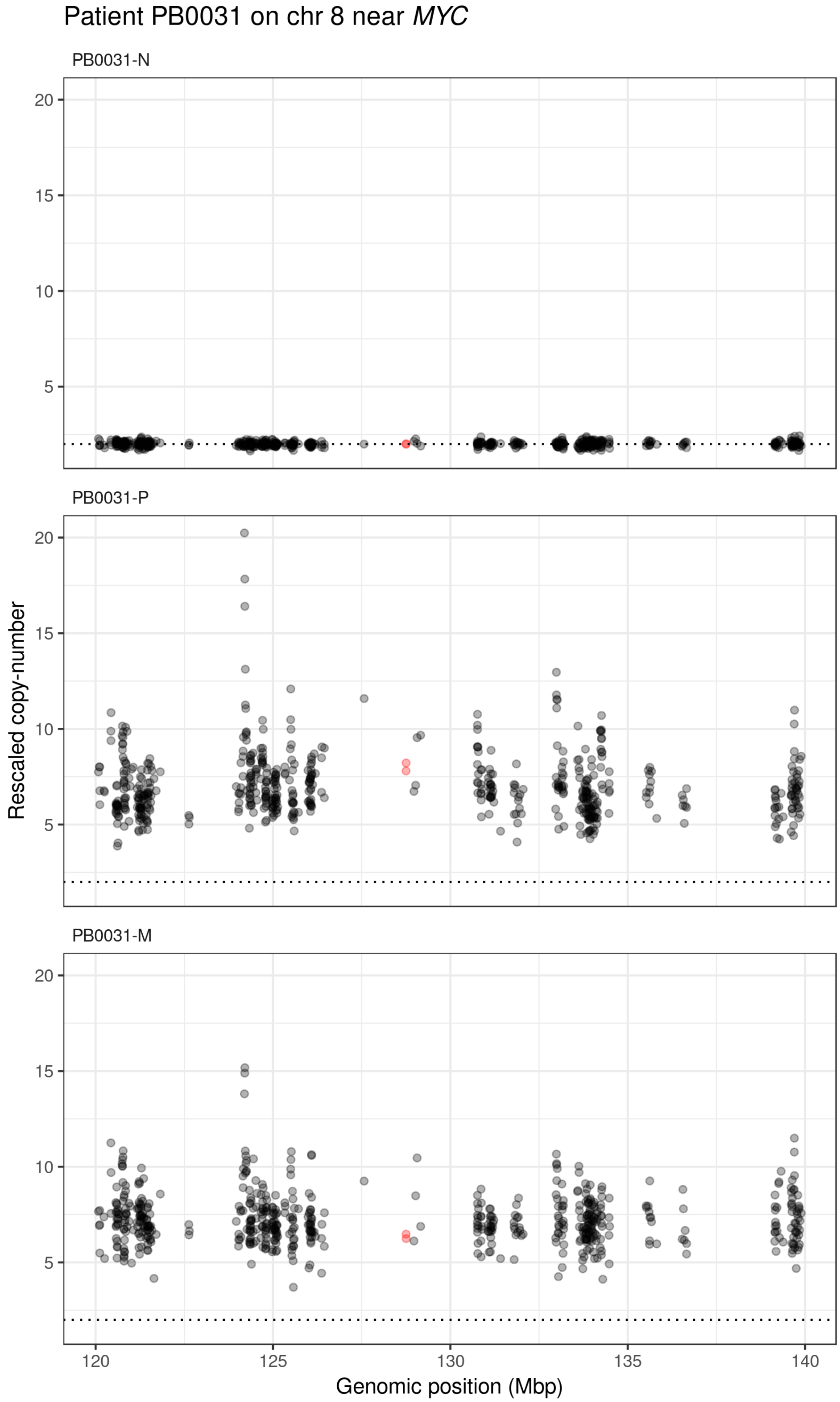

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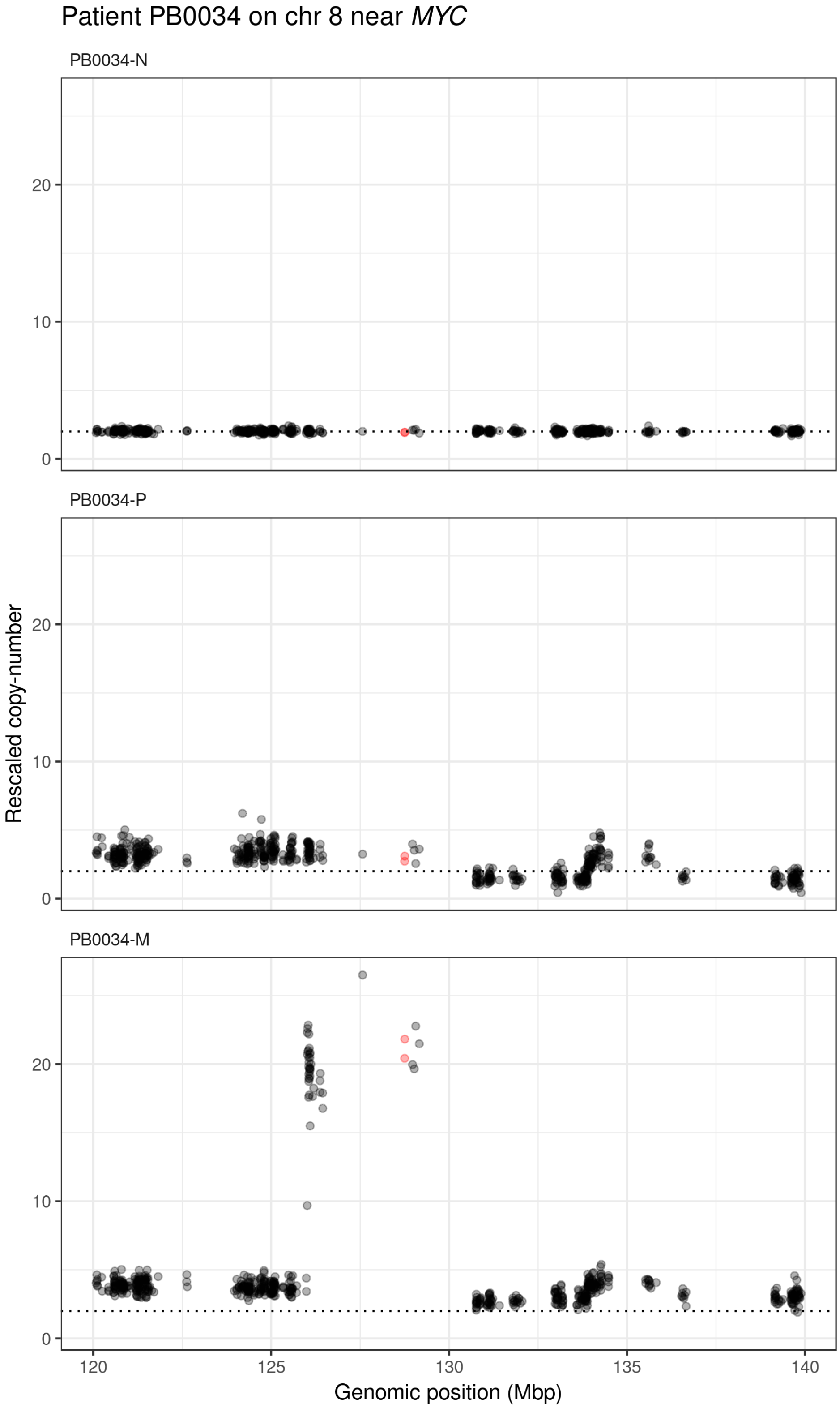

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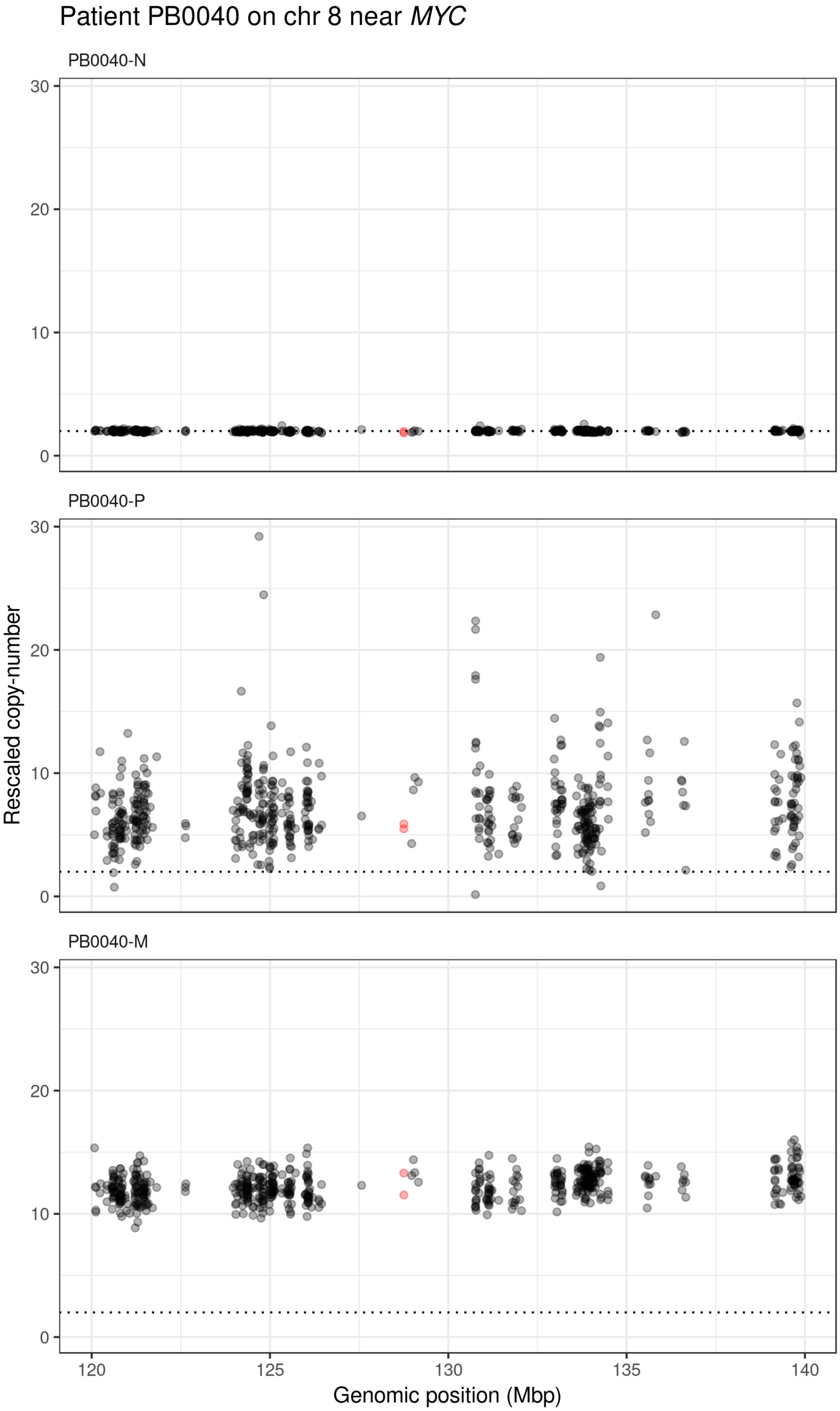

