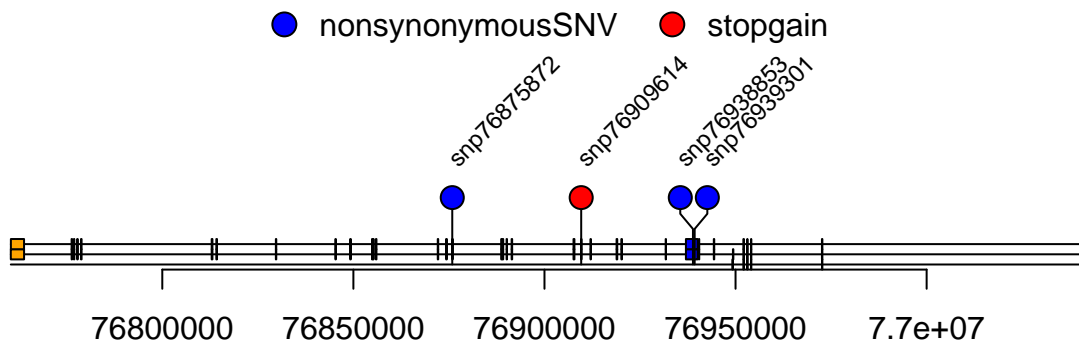
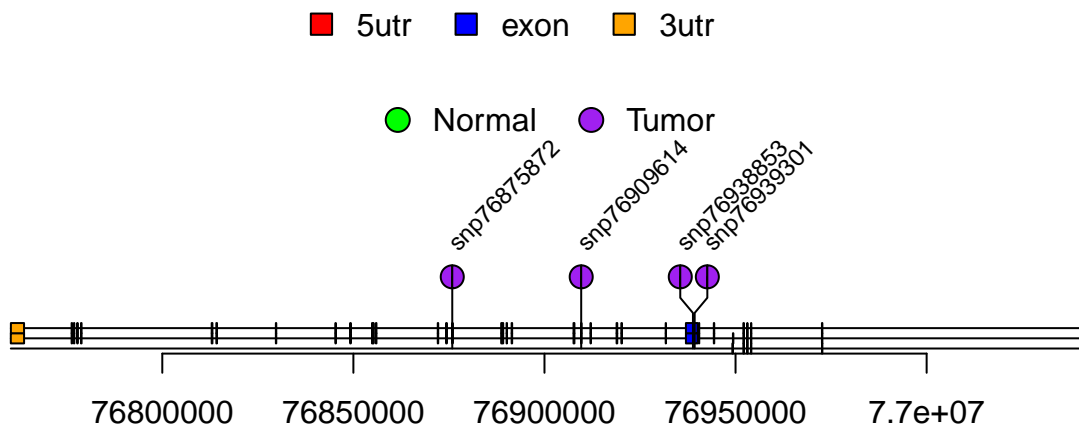


