

Supplementary Materials for

Personalized genomic analyses for cancer mutation discovery and interpretation

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This PDF file includes:

Fig. S1. Bioinformatic approach to classify somatic and germline mutations on the basis of the consequence of the alteration.

Fig. S2. Bioinformatic approach to classify somatic and germline mutations based on the affected protein domain.

Other Supplementary Material for this manuscript includes the following:

(available at www.sciencetranslationalmedicine.org/cgi/content/full/7/283/283ra53/DC1)

Table S1. Genes analyzed in the targeted approach (provided in a separate Excel file).

Table S2. Summary of sequencing statistics (provided in a separate Excel file).

Table S3. Summary of performance characteristics of whole-exome and targeted analyses (provided in a separate Excel file).

Table S4. Characteristics of the tumor and normal samples (provided in a separate Excel file).

Table S5. Fraction of cases with somatic mutations in actionable genes (provided in a separate Excel file).

Table S6. Fraction of cases with evidence for clinical actionability in different tumor types (provided in a separate Excel file).

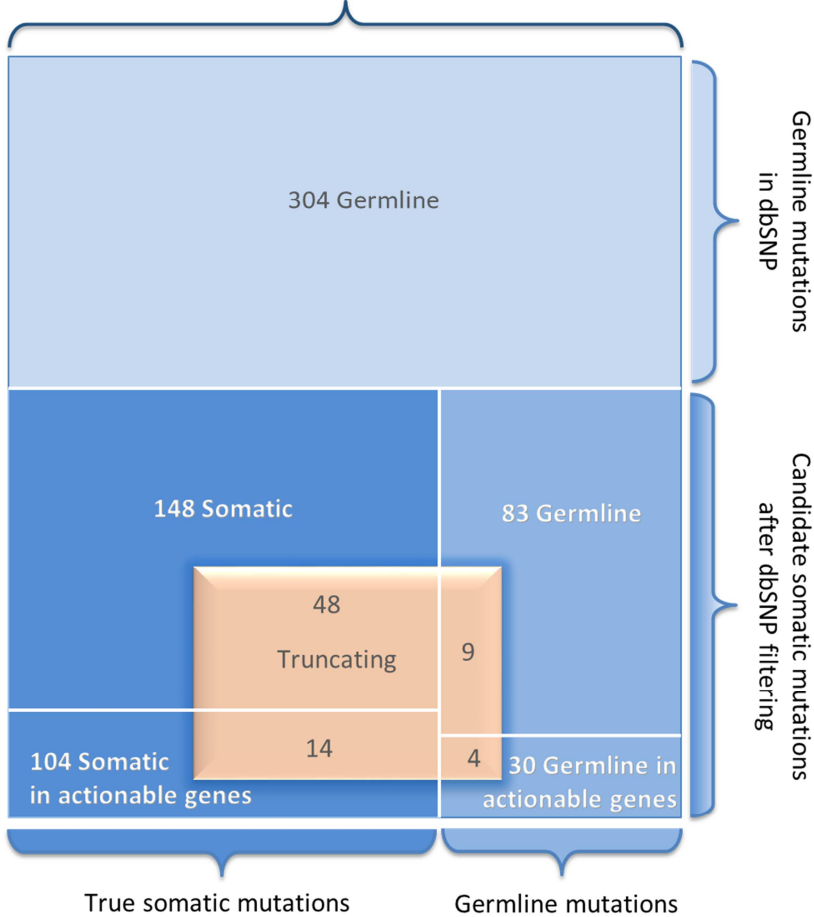
Table S7. Hereditary cancer predisposition genes (provided in a separate Excel file).

Table S8. Putative germline predisposing mutations (provided in a separate Excel file).

Table S9. Germline false-positive mutations in actionable genes (provided in a separate Excel file).

A.

669 Somatic Candidate Mutations from Targeted Analyses



B.

