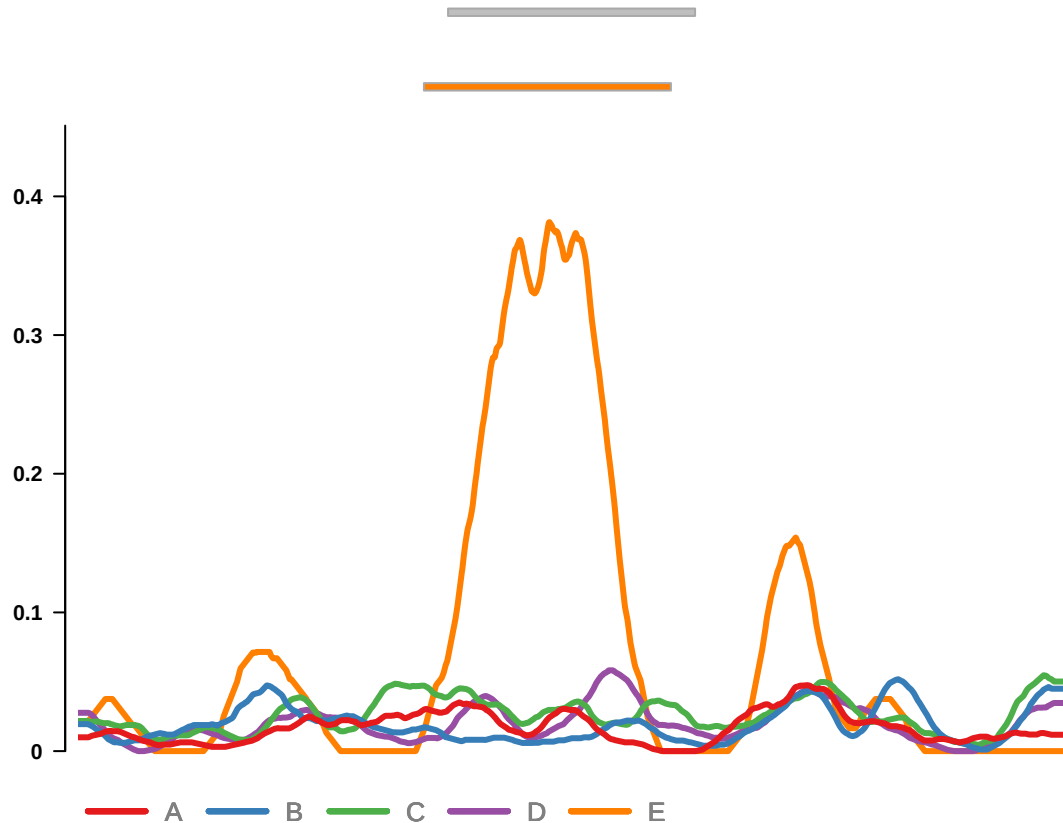
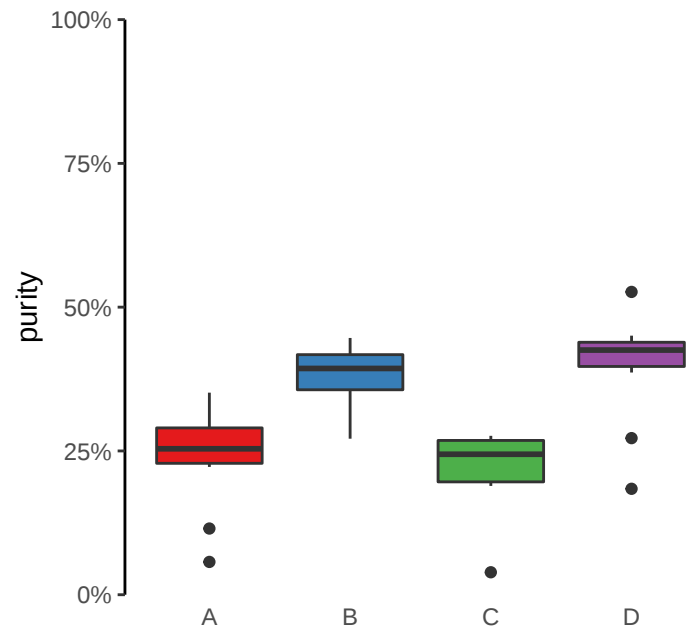


FAM83G (GH17J019010) enhancer loss
chr17:19011073–19011573



Putatively Subclonal (logFC = -1.06)

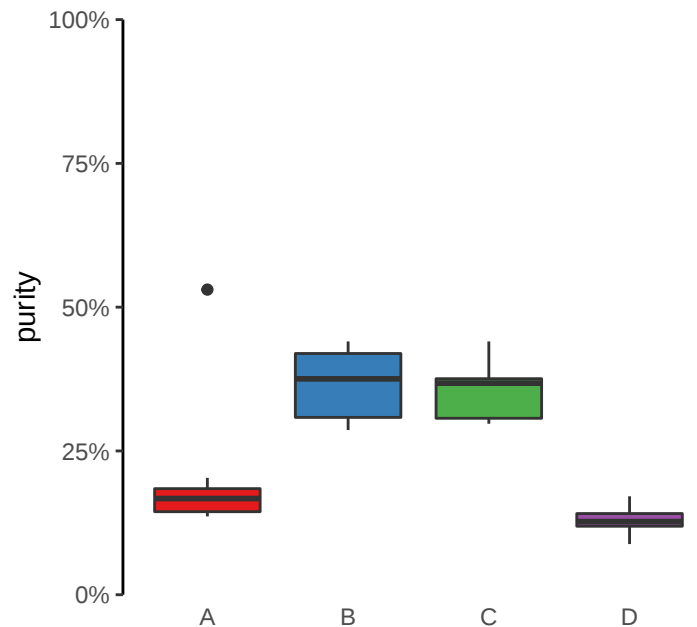
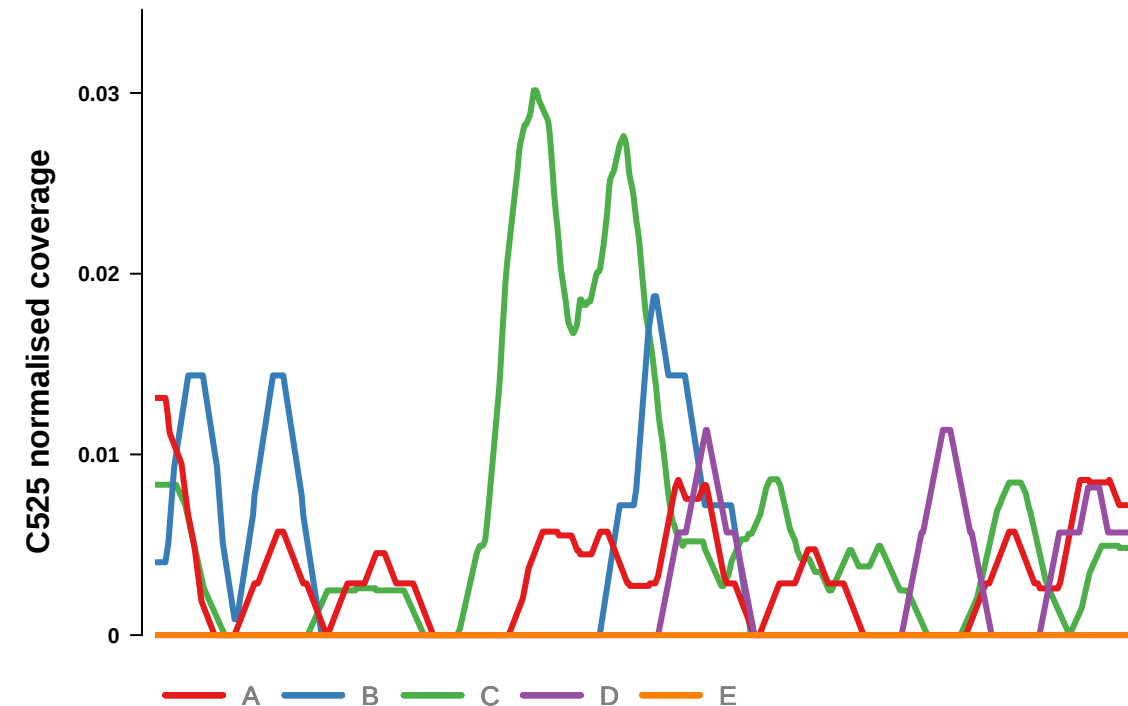
	P.	Adjusted P.
<i>~region vs. ~</i>	1.33e-03 **	3.91e-02 *
<i>~purity vs ~</i>	4.7e-01	8.48e-01
<i>~purity+region vs ~purity</i>	1.06e-03 **	3.34e-02 *
<i>Carcinoma vs. normal</i>	1.25e-01	1.25e-01



ACAP2, PPP1R2 (GH03J195537) enhancer loss
chr3:195537917–195538417

Putatively Subclonal (logFC = -1.47)

	P.	Adjusted P.
~region vs. ~	8.63e-04 ***	4.64e-03 **
~purity vs ~	8.21e-02	7.18e-01
~purity+region vs ~purity	4.04e-03 **	1.98e-02 *
Carcinoma vs. normal	1.16e-01	1.16e-01

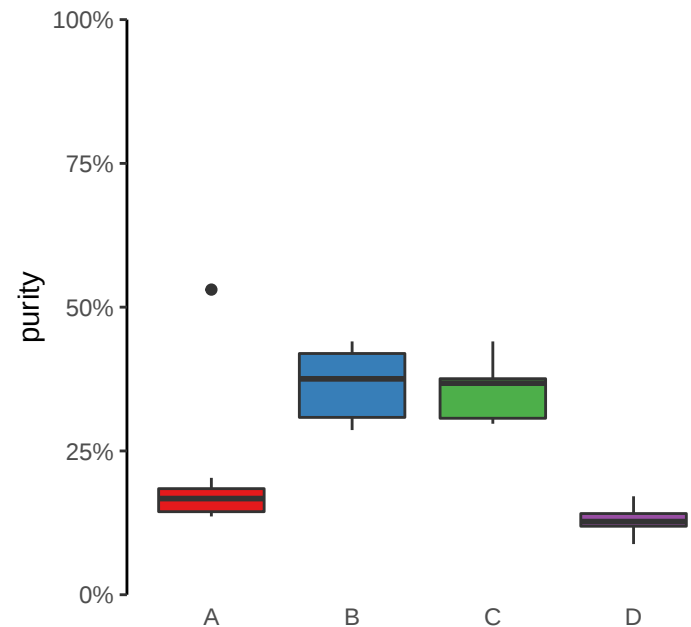
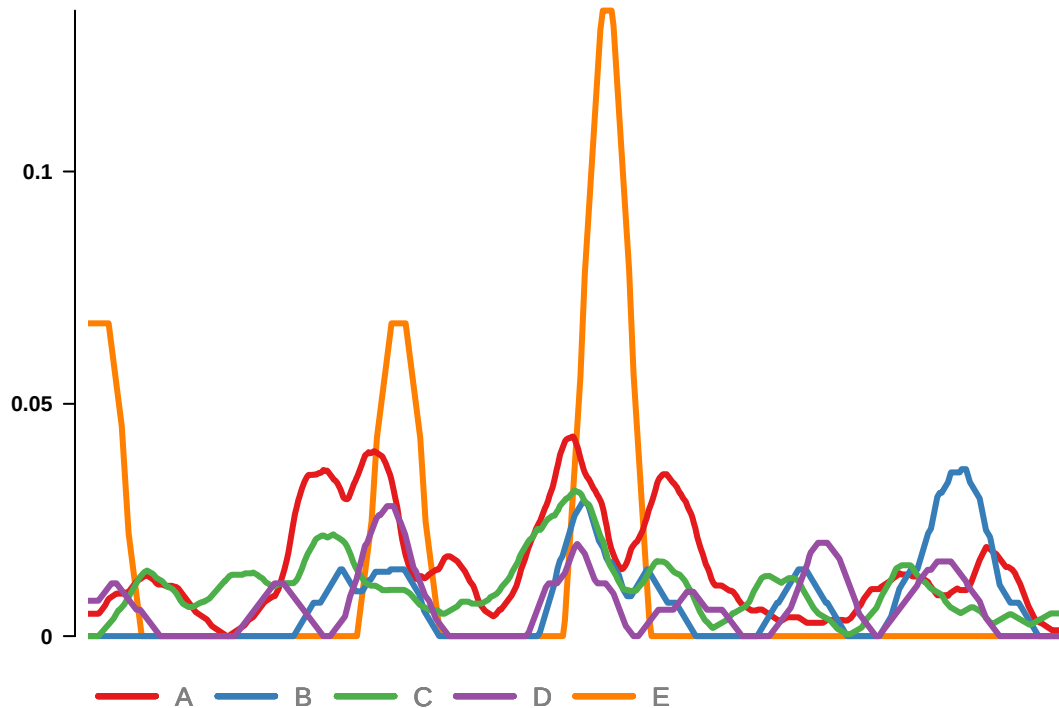


CNST (GH01J246591) enhancer loss
chr1:246591917-246592417

Putatively Subclonal (logFC = -0.73)

	P.	Adjusted P.
<i>~region vs. ~</i>	1.68e-02 *	4.62e-02 *
<i>~purity vs ~</i>	5.16e-01	8.63e-01
<i>~purity+region vs ~purity</i>	7.48e-03 **	2.53e-02 *
<i>Carcinoma vs. normal</i>	NA	NA