SNP



normal & tumor amount



5utr exon 3utr

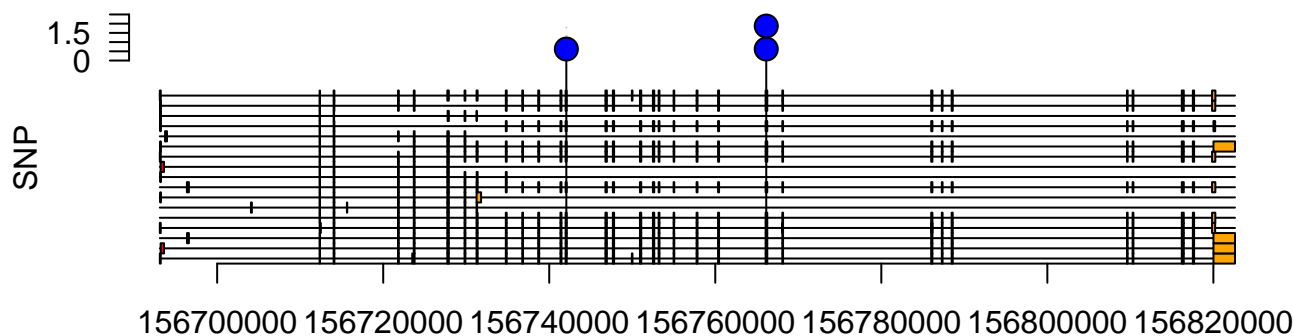
ATRX – Chr.23

Input data set used for plotting gene ATRX

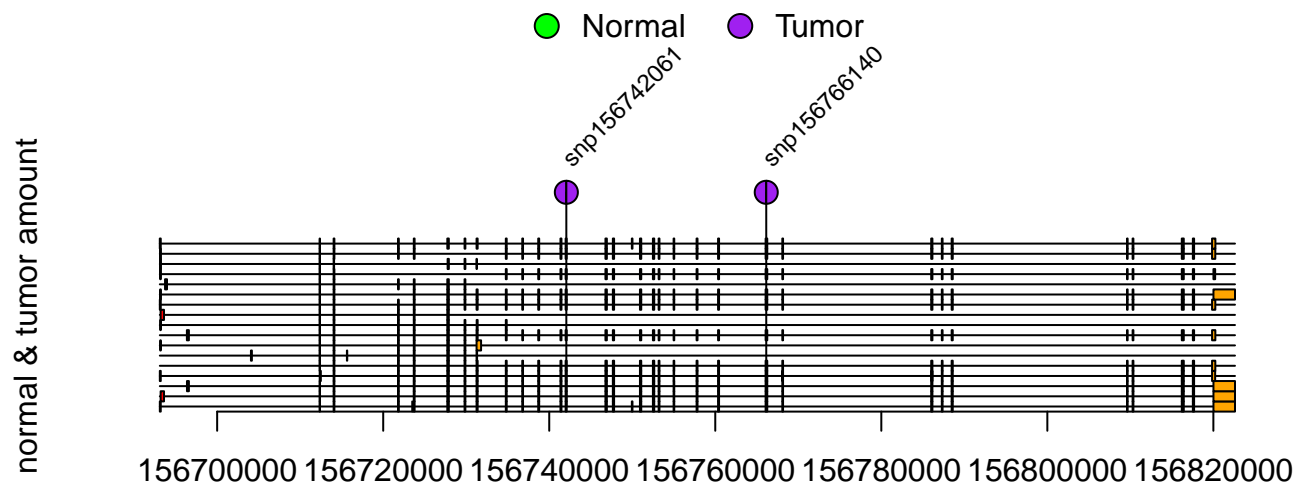
(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	ch15	ch13	r9t	r14t
ATRX_76875872_G_C_nonsynonymousSNV_NONE_.	0.8156	0	0	0
ATRX_76909614_G_A_stopgain_NONE_.	0	0.3556	0	0
ATRX_76938853_T_C_nonsynonymousSNV_EXON_.	0	0	0.0635	0
ATRX_76939301_G_C_nonsynonymousSNV_EXON_.	0	0	0	0.2898

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
ATRX_76875872_G_C_nonsynonymousSNV_NONE_.	ATRX	nonsynonymousSNV	76875872	1	blue	0	1
ATRX_76909614_G_A_stopgain_NONE_.	ATRX	stopgain	76909614	1	red	0	1
ATRX_76938853_T_C_nonsynonymousSNV_EXON_.	ATRX	nonsynonymousSNV	76938853	1	blue	0	1
ATRX_76939301_G_C_nonsynonymousSNV_EXON_.	ATRX	nonsynonymousSNV	76939301	1	blue	0	1



5utr exon 3utr



5utr exon 3utr

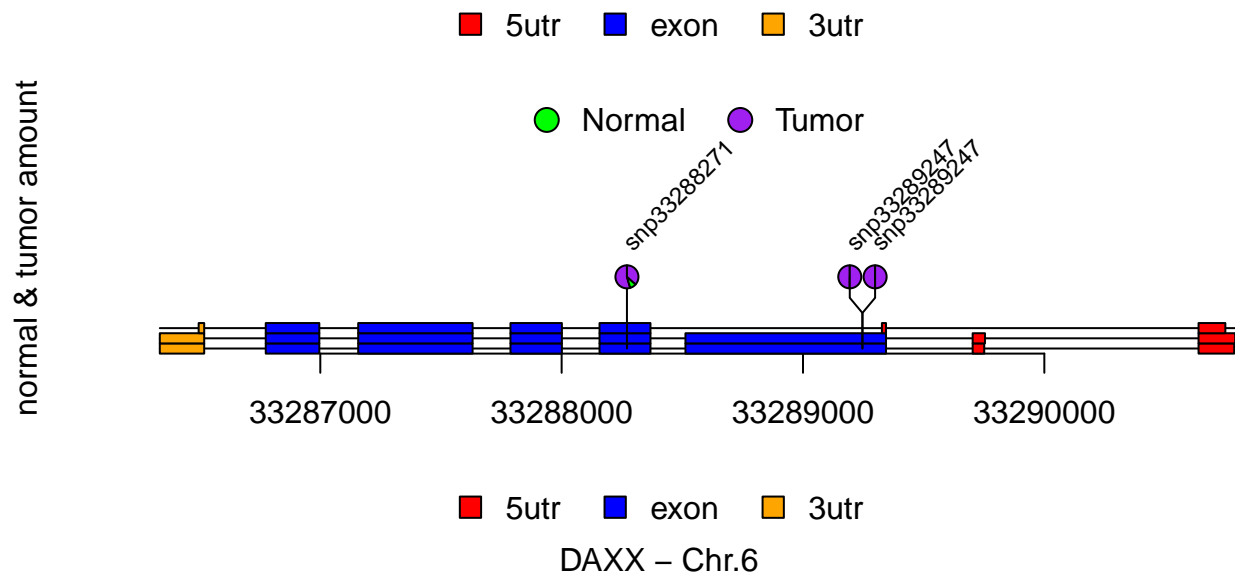
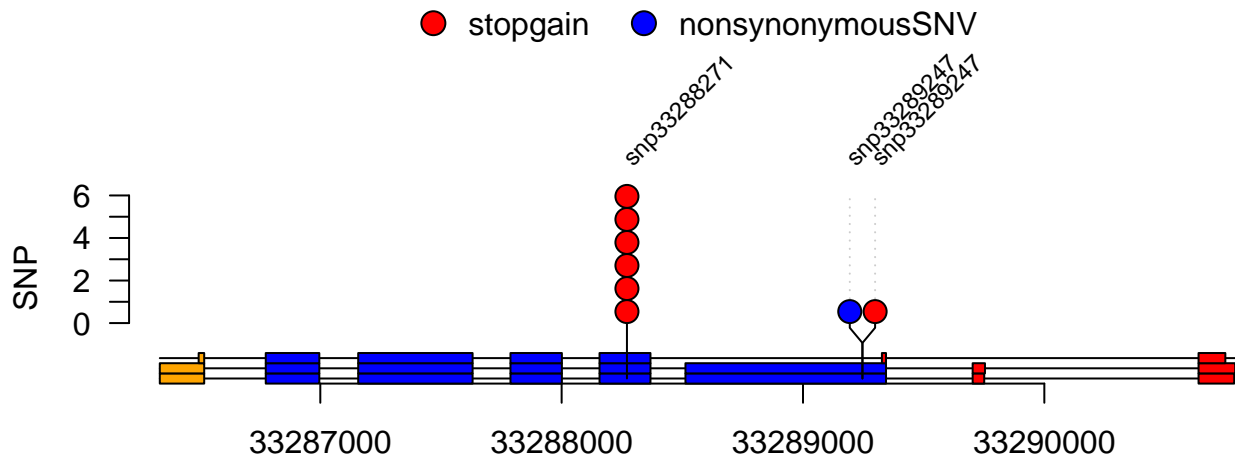
Input data set used for plotting gene CYFIP2

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	r20t	r8t	r19t
CYFIP2_156742061_C_T_nonsynonymousSNV_DOWNSTREAM_	0.0552	0	0
CYFIP2_156766140_G_A_nonsynonymousSNV_DOWNSTREAM_	0	0.3816	0.3816

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
CYFIP2_156742061_C_T_nonsynonymousSNV_DOWNSTREAM_	CYFIP2	nonsynonymousSNV	156742061	1	blue	0	1
CYFIP2_156766140_G_A_nonsynonymousSNV_DOWNSTREAM_	CYFIP2	nonsynonymousSNV	156766140	2	blue	0	2

Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda

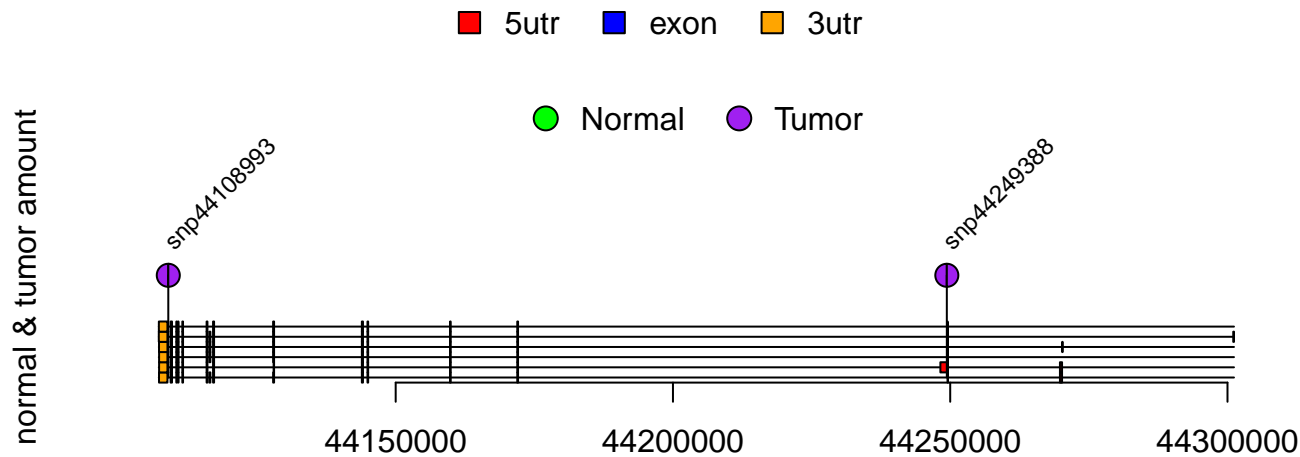
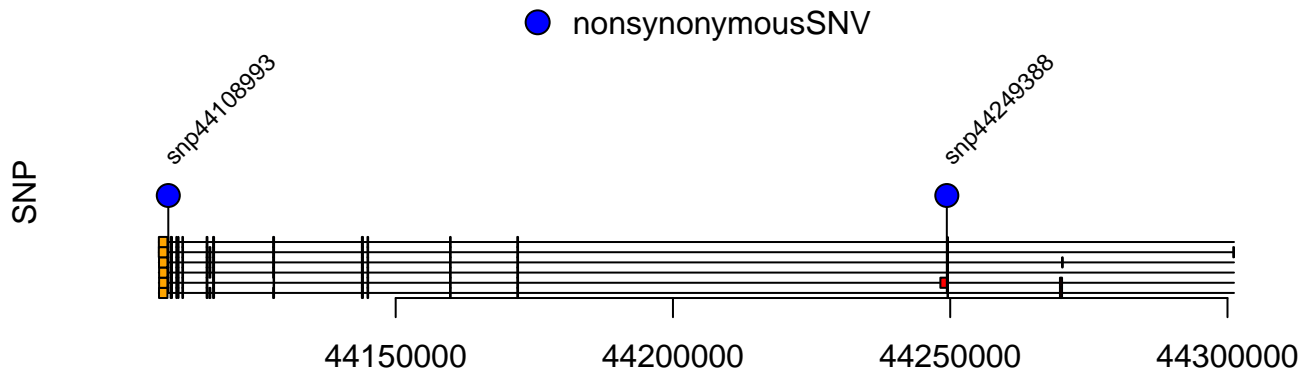


Input data set used for plotting gene DAXX

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	ch13	r3t	r5t	r4n	b1	r1t	ch7	r4t
DAXX_33288271_A_C_stopgain_DOWNSTREAM_	0.0763	0.4883	0.3262	0.168	0.1086	0.3333	0	0
DAXX_33289247_G_A_nonsynonymousSNV_DOWNSTREAM_	0	0	0	0	0	0	0.6103	0
DAXX_33289247_G_T_stopgain_DOWNSTREAM_	0	0	0	0	0	0	0	0.4555

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
DAXX_33288271_A_C_stopgain_DOWNSTREAM_	DAXX	stopgain	33288271	6	red	1	4
DAXX_33289247_G_A_nonsynonymousSNV_DOWNSTREAM_	DAXX	nonsynonymousSNV	33289247	1	blue	0	1
DAXX_33289247_G_T_stopgain_DOWNSTREAM_	DAXX	stopgain	33289247	1	red	0	1