140,107 Somatic Candidate Mutations from Whole Exome Analyses

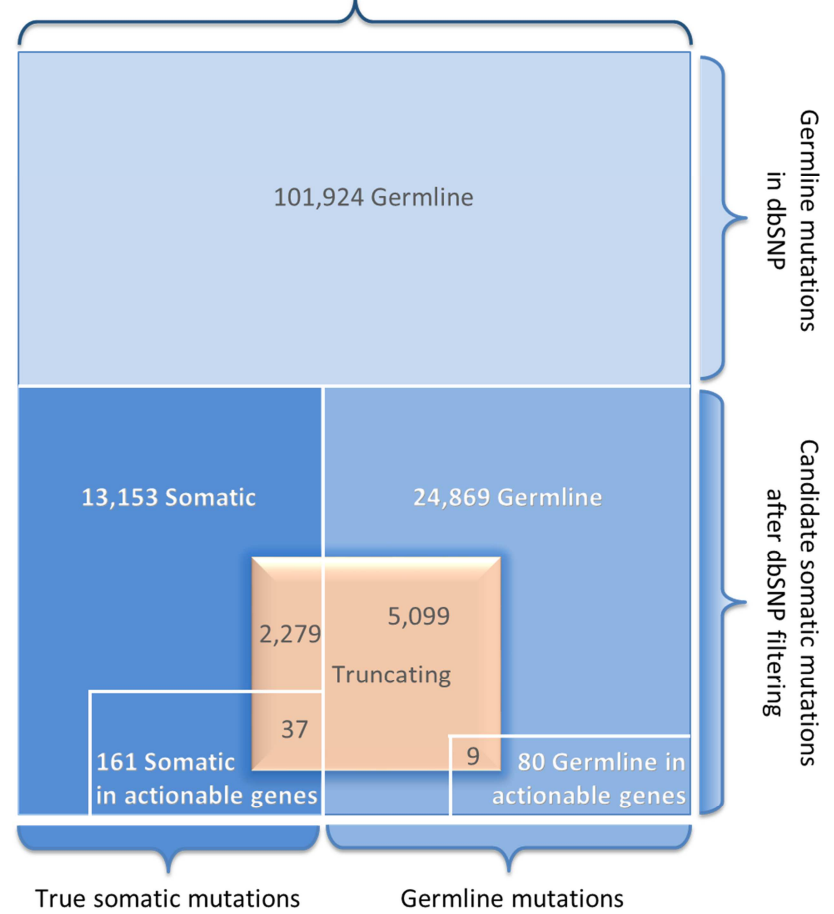
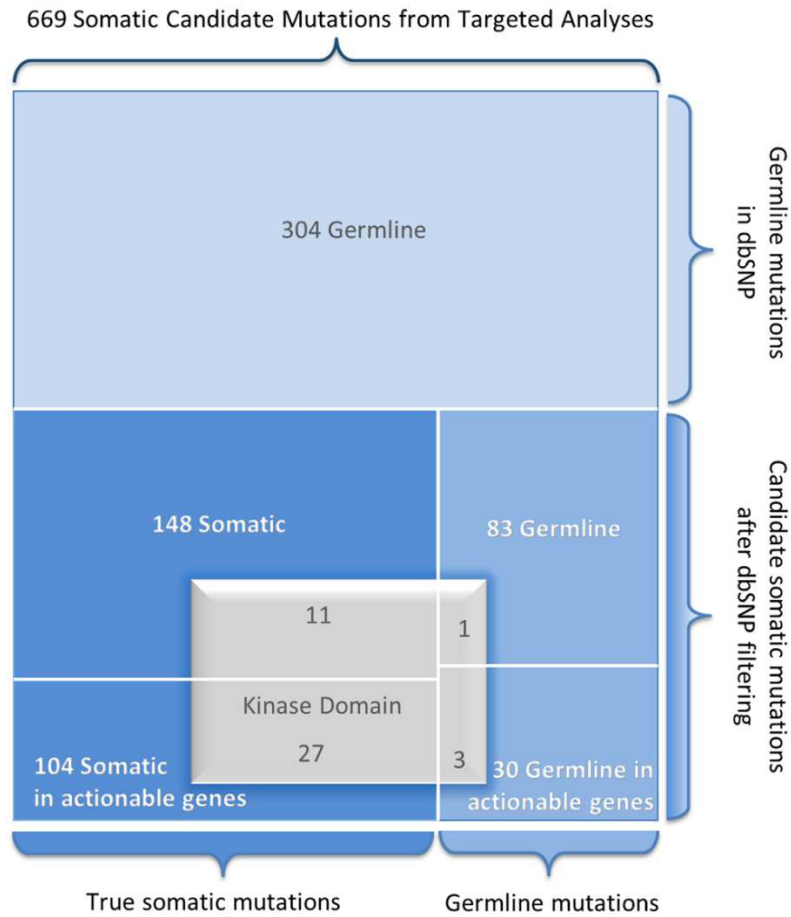