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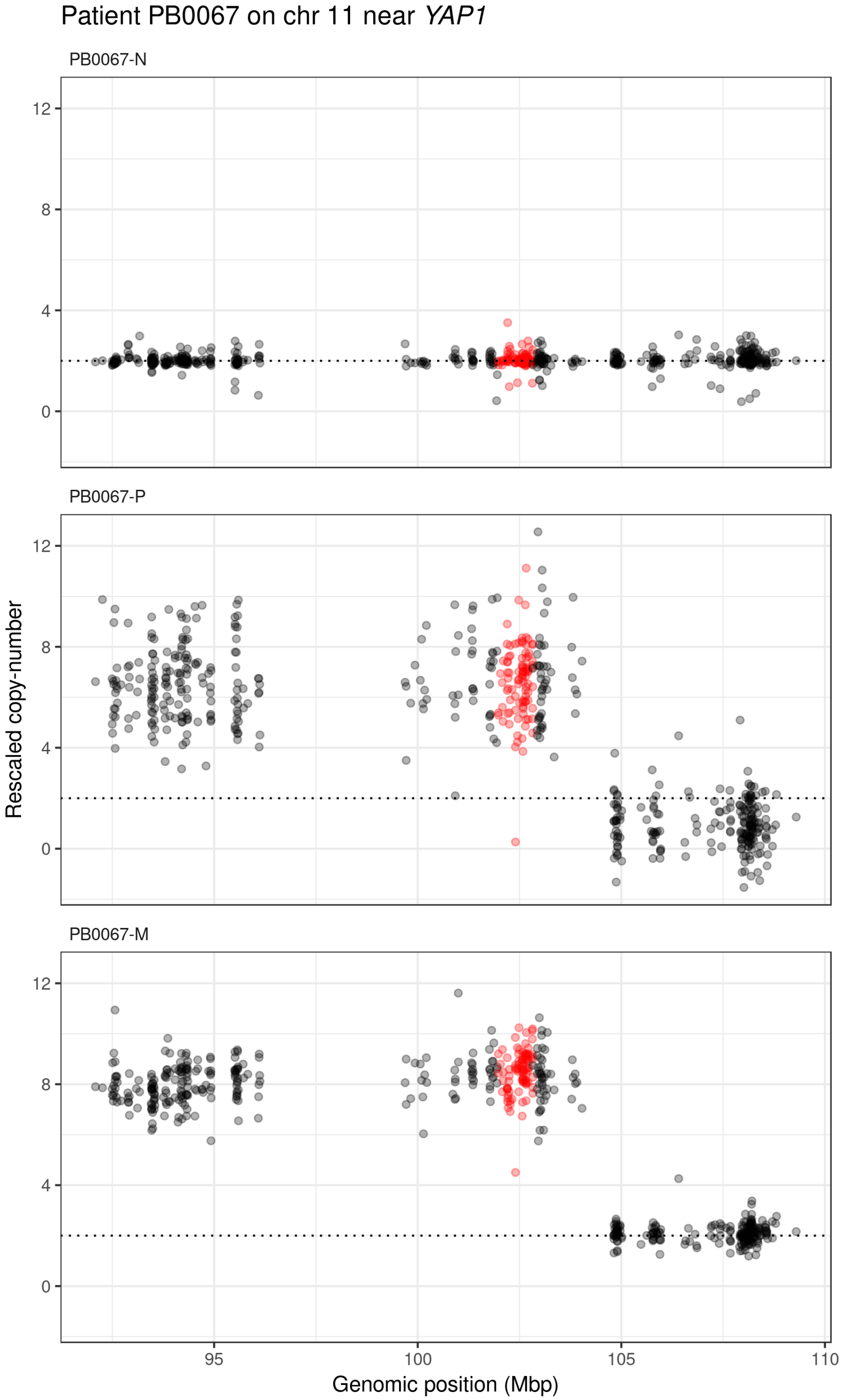

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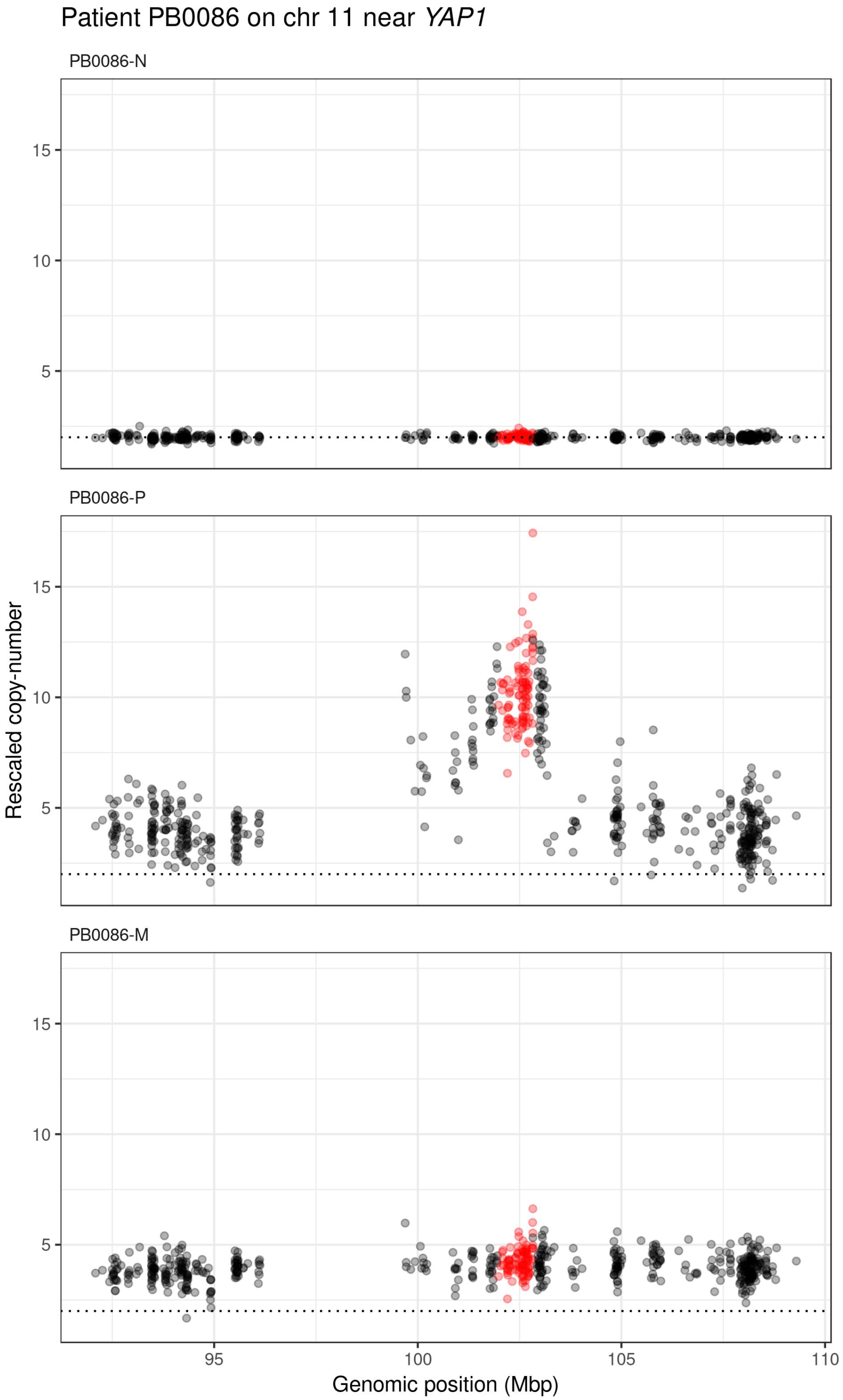

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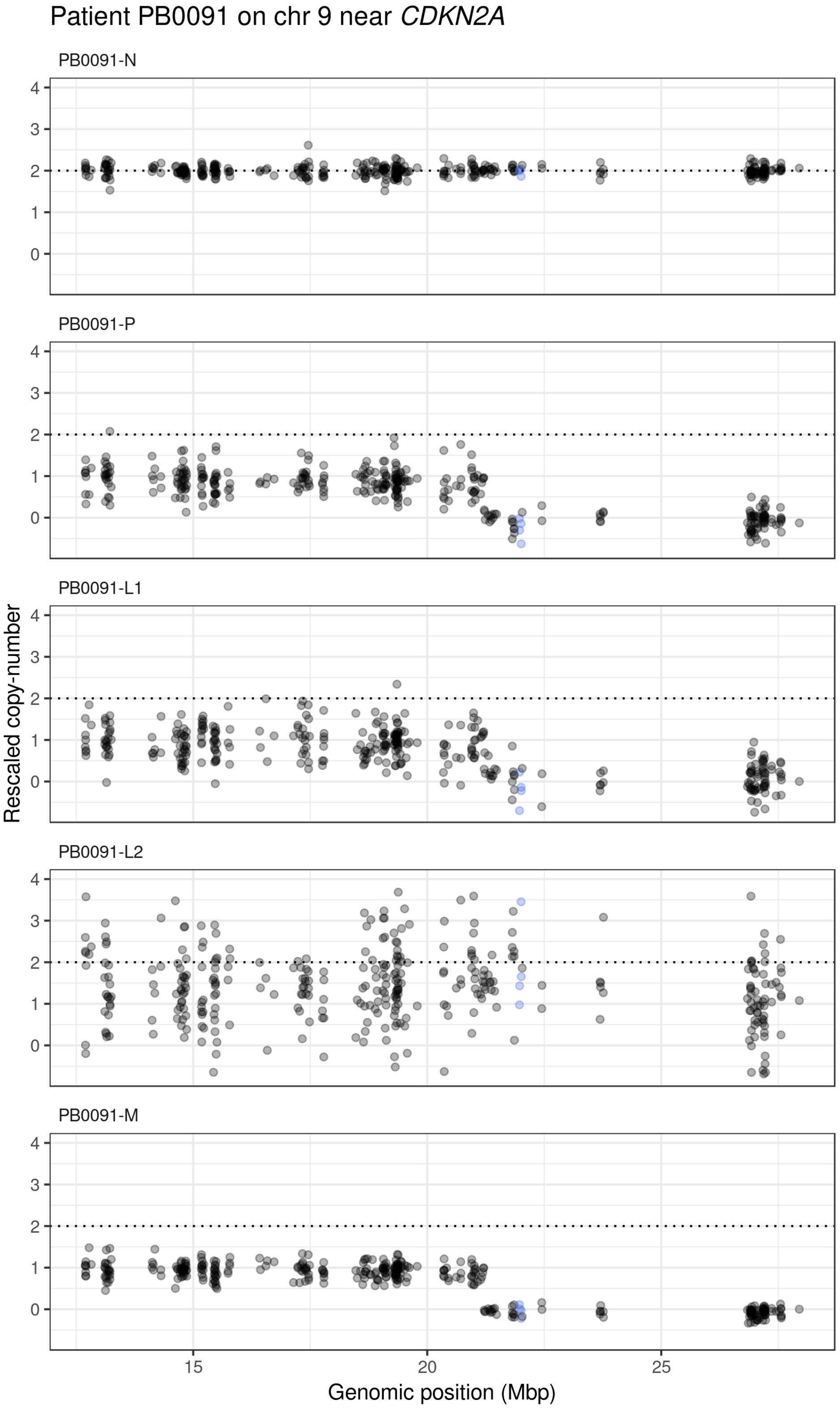

