

Supplementary Figure S1

.fastq data from HiSeq 2000 (100bp pair end read)

Align to the human genome reference (hg19) using BWA

Remove PCR duplicates by Picard MarkDuplicates

Discard low-quality reads and low-quality bases:

- Reads with 5 or more mismatches
- Reads with < 25 mapping quality
- Bases with < 30 base quality

Detect variants fulfilling the criteria:

- with 10 or more total reads
- with 6 or more supporting reads
- with supporting read(s) from both direction
- with > 0.02 allele frequency

Remove synonymous SNVs / ambiguous candidates

Remove Missense SNVs registered in known polymorphisms database:

- In-house SNP database
- dbSNP131
- 1000 genomes as of 2011/05/21
- ESP 6500

Remove candidates fulfilling the criteria:

- Missense SNVs with 0.45 ~ 0.55 allele frequency or on copy number change

Rescue candidates registered in COSMIC V60 except for novel recurrent variants ($n \geq 2$) not reported somatic origins in the literature.

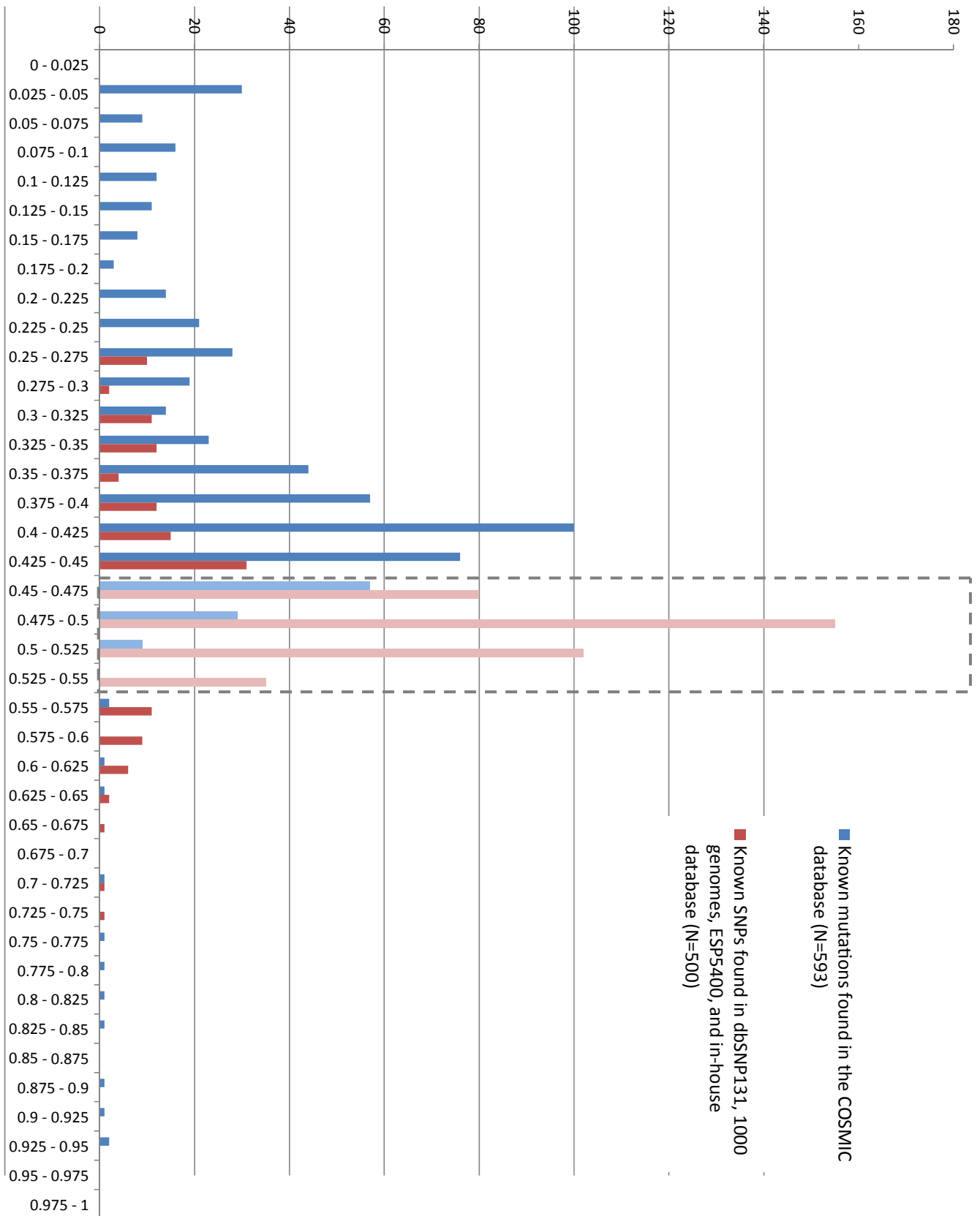
Remove candidates, if the same variant allele is also detected in 53 normal samples with 0.25% allele frequency on average or identical candidates in 53 normal samples

Remove mapping errors by visual inspection with IGV

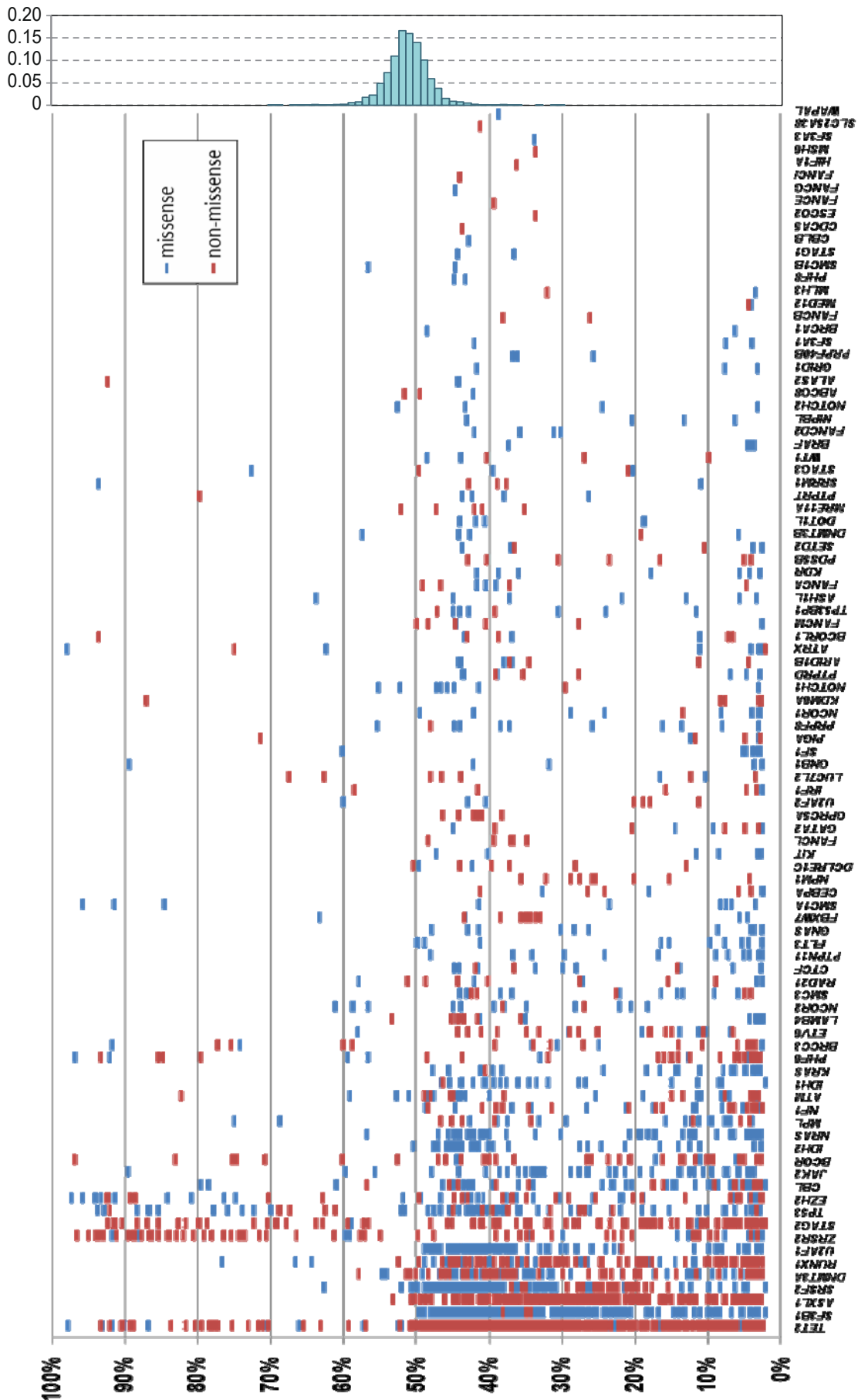
Final list of variants

Supplementary Figure S2

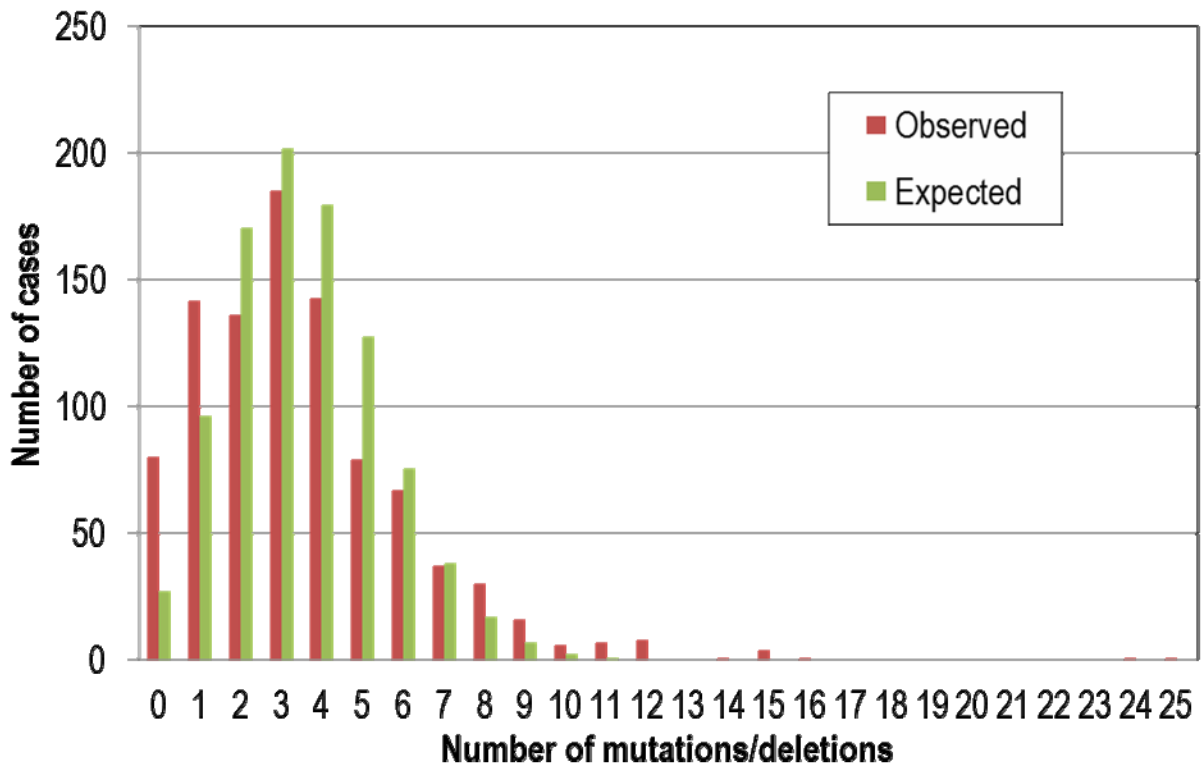
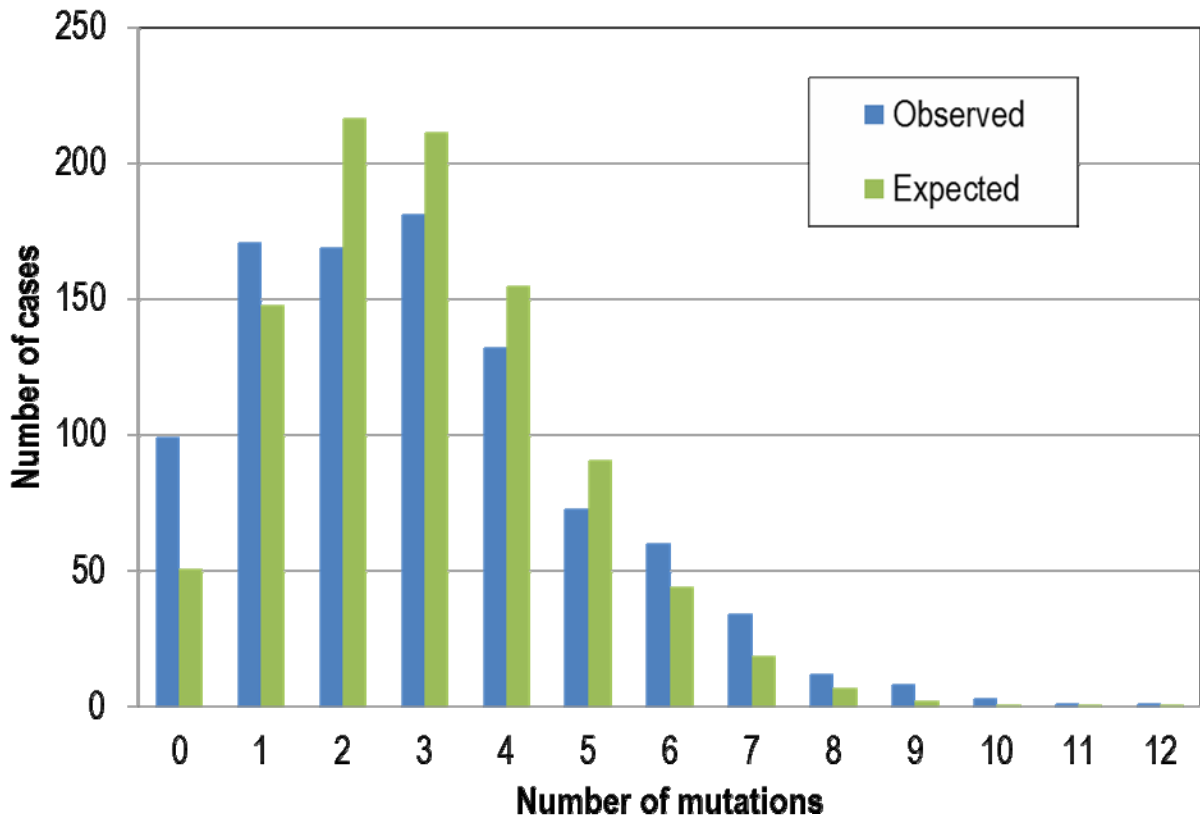
Number of variants