Figure S1. Bioinformatic approach to classify somatic and germline mutations on the basis of the consequence of the alteration.

A.



B.

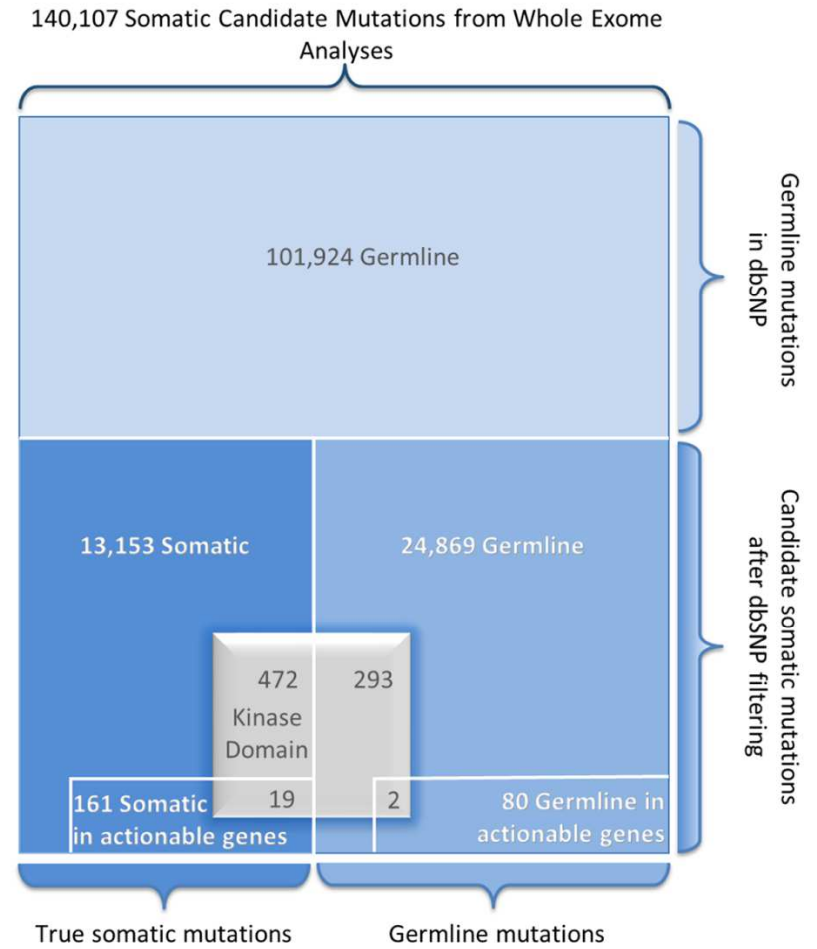


Figure S2. Bioinformatic approach to classify somatic and germline mutations based on the affected protein domain.