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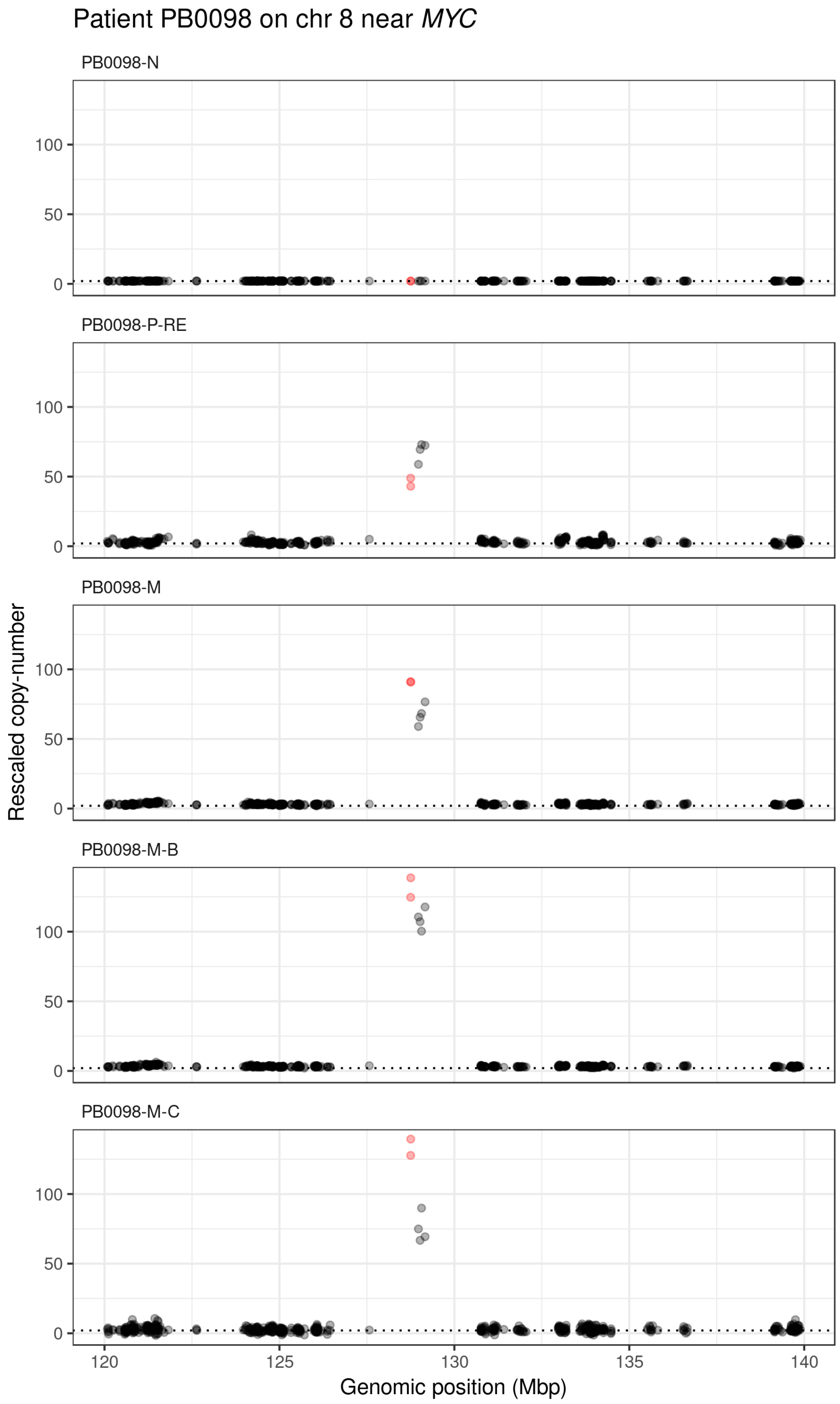

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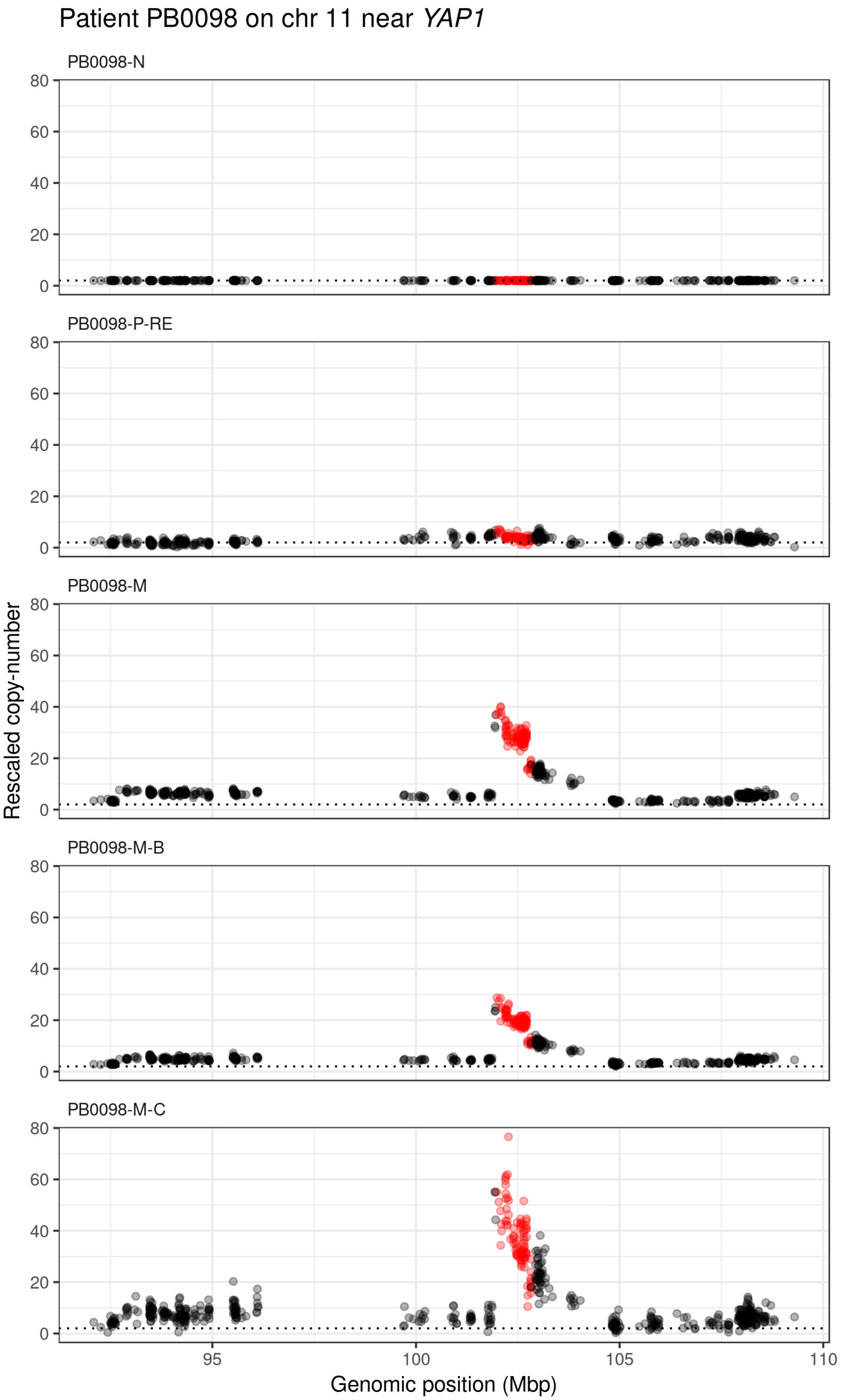

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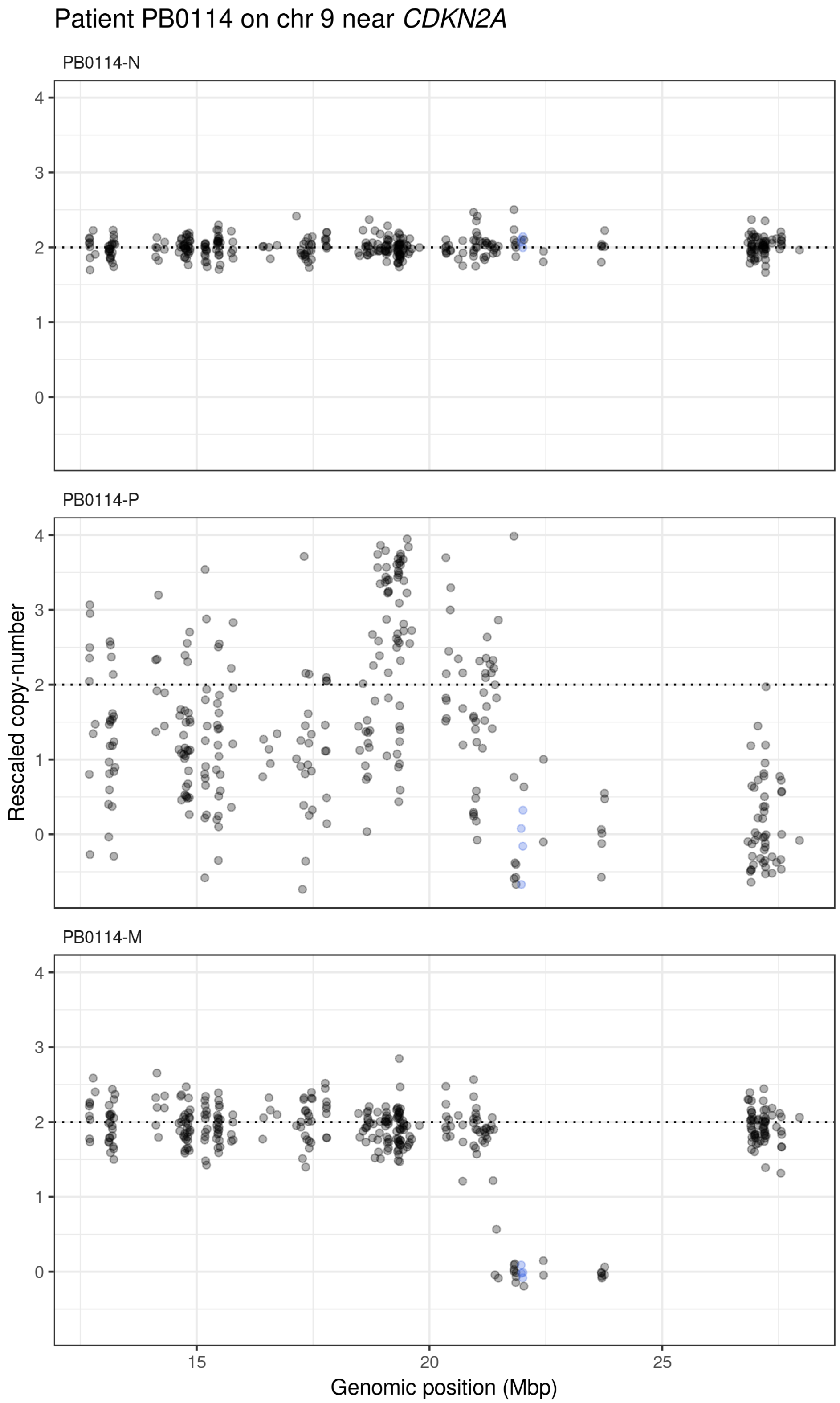