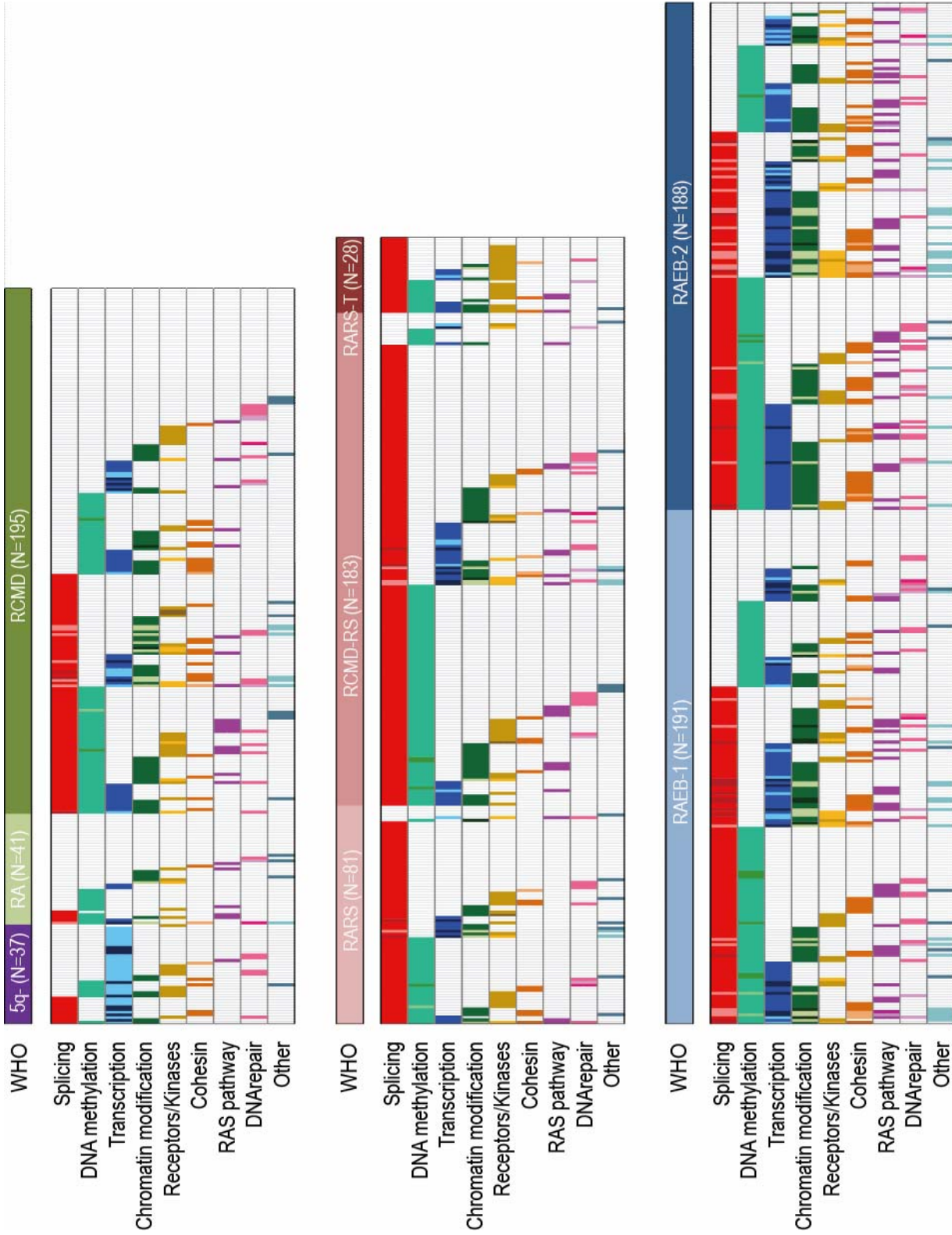
Supplementary Figure S3



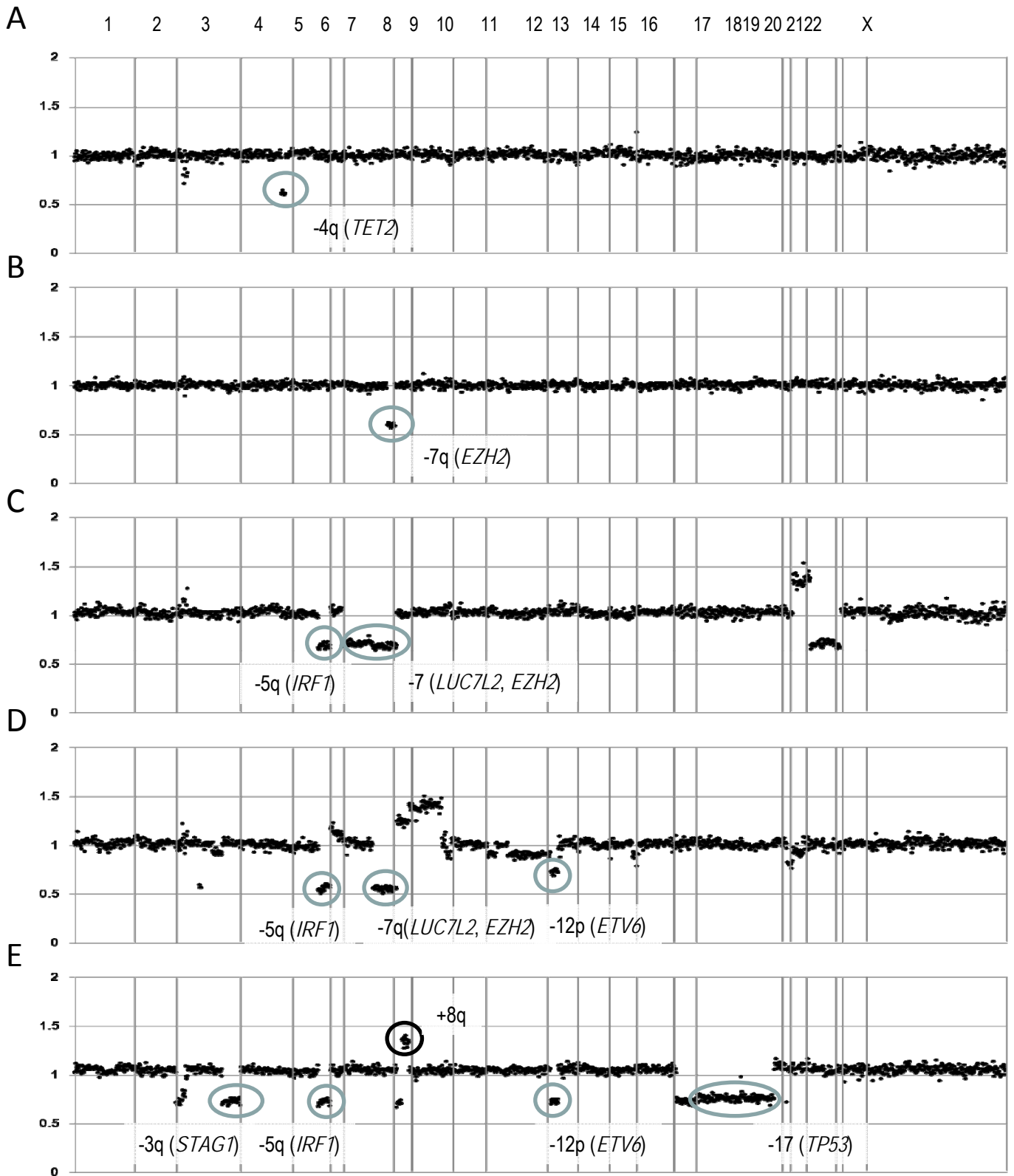
Supplementary Figure S4



Supplementary Figure S5

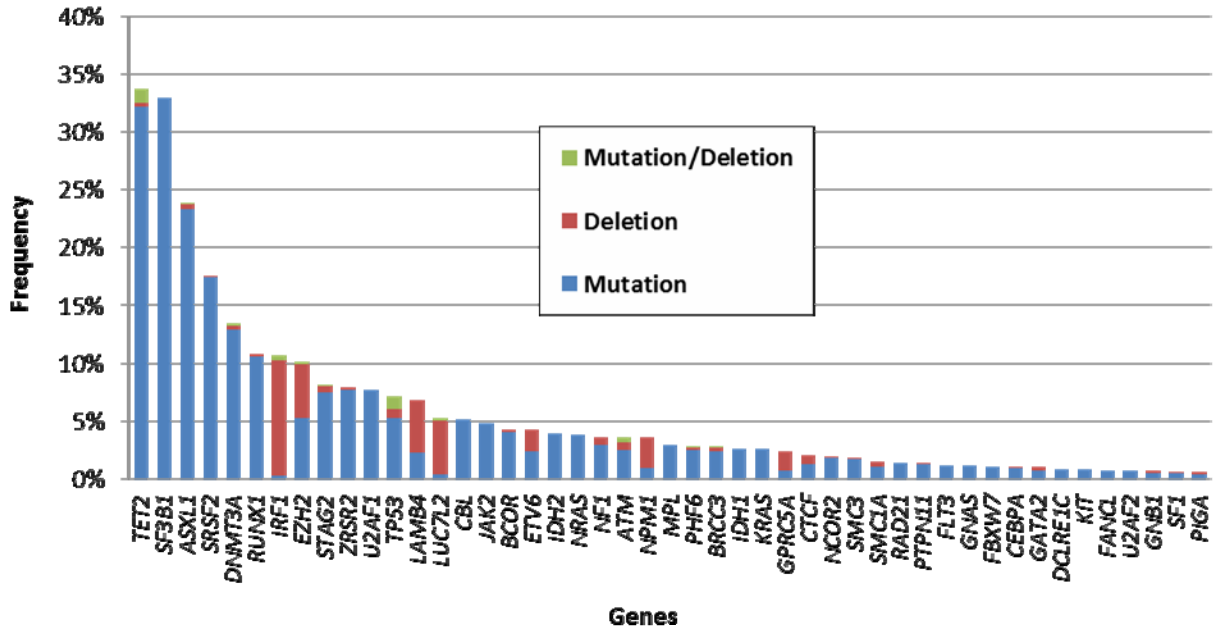


Supplementary Figure S6

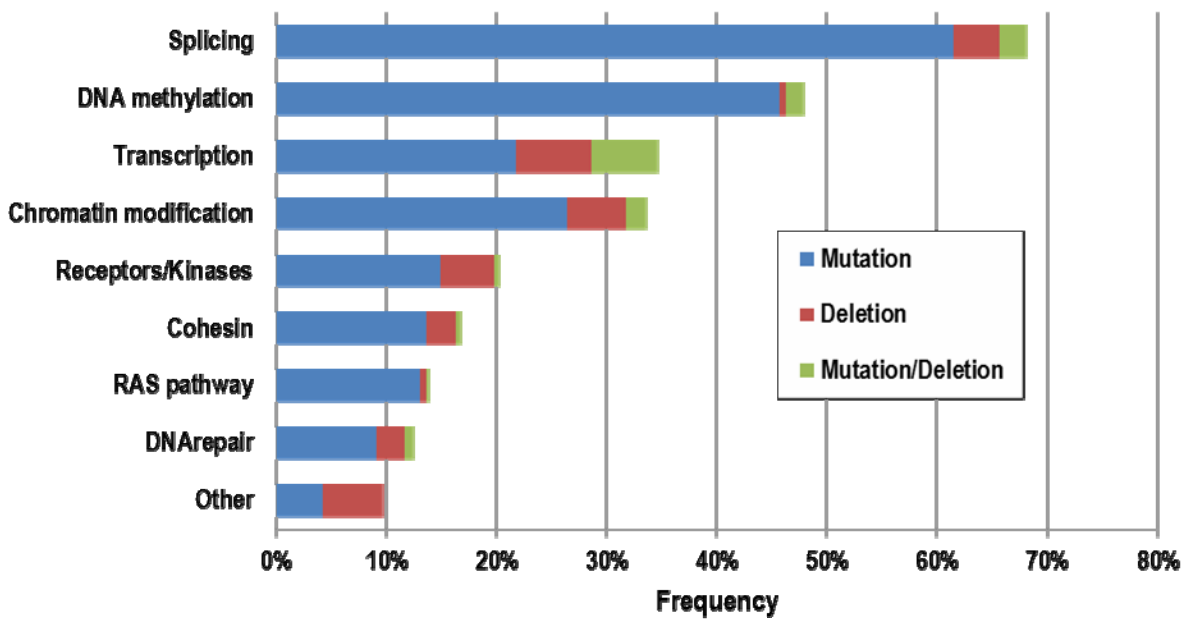


Supplementary Figure S7

A

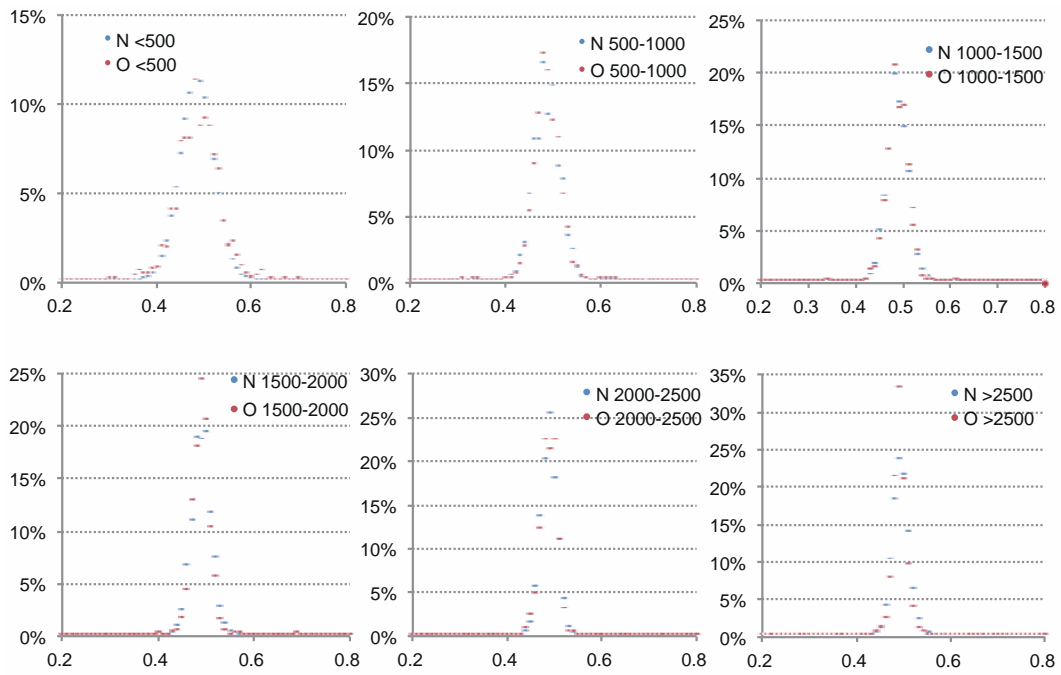


B

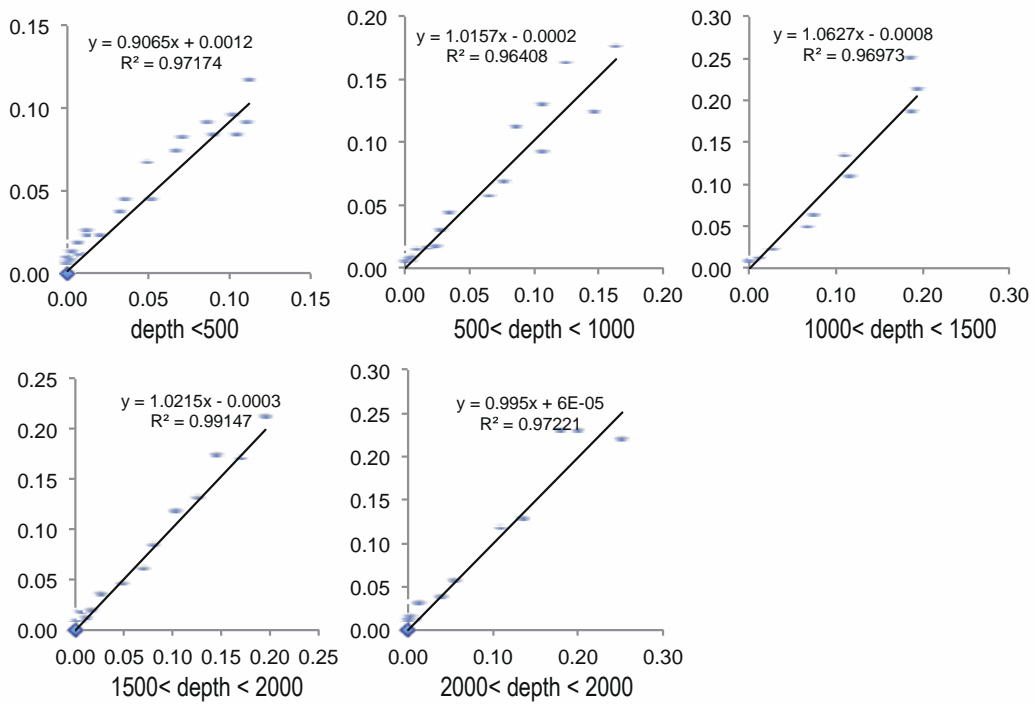


Supplementary Figure S8A-B

A

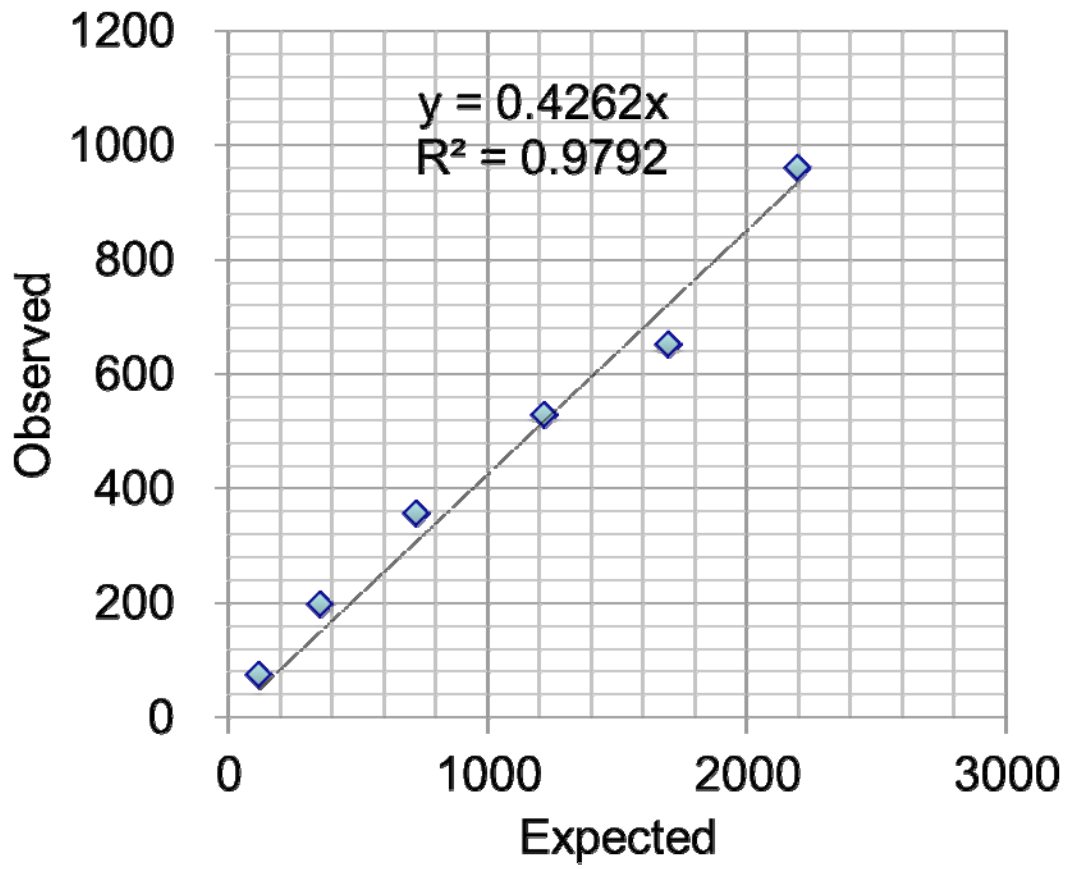


B

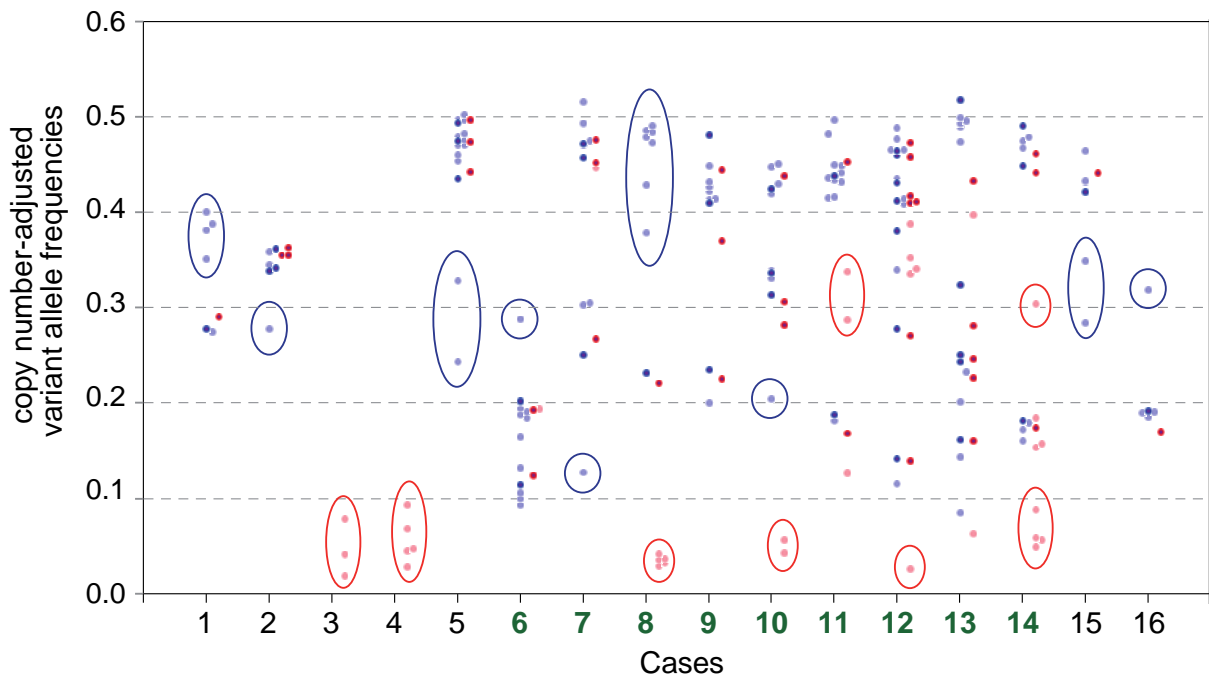


Supplementary Figure S8C-D

C