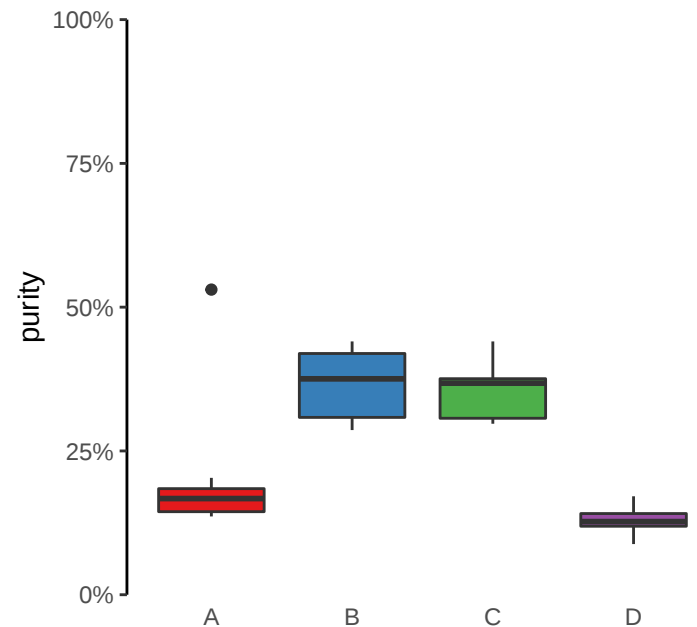
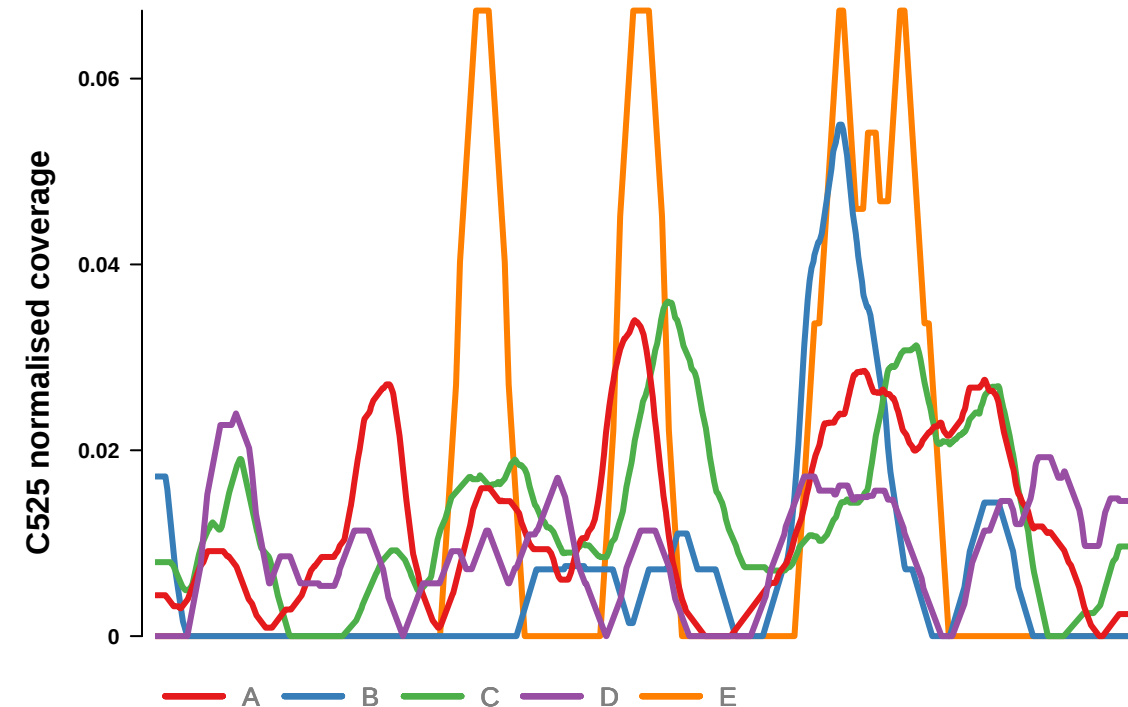
C525 normalised coverage



DNAH7, ENSG00000272211 (GH02J196100) enhancer loss
chr2:196101142–196101642

Putatively Subclonal (logFC = -0.99)

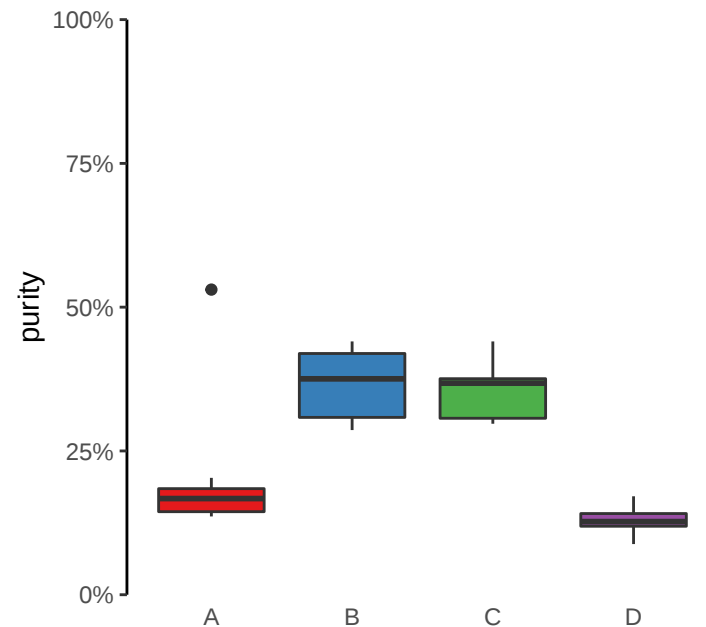
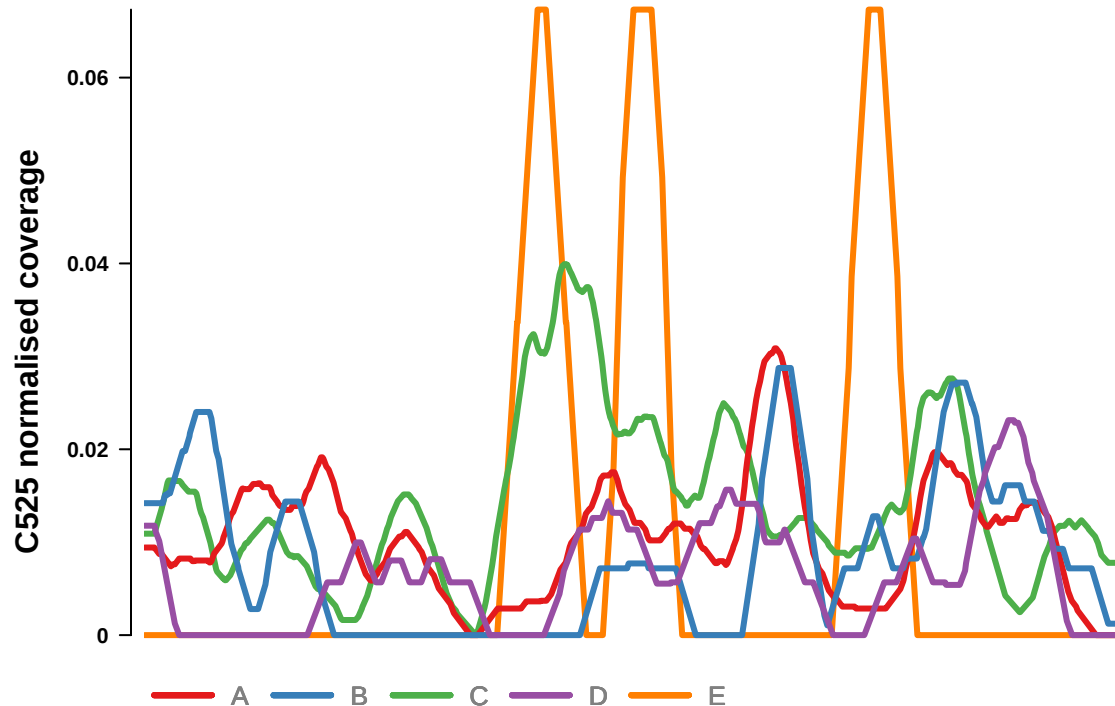
	P.	Adjusted P.
~region vs. ~	2.27e-03 **	9.28e-03 **
~purity vs. ~	7.81e-01	8.93e-01
~purity+region vs ~purity	6.57e-04 ***	4.82e-03 **
Carcinoma vs. normal	NA	NA



FABP1, THNSL2 (GH02J088144) enhancer loss
chr2:88144817–88145317

Putatively Subclonal (logFC = -1.92)

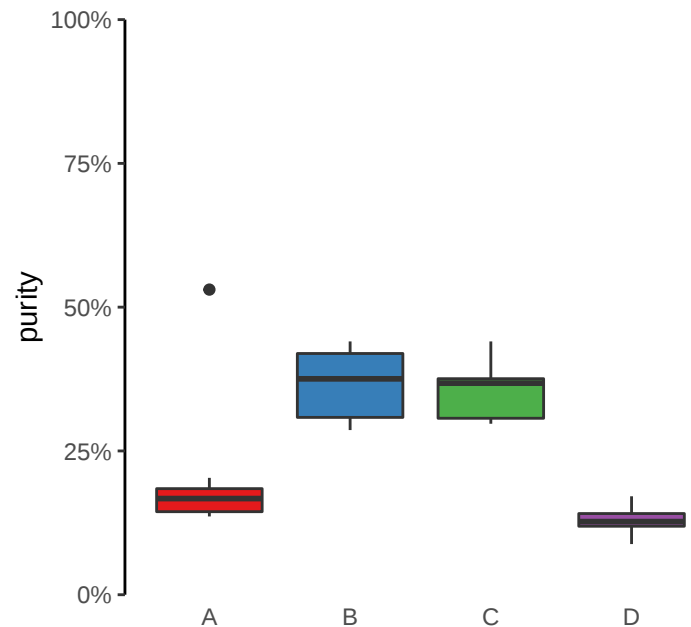
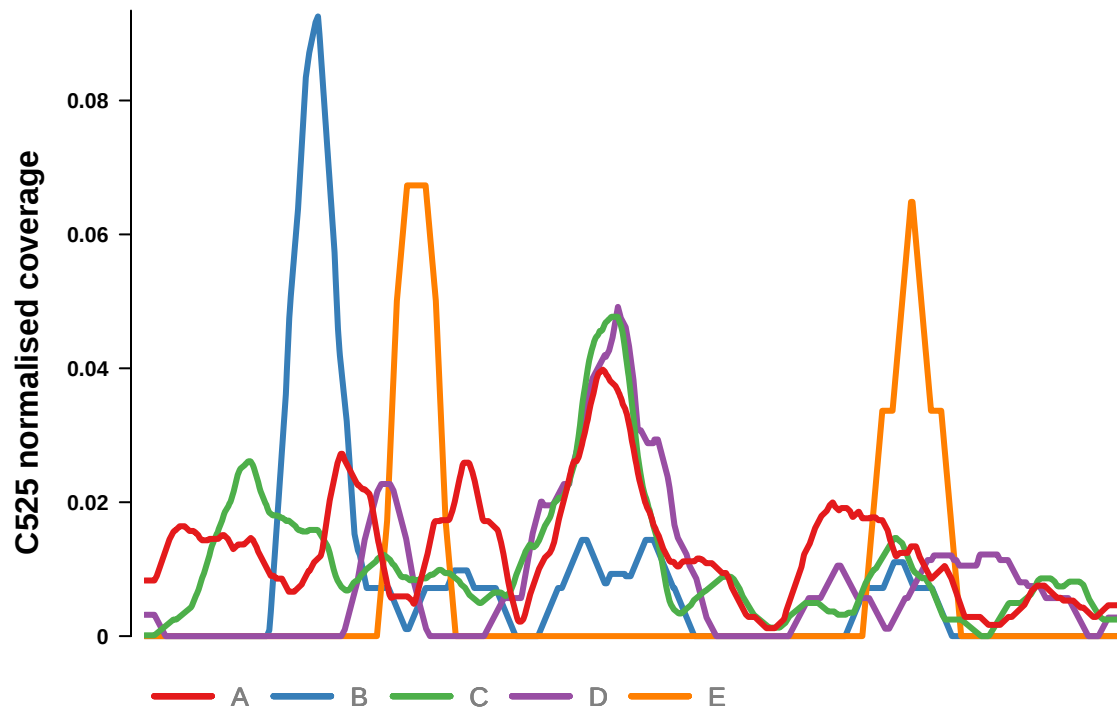
	P.	Adjusted P.
<i>~region vs. ~</i>	7.41e-05 ****	7.83e-04 ***
<i>~purity vs ~</i>	2.43e-01	7.37e-01
<i>~purity+region vs ~purity</i>	3.02e-04 ***	2.95e-03 **
<i>Carcinoma vs. normal</i>	1.54e-02 *	1.54e-02 *



MAP3K1, LINC01948 (GH05J056411) enhancer loss
chr5:56412924-56413424

Putatively Subclonal (logFC = -1.04)