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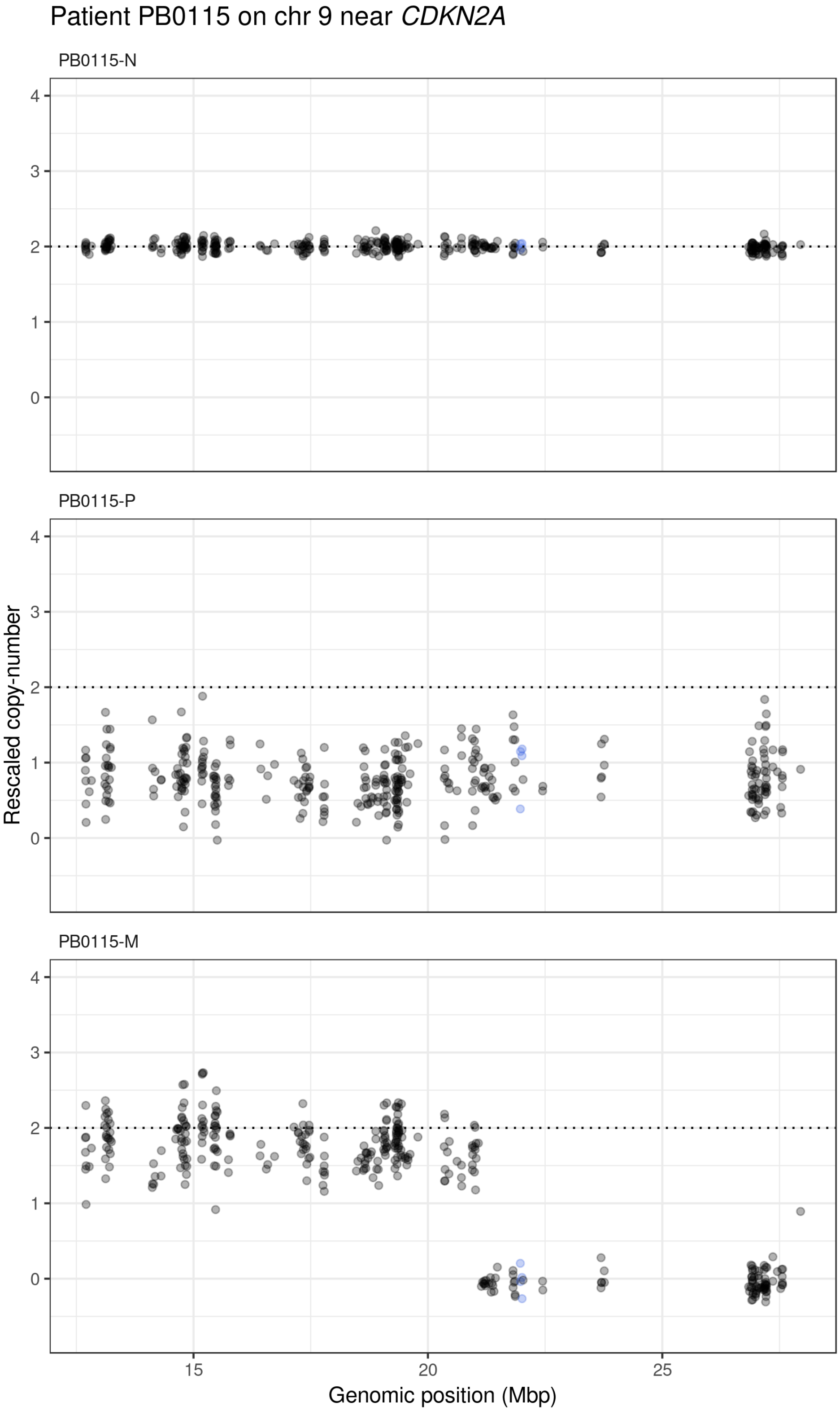

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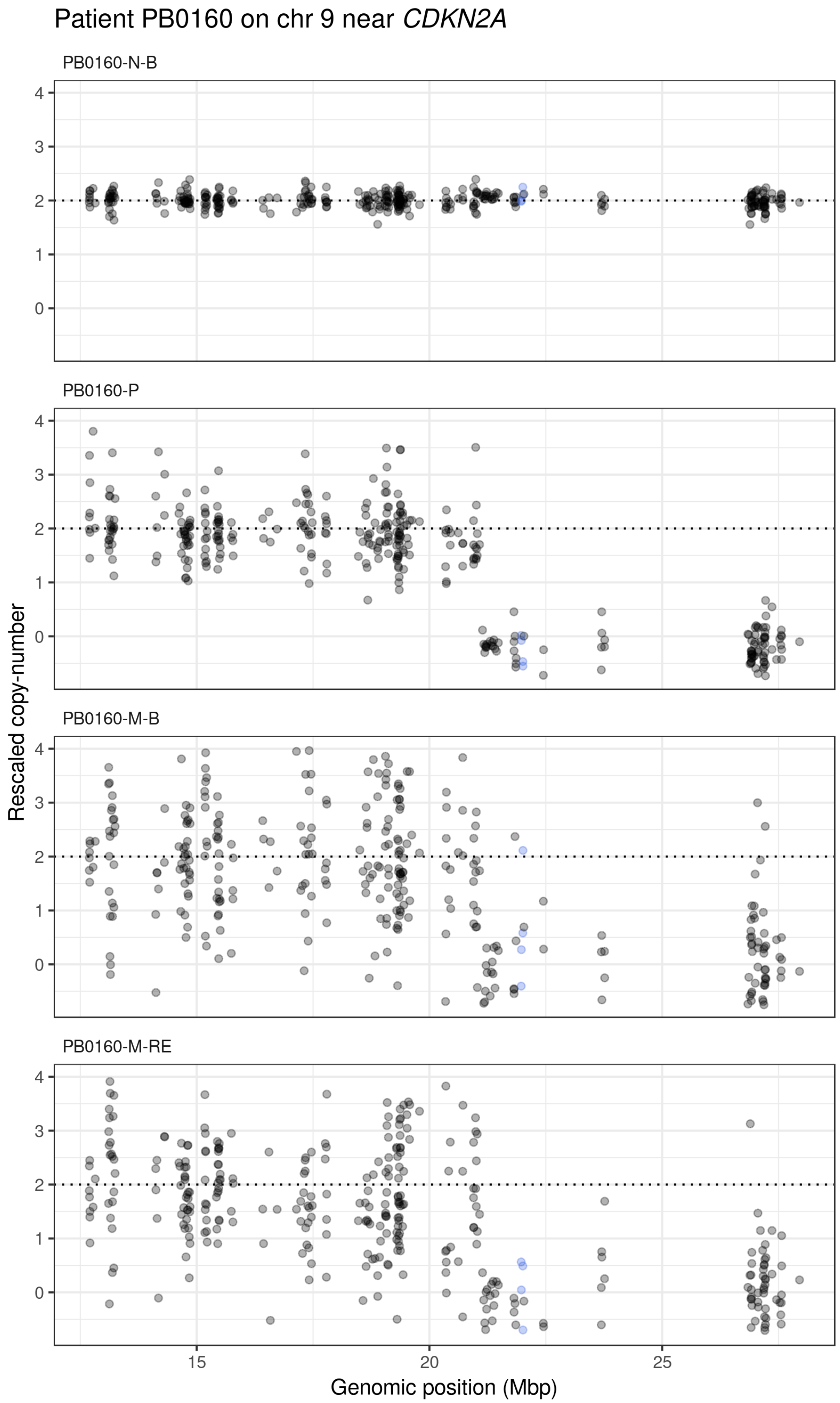

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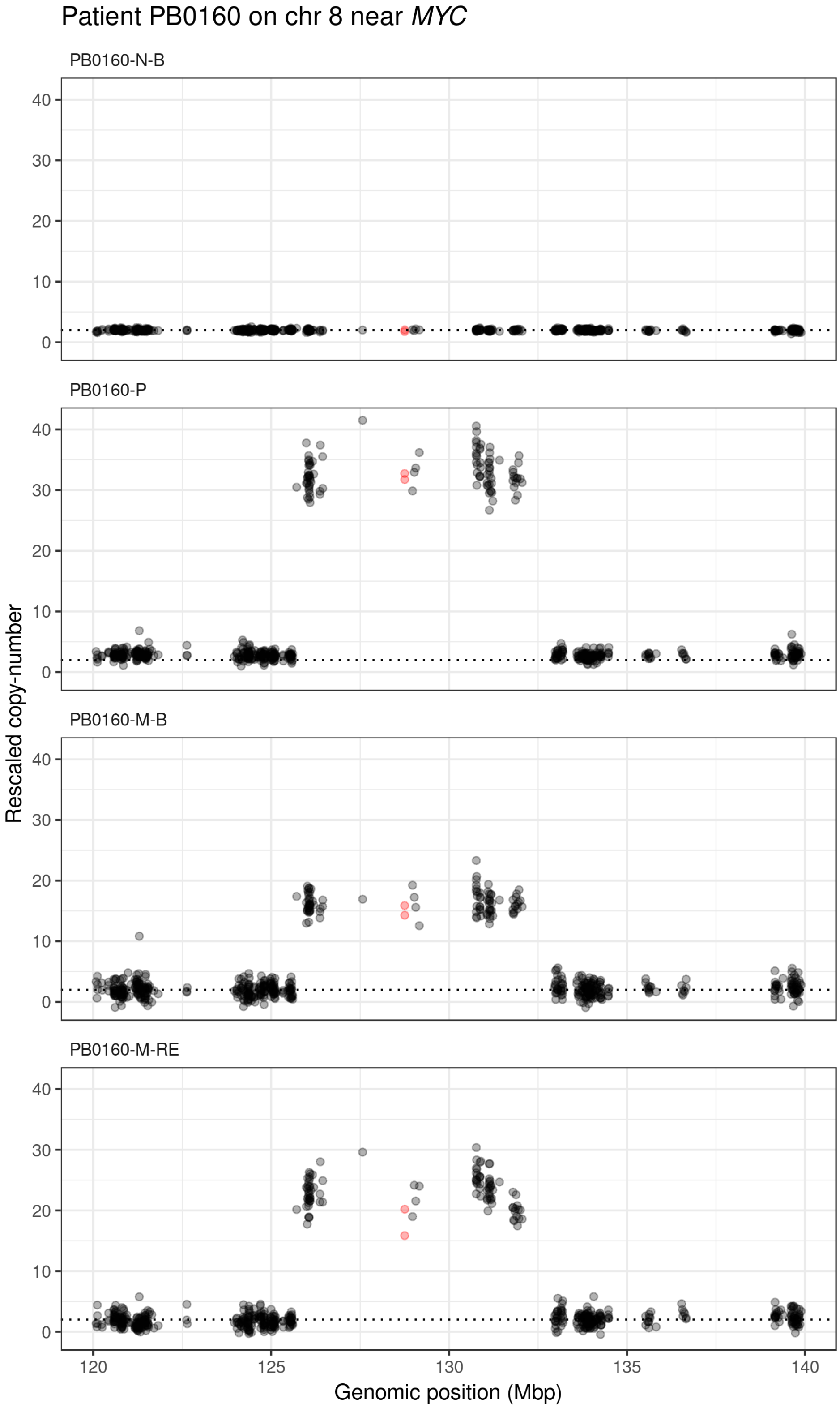

