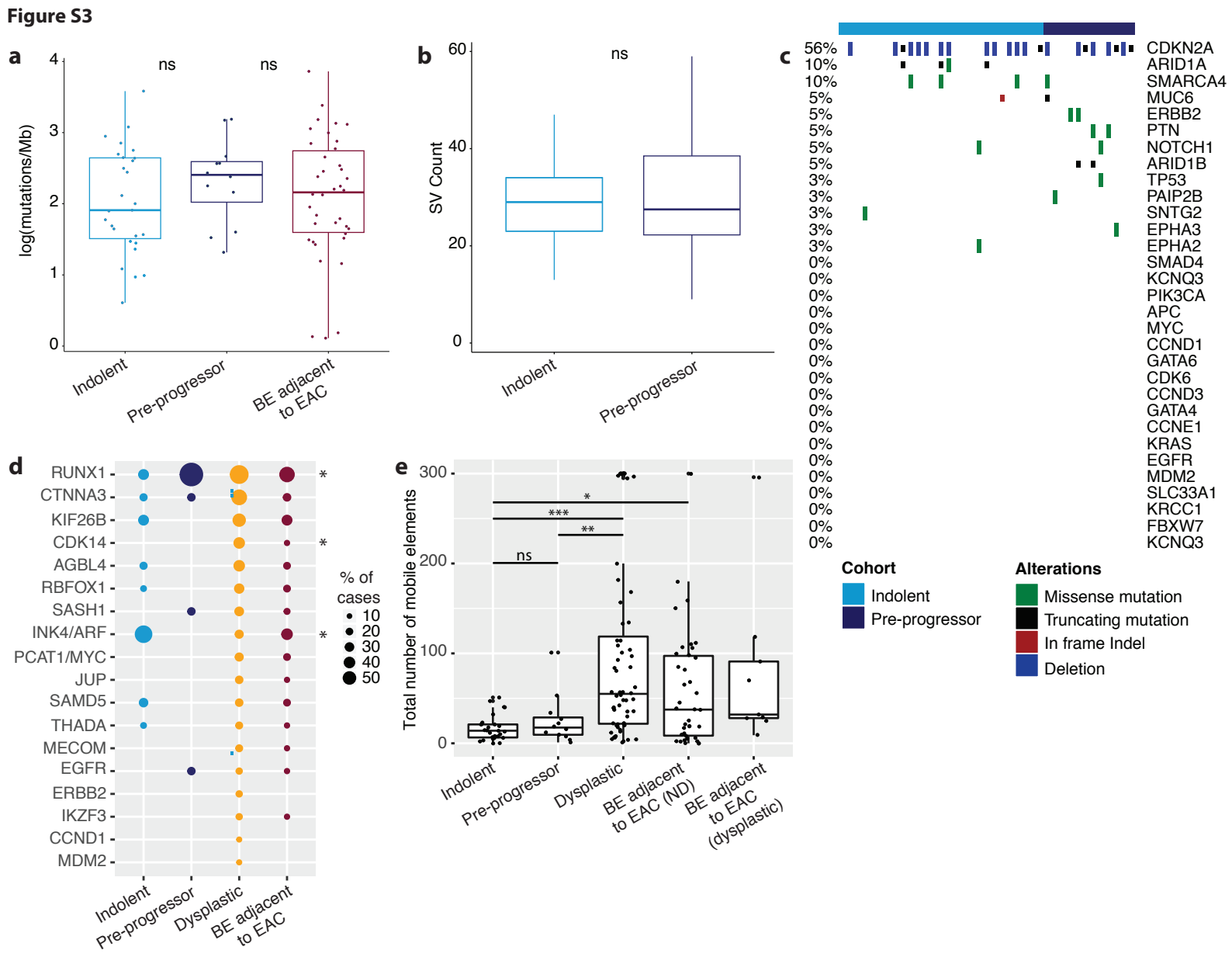
Figure S3


a
log(mutations/Mb)
ns
ns
Indolent
Pre-progressor
BE adjacent to EAC
b
SV Count
ns
Indolent
Pre-progressor
c
CDKN2A
ARID1A
SMARCA4
MUC6
ERBB2
PTN
NOTCH1
ARID1B
TP53
PAIP2B
SNTG2
EPHA3
EPHA2
SMAD4
KCNQ3
PIK3CA
APC
MYC
CCND1
GATA6
CDK6
CCND3
GATA4
CCNE1
KRAS
EGFR
MDM2
SLC33A1
KRCC1
FBXW7
KCNQ3
Cohort
Indolent
Pre-progressor
Alterations
Missense mutation
Truncating mutation
In frame Indel
Deletion

d
RUNX1
CTNNA3
KIF26B
CDK14
AGBL4
RBFOX1
SASH1
INK4/ARF
PCAT1/MYC
JUP
SAMD5
THADA
MECOM
EGFR
ERBB2
IKZF3
CCND1
MDM2
% of cases
10
20
30
40
50
Indolent
Pre-progressor
Dysplastic
BE adjacent to EAC
e
Total number of mobile elements
ns
*
***
**
Indolent
Pre-progressor
Dysplastic
BE adjacent to EAC (ND)
BE adjacent to EAC (dysplastic)