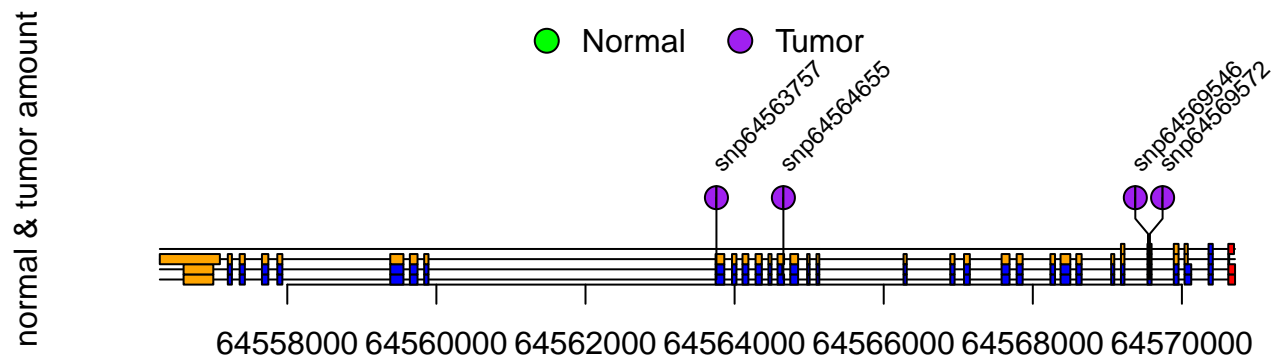
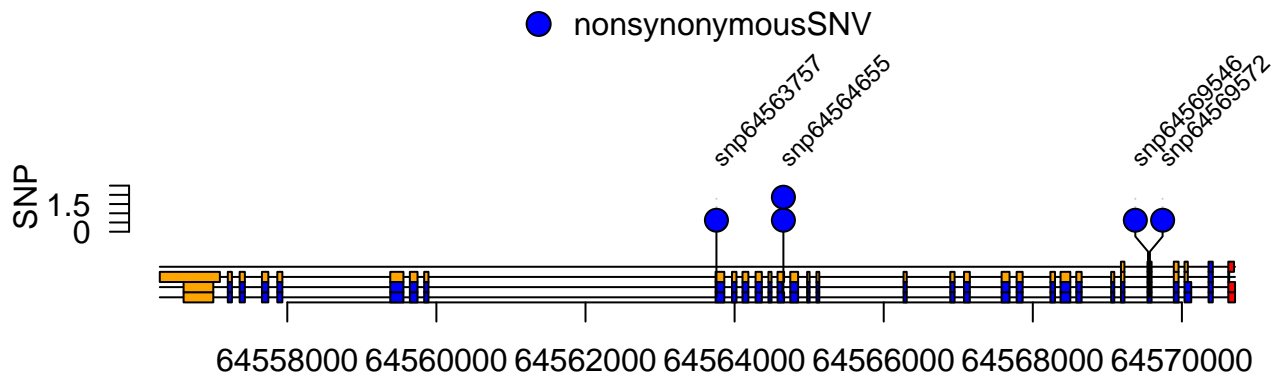
Input data set used for plotting gene KANSL1

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	r9t	b12
KANSL1_44108993_G_A_nonsynonymousSNV_DOWNSTREAM_	0.4727	0
KANSL1_44249388_T_C_nonsynonymousSNV_NON_SYNONYMOUS_CODING_N41S	0	0.2336

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
KANSL1_44108993_G_A_nonsynonymousSNV_DOWNSTREAM_	KANSL1	nonsynonymousSNV	44108993	1	blue	0	1
KANSL1_44249388_T_C_nonsynonymousSNV_NON_SYNONYMOUS_CODING_N41S	KANSL1	nonsynonymousSNV	44249388	1	blue	0	1

Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda



MAP4K2 – Chr.11

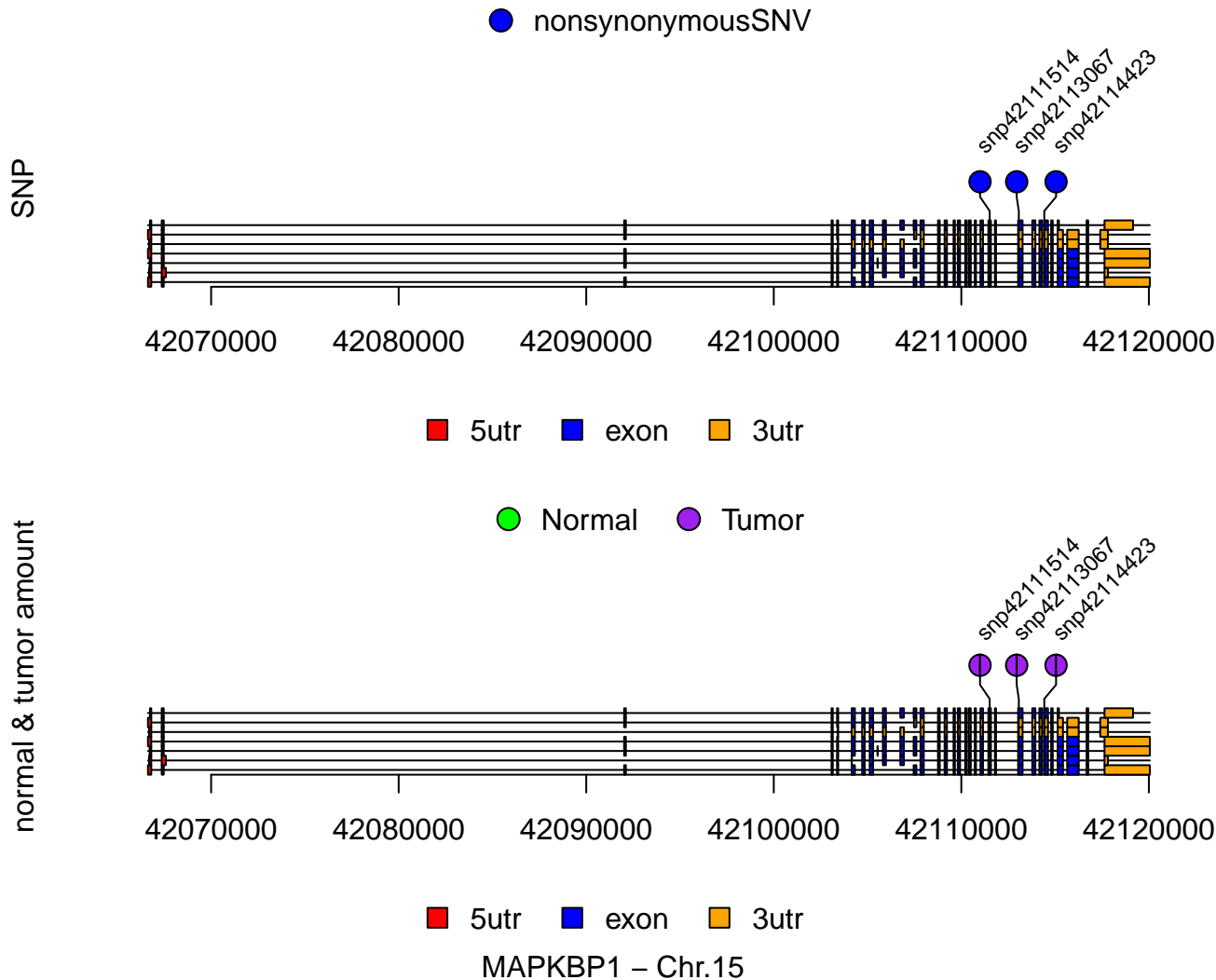
Input data set used for plotting gene MAP4K2