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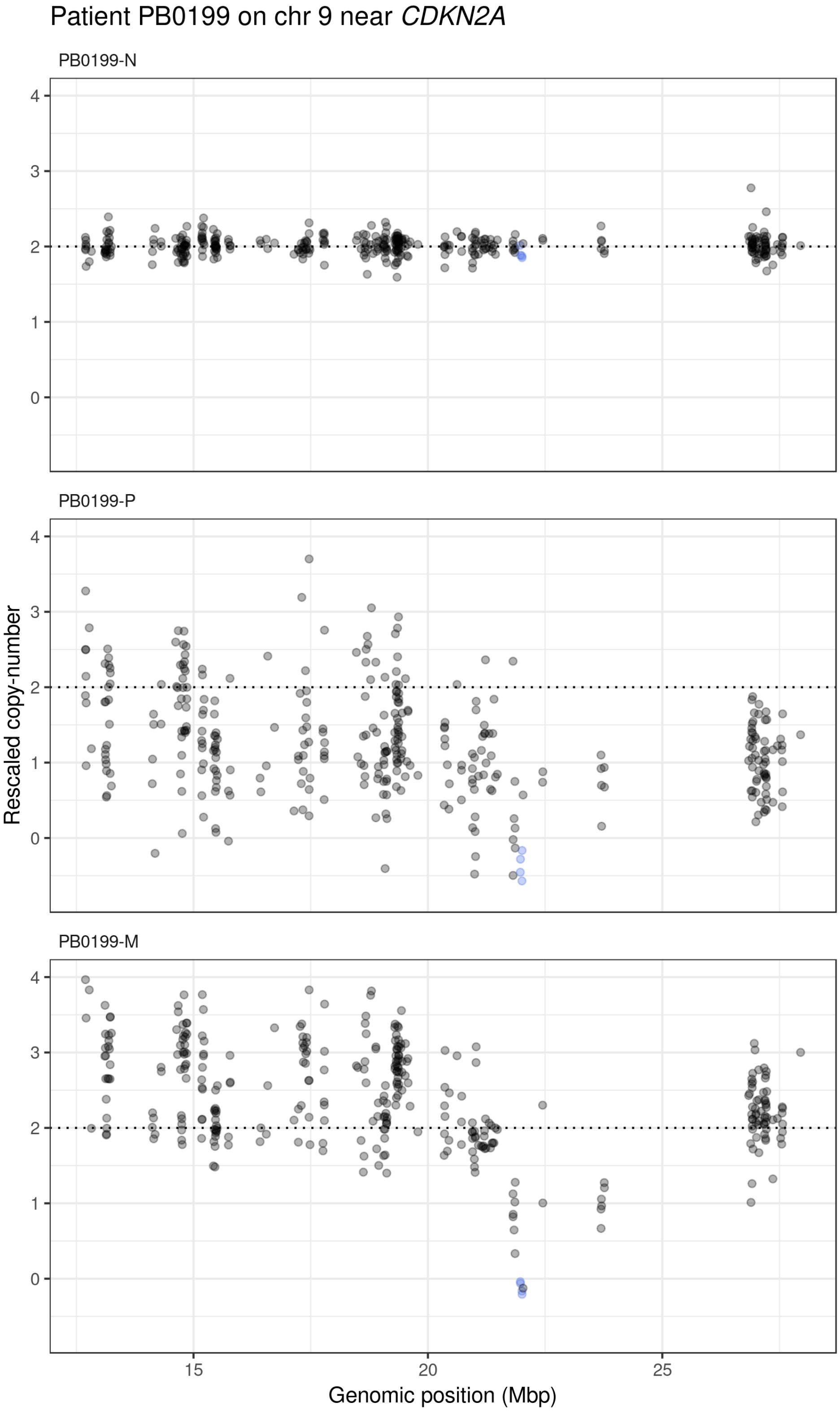

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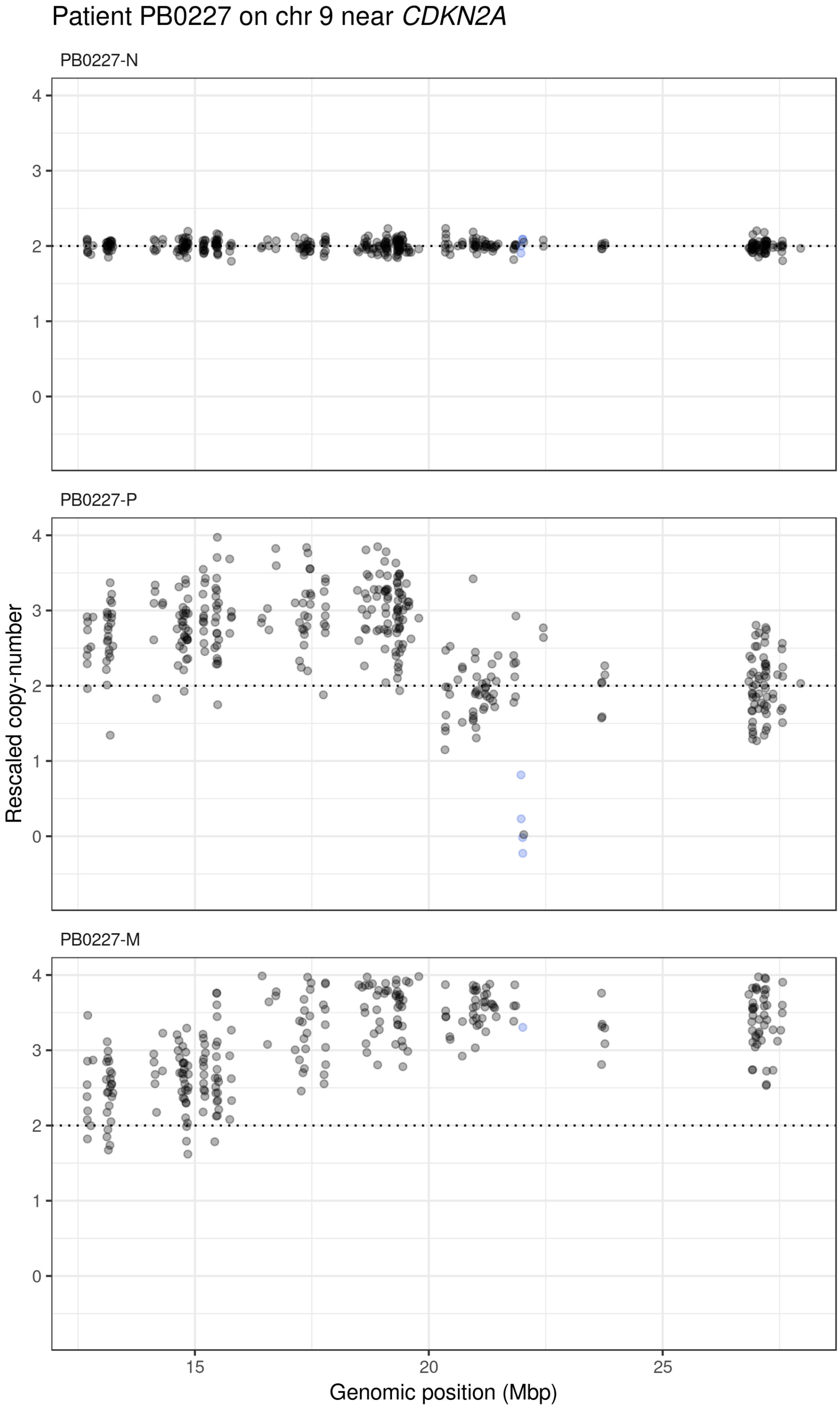