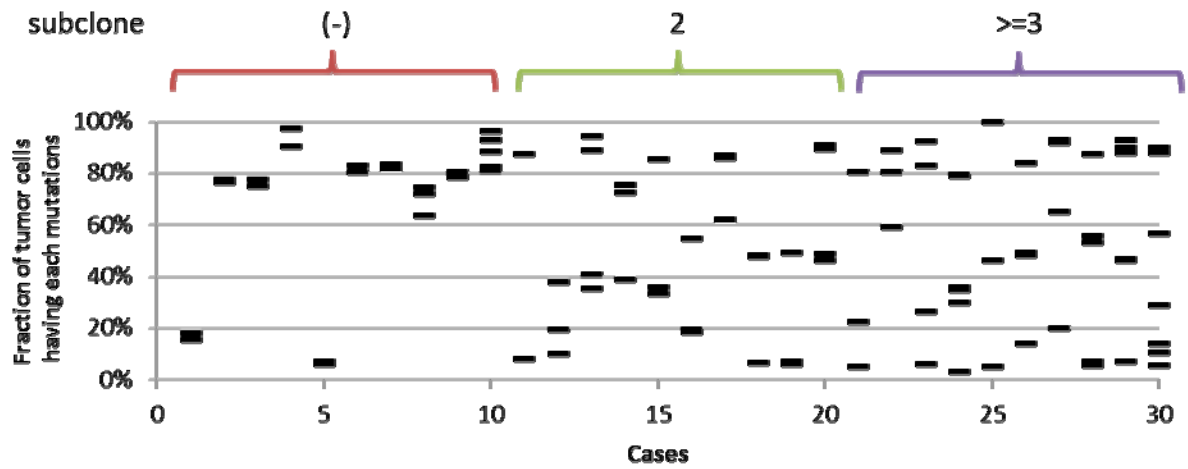


D

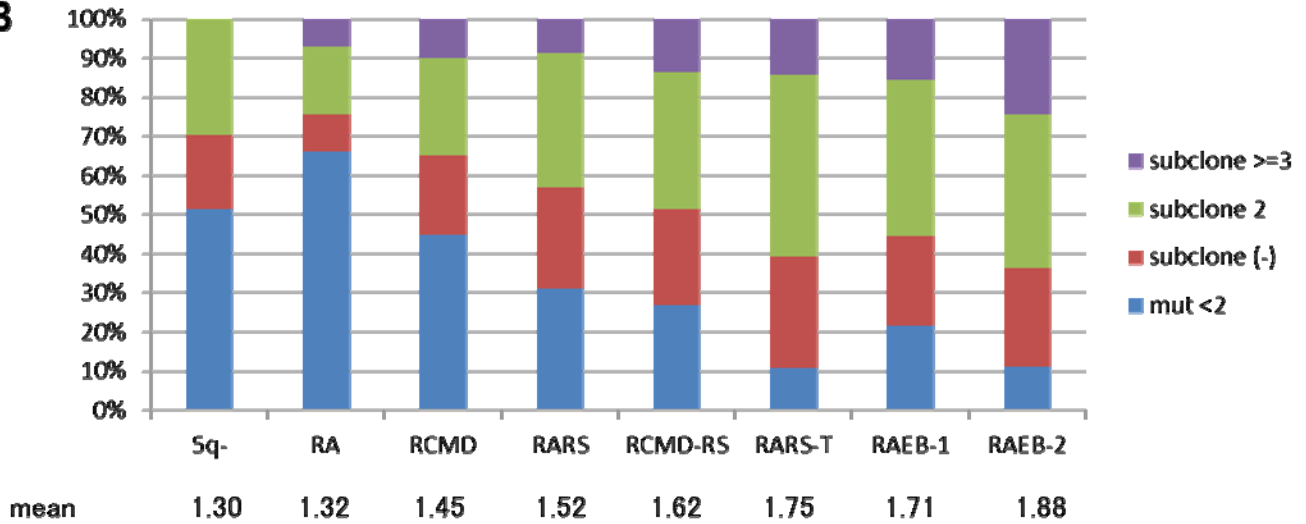


Supplementary Figure S9

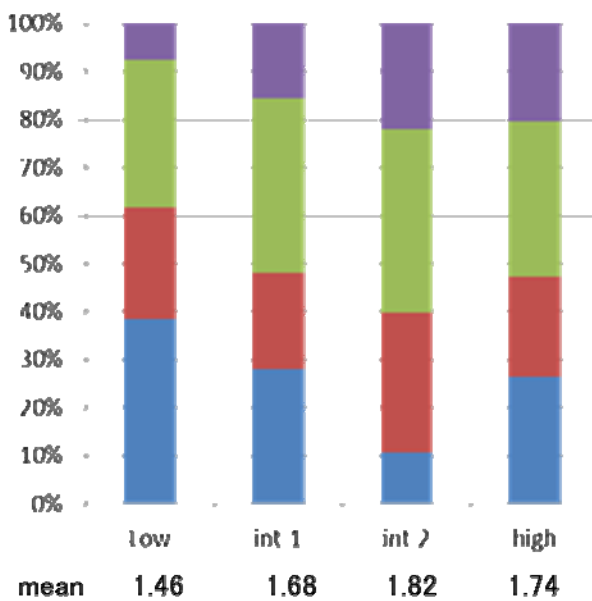
A



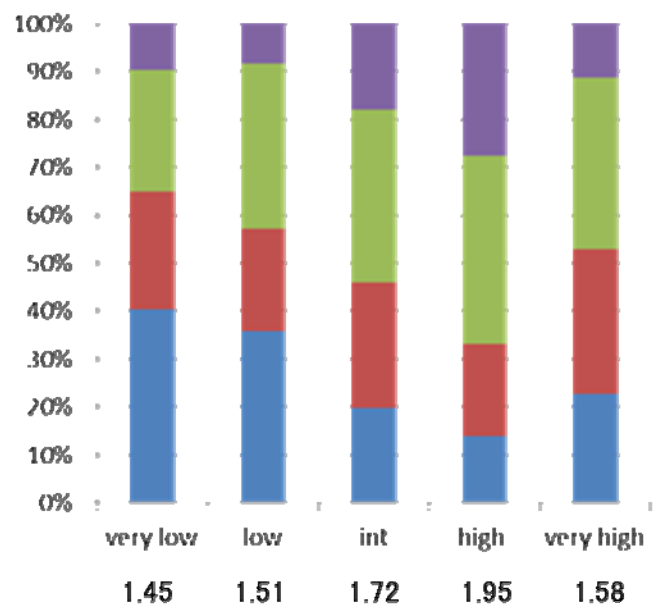
B



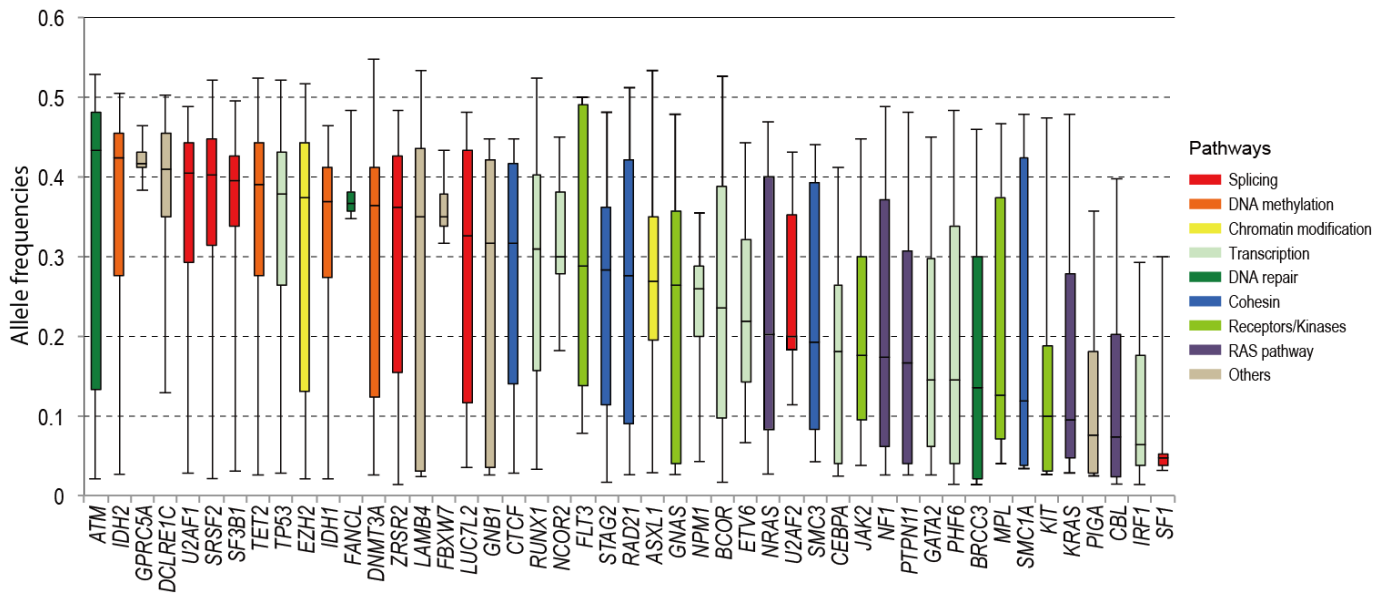
C



D

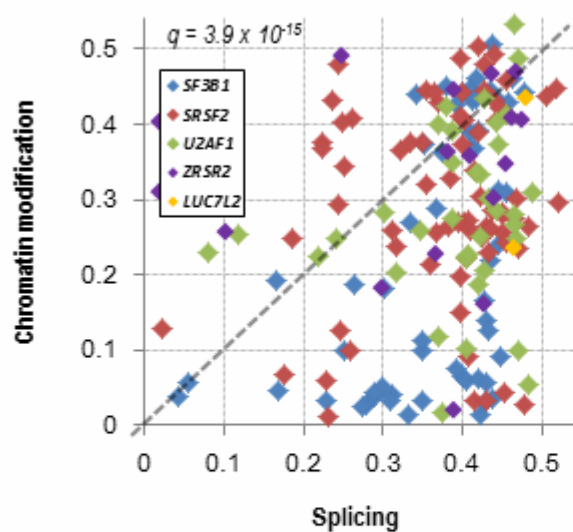


Supplementary Figure S10

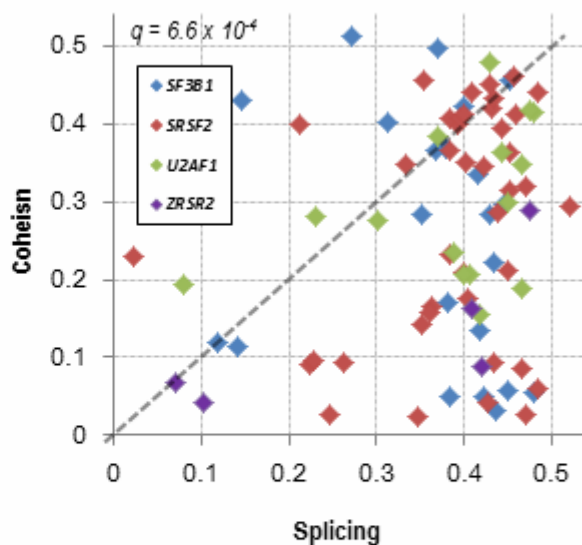


Supplementary Figure S11 A-F

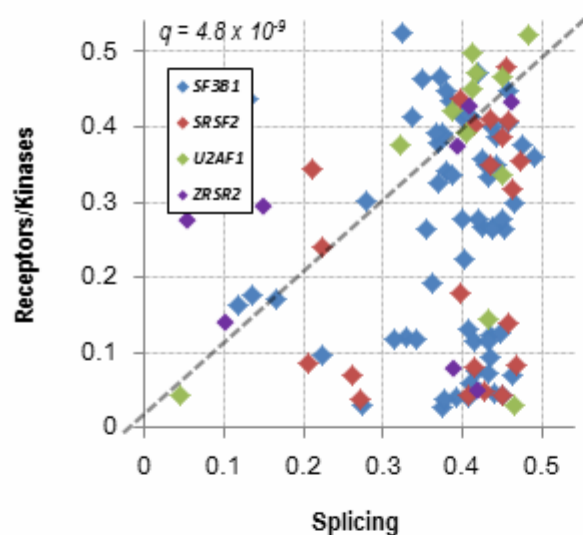
A



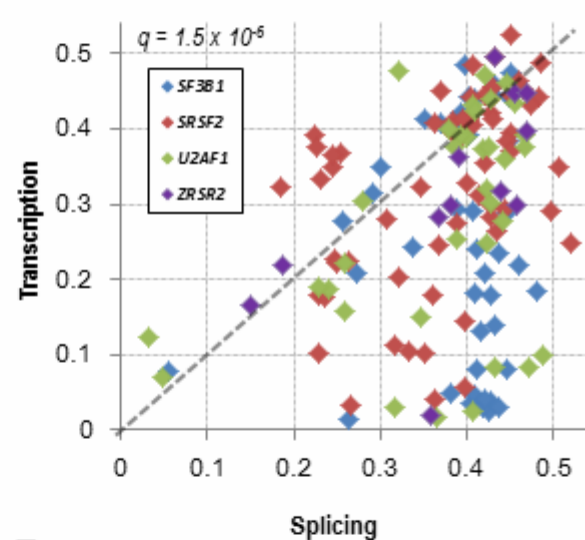
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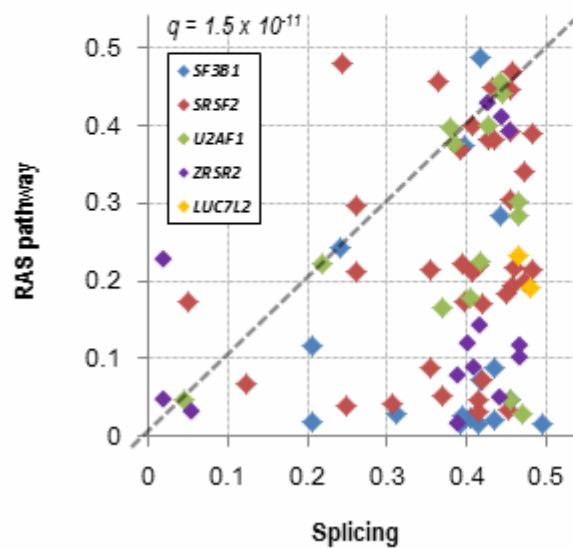
