Final model **Breast** Cervix CNS_Glioma CNS_Medullo sigs. SBS2 sigs. SBS2 sigs. DBS11 sigs. SBS35 mrd. HeadAndNeck_Other.2 sigs. ID2 sigs. SBS38 sigs. SBS6 sigs. SBS6 sigs. SBS6 DMPLEX.largest_clus sv.DUP [1e+04,1e+05) sigs.SBS16 sigs.SBS13 gene.MLH1.deep_del rmd.Pancreas.2 ags.SB\$1 md.CNS_Glioma.1 gene.DH1.monoall S. SBS44 S. SBS44 S. SBS42 S. SBS48 S. SBS41 I load indel sigs. SB S1 sigs. DB S7 sigs. SB S91 md.CNS. Ciloma.2 sigs. SB S37 genome. diploid_proposigs. DB S3 sigs. SB S8 40 rmd.CNS_Gloma.3 rmd.CNS_Glioma.2 sigs.ID6 gene.ZNF703.amp 20 CNS_PiloAstro Colorectal Gastroesophageal HeadAndNeck_Other HeadAndNeck_SalivaryGland 60 rmd.HeadAndNeck_Other.2 rmd.HeadAndNeck_Other.1 svLINEs viral_ins.EBV viral_ins.HPV sigs.BB13 sigs.SB39 sigs.SB239 gene.AJUBA.biall sigs.SB239 sv.sv_load sv.DUP_[1e+05,1e+06) sigs.SBS10 IAA1549_BRAF D4 n.CTNNB1_PLAG1 .CRTC1_MAML2 rmd.CNS PiloAstro.1 mul load.dbs gerlome.diploid_proposities.SBS22 sigs.SBS8 sigs.ID10 sigs.DBS7 sigs.SBS7 md.CNS_Glioma.2 sigs.SBS38 gerlome.ploidy on.LIFR_PLAG1 s.DBS9 t_load.indel s.SBS32 s.SBS31 40 20 0 Liver Lung_NonSmallCell Kidney_Chromophobe Kidney_ClearCell Kidney_Papillary Papillary.1 ClearCell.1 hrom_arm.loss.20q igs.SBS29 hrom_arm.loss.7p lgs.ID11 40 rom_arm.loss.1q ut_load.dbs js.ID5 20 Feature type Myeloid Lung_SmallCell NET_Gastrointestinal Lymphoid Mesothelium 60 .MEN1.deep_del HeadAndNeck_Other.2 fusion RUNX1_RUNX1T1 sigs.SBS84 sigs.SBS19 fusion.@IGL_MYC sigs.SBS9 sigs.SBS9 fusion.CBFB_MYH11 mut_load.indel sigs.SBS1 gene_JAK2.biall sigs.SBS32 sigs.SBS32 genome.diploid_proportion sigs.ID11 sigs.SBS30 SV. DEL_[1e+03,1e+04) SV. DEL_[1e+04,1e+05) SIS.ID5 SV. DEL_[0,300) rmd.Mesothelium.1 gene.NF2.deep_del gene.BAP1.deep_del 40 chrom_arm.gain.4q sgs.ID10 NET_Pancreas NET_Lung Pancreas Prostate Ovarian e.WEE1.amp ome.diploid_proportion .SBS5 s. SBS40 le. CHD1.deep_del s. SBS15 le. PTEN.deep_del nrom_arm.gain.12q nrom_arm.gain.4p 40 load.indel SBS8 SBS85 Load.snv SID10 SBS16 SBS12 20 -0 Sarcoma_GIST Sarcoma_Osteo Sarcoma_Leiomyo Sarcoma_Lipo Sarcoma_Other 60 .comPLEX.largest_clus OMPLEX_[800,Inf) e.MDM2.amp s.SBS89 s.SBS19 ne.ATRX.deep_del s.SBS12 t oad.dbs COMPLEX_[0,25) t load.indel rcoma_Osteo. Sarcoma_Other. rmd.Sarcoma_GIST. gs.ID10 gs.SBS40 gs.SBS86 gs.SBS16 hrom_arm.loss.1q 40 CDK4.amp 20 Uterus Skin_Carcinoma Skin_Melanoma Thyroid Urothelial 60 rmd.Thyroid.1 fusion.THADA_IGF2BP3 mut_load.indel mut_load.snv mut_load.shv sy_DUP_[1e+04,1e+05) sigs.SBS1 sigs.SBS1 sigs.DBS10 sigs.ID12 gene.PIK3R1.monoall rmd.Ovarian.3 drrom_arm.gain.1q sigs.SBS32 sigs.SBS32 sigs.SBS88 mut load.snv gene.SOX4.amp sv.DEL_[1e+05,1e+06) sigs.SBS19 .SPRED1.deep_del rmd.Skin_Carcinoma.1 sigs.SBS28 sigs.ID10 gene.NOTCH1.biall rmd.Skin_Melanoma.1 chrom_arm.gain.14q sigs.ID13 gene.SMTNL2.biall sigs.ID8 gene.BRAF.monoall sigs.ID14 chrom_arm.gain.22q nrom_arm.loss.6p nrom_arm.loss.3q 40 ERT.monoall 20 0 -

15

Ö

10

Rank

15

Ö

10

10

15 0 15

0

10

15

10

rmd

sigs

gene

fusion

viral_ins

mut_load

chrom_arm genome gender sv

Feature importance (mean decrease in accuracy)