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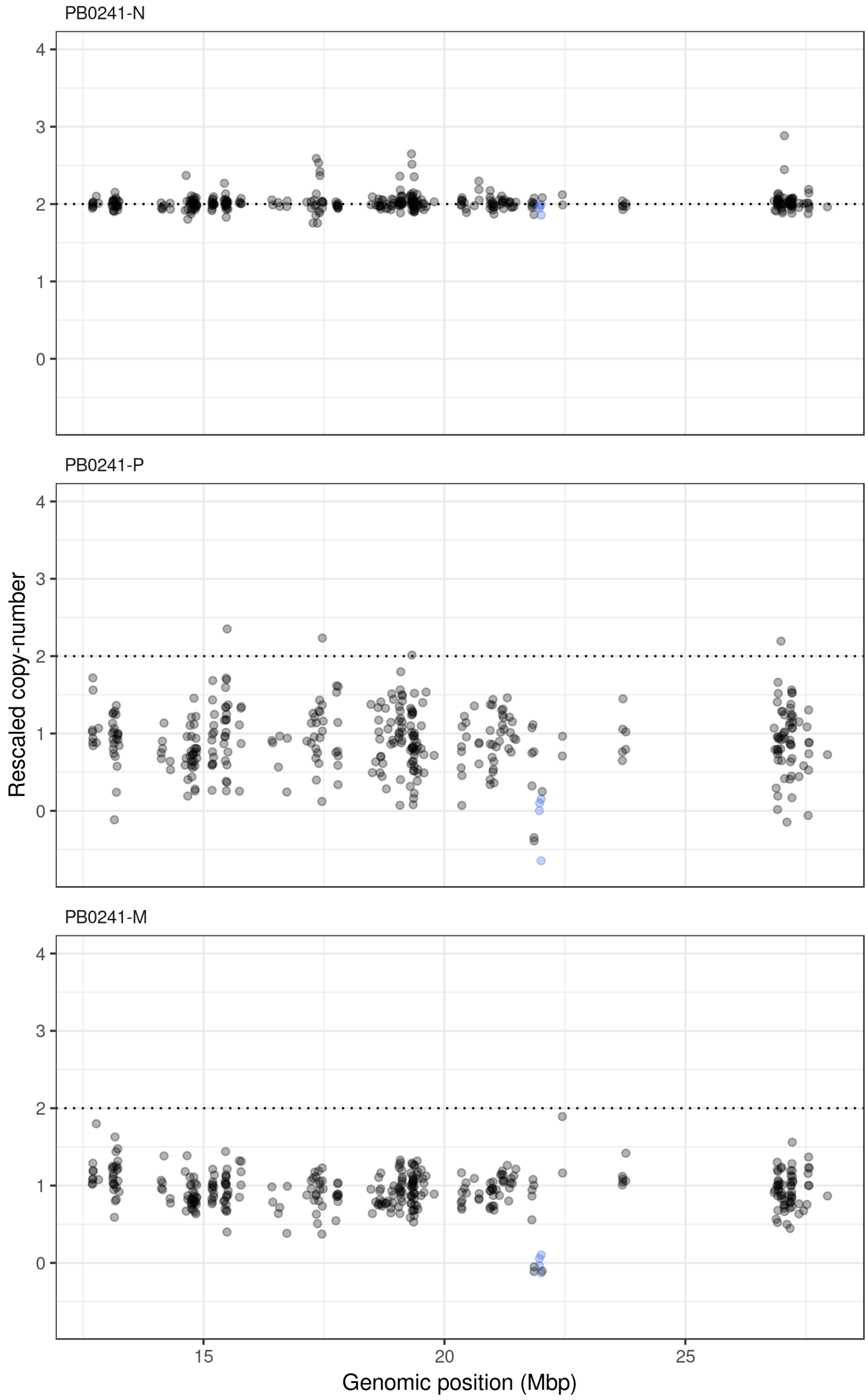
Patient PB0241 on chr 9 near *CDKN2A*



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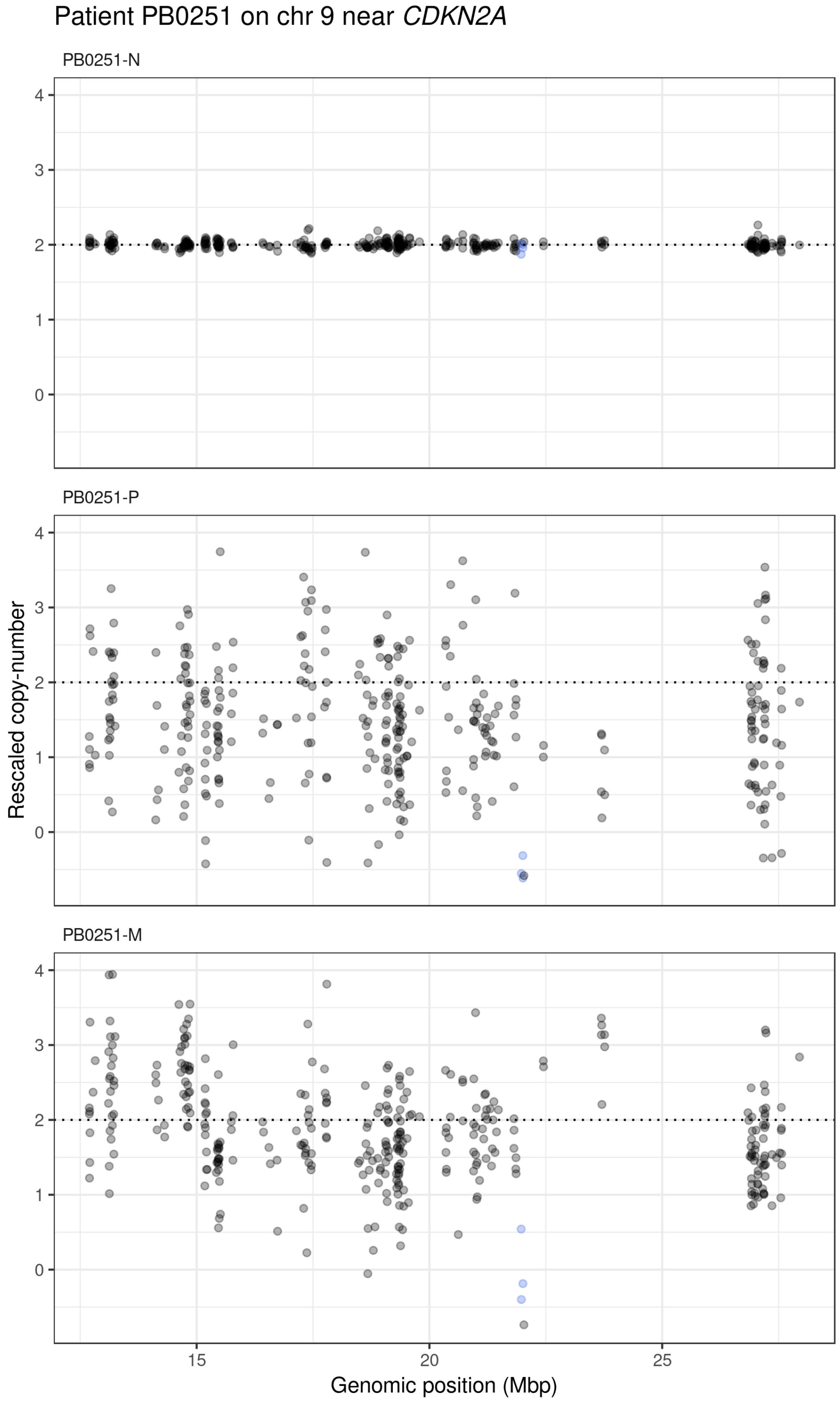

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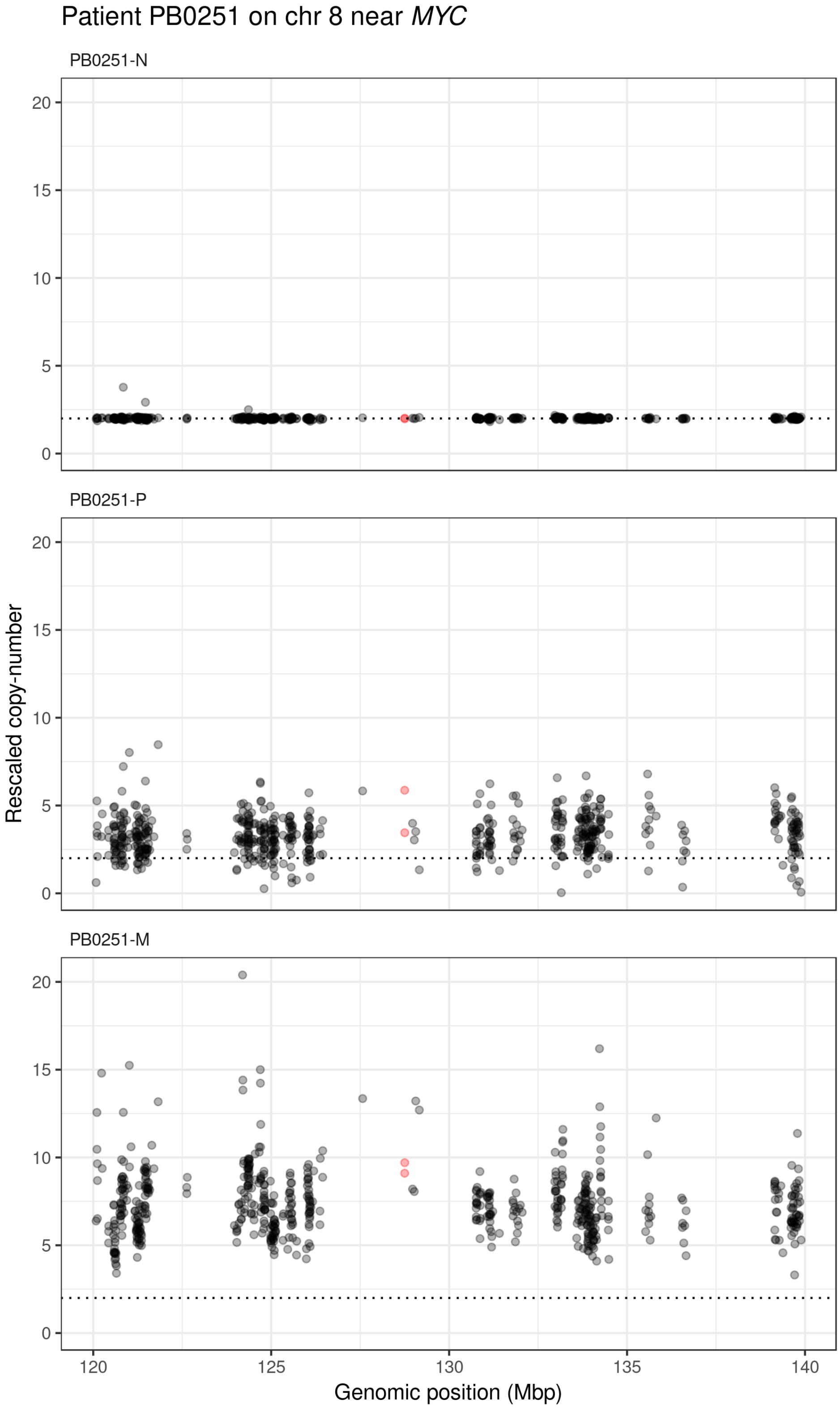