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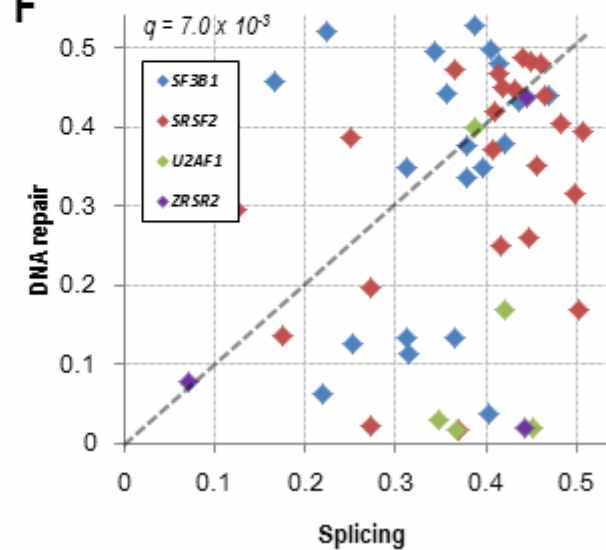
E



C

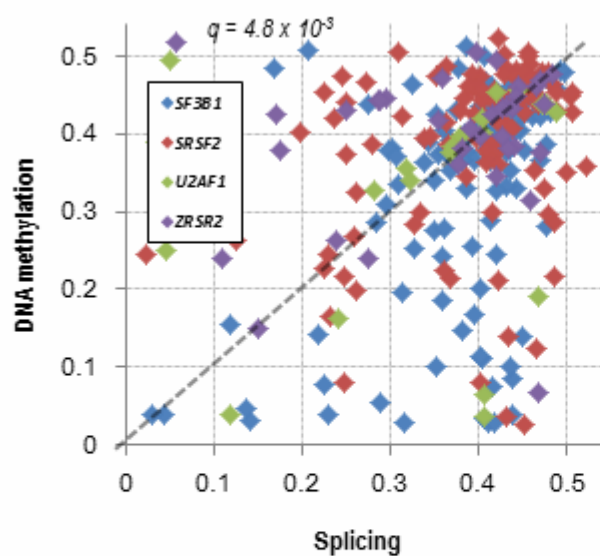


F

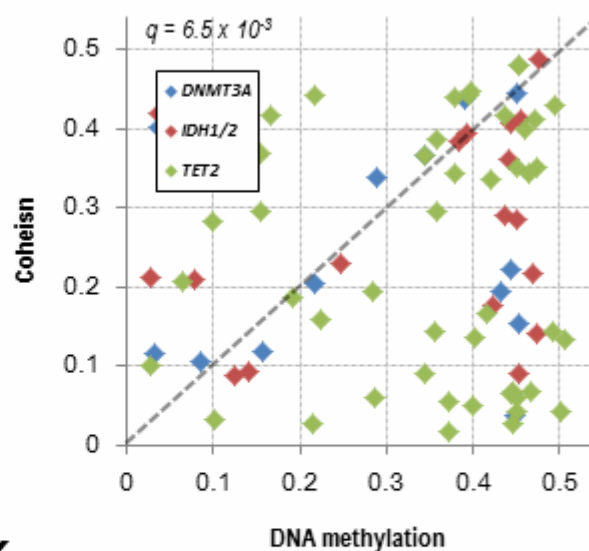


Supplementary Figure S11 G-L

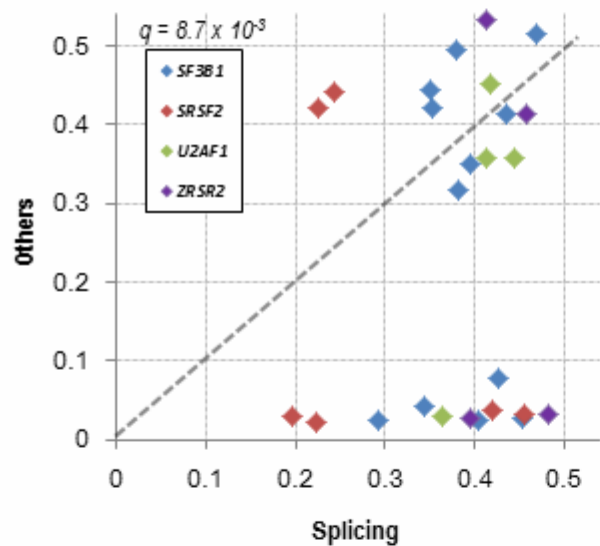
G



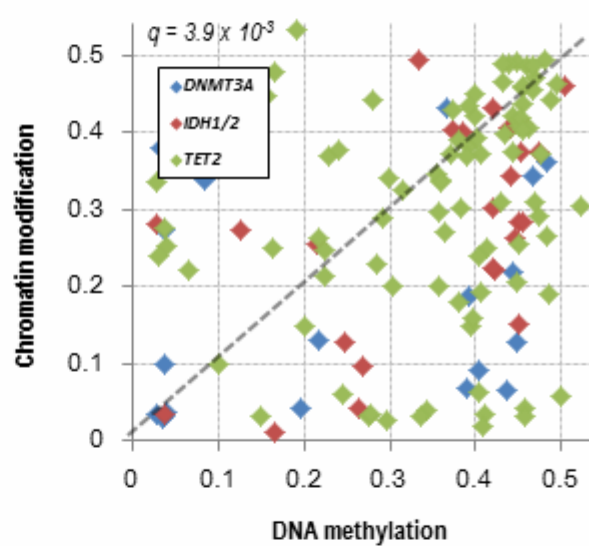
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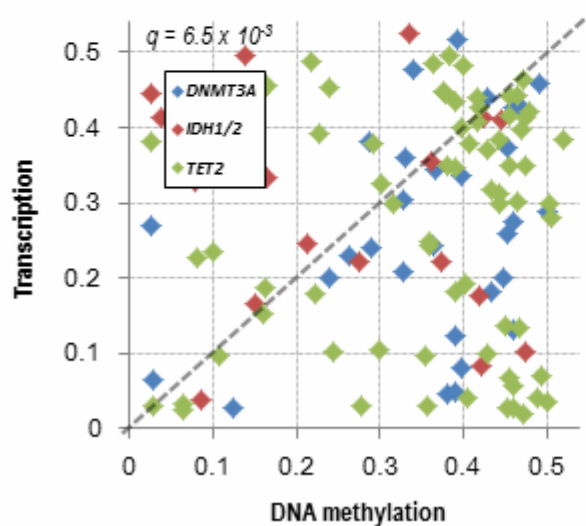
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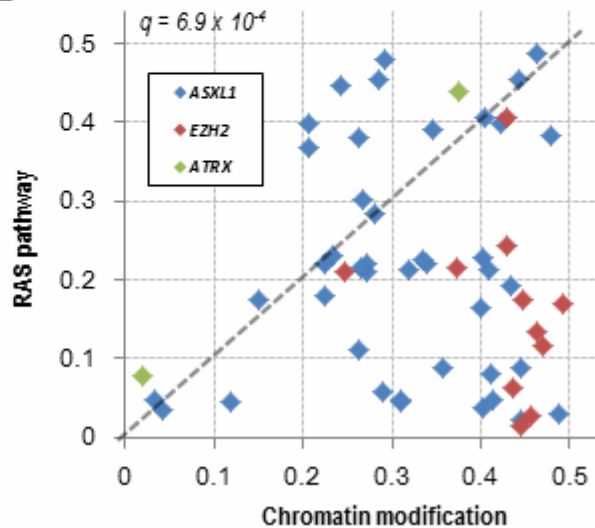
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I