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	r8t	r19t	b13	b8
MAP4K2_64563757_C_T_nonsynonymousSNV_DOWNSTREAM_.	0	0	0.9104	0
MAP4K2_64564655_G_T_nonsynonymousSNV_DOWNSTREAM_.	0.6896	0.6896	0	0
MAP4K2_64569546_C_A_nonsynonymousSNV_DOWNSTREAM_.	0	0	0.7769	0
MAP4K2_64569572_C_G_nonsynonymousSNV_DOWNSTREAM_.	0	0	0	0.5062

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
MAP4K2_64563757_C_T_nonsynonymousSNV_DOWNSTREAM_.	MAP4K2	nonsynonymousSNV	64563757	1	blue	0	1
MAP4K2_64564655_G_T_nonsynonymousSNV_DOWNSTREAM_.	MAP4K2	nonsynonymousSNV	64564655	2	blue	0	2
MAP4K2_64569546_C_A_nonsynonymousSNV_DOWNSTREAM_.	MAP4K2	nonsynonymousSNV	64569546	1	blue	0	1
MAP4K2_64569572_C_G_nonsynonymousSNV_DOWNSTREAM_.	MAP4K2	nonsynonymousSNV	64569572	1	blue	0	1

Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda

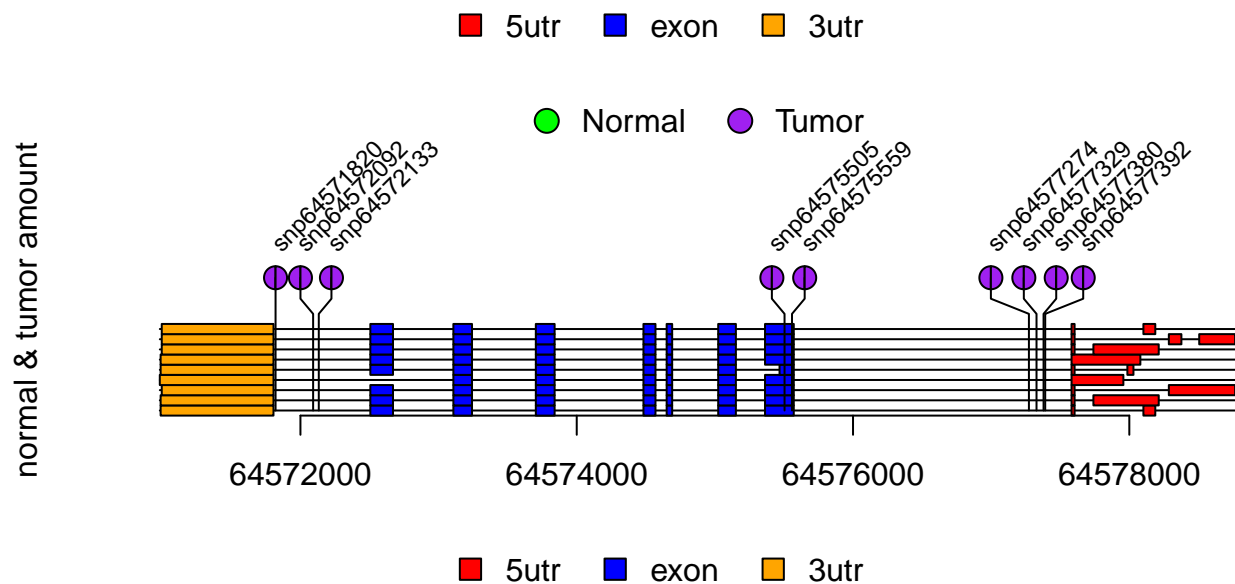
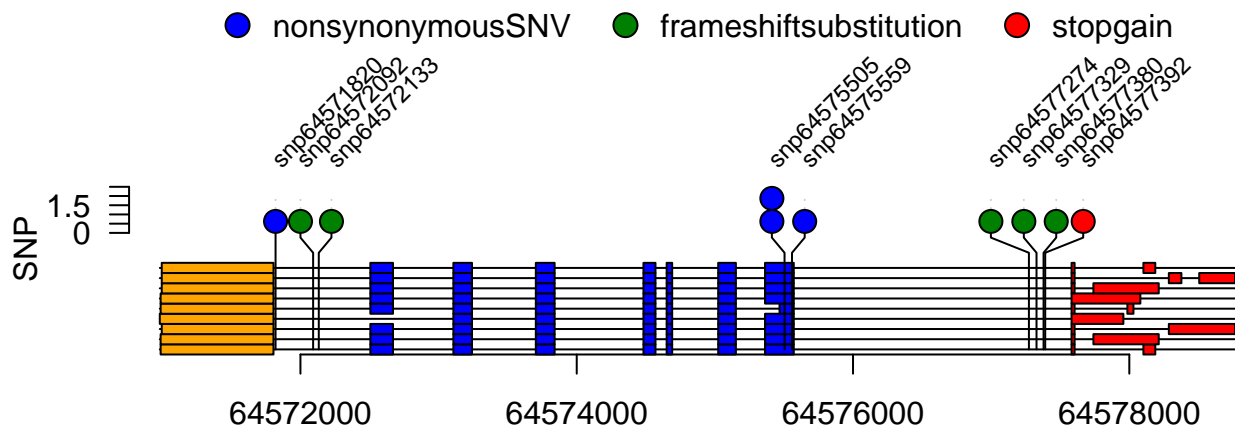


Input data set used for plotting gene MAPKBP1
(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	r5t	r7t	b16
MAPKBP1_42111514_G_A_nonsynonymousSNV_DOWNSTREAM_.	0	0.3087	0
MAPKBP1_42113067_C_A_nonsynonymousSNV_DOWNSTREAM_.	0.135	0	0
MAPKBP1_42114423_A_C_nonsynonymousSNV_DOWNSTREAM_.	0	0	0.3747

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
MAPKBP1_42111514_G_A_nonsynonymousSNV_DOWNSTREAM_.	MAPKBP1	nonsynonymousSNV	42111514	1	blue	0	1
MAPKBP1_42113067_C_A_nonsynonymousSNV_DOWNSTREAM_.	MAPKBP1	nonsynonymousSNV	42113067	1	blue	0	1
MAPKBP1_42114423_A_C_nonsynonymousSNV_DOWNSTREAM_.	MAPKBP1	nonsynonymousSNV	42114423	1	blue	0	1

Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda



MEN1 – Chr.11

Input data set used for plotting gene MEN1

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	ch15	r20t	ch7	b8	r2t	r10t	ch1	ch19	r17t	r15t
MEN1_64571820_G_A_nonsynonymousSNV_DOWNSTREAM_.	0	0.0593	0	0	0	0	0	0	0	0
MEN1_64572092_C_CG_frameshiftsubstitution_DOWNSTREAM_.	0	0	0	0	0.0672	0	0	0	0	0
MEN1_64572133_CT_C_frameshiftsubstitution_DOWNSTREAM_.	0	0	0	0	0	0.2016	0	0	0	0
MEN1_64575505_C_T_nonsynonymousSNV_DOWNSTREAM_.	0	0	0	0	0	0	0.4581	0.5033	0	0
MEN1_64575559_T_A_nonsynonymousSNV_DOWNSTREAM_.	0	0	0	0	0	0	0	0	0.2648	0
MEN1_64577274_AG_A_frameshiftsubstitution_UPSTREAM_.	0	0	0.6511	0	0	0	0	0	0	0
MEN1_64577329_TAGAC_T_frameshiftsubstitution_UPSTREAM_.	0.0995	0	0	0	0	0	0	0	0	0
MEN1_64577380_C_CG_frameshiftsubstitution_FRAME_SHIFT_P67P?	0	0	0	0	0	0	0	0	0	0.1513
MEN1_64577392_G_A_stopgain_STOP_GAINED_Q64*	0	0	0	0.3592	0	0	0	0	0	0