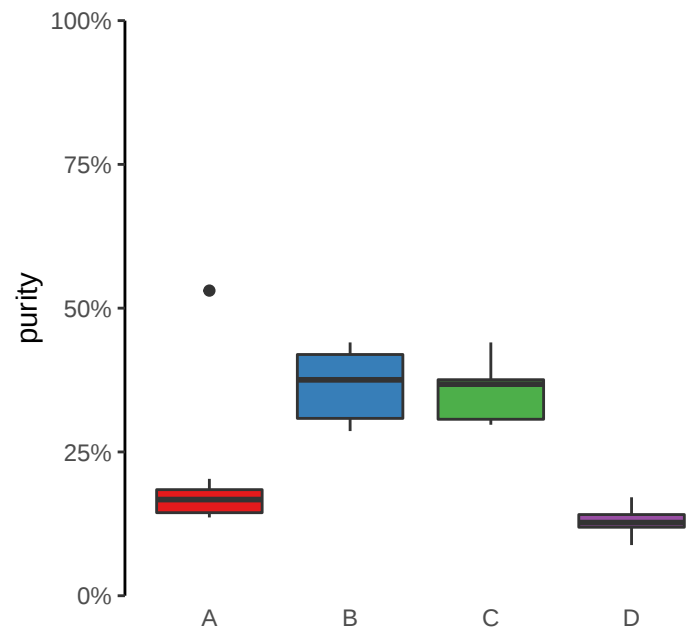
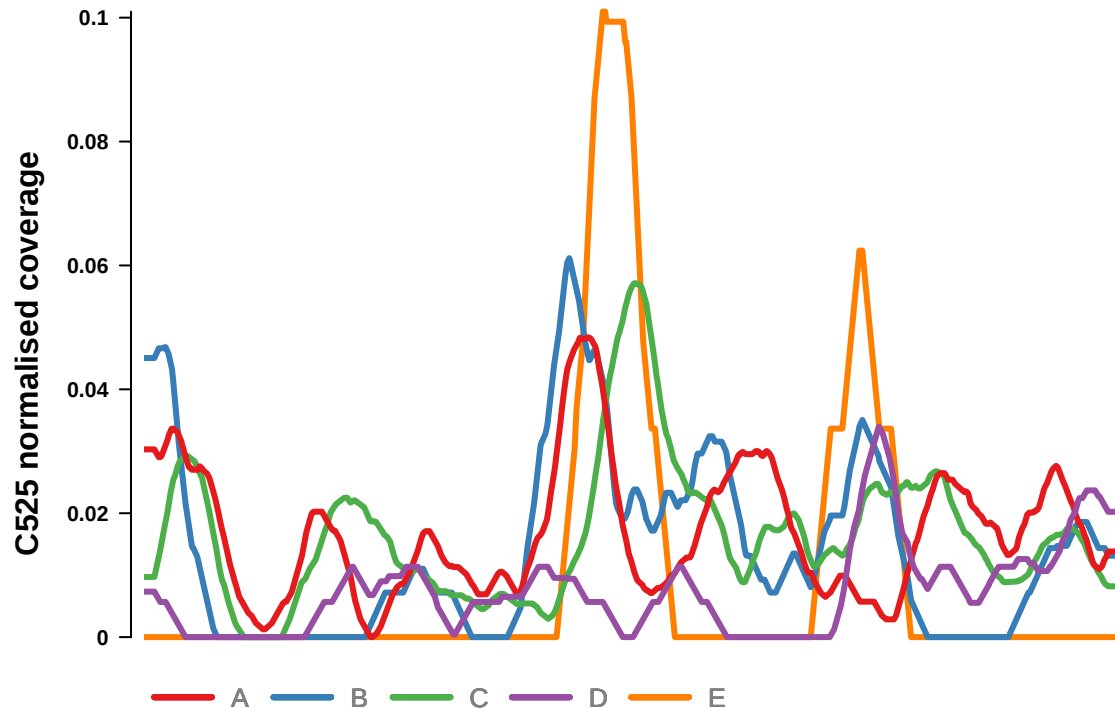
	P.	Adjusted P.
<i>~region vs. ~</i>	2.64e-03 **	1.03e-02 *
<i>~purity vs ~</i>	4.77e-01	8.63e-01
<i>~purity+region vs ~purity</i>	4.02e-03 **	1.98e-02 *
<i>Carcinoma vs. normal</i>	2.11e-01	2.11e-01



PPP2CB (GH08J030800) enhancer loss
chr8:30804244–30804744

Putatively Subclonal (logFC = -0.8)

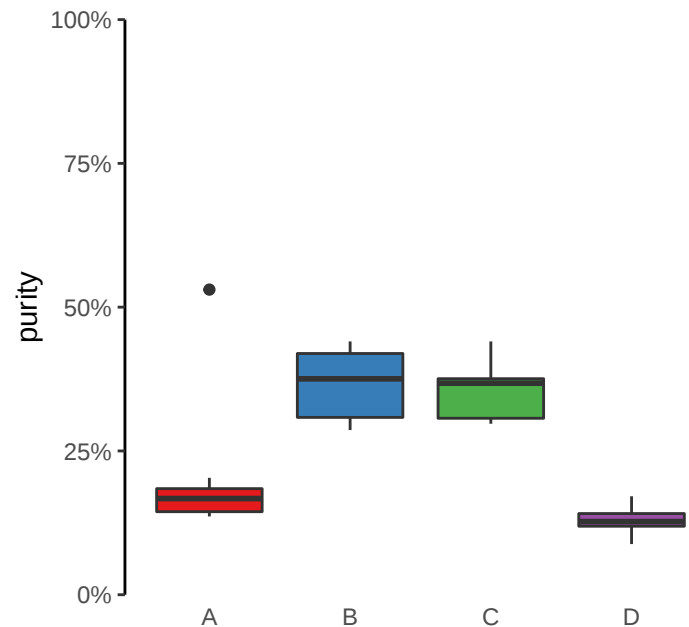
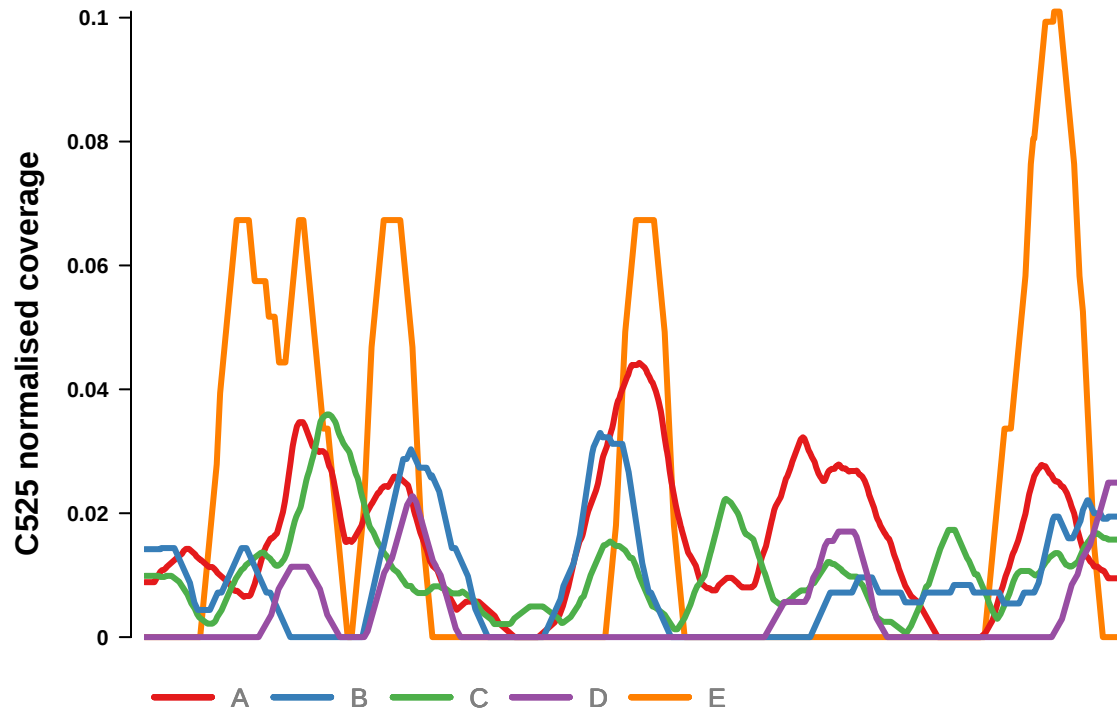
	P.	Adjusted P.
<i>~region vs. ~</i>	3.81e-03 **	1.37e-02 *
<i>~purity vs ~</i>	3.05e-01	7.48e-01
<i>~purity+region vs ~purity</i>	6.71e-03 **	2.37e-02 *
<i>Carcinoma vs. normal</i>	NA	NA



PPP3CA (GH04J101183) enhancer loss
chr4:101183634-101184134

Putatively Subclonal (logFC = -0.85)

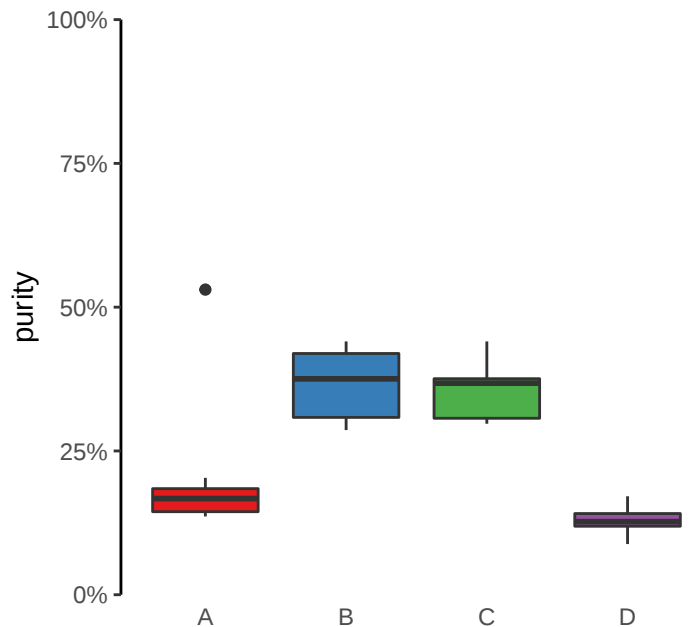
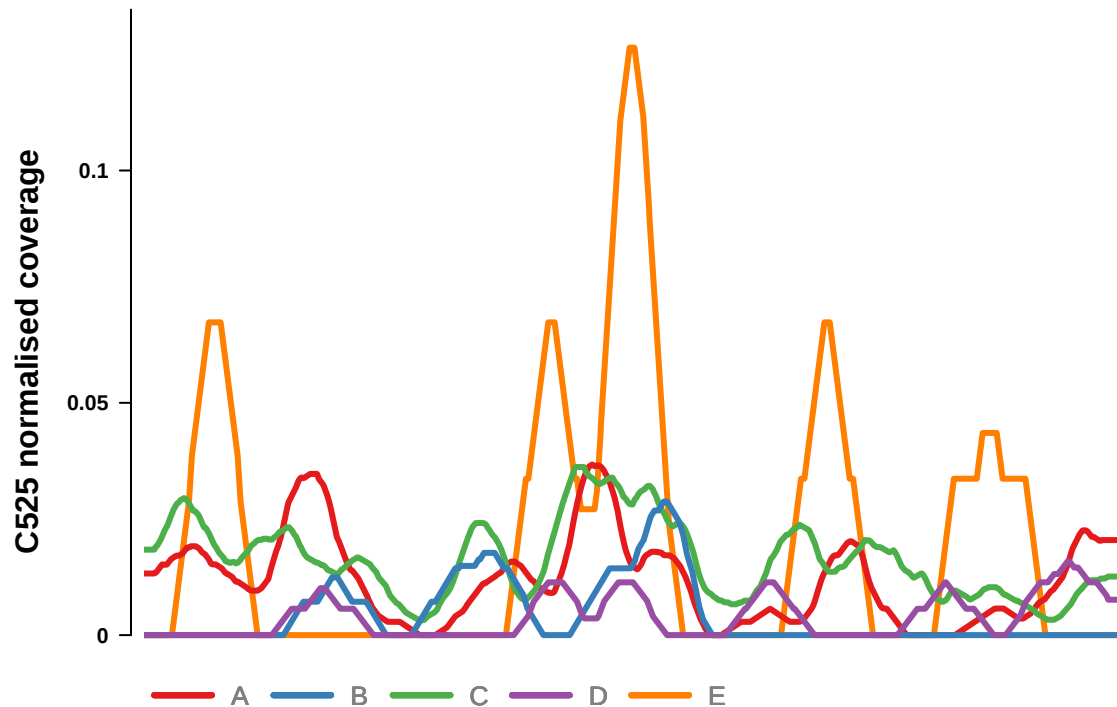
	P.	Adjusted P.
<i>~region vs. ~</i>	1.72e-03 **	7.63e-03 **
<i>~purity vs ~</i>	8.83e-01	9.48e-01
<i>~purity+region vs ~purity</i>	2.13e-03 **	1.25e-02 *
<i>Carcinoma vs. normal</i>	NA	NA



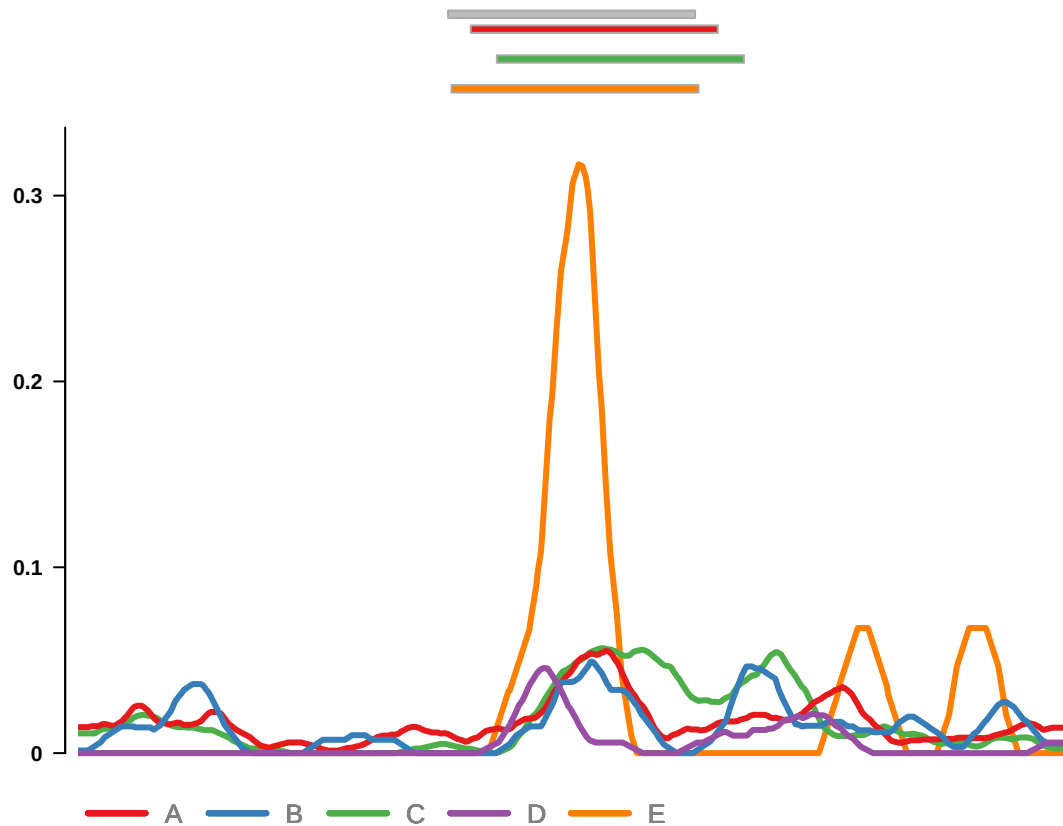
SDHB (GH01J017108) enhancer loss
chr1:17108338–17108838

Putatively Subclonal (logFC = -1)

	P.	Adjusted P.
<i>~region vs. ~</i>	1.46e-03 **	6.96e-03 **
<i>~purity vs ~</i>	1.91e-01	7.37e-01
<i>~purity+region vs ~purity</i>	5.71e-03 **	2.21e-02 *
<i>Carcinoma vs. normal</i>	1.9e-01	1.9e-01