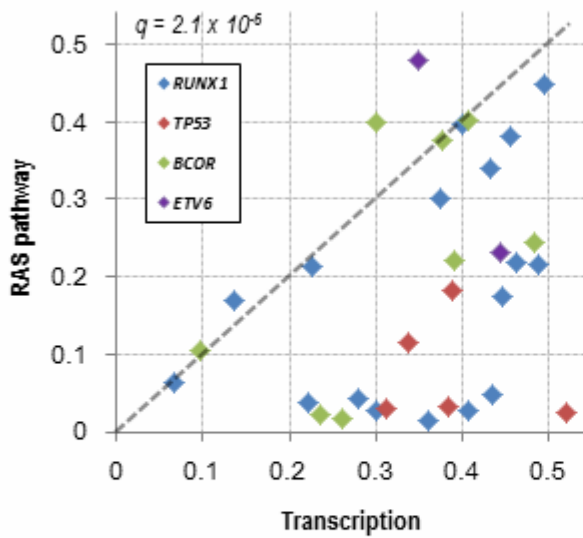


L

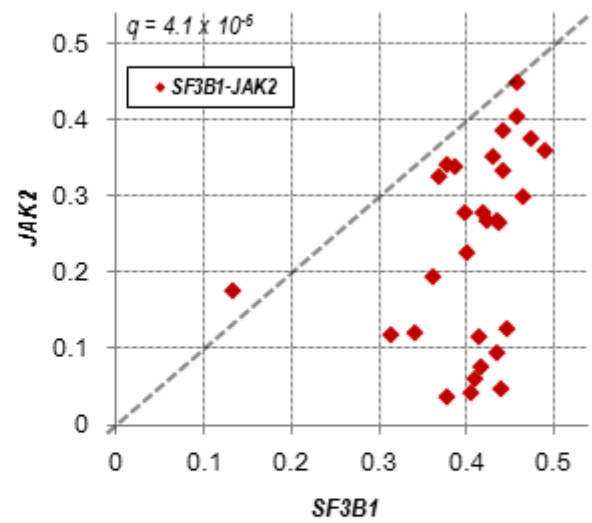


Supplementary Figure S11 M-R

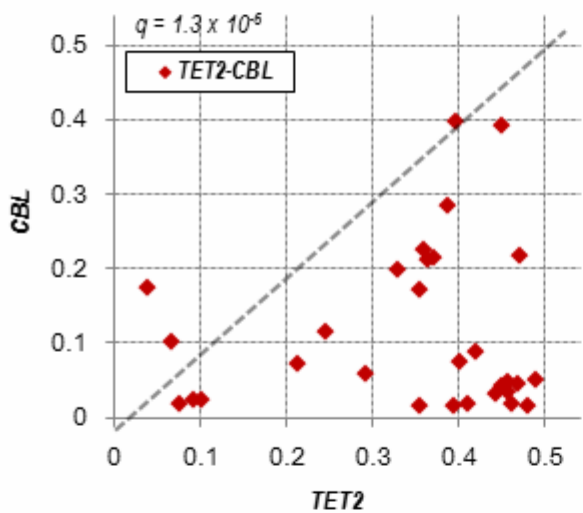
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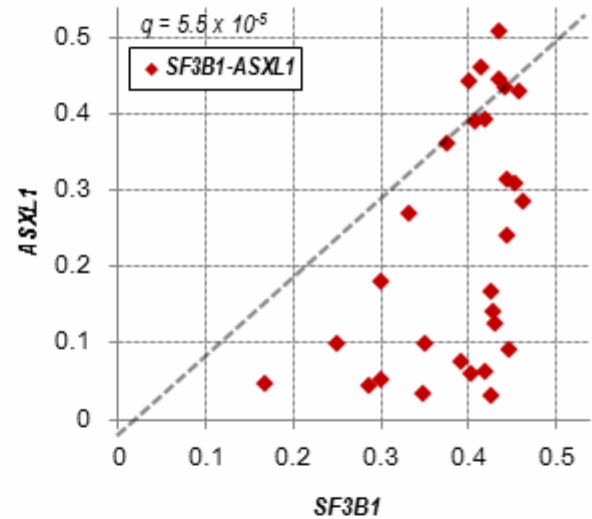
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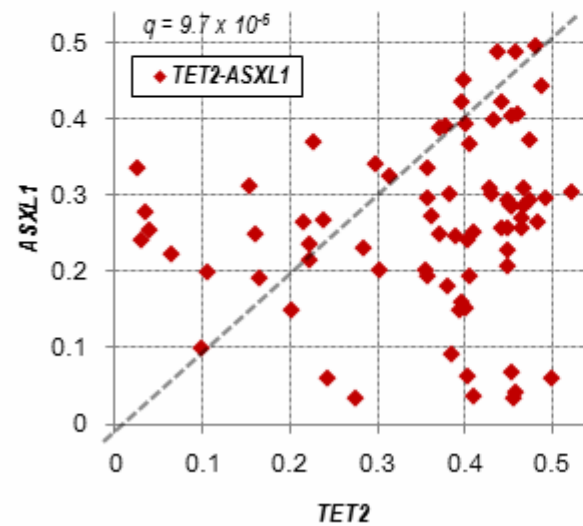
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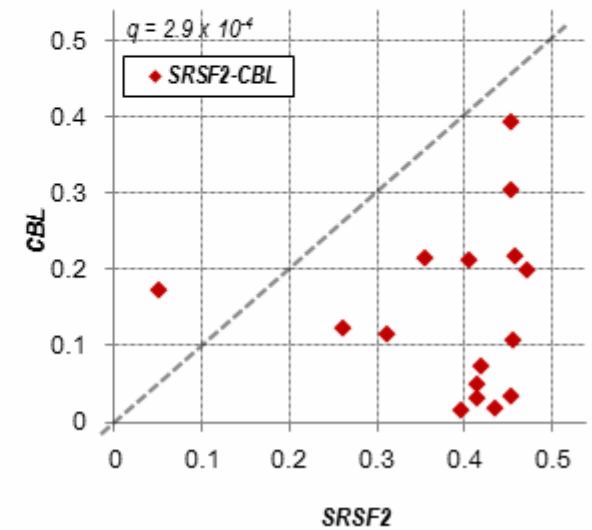
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O

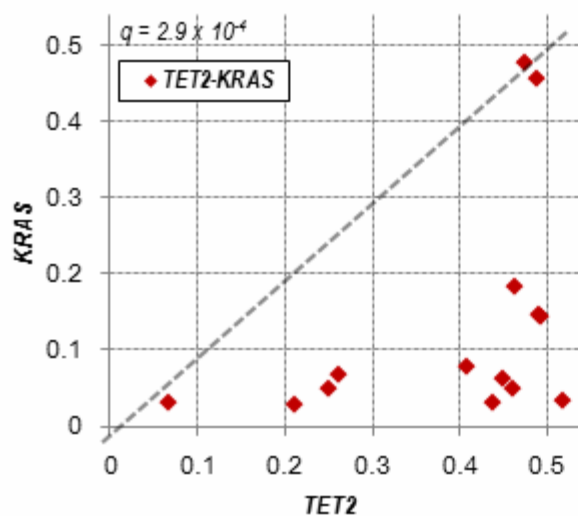


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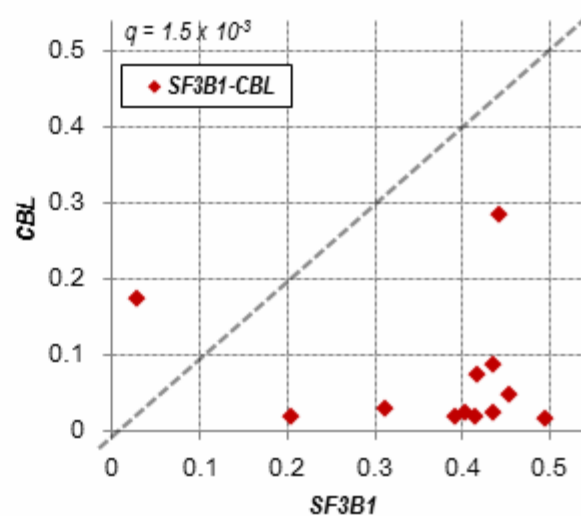


Supplementary Figure S11 S-X

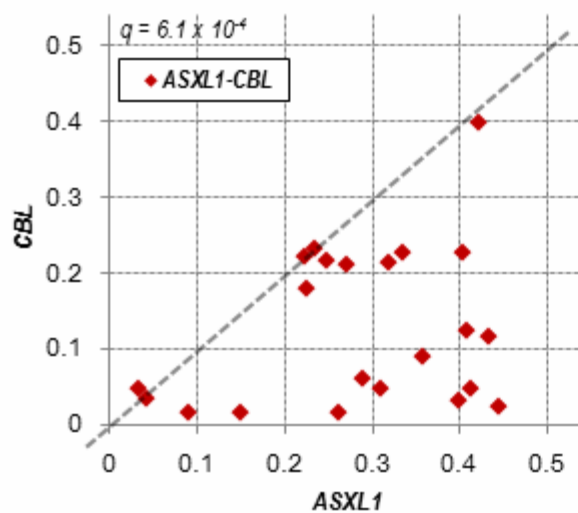
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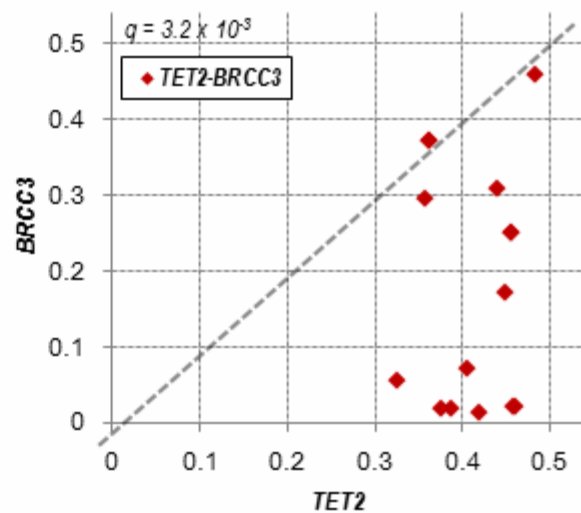
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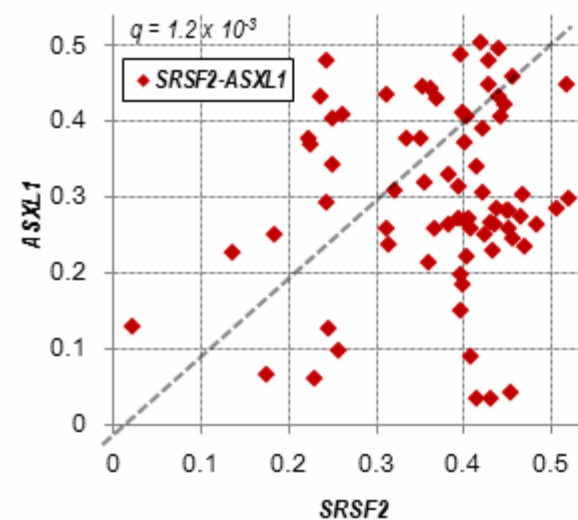
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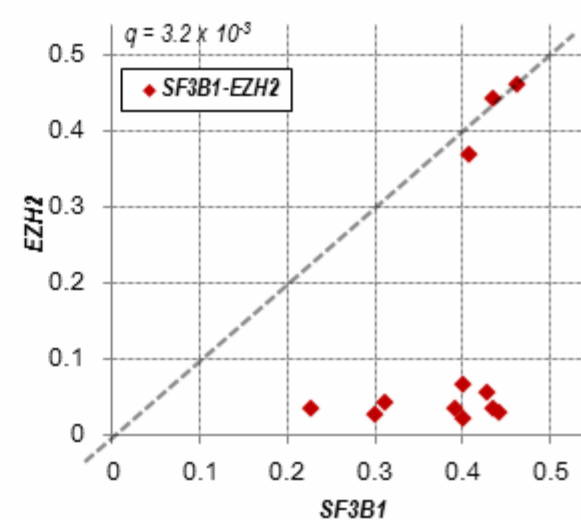
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U

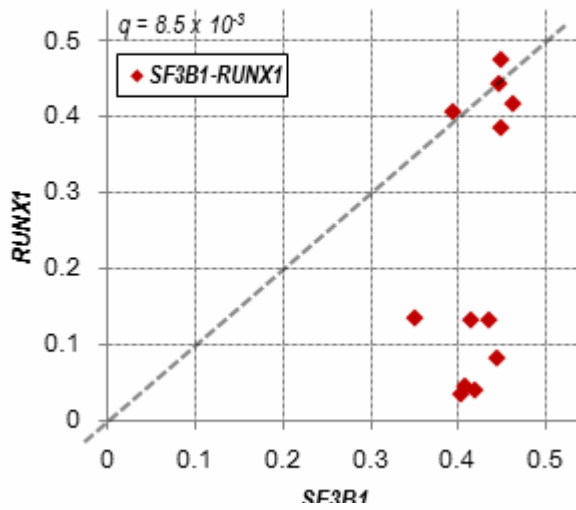


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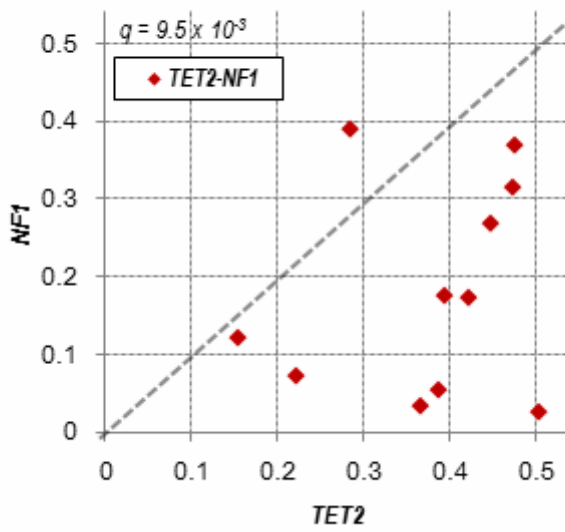