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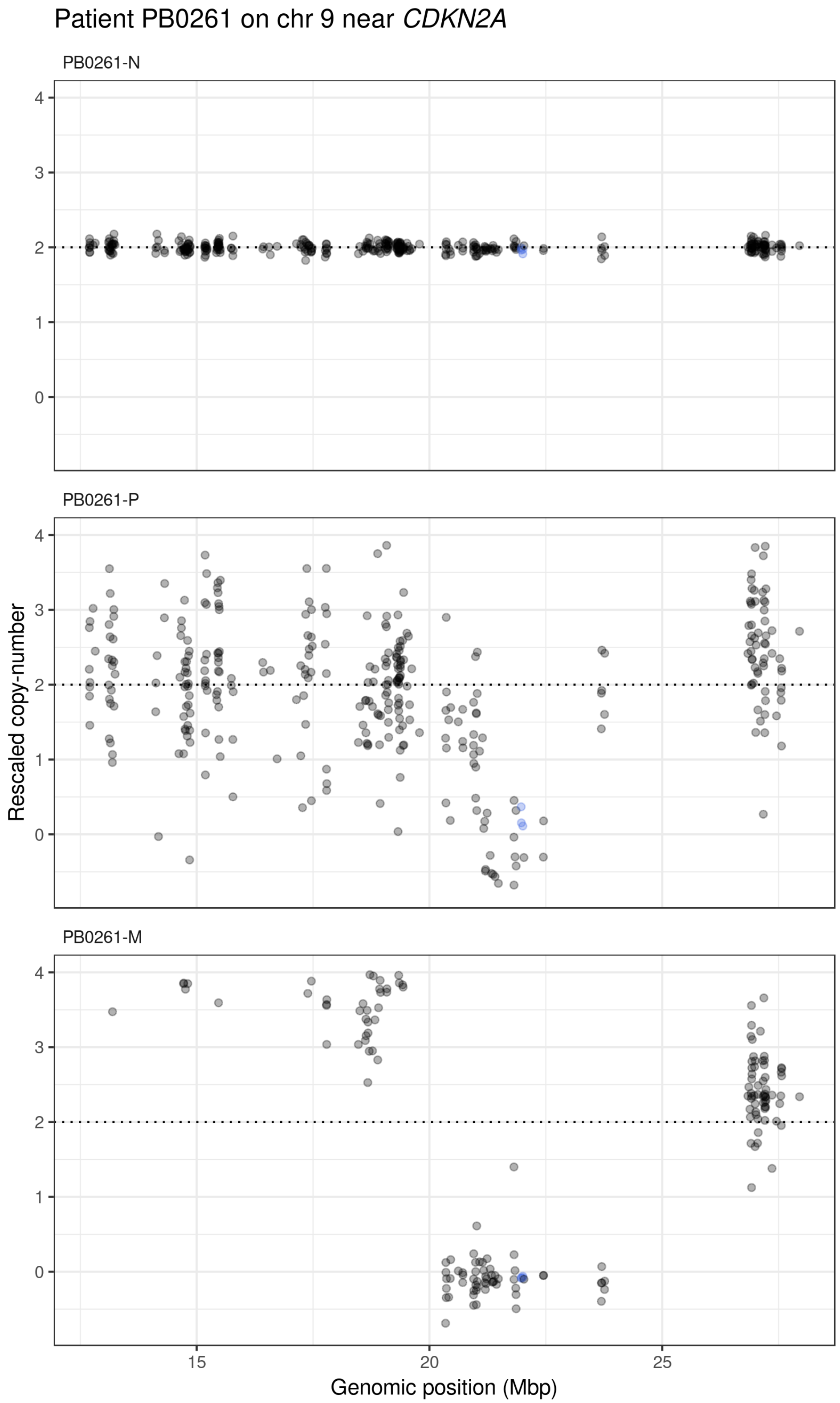

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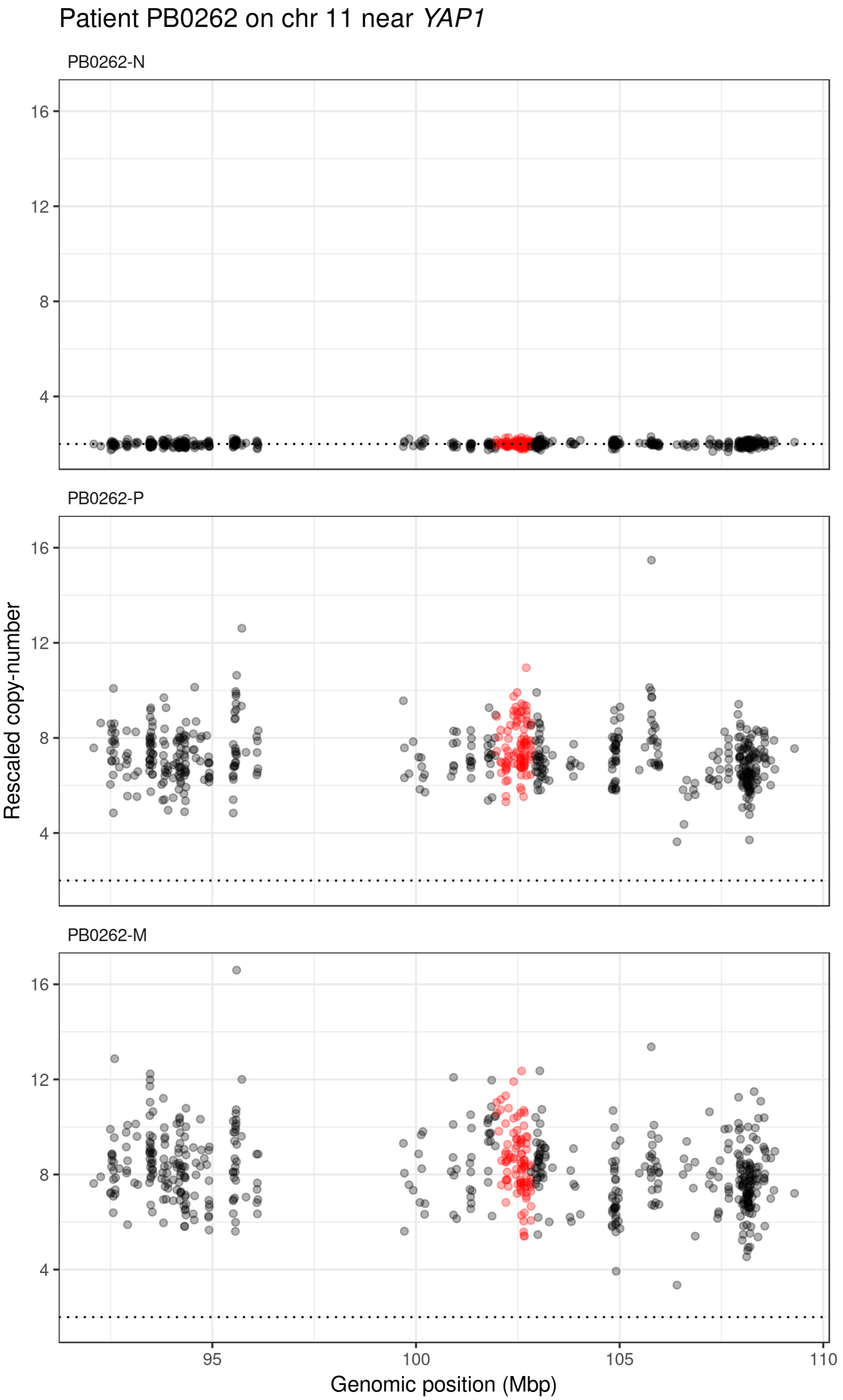

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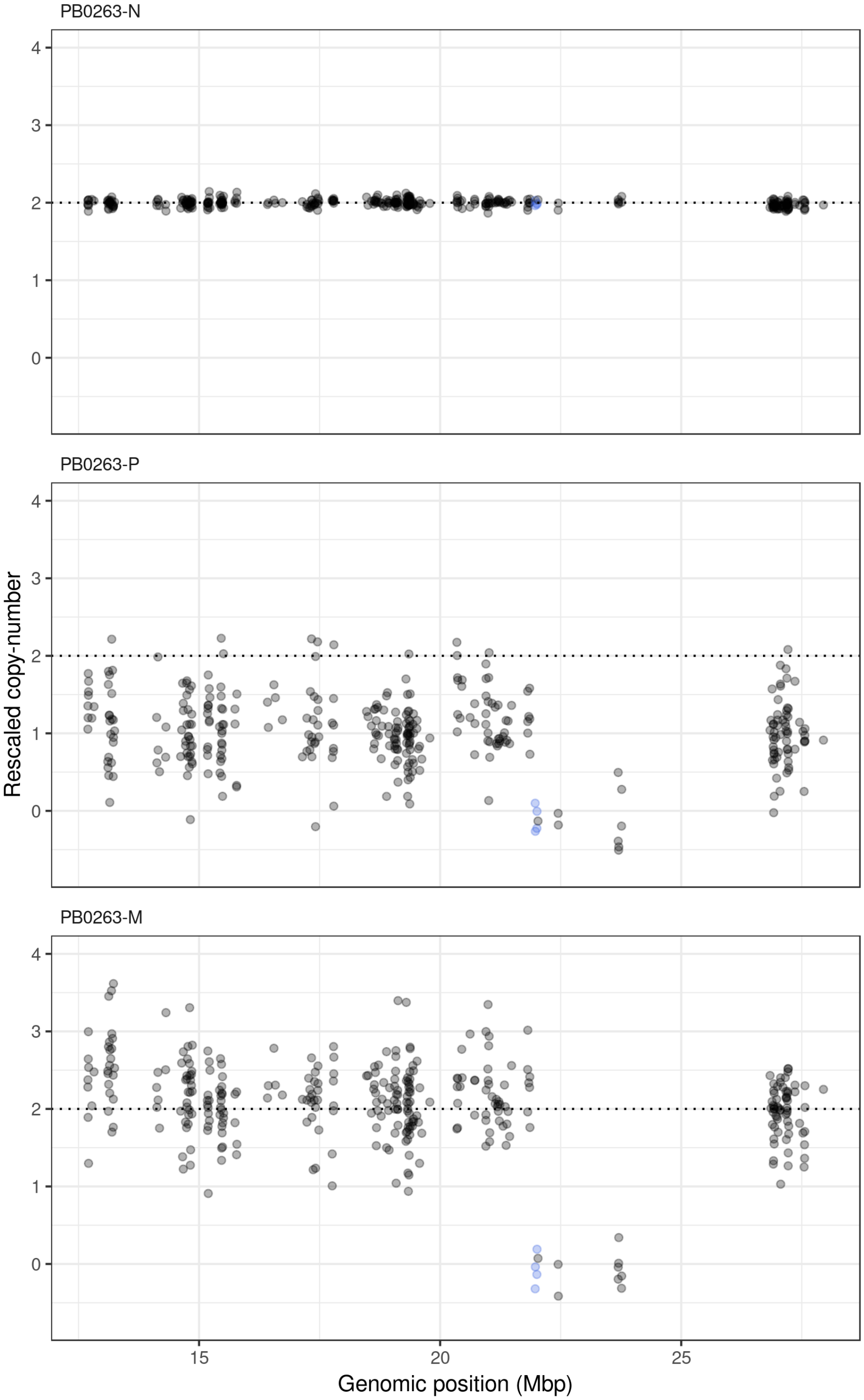
Patient PB0263 on chr 9 near *CDKN2A*