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
MEN1_64571820_G_A_nonsynonymousSNV_DOWNSTREAM_.	MEN1	nonsynonymousSNV	64571820	1	blue	0	1
MEN1_64572092_C_CG_frameshiftsubstitution_DOWNSTREAM_.	MEN1	frameshiftsubstitution	64572092	1	#008000	0	1
MEN1_64572133_CT_C_frameshiftsubstitution_DOWNSTREAM_.	MEN1	frameshiftsubstitution	64572133	1	#008000	0	1
MEN1_64575505_C_T_nonsynonymousSNV_DOWNSTREAM_.	MEN1	nonsynonymousSNV	64575505	2	blue	0	2
MEN1_64575559_T_A_nonsynonymousSNV_DOWNSTREAM_.	MEN1	nonsynonymousSNV	64575559	1	blue	0	1
MEN1_64577274_AG_A_frameshiftsubstitution_UPSTREAM_.	MEN1	frameshiftsubstitution	64577274	1	#008000	0	1
MEN1_64577329_TAGAC_T_frameshiftsubstitution_UPSTREAM_.	MEN1	frameshiftsubstitution	64577329	1	#008000	0	1
MEN1_64577380_C_CG_frameshiftsubstitution_FRAME_SHIFT_P67P?	MEN1	frameshiftsubstitution	64577380	1	#008000	0	1
MEN1_64577392_G_A_stopgain_STOP_GAINED_Q64*	MEN1	stopgain	64577392	1	red	0	1

SNP

normal & tumor amount

nonsynonymousSNV

snp11308007

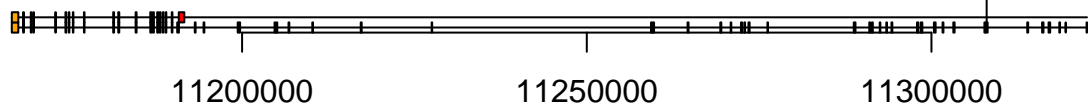
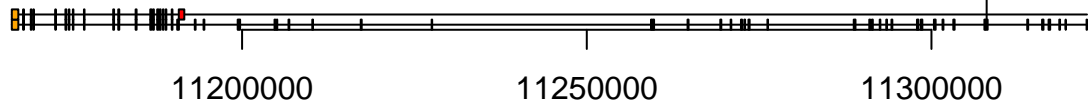
5utr exon 3utr

Normal Tumor

snp11308007

5utr exon 3utr

MTOR – Chr.1



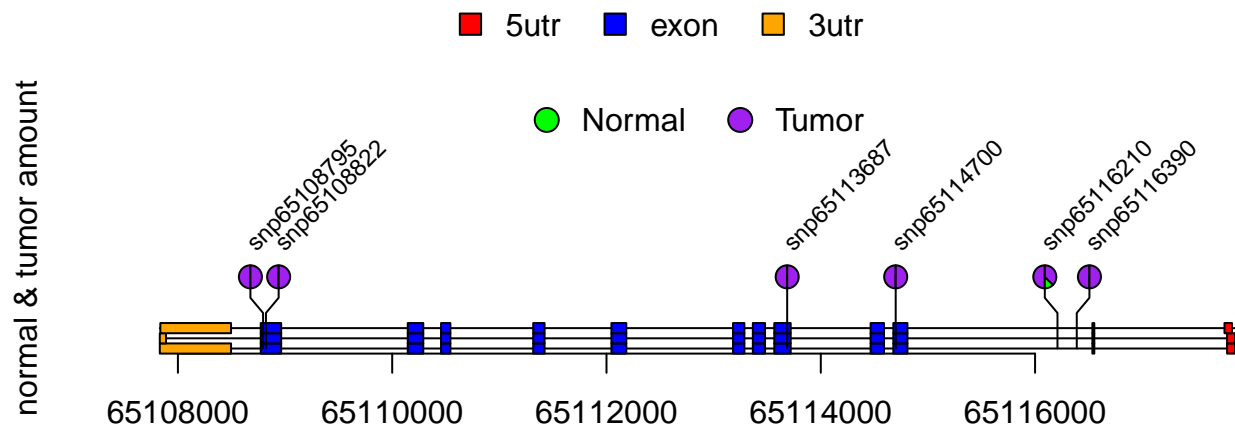