Supplementary Figure S11 Y-Z

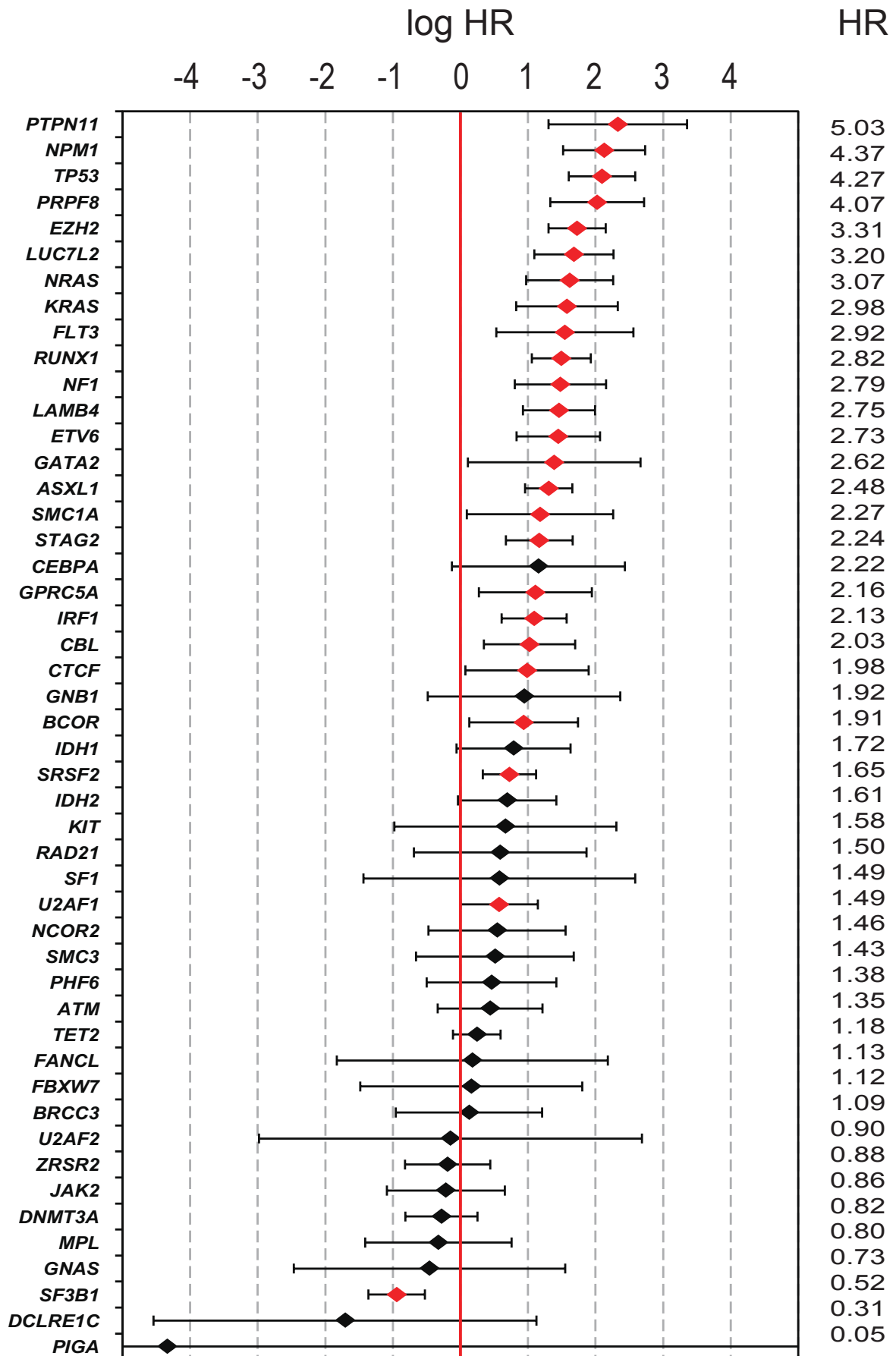
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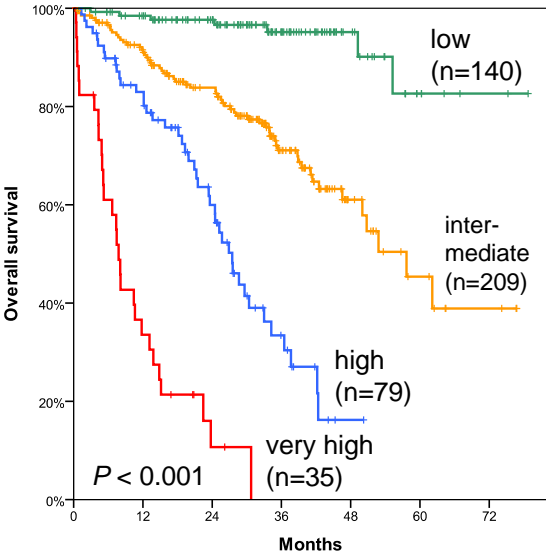
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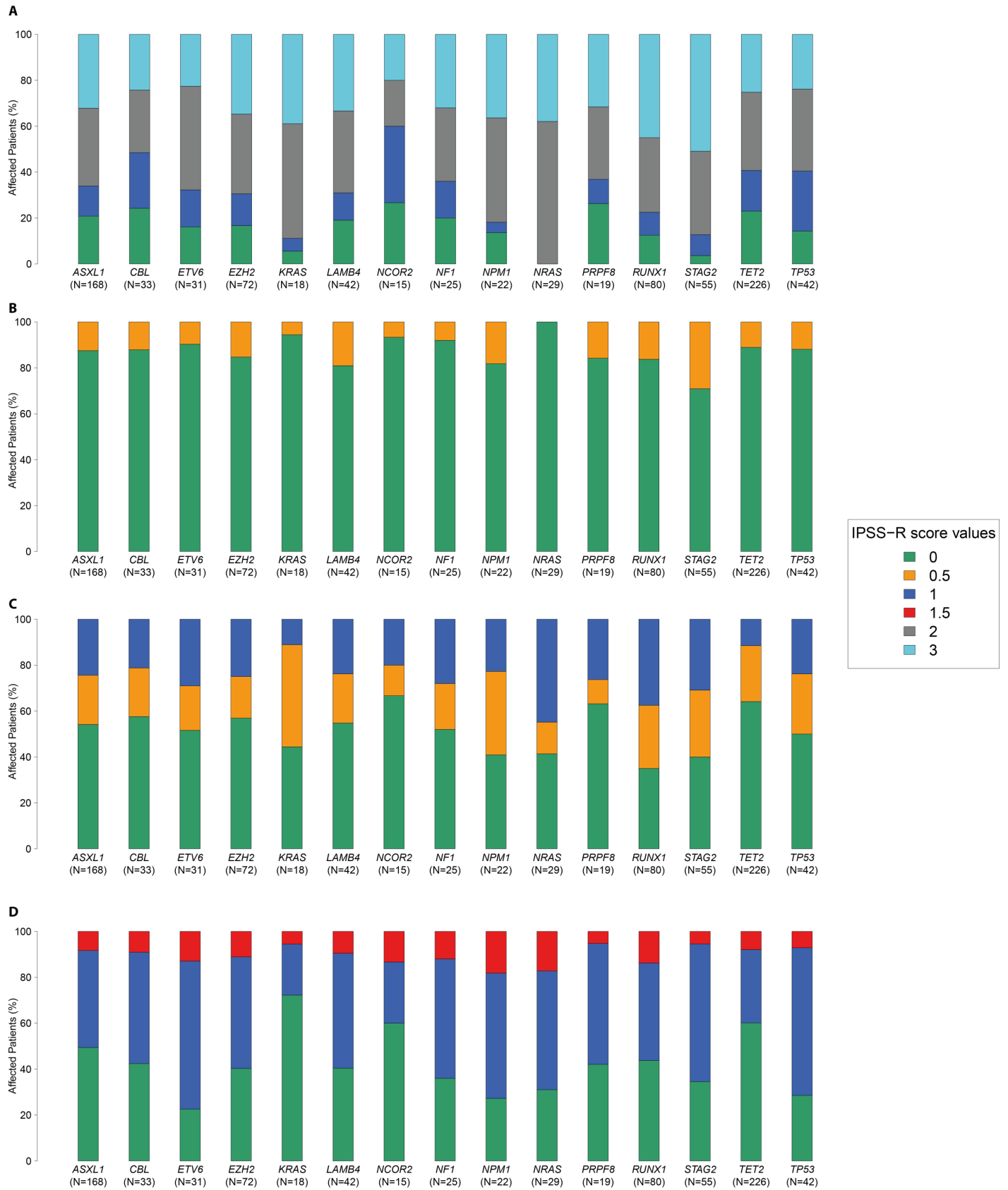
Supplementary Figure S12



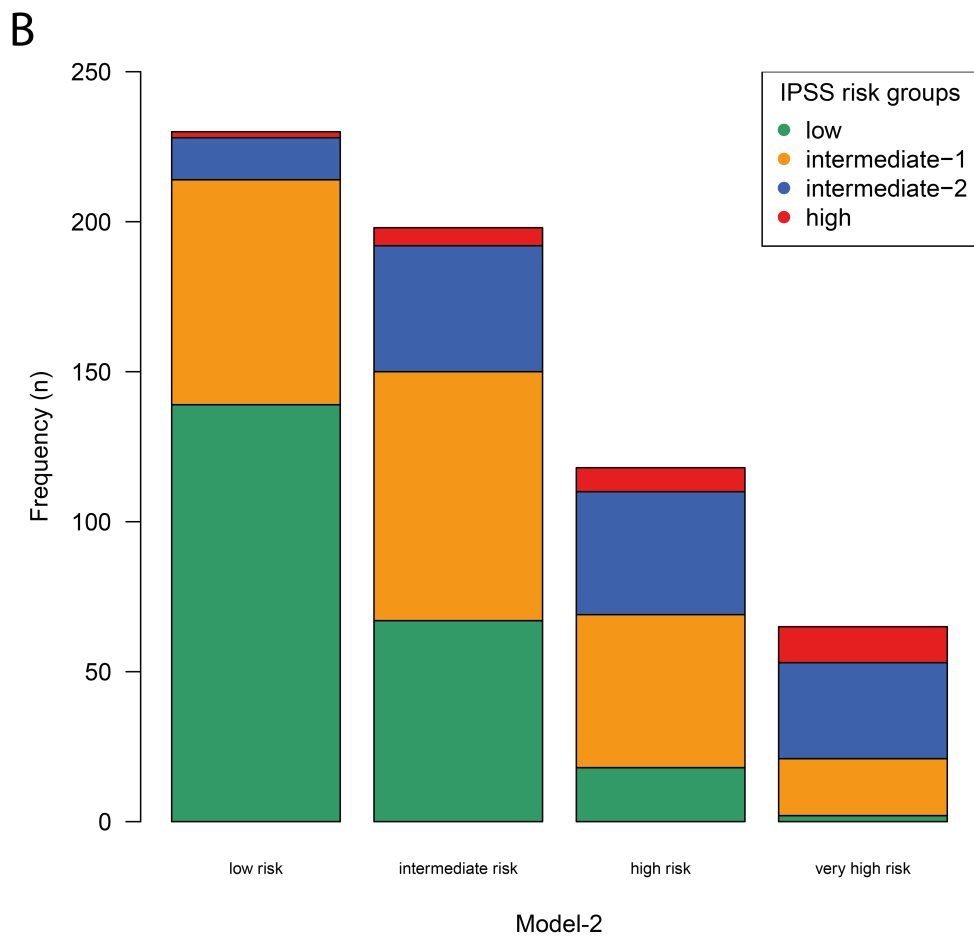
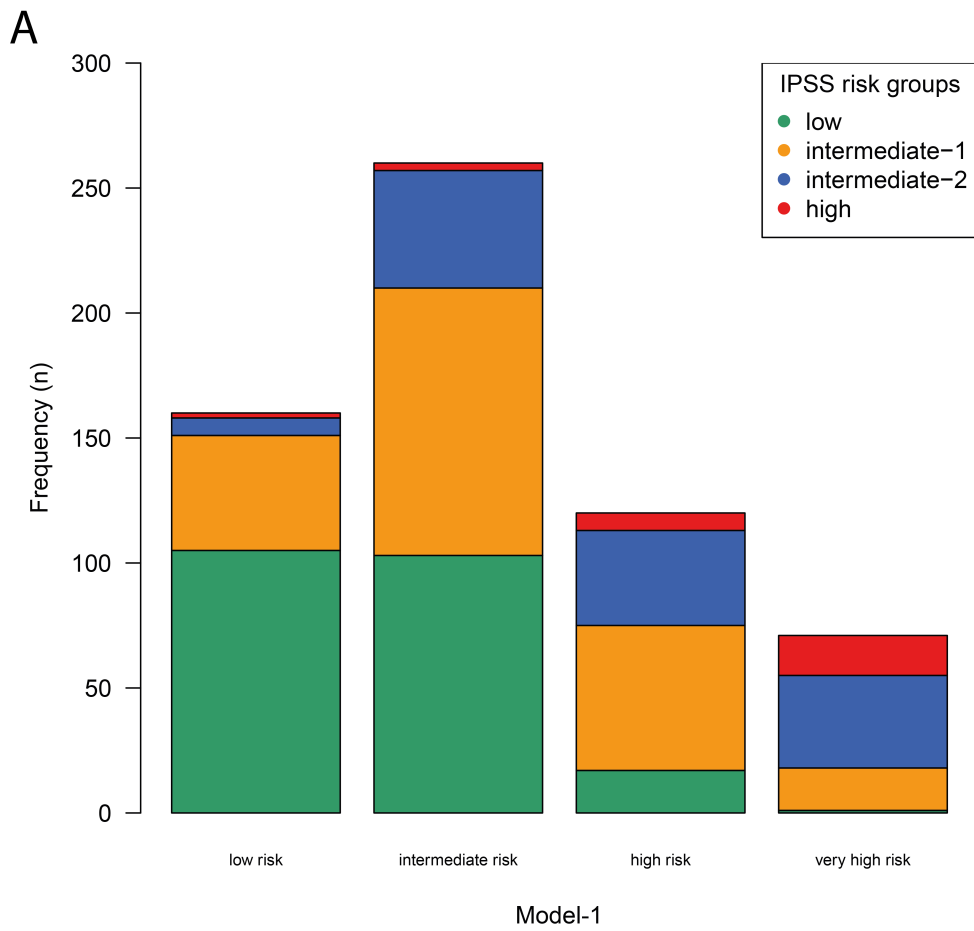
Supplementary Figure S13