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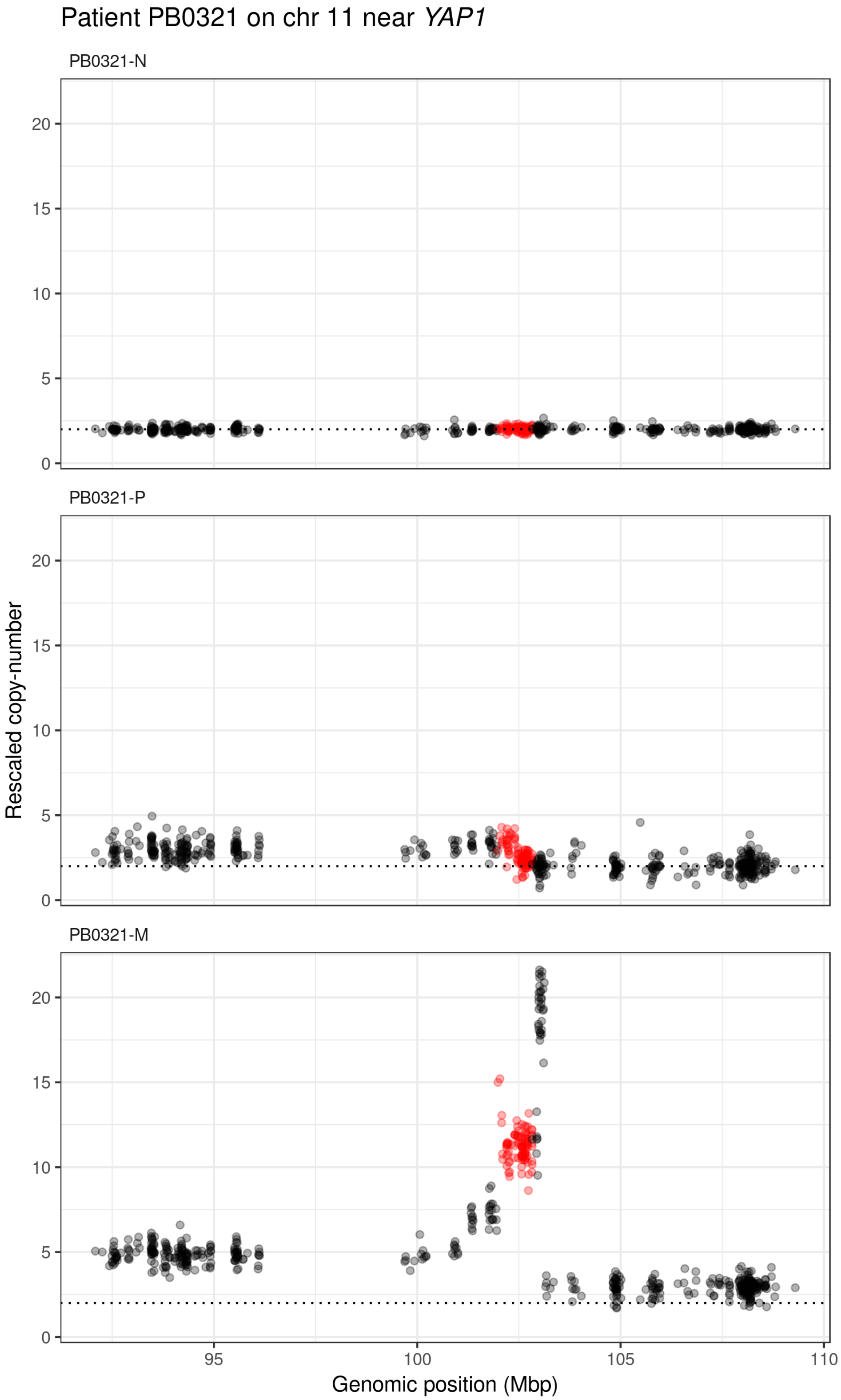

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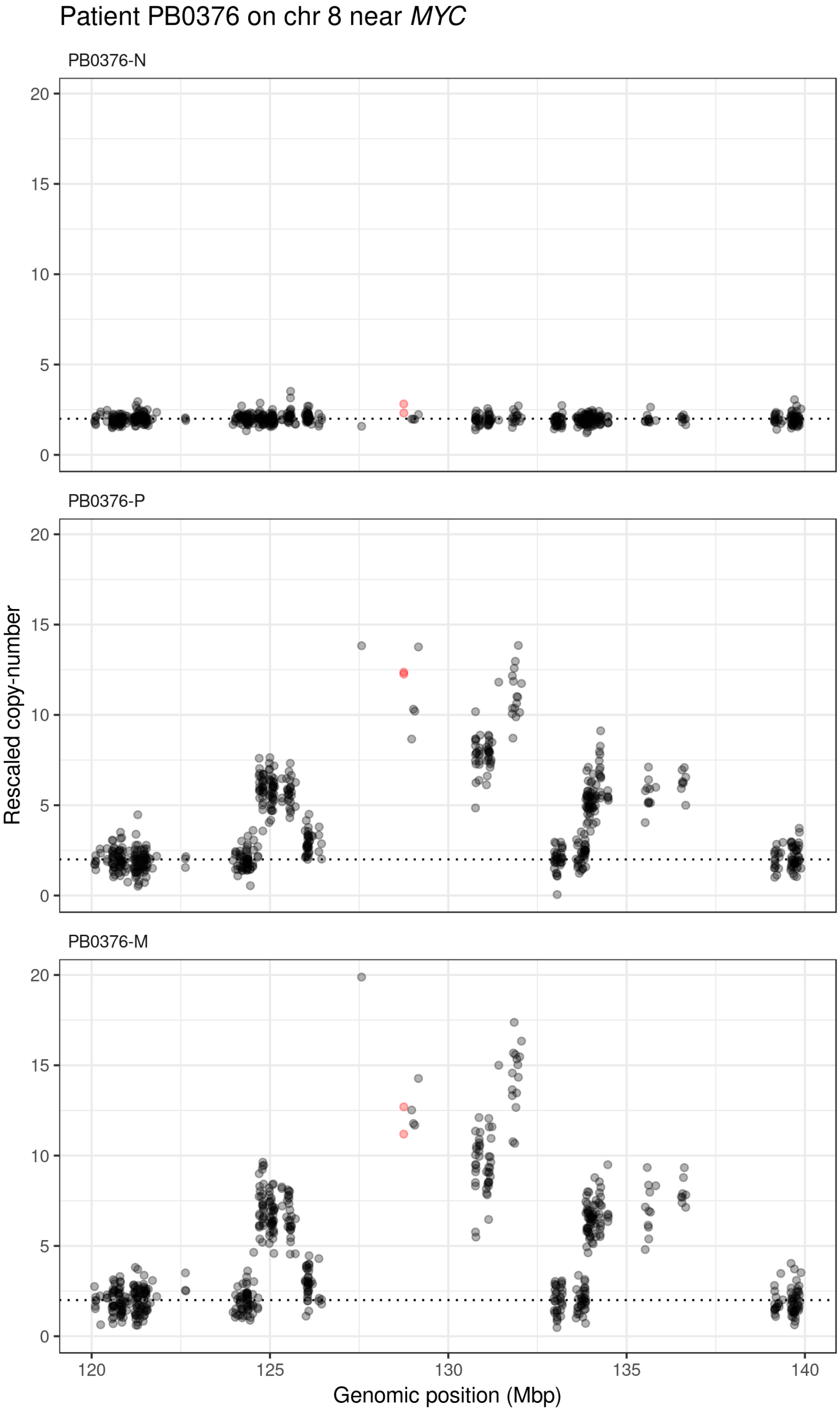

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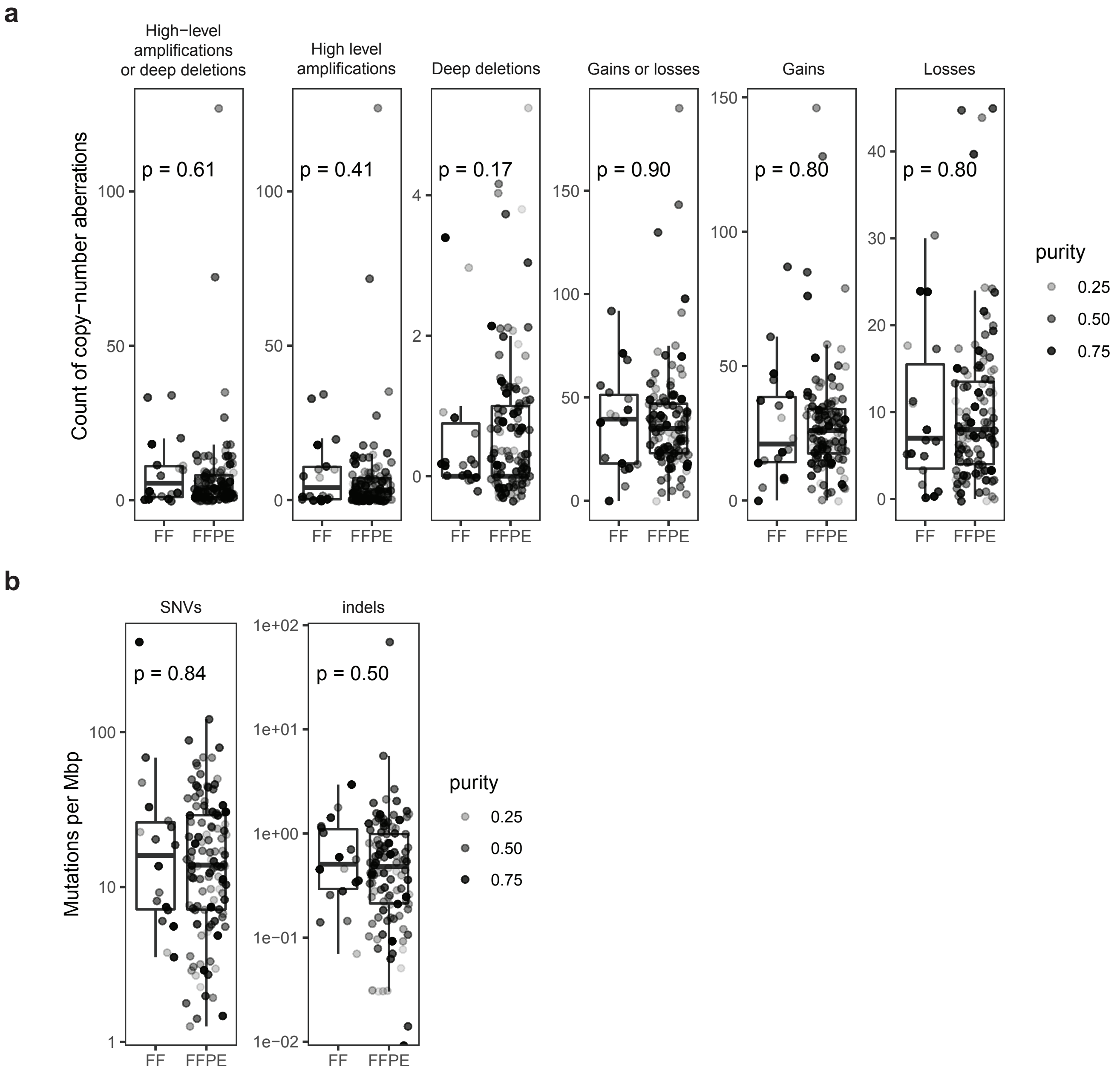

Supplementary Fig. 2 | Comparable detections of CNAs on fresh frozen vs. formalin-fixed tissues.
a, Frequencies of copy-number aberrations detected in fresh frozen vs. formalin-fixed tissues. Box represents interquartile range; middle line represents median. Each point represents the frequency of copy-number 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.