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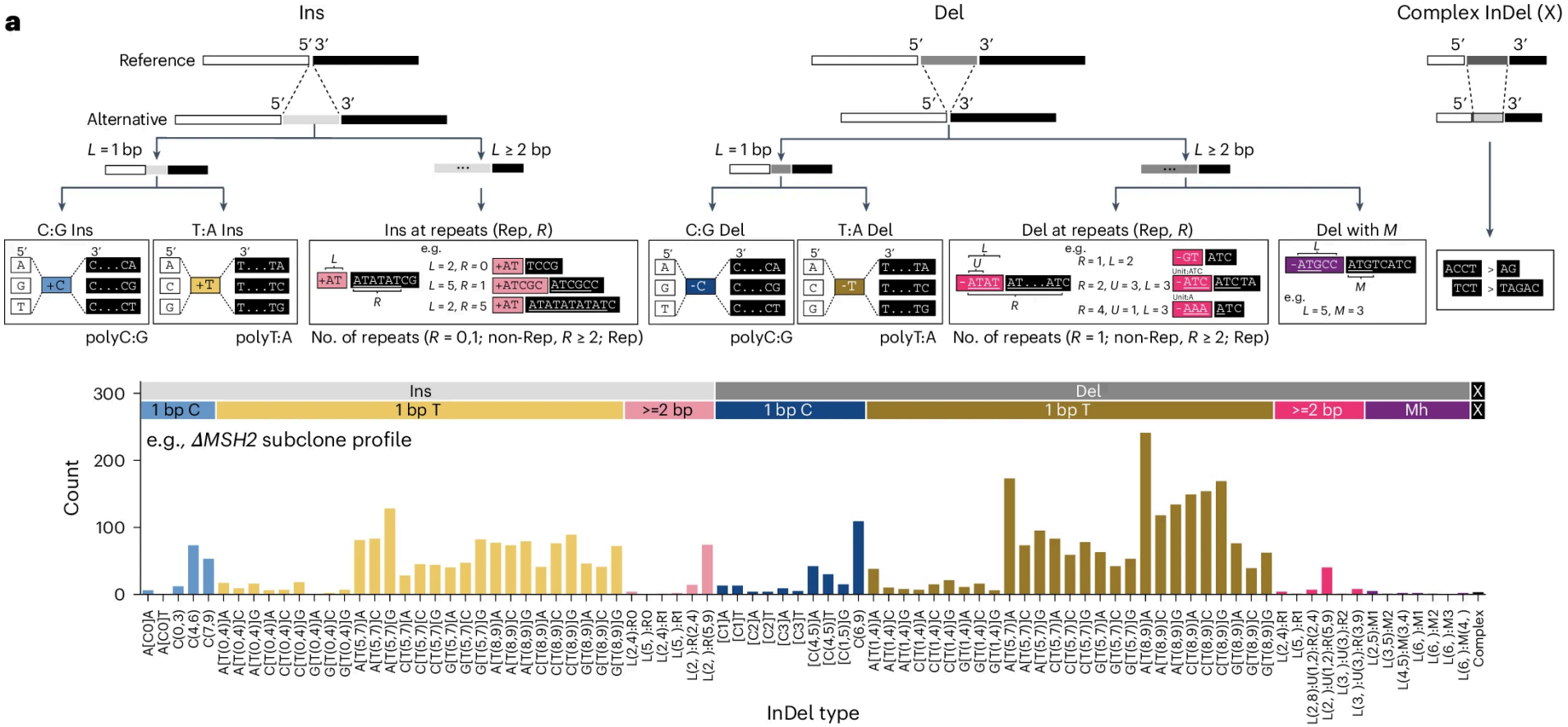
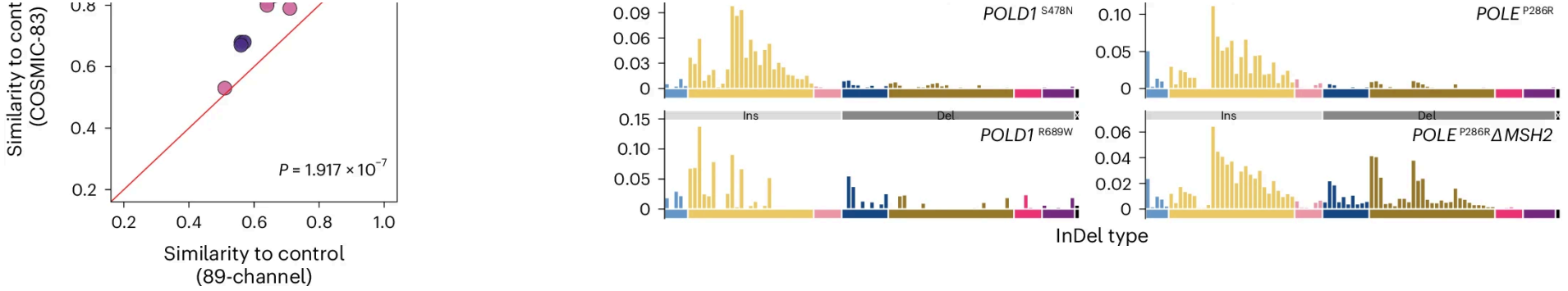
Fig. 2: Redefined InDel taxonomy improves discriminatory power and reveals differential InDel patterns associated with PRR gene edits.

From: A redefined InDel taxonomy provides insights into mutational signatures


a
Ins
Del
Complex InDel (X)
Reference
Alternative
L = 1 bp
L ≥ 2 bp
C:G Ins
T:A Ins
Ins at repeats (Rep, R)
C:G Del
T:A Del
Del at repeats (Rep, R)
Del with M
polyC:G
polyT:A
No. of repeats (R = 0,1; non-Rep, R ≥ 2; Rep)
e.g., ΔMSH2 subclone profile
Count
InDel type
1 bp C
1 bp T
>=2 bp
Mh
b
89-channel
Cosine similarity
InDel count
Gene edits
ΔMLH1
ΔMSH2
ΔMSH3
POLD1R689W
POLD1S478N
POLD1S478N/+ΔMLH1
POLD1S478N/+ΔMSH2
POLEL424V
POLEP286RΔMSH2
POLEP286R
ΔSETD2
Control
c
d
Proportion
ΔMLH1
POLD1 S478N/+ΔMLH1
ΔMSH2
POLD1 S478N/+ΔMSH2
ΔMSH3
POLE L424V



a, Proposed InDel classification schema and an example 89-channel InDel profile of an *ΔMSH2* subclone. **b**, Distinguishing 89-channel InDel profiles of edited subclones from background control. Light blue error bars depict the mean ± 3 s.d. of cosine similarities between $n = 100$ bootstrapped InDel profiles of unedited controls and the background profile (Extended Data Fig. 5b) aggregated from $n = 7$ unedited subclones. The x axis shows the InDel count in log scale. **c**, Cosine similarities of edited subclones and bootstrapped controls in COSMIC-83 InDel profiles against 89-channel InDel profiles. Two-tailed Wilcoxon signed-rank test, $P = 1.917 \times 10^{-7}$). **d**, The 89-channel InDel mutational signatures associated with PRRd gene edits following background subtraction (Supplementary Table 4; https://signal.mutationalsignatures.com/explore/main/experimental/experiments?study=7). Ins, insertion; Del, deletion.

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