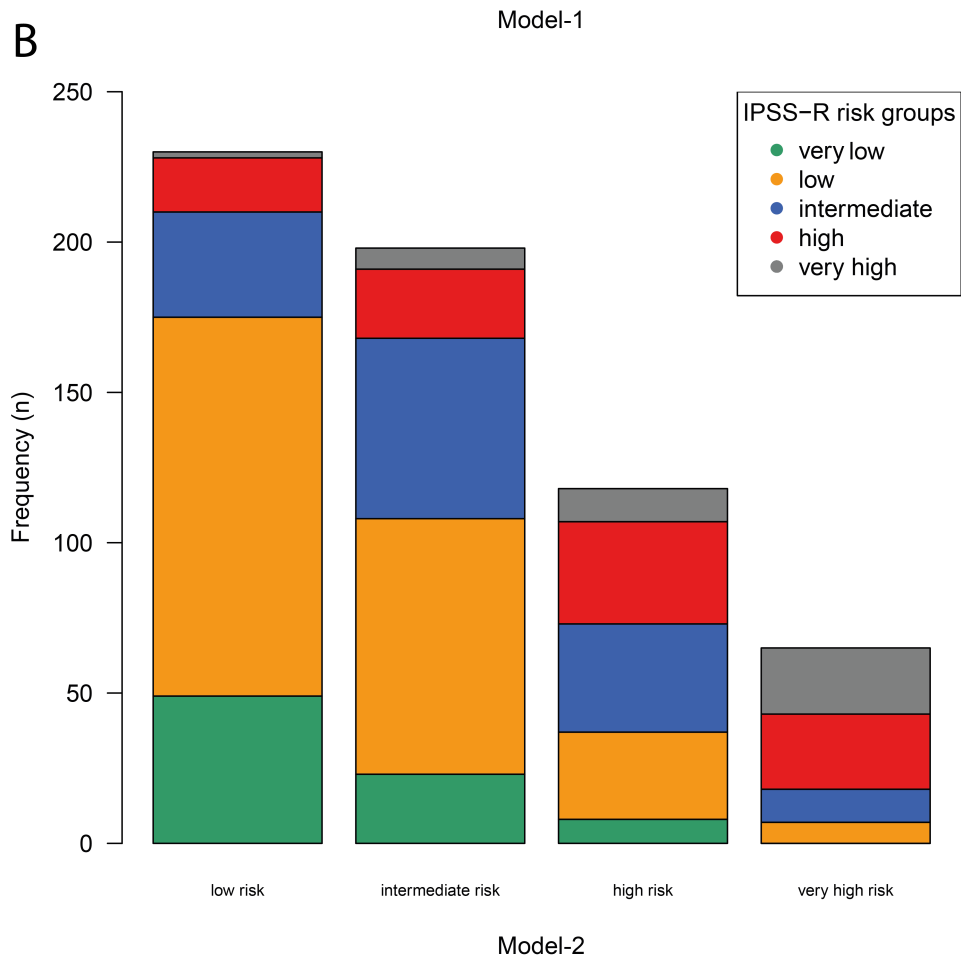
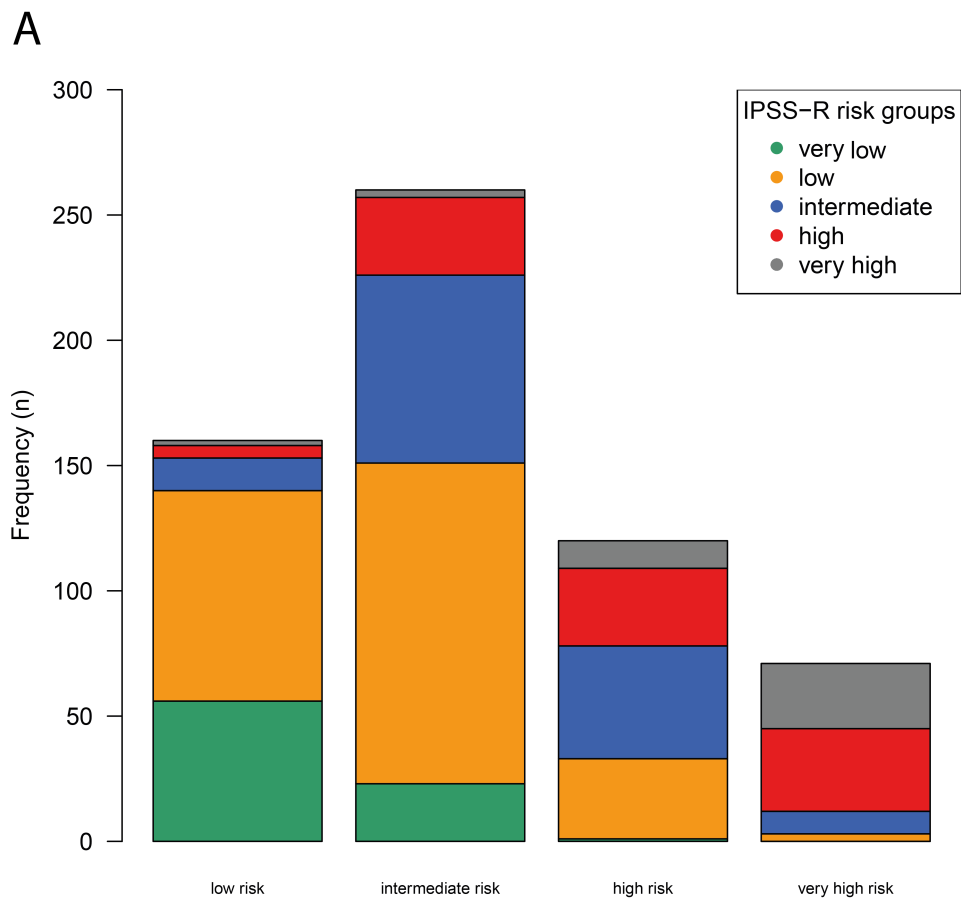
Supplementary Figure S14



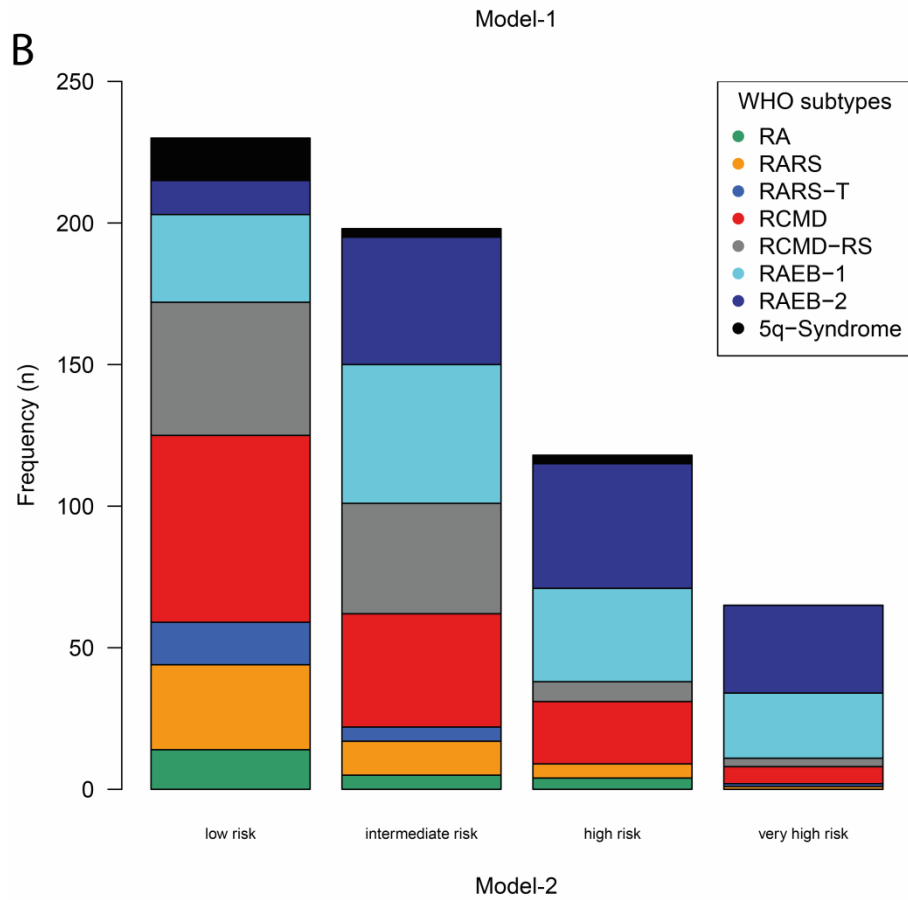
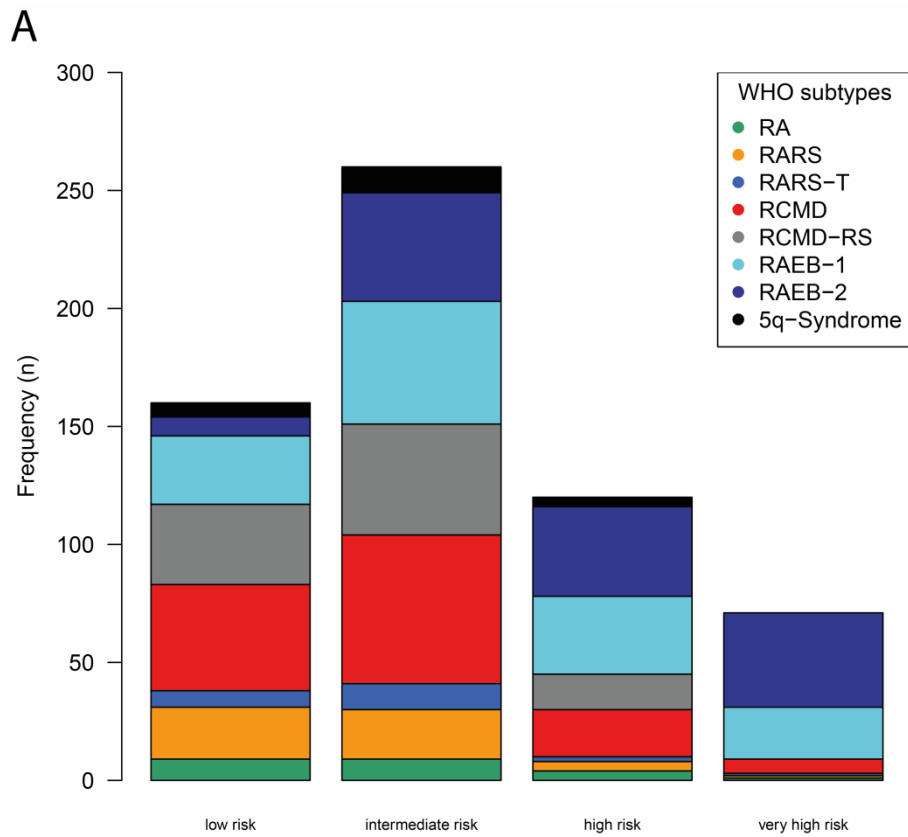
Supplementary Figure S15



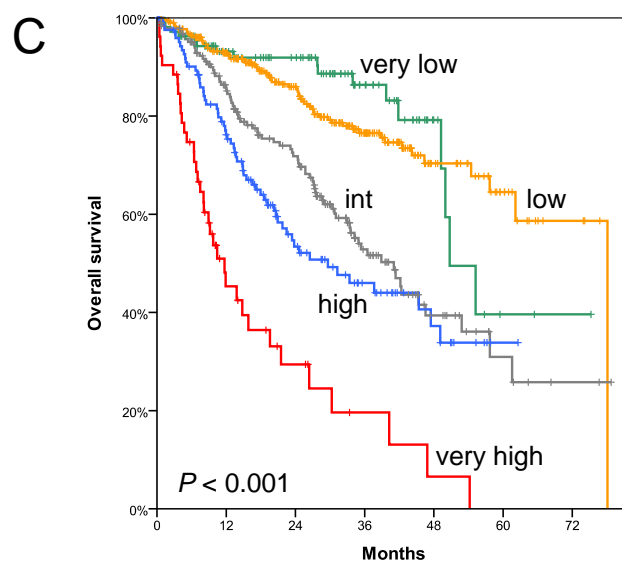
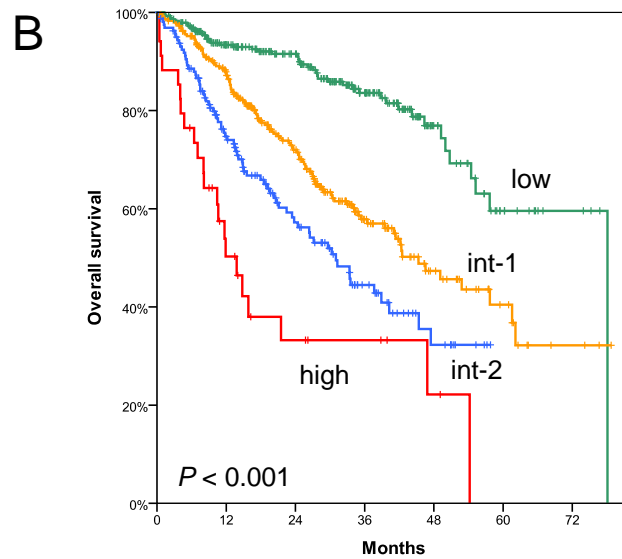
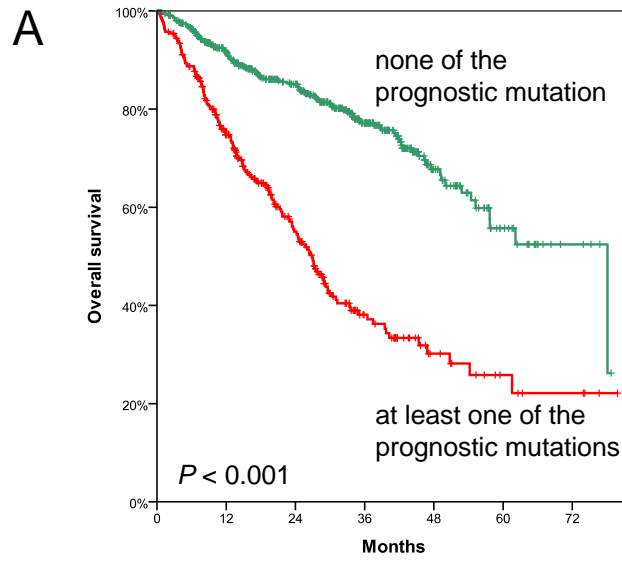
Supplementary Figure S16



Supplementary Figure S17

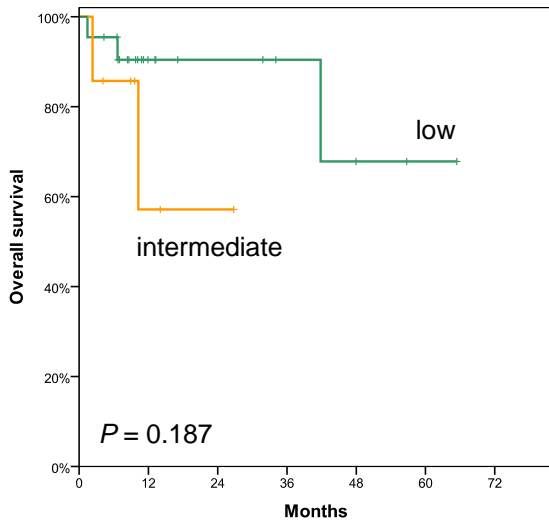


Supplementary Figure S18

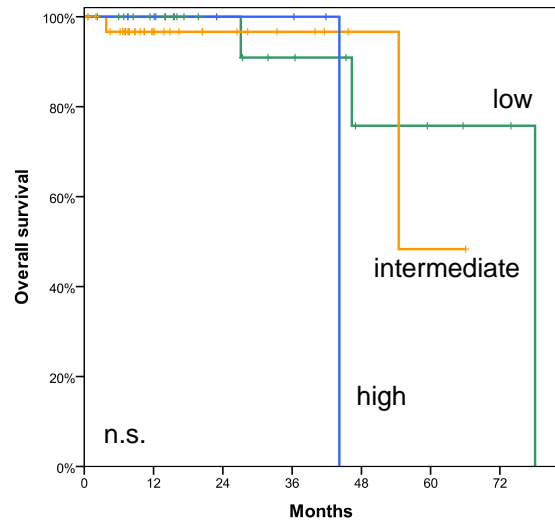


Supplementary Figure S19

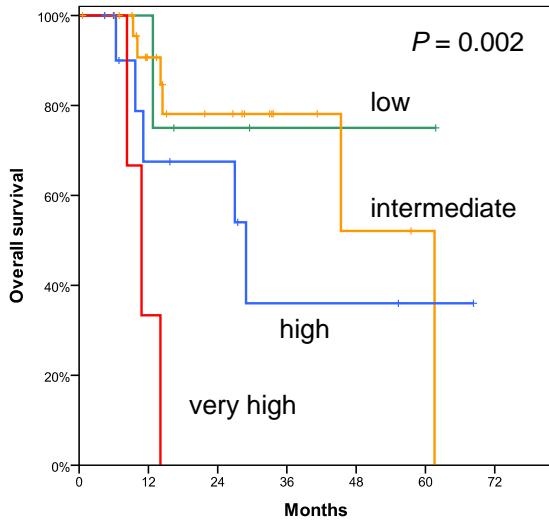
A



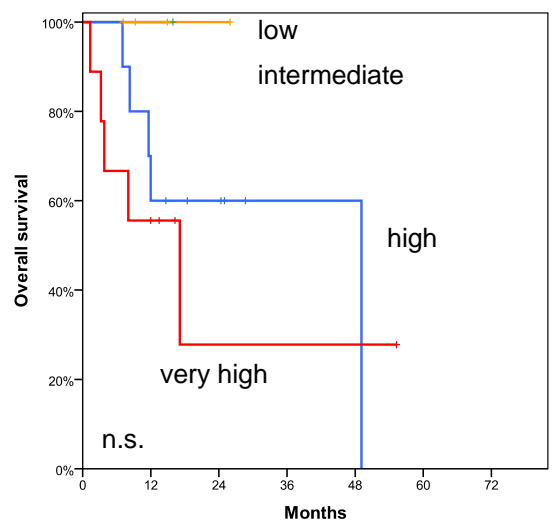
B



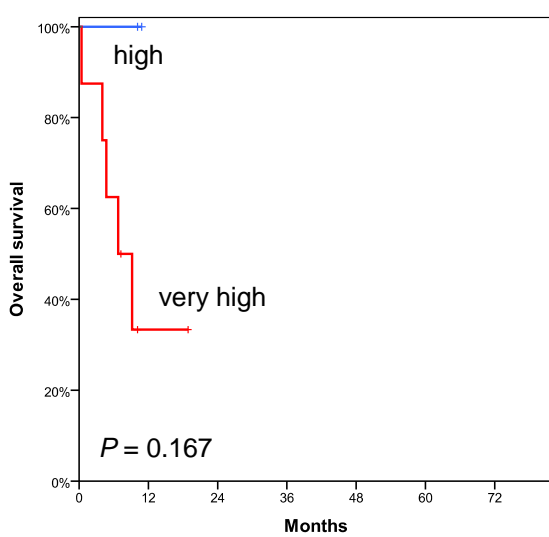
C



D

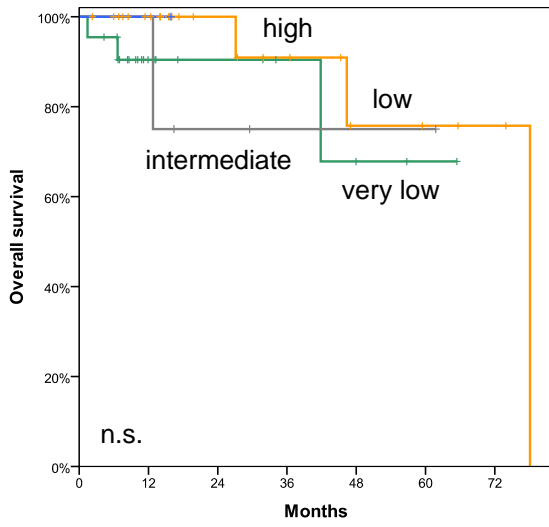


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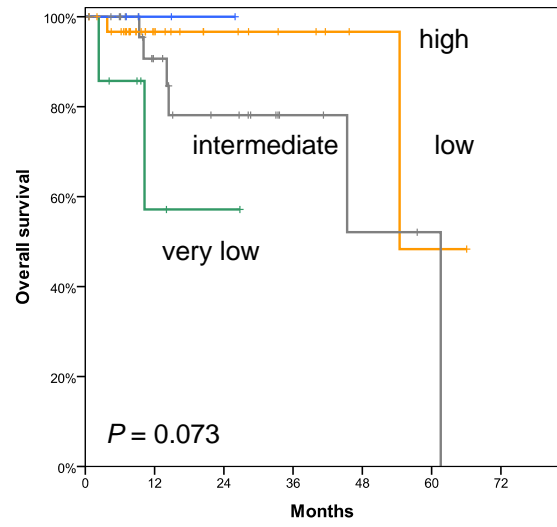


Supplementary Figure S20

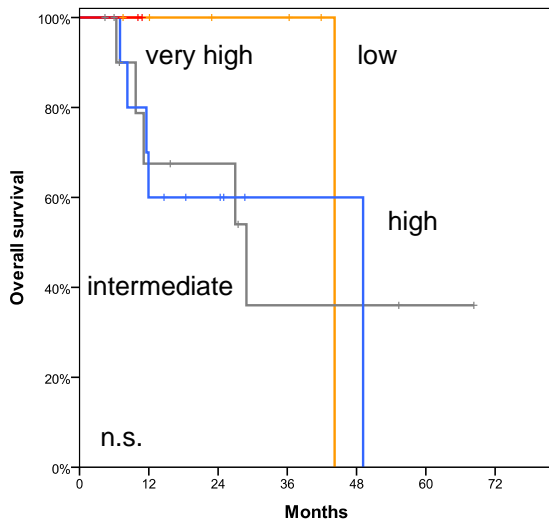
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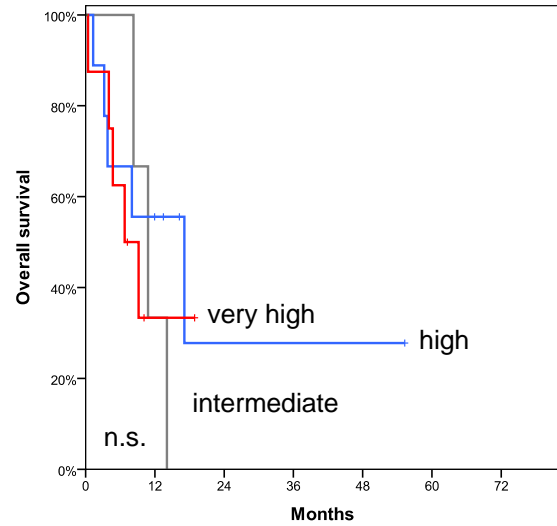
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C

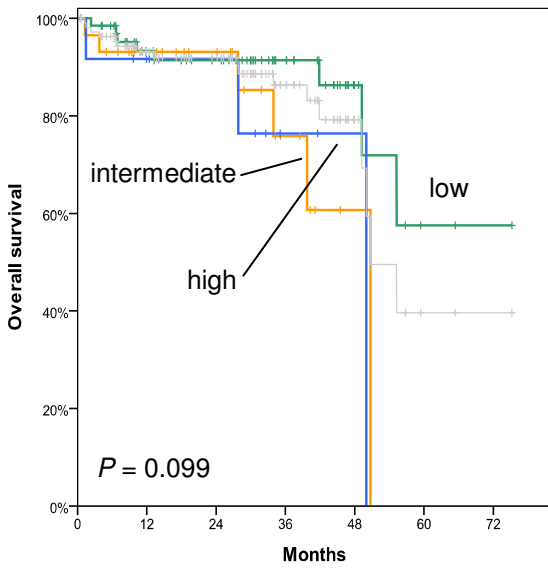


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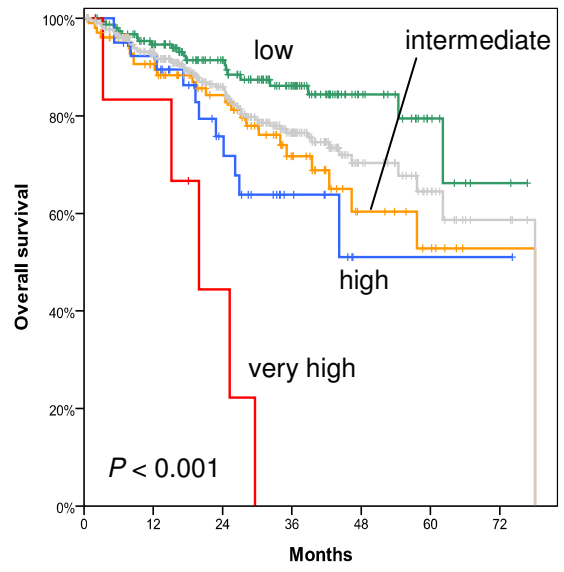


Supplementary Figure S21

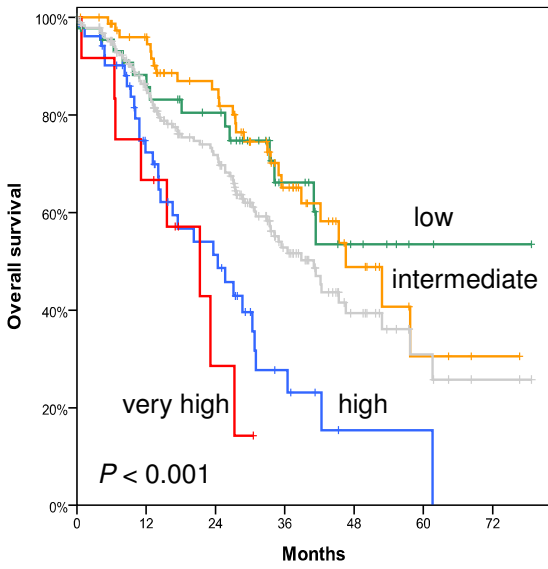
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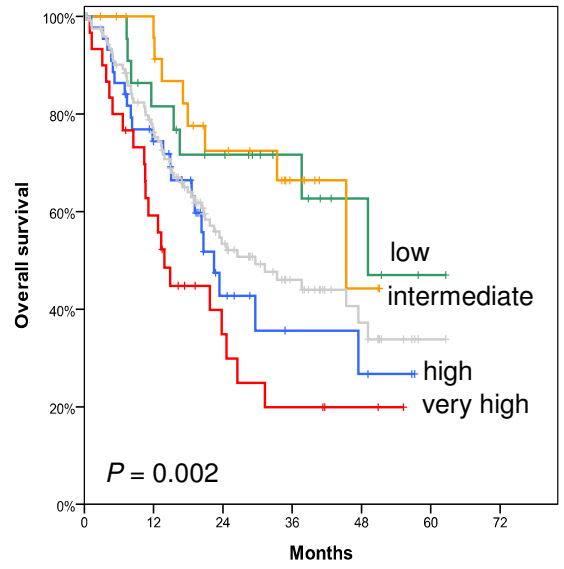
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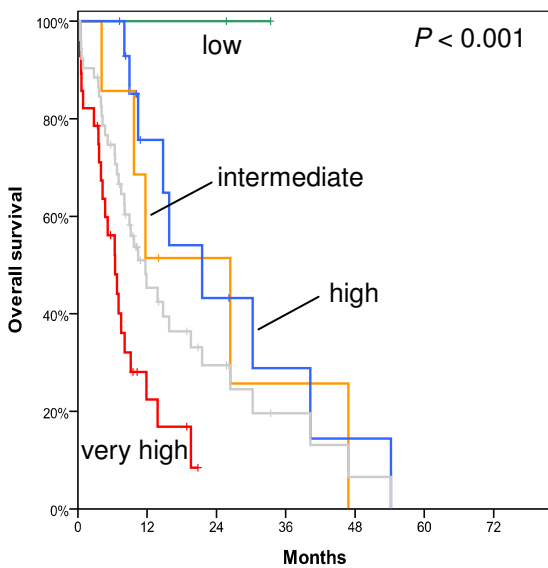
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D

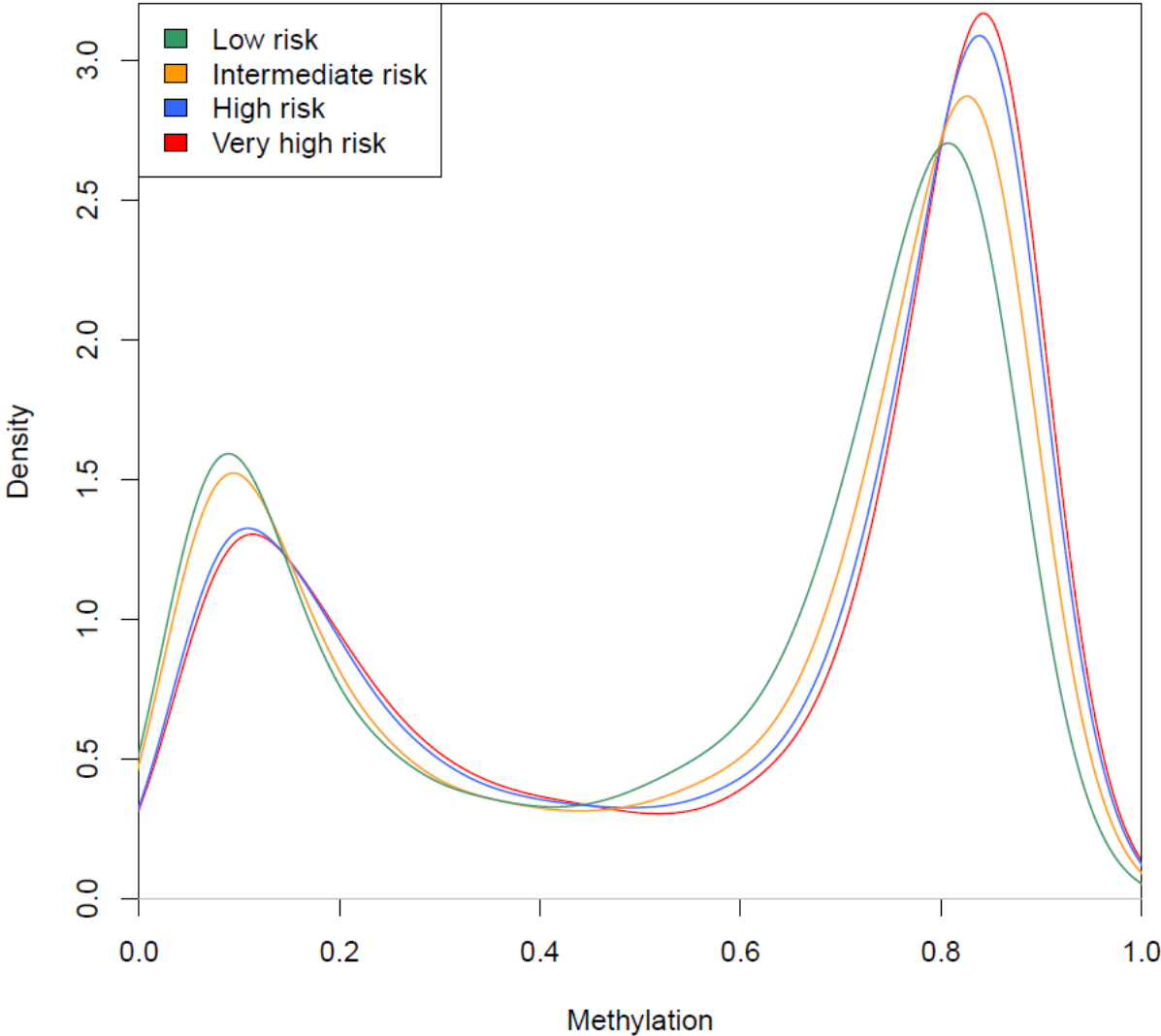


E



Supplementary Figure S22

A



Supplementary Figure S22

B

