5A
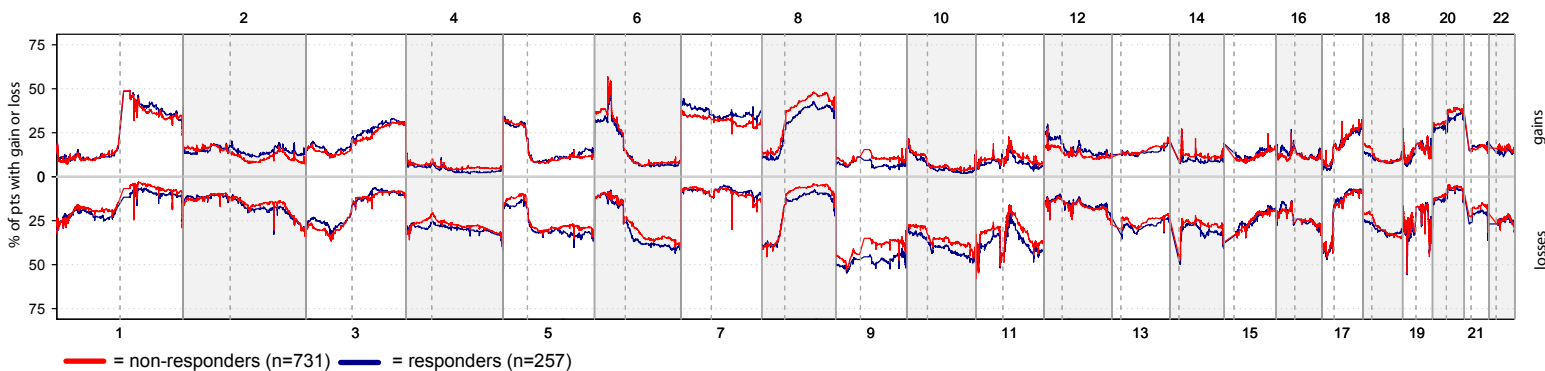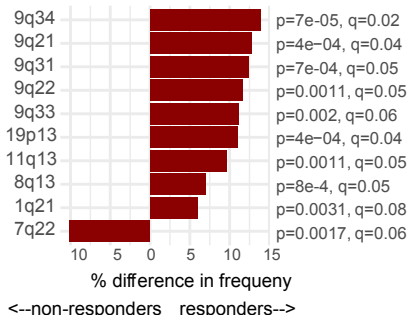
Pan-cancer genome-wide somatic copy number alteration profile: responders (CR/PR) vs non-responders (SD/PD)
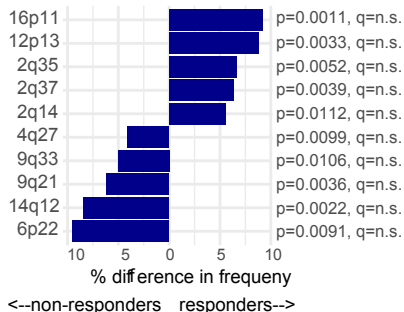
= non-responders (n=731) = responders (n=257)

B

differentially lost cytobands:

	% difference in frequency	p-value
9q34		p=7e-05, q=0.02
9q21		p=4e-04, q=0.04
9q31		p=7e-04, q=0.05
9q22		p=0.0011, q=0.05
9q33		p=0.002, q=0.06
19p13		p=4e-04, q=0.04
11q13		p=0.0011, q=0.05
8q13		p=8e-4, q=0.05
1q21		p=0.0031, q=0.08
7q22		p=0.0017, q=0.06

<--non-responders   responders-->

differentially gained cytobands:

	% difference in frequency	p-value
16p11		p=0.0011, q=n.s.
12p13		p=0.0033, q=n.s.
2q35		p=0.0052, q=n.s.
2q37		p=0.0039, q=n.s.
2q14		p=0.0112, q=n.s.
4q27		p=0.0099, q=n.s.
9q33		p=0.0106, q=n.s.
9q21		p=0.0036, q=n.s.
14q12		p=0.0022, q=n.s.
6p22		p=0.0091, q=n.s.

<--non-responders   responders-->

C

9q34

NR (SD/PD) =40.1%
R (CR/PR) =44.4%

NR (SD/PD) =30.5%
R (CR/PR) =44.4%

chr9 base position hg19 (Mb)

9q34.3

MAMDC4   EDF1   TRAF2
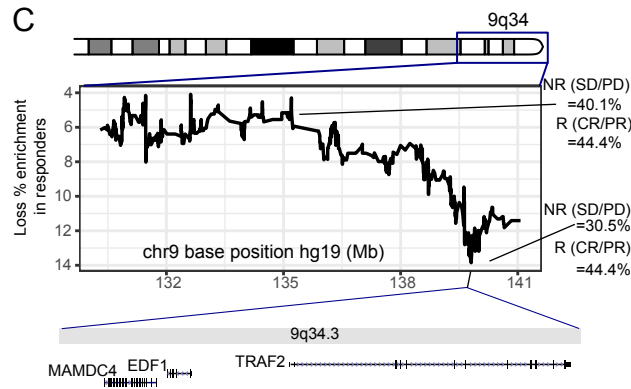
D

responder   non-responder

	TRAF2 loss %	p-value
Pan−cancer		p=0.00018
Urothelial		p=0.008
Melanoma		p=0.032
Other		p=0.070
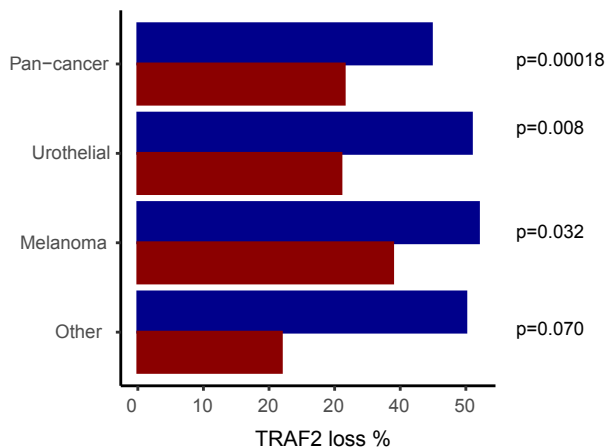
E

gnomAD/ExAC human germline data (n=125,748)
pLI>0.9 is strongly haploinsufficient

TRAF2

probability haploinsufficient

genes (ordered based on haploinsuff. score)