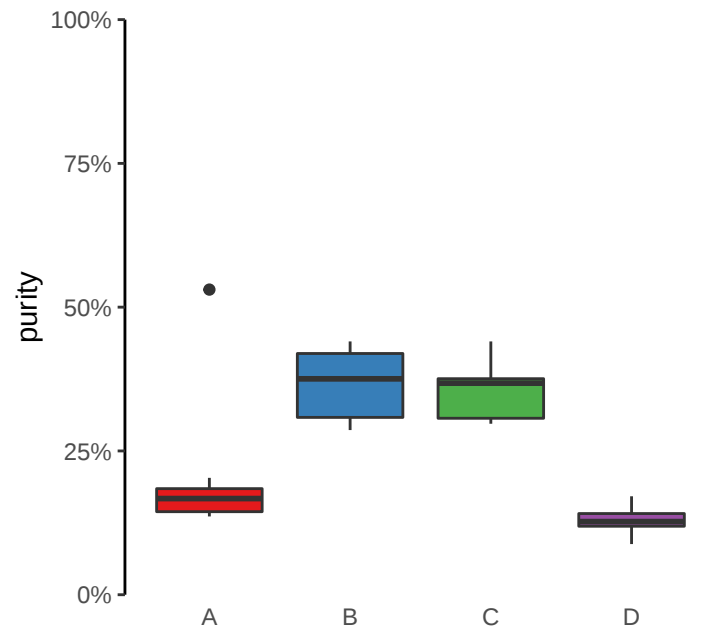


ZNF431 (GH19J020999) enhancer loss
chr19:20999605–21000105

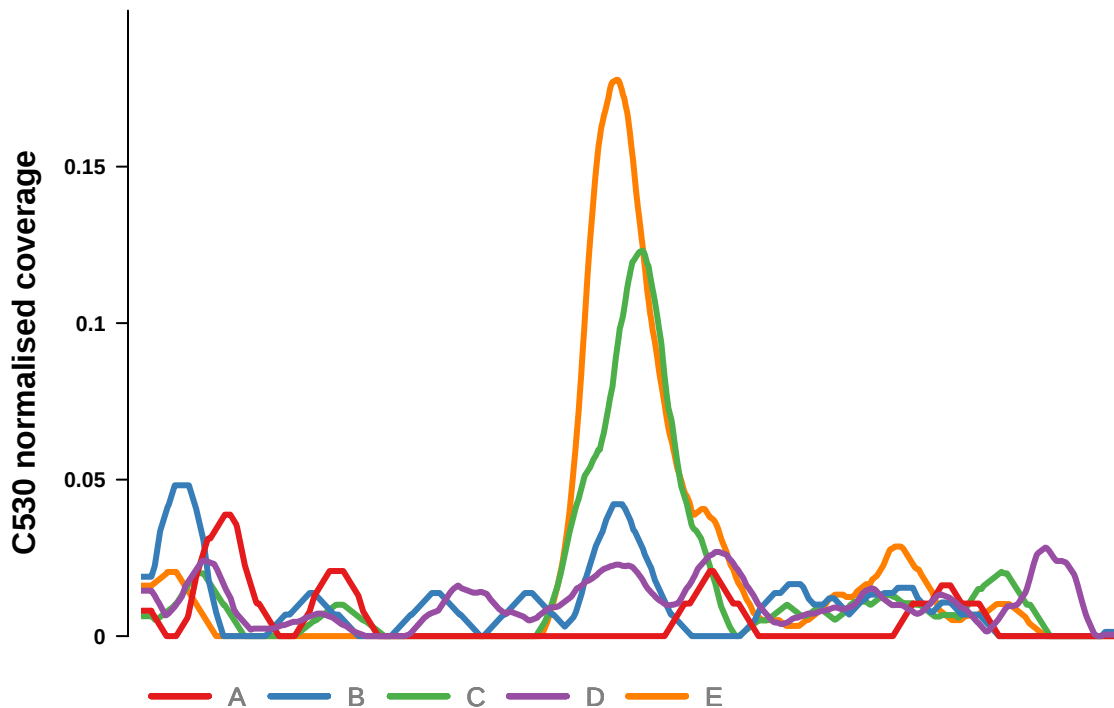


Putatively Subclonal (logFC = -0.82)

	P.	Adjusted P.
<i>~region vs. ~</i>	5.02e-05 ****	7.46e-04 ***
<i>~purity vs ~</i>	2.85e-01	7.48e-01
<i>~purity+region vs ~purity</i>	1.86e-04 ***	2.95e-03 **
<i>Carcinoma vs. normal</i>	NA	NA

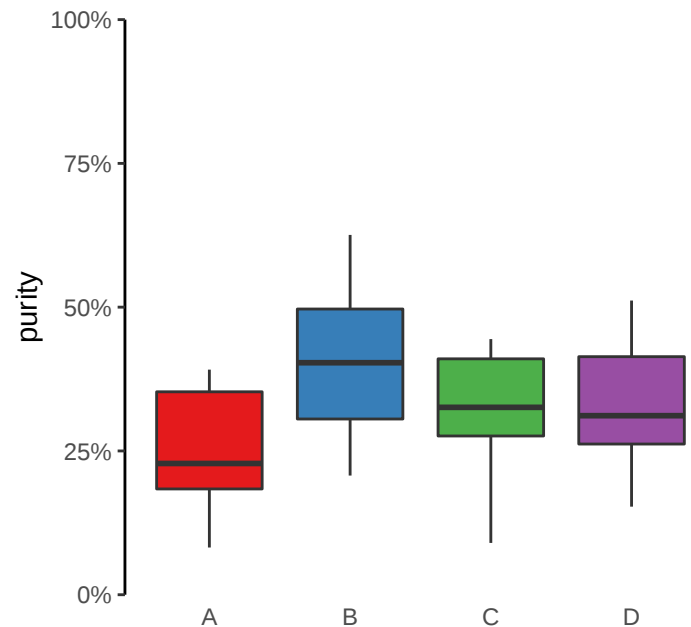


CCDC6 (GH10J059885) enhancer loss
chr10:59885378–59885878



Putatively Subclonal (logFC = -0.51)

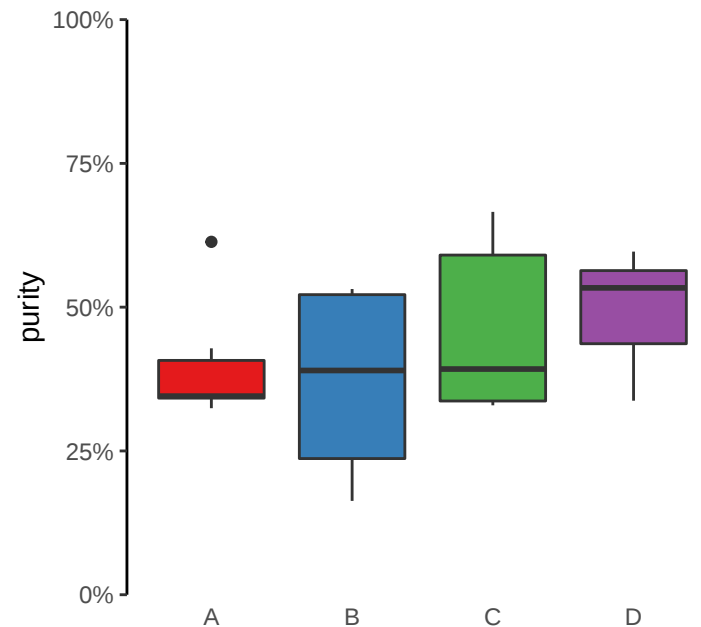
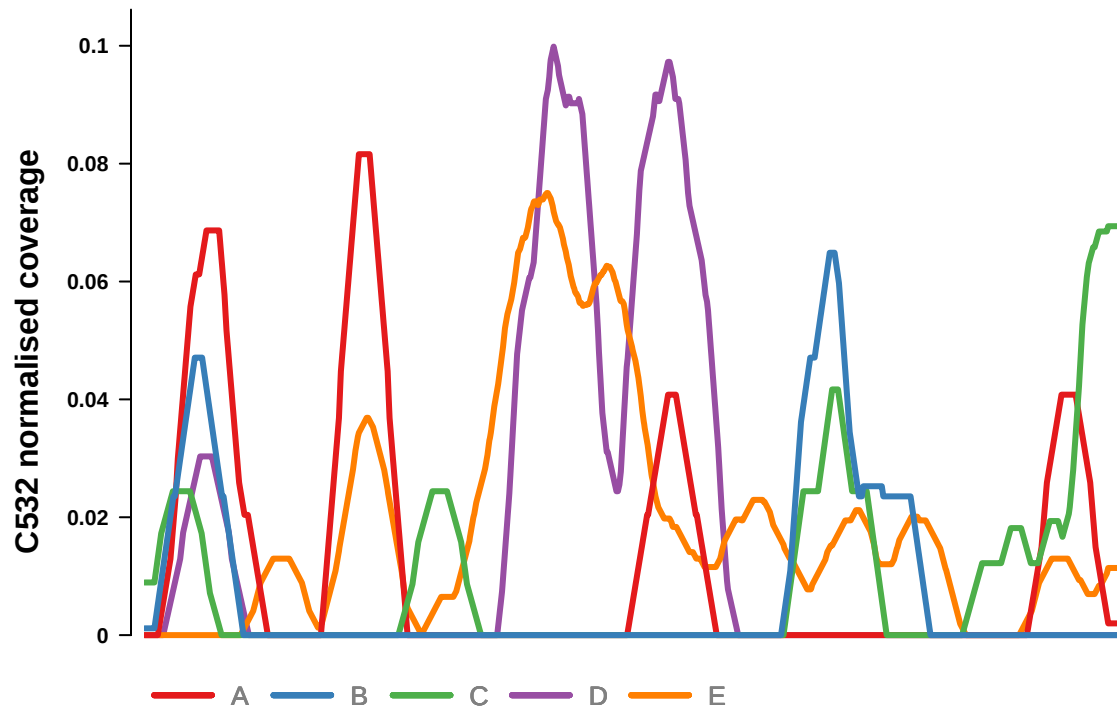
	P.	Adjusted P.
<i>~region vs. ~</i>	1.18e-03 **	5.12e-02
<i>~purity vs ~</i>	8.75e-01	9.62e-01
<i>~purity+region vs ~purity</i>	1.54e-03 **	4.52e-02 *
<i>Carcinoma vs. normal</i>	NA	NA



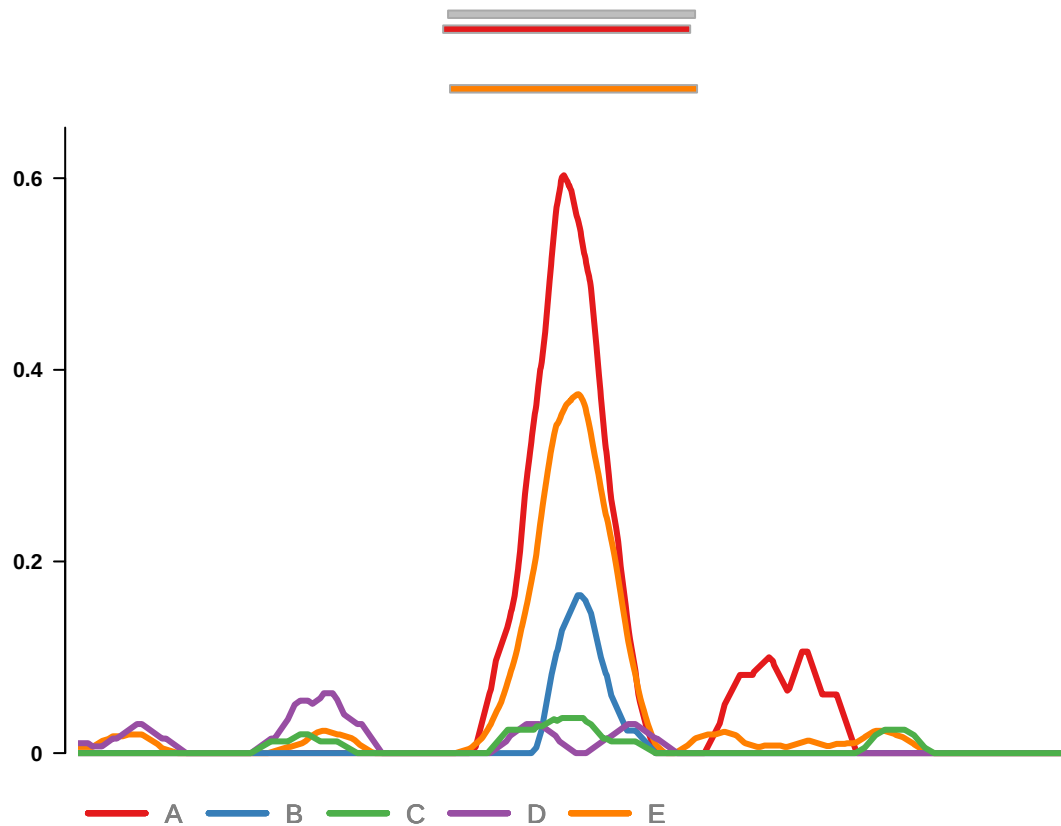
SMAD3 (GH15J067079) enhancer loss
chr15:67081050–67081550

Putatively Subclonal (logFC = -0.57)

	P.	Adjusted P.
<i>~region vs. ~</i>	6.8e-05 ****	2.99e-03 **
<i>~purity vs ~</i>	3.35e-01	8.63e-01
<i>~purity+region vs ~purity</i>	3.83e-04 ***	1.69e-02 *
<i>Carcinoma vs. normal</i>	NA	NA

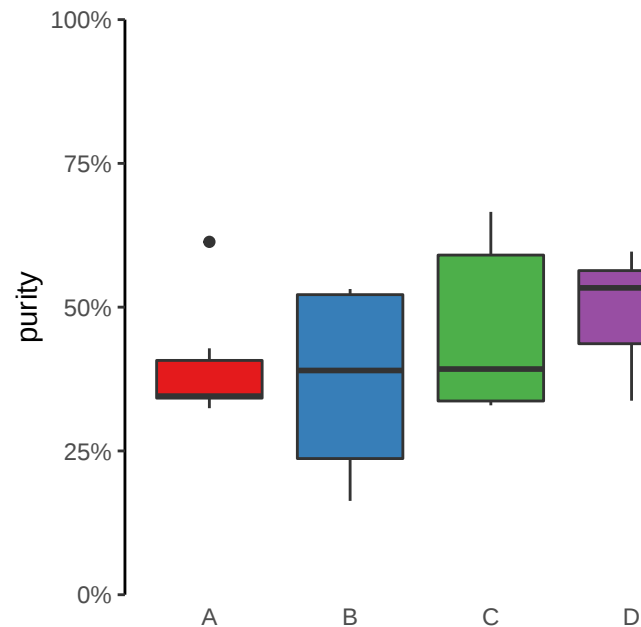


ZNF431 (GH19J020999) enhancer loss
chr19:20999605–21000105

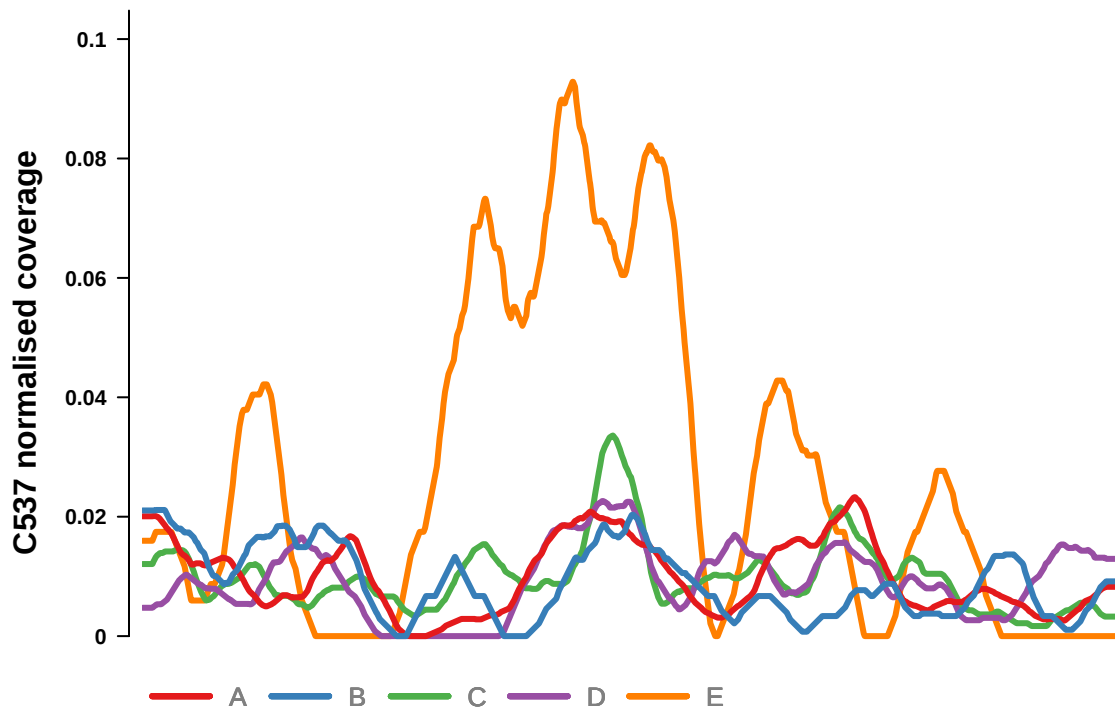


Putatively Subclonal ($\log FC = -1.3$)

	P.	Adjusted P.
<i>~region vs. ~</i>	6.69e-07 ****	5.88e-05 ****
<i>~purity vs ~</i>	5.27e-01	9.09e-01
<i>~purity+region vs ~purity</i>	1.62e-06 ****	1.42e-04 ***
<i>Carcinoma vs. normal</i>	6.85e-02	6.85e-02

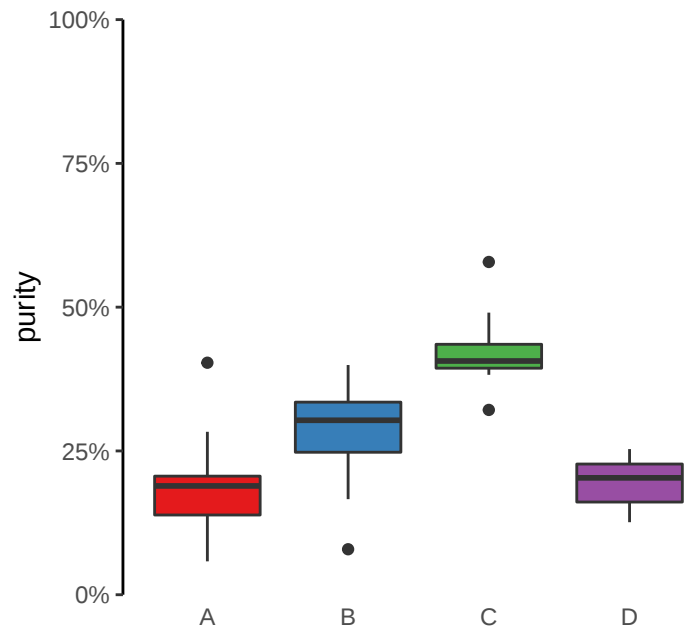


SDHB (GH01J017108) enhancer loss
chr1:17108338–17108838

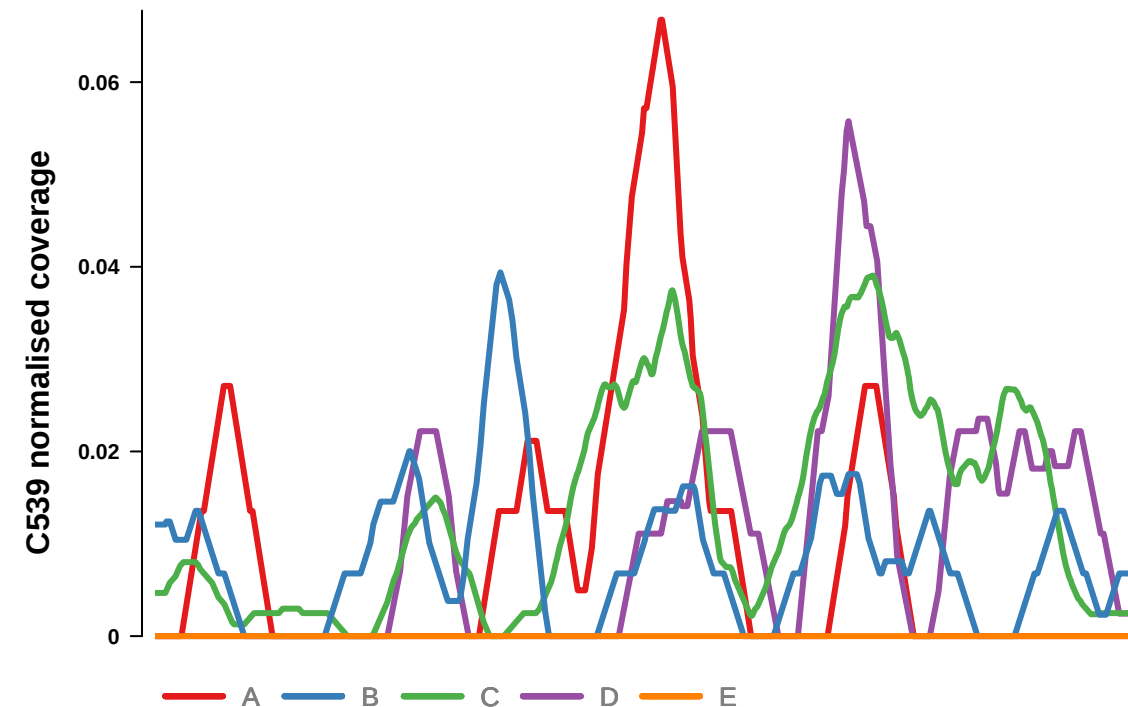


Putatively Subclonal (logFC = -1.93)

	P.	Adjusted P.
<i>~region vs. ~</i>	2.17e-02 *	7.18e-02
<i>~purity vs ~</i>	8.42e-01	8.78e-01
<i>~purity+region vs ~purity</i>	2.46e-03 **	3.88e-02 *
<i>Carcinoma vs. normal</i>	8.66e-03 **	8.66e-03 **

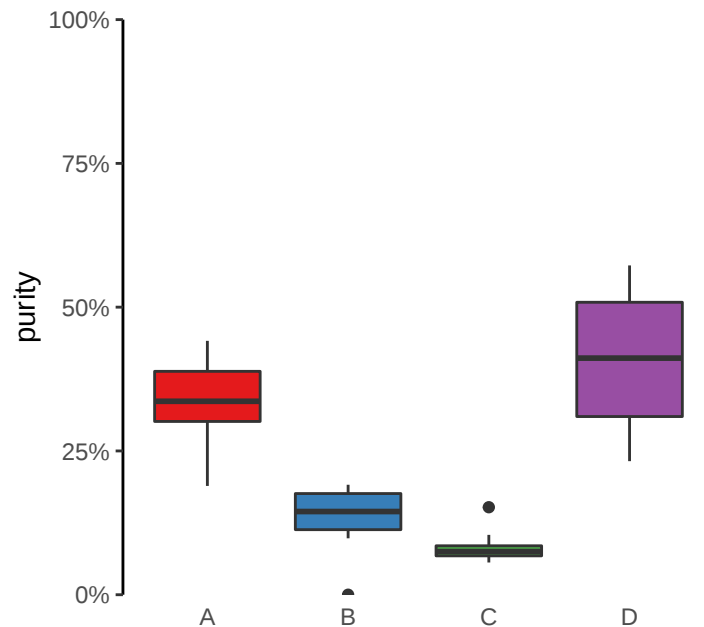


ANTXR2 (GH04J080057) enhancer loss
chr4:80058687–80059187

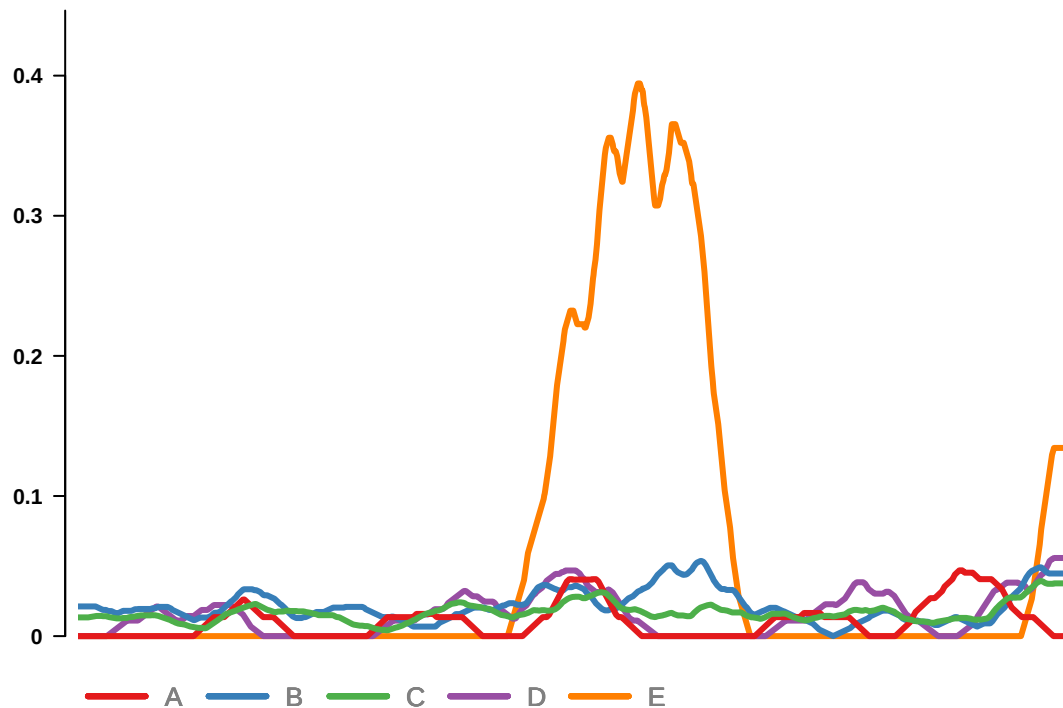


Putatively Subclonal (logFC = -0.68)

	P.	Adjusted P.
<i>~region vs. ~</i>	1.94e-05 ****	1.71e-04 ***
<i>~purity vs ~</i>	9.26e-04 ***	3.54e-03 **
<i>~purity+region vs ~purity</i>	1.65e-03 **	1.45e-02 *
<i>Carcinoma vs. normal</i>	NA	NA

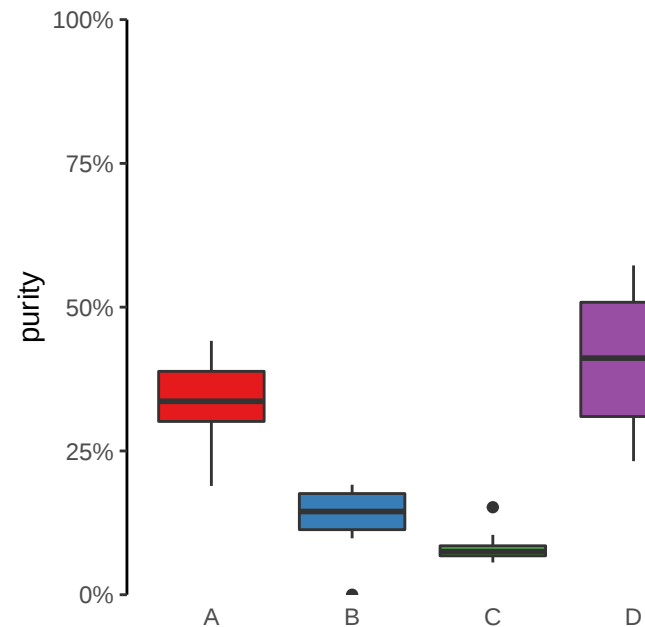


ENSG00000228035, NGF (GH01J115322) enhancer loss
chr1:115323237-115323737

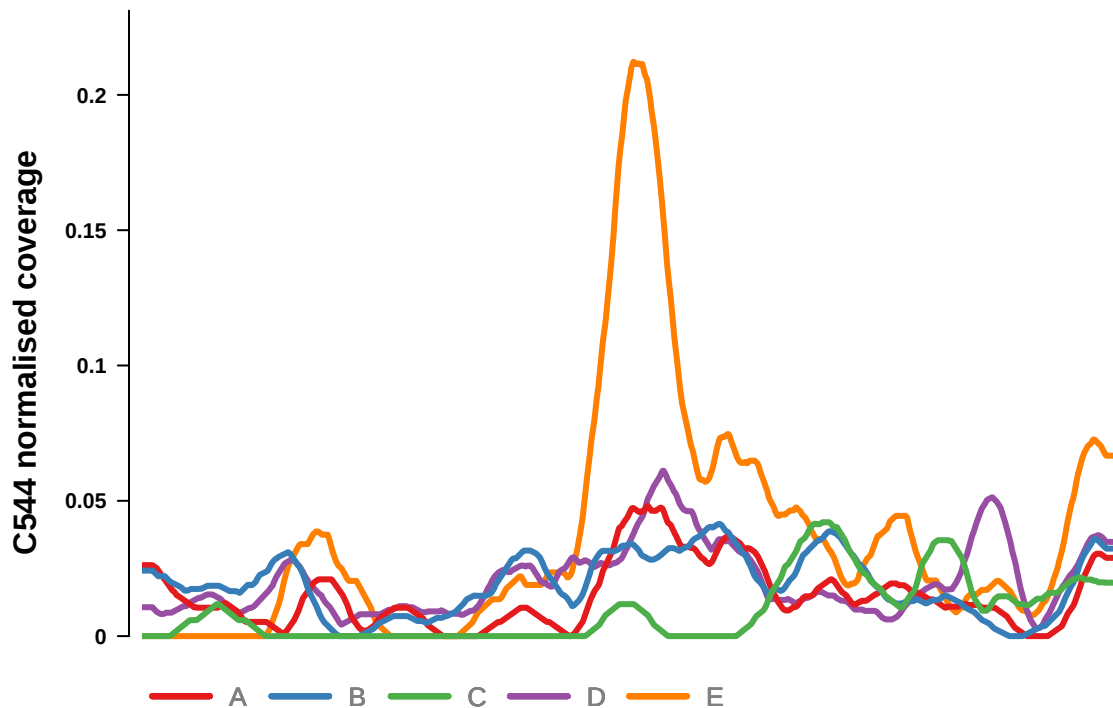


Putatively Subclonal (logFC = -0.46)

	P.	Adjusted P.
<i>~region vs. ~</i>	1.66e-06 ****	2.92e-05 ****
<i>~purity vs ~</i>	8.85e-05 ****	6.48e-04 ***
<i>~purity+region vs ~purity</i>	9.37e-03 **	4.35e-02 *
<i>Carcinoma vs. normal</i>	NA	NA

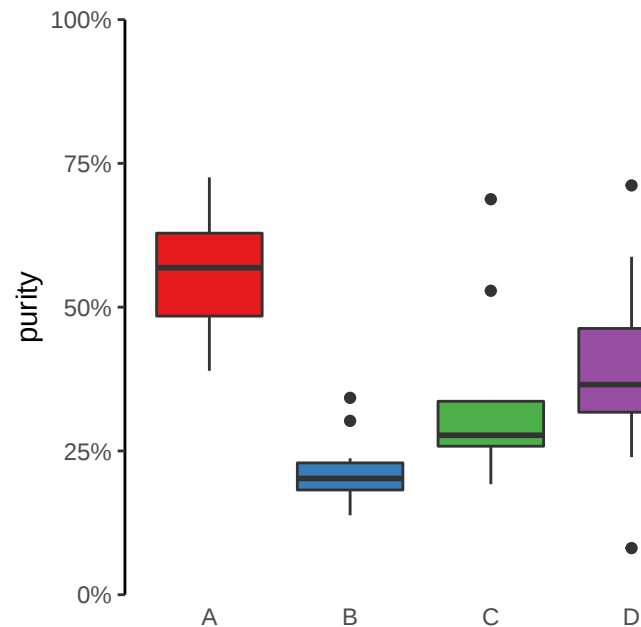


ENSG00000228035, NGF (GH01J115322) enhancer loss
chr1:115323237-115323737

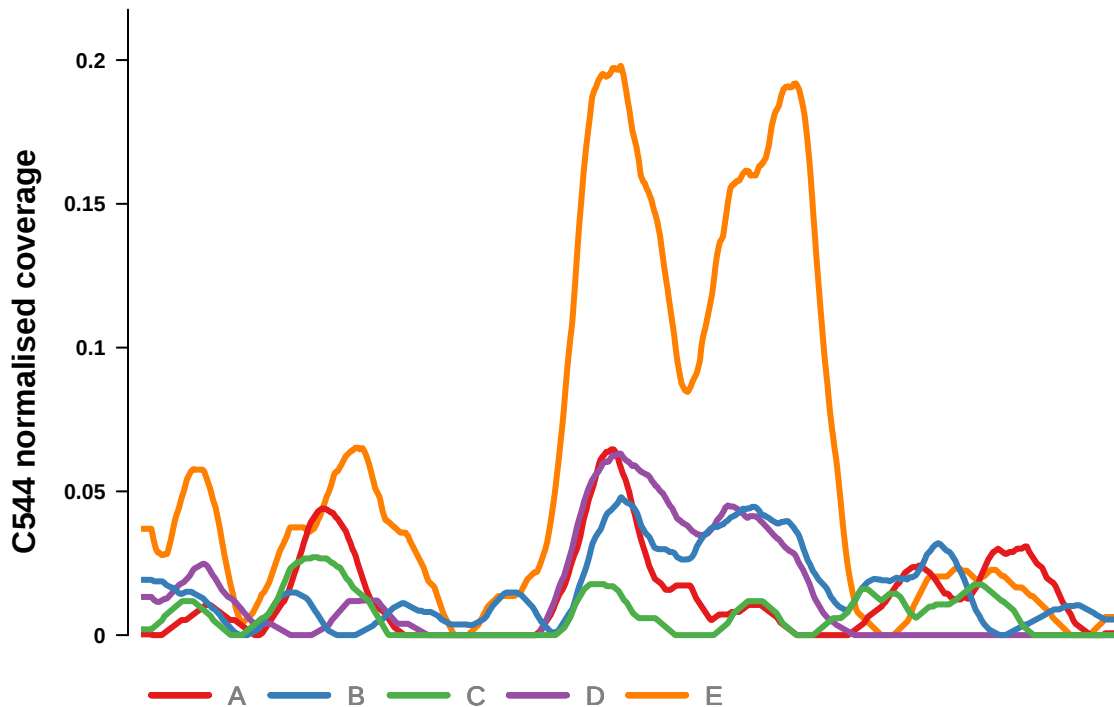


Putatively Subclonal (logFC = -0.7)

	P.	Adjusted P.
~region vs. ~	1.53e-03 **	7.73e-03 **
~purity vs ~	4.64e-01	6.09e-01
~purity+region vs ~purity	1.75e-04 ***	9.1e-03 **
Carcinoma vs. normal	NA	NA

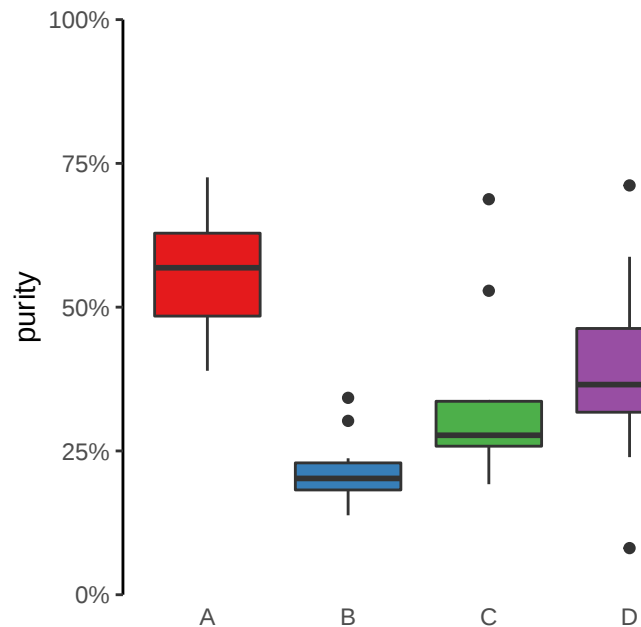


FABP1, THNSL2 (GH02J088144) enhancer loss chr2:88144817-88145317

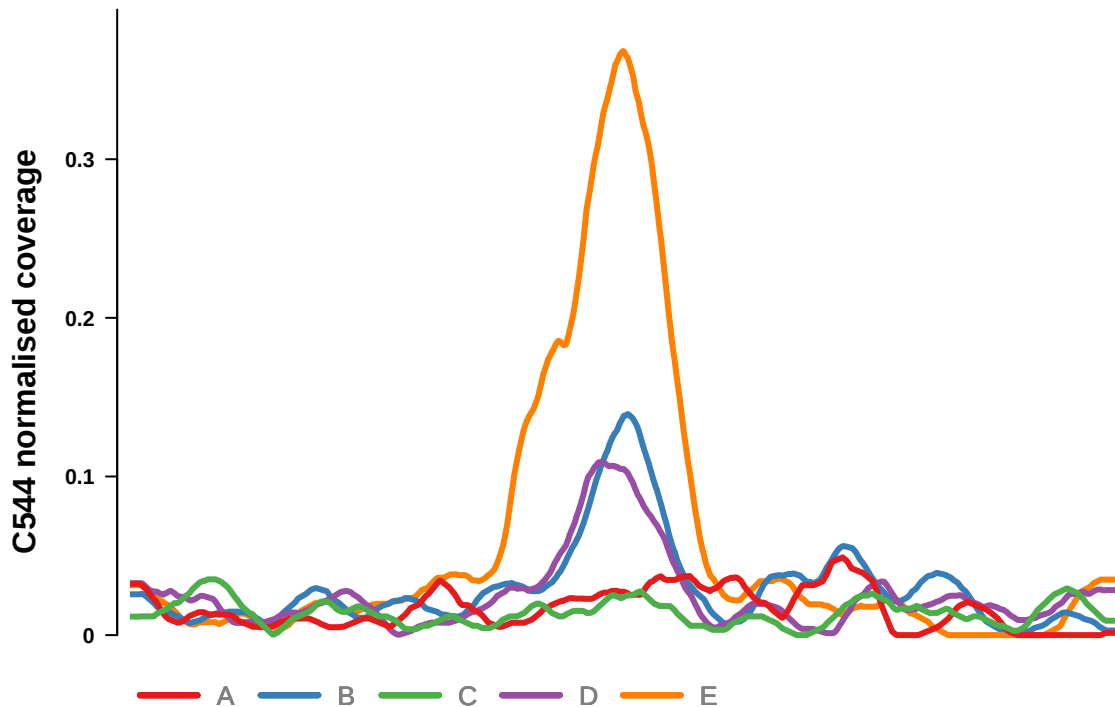


Putatively Subclonal (logFC = -1.25)

	P.	Adjusted P.
<i>~region vs. ~</i>	5.88e-03 **	2.06e-02 *
<i>~purity vs ~</i>	8.86e-01	9.1e-01
<i>~purity+region vs ~purity</i>	4.97e-03 **	2.83e-02 *
<i>Carcinoma vs. normal</i>	8.04e-02	8.04e-02

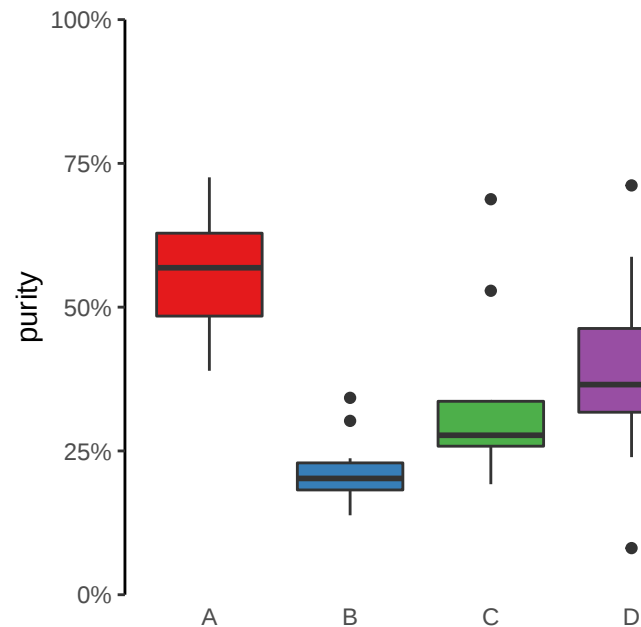


FAM83G (GH17J019010) enhancer loss
chr17:19011073–19011573



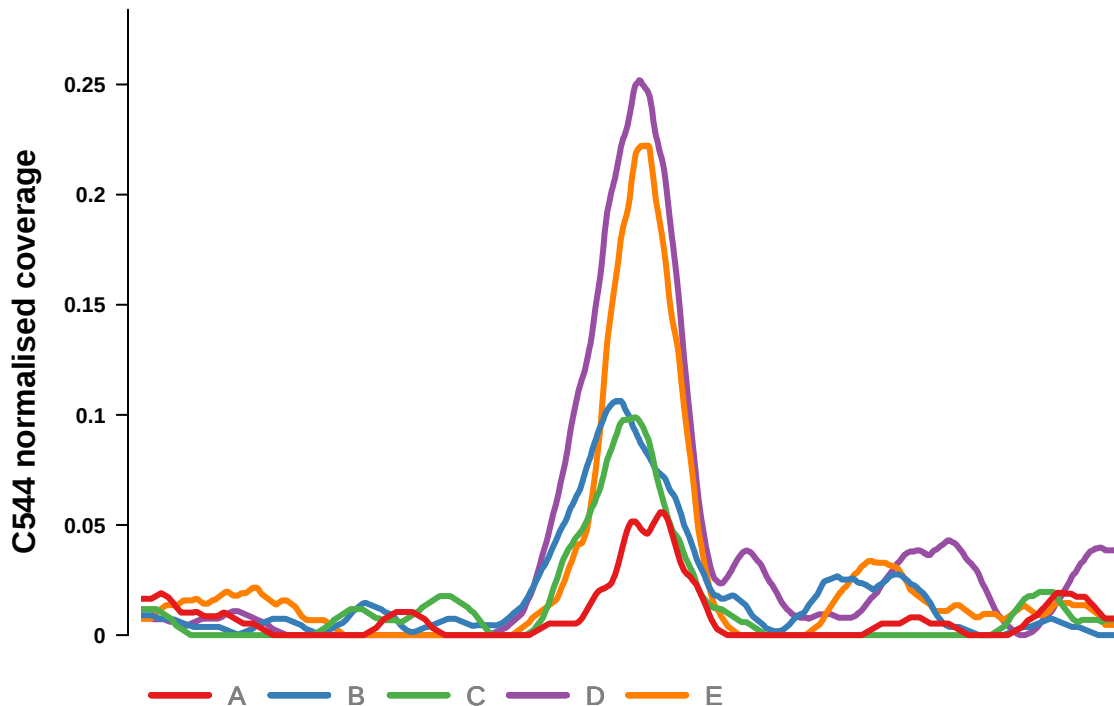
Putatively Subclonal (logFC = -1.51)

	P.	Adjusted P.
<i>~region vs. ~</i>	3.46e-03 **	1.6e-02 *
<i>~purity vs ~</i>	1.97e-01	3.54e-01
<i>~purity+region vs ~purity</i>	9.87e-03 **	4.65e-02 *
<i>Carcinoma vs. normal</i>	3.3e-02 *	3.3e-02 *



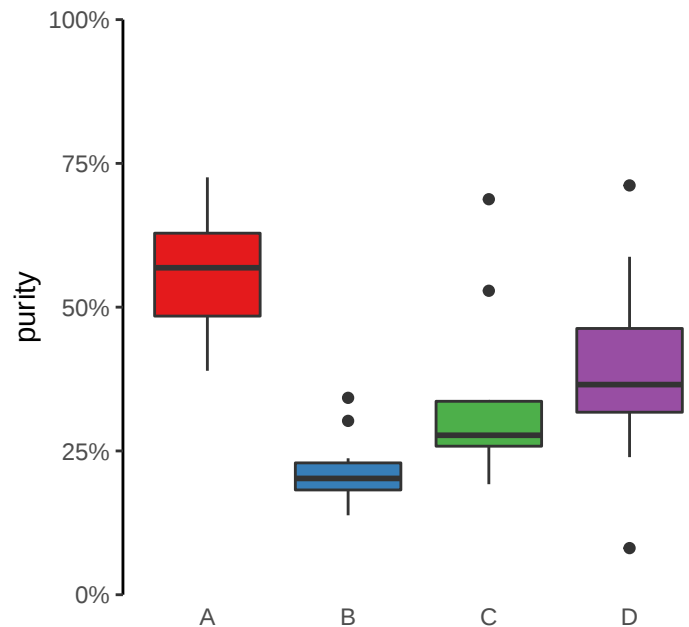
HMGN2, ARID1A, PIGV (GH01J026739) enhancer loss

chr1:26743976-26744476

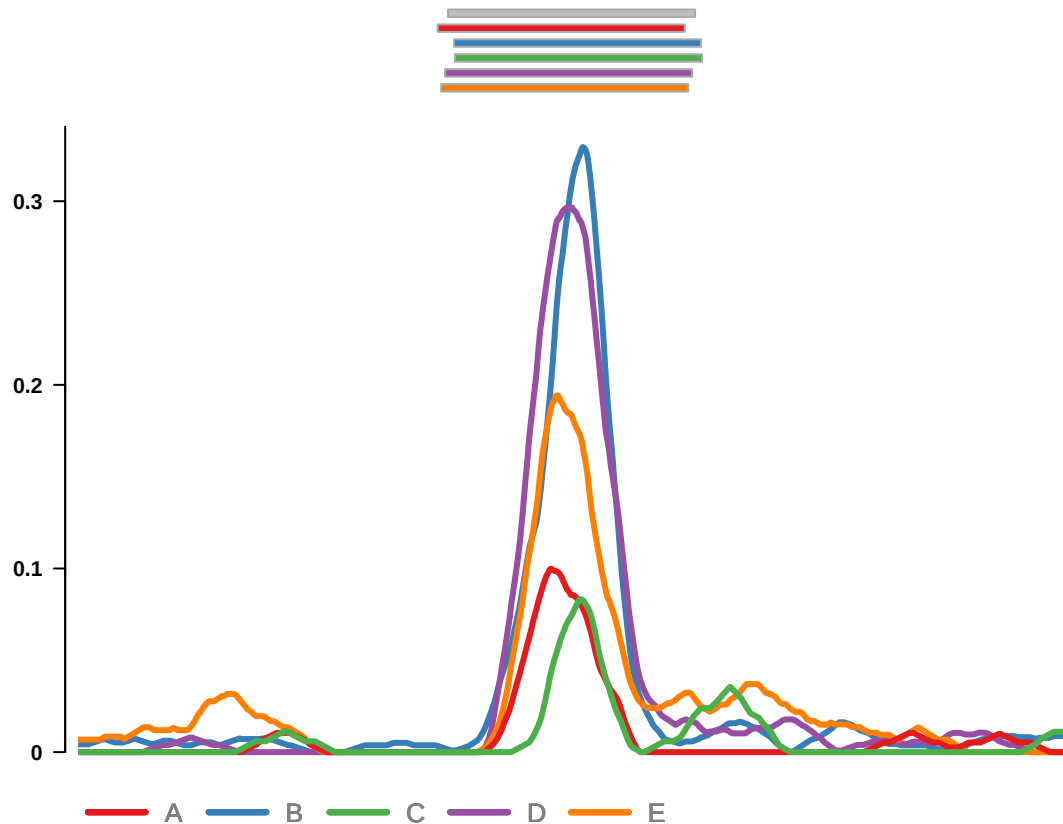


Putatively Subclonal (logFC = -1.72)

	P.	Adjusted P.
<i>~region vs. ~</i>	1.19e-03 **	6.55e-03 **
<i>~purity vs ~</i>	1.6e-02 *	7.18e-02
<i>~purity+region vs ~purity</i>	1.02e-02 *	4.65e-02 *
<i>Carcinoma vs. normal</i>	1.62e-02 *	1.62e-02 *

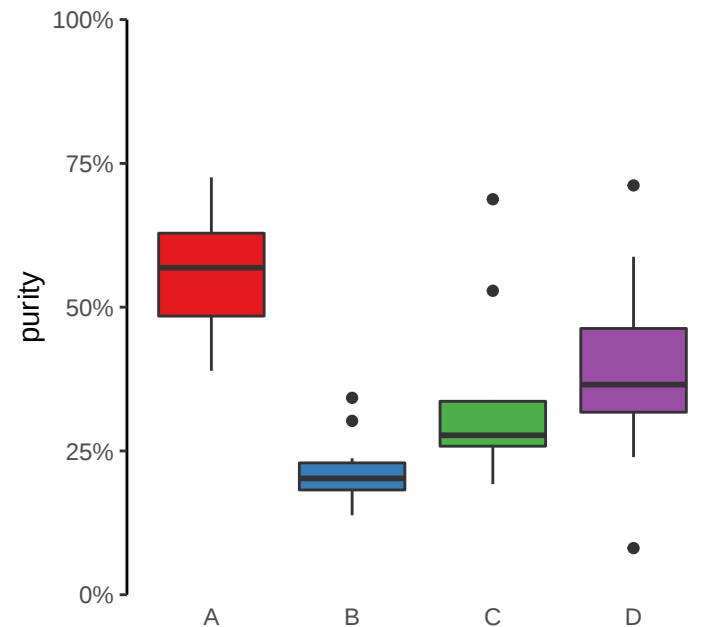


ZNF431 (GH19J020999) enhancer loss chr19:20999605–21000105



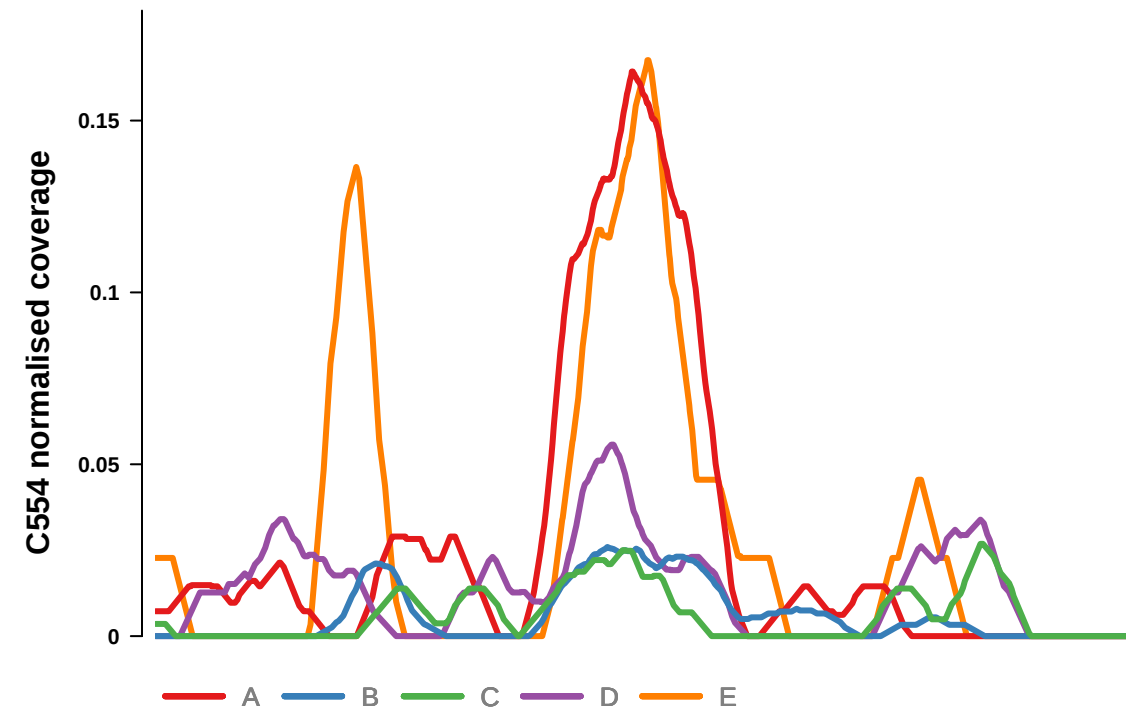
Putatively Subclonal (logFC = -1.01)

	P.	Adjusted P.
<i>~region vs. ~</i>	2.72e-05 ****	3.48e-04 ***
<i>~purity vs ~</i>	6.29e-03 **	3.4e-02 *
<i>~purity+region vs ~purity</i>	1.1e-03 **	1.17e-02 *
<i>Carcinoma vs. normal</i>	1.49e-01	1.49e-01



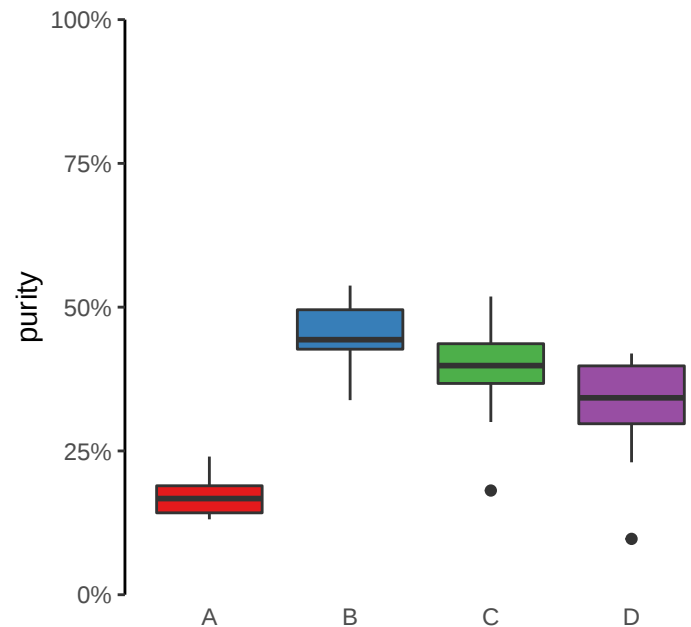
CLASP2, ENSG00000271324 (GH03J033790) enhancer loss

chr3:33791629-33792129



Putatively Subclonal (logFC = -2.18)

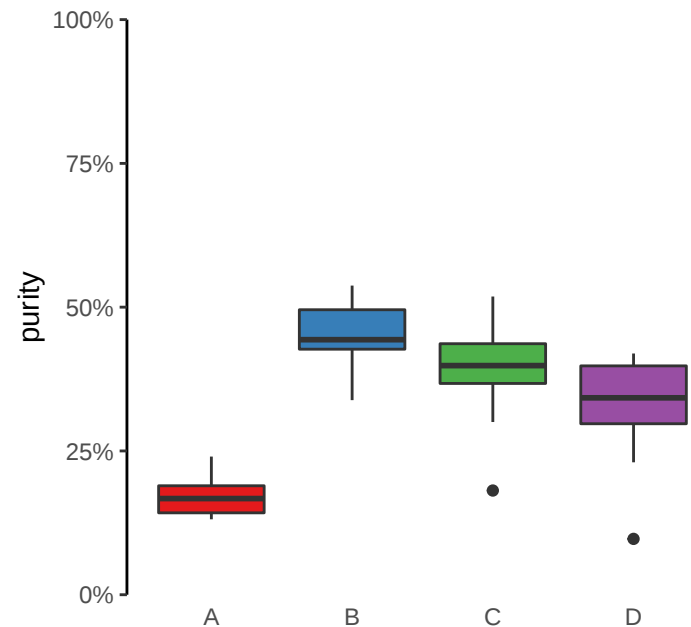
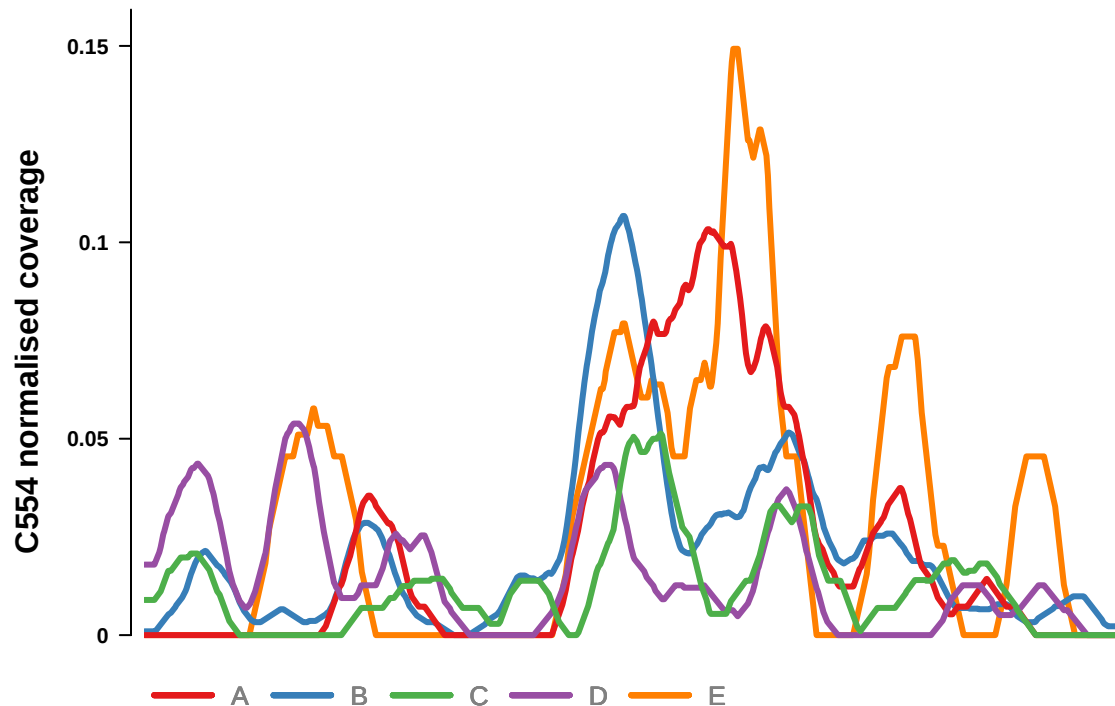
	P.	Adjusted P.
<i>~region vs. ~</i>	1.53e-03 **	7.35e-03 **
<i>~purity vs ~</i>	2.42e-02 *	9.72e-02
<i>~purity+region vs ~purity</i>	1.12e-02 *	4.35e-02 *
<i>Carcinoma vs. normal</i>	2.41e-03 **	2.41e-03 **



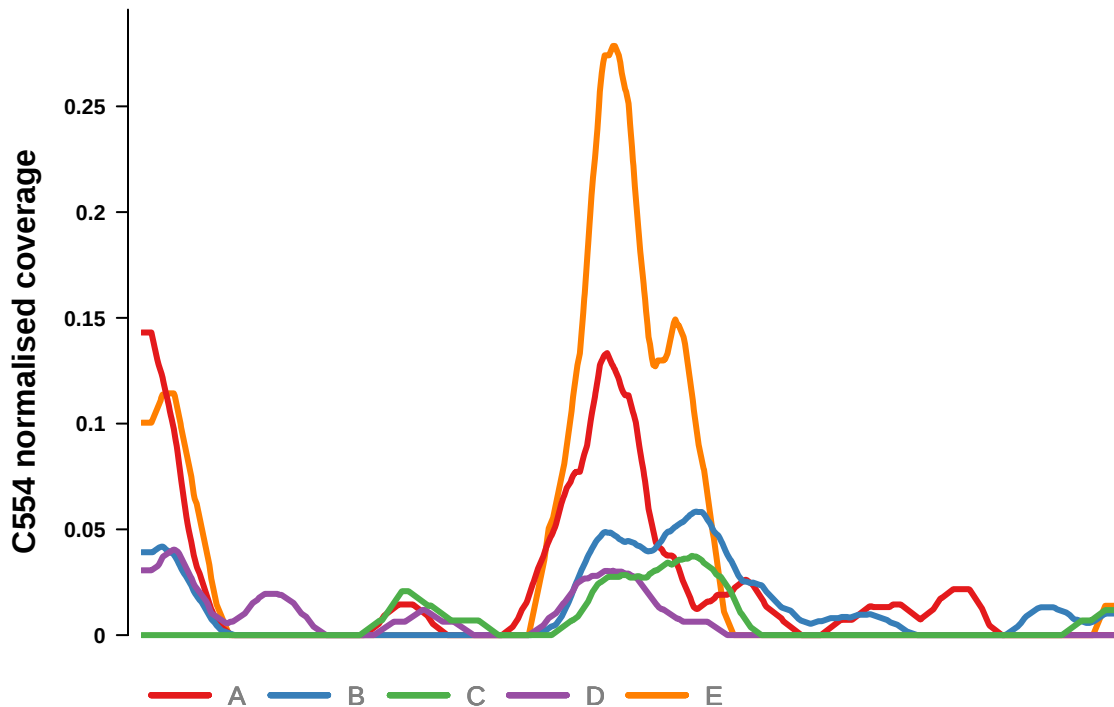
FABP1, THNSL2 (GH02J088144) enhancer loss
chr2:88144817–88145317

Putatively Subclonal (logFC = -0.86)

	P.	Adjusted P.
<i>~region vs. ~</i>	3.08e-03 **	1.05e-02 *
<i>~purity vs ~</i>	6.67e-01	7.93e-01
<i>~purity+region vs ~purity</i>	3.78e-03 **	2.79e-02 *
<i>Carcinoma vs. normal</i>	NA	NA

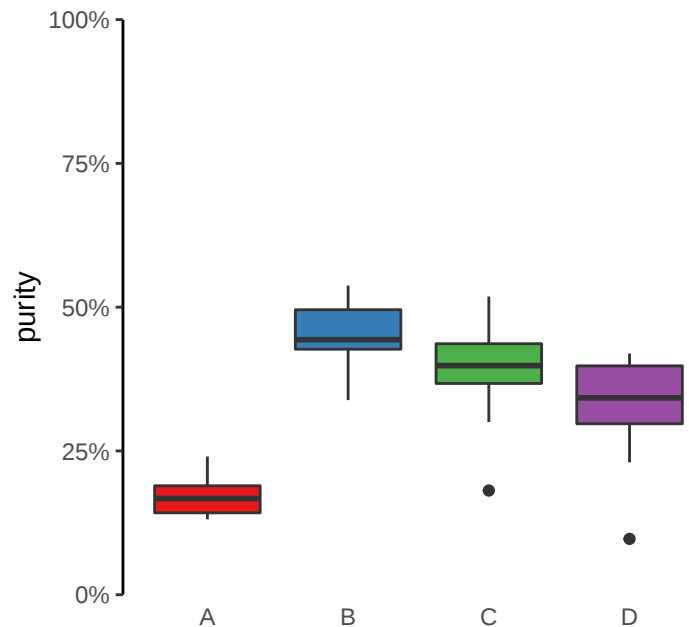


PPP2CB (GH08J030800) enhancer loss
chr8:30804244–30804744



Putatively Subclonal (logFC = -1.19)

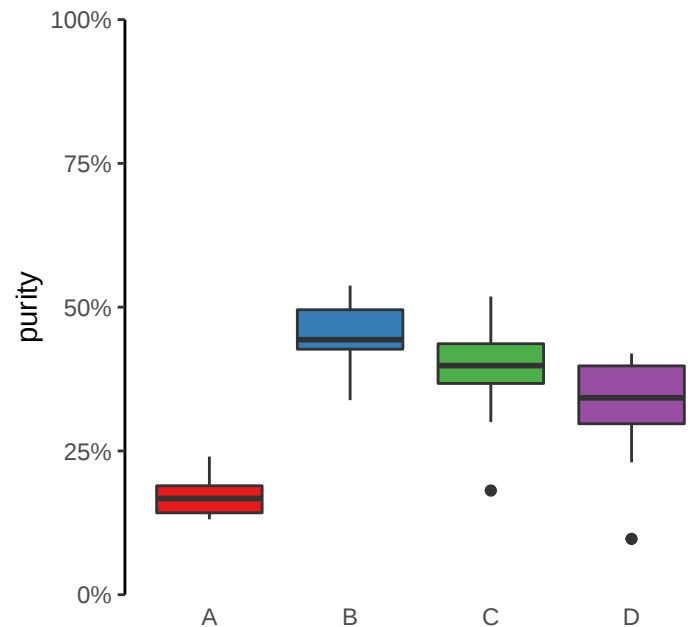
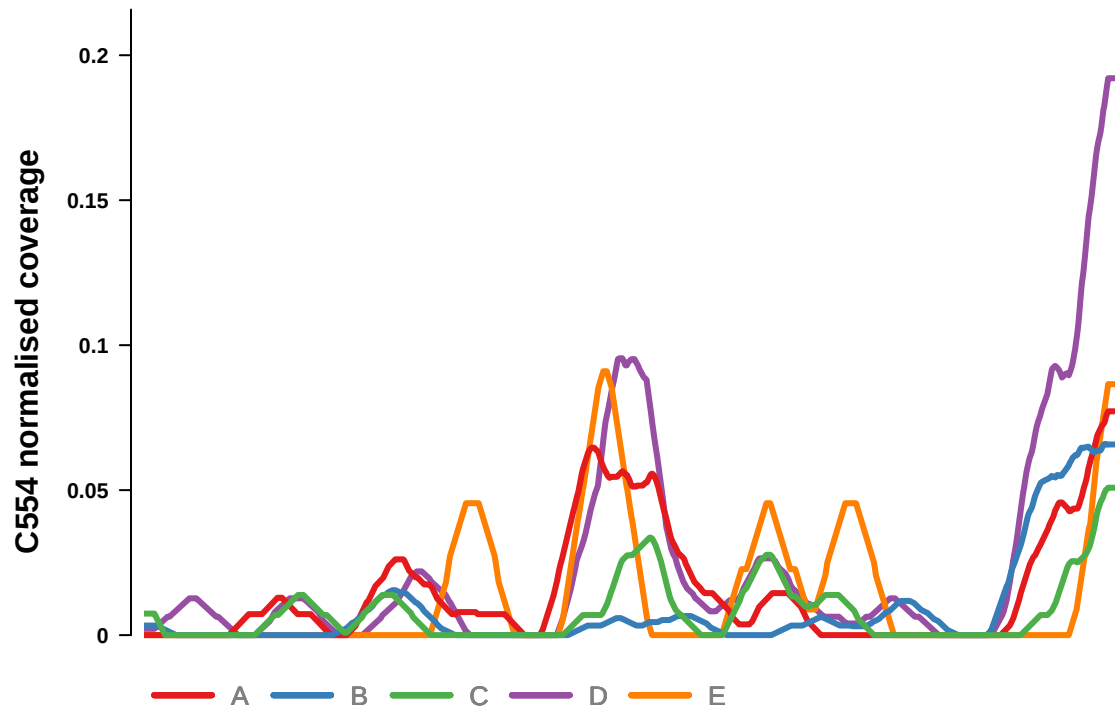
	P.	Adjusted P.
<i>~region vs. ~</i>	1.06e-02 *	3.1e-02 *
<i>~purity vs ~</i>	9.09e-01	9.43e-01
<i>~purity+region vs ~purity</i>	9.43e-03 **	3.88e-02 *
<i>Carcinoma vs. normal</i>	8.76e-02	8.76e-02



PPP3CA (GH04J101183) enhancer loss
chr4:101183634-101184134

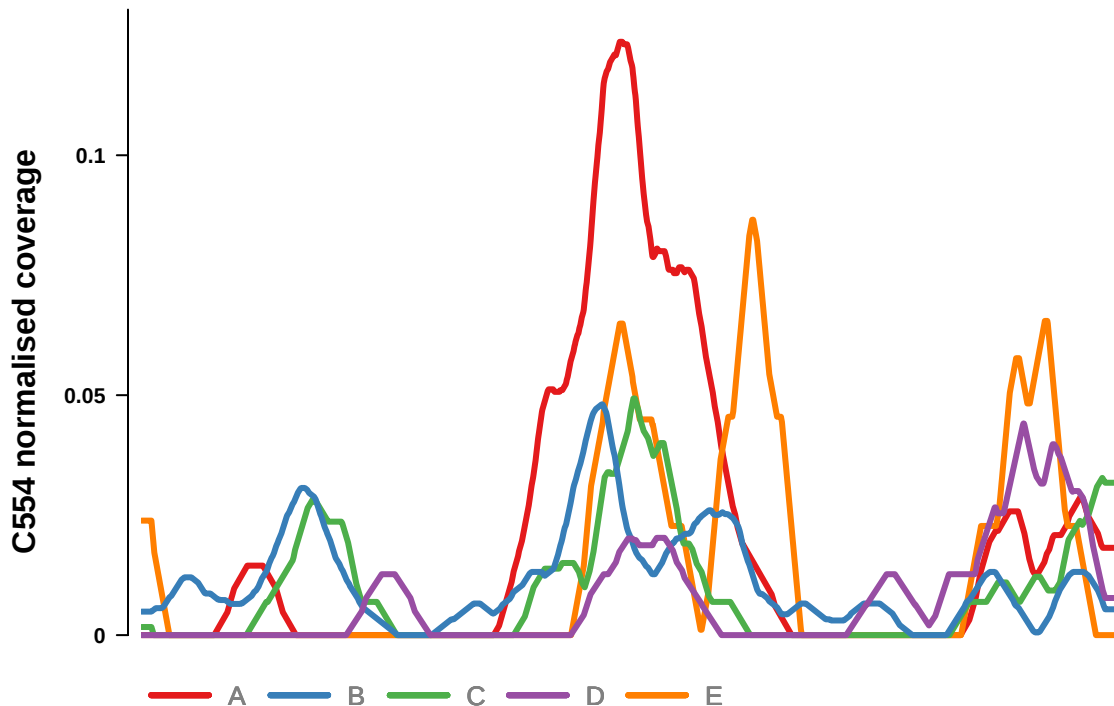
Putatively Subclonal (logFC = -2.31)

	P.	Adjusted P.
~region vs. ~	5.81e-04 ***	3.17e-03 **
~purity vs ~	1.8e-01	3.72e-01
~purity+region vs ~purity	2.09e-03 **	1.9e-02 *
Carcinoma vs. normal	3.22e-03 **	3.22e-03 **



STAG1, RNU6-789P (GH03J136616) enhancer loss

chr3:136617156-136617656



Putatively Subclonal (logFC = -1.45)

	P.	Adjusted P.
~region vs. ~	4.69e-04 ***	2.75e-03 **
~purity vs ~	3.06e-01	5.23e-01
~purity+region vs ~purity	1.02e-03 **	1.08e-02 *
Carcinoma vs. normal	3.84e-02 *	3.84e-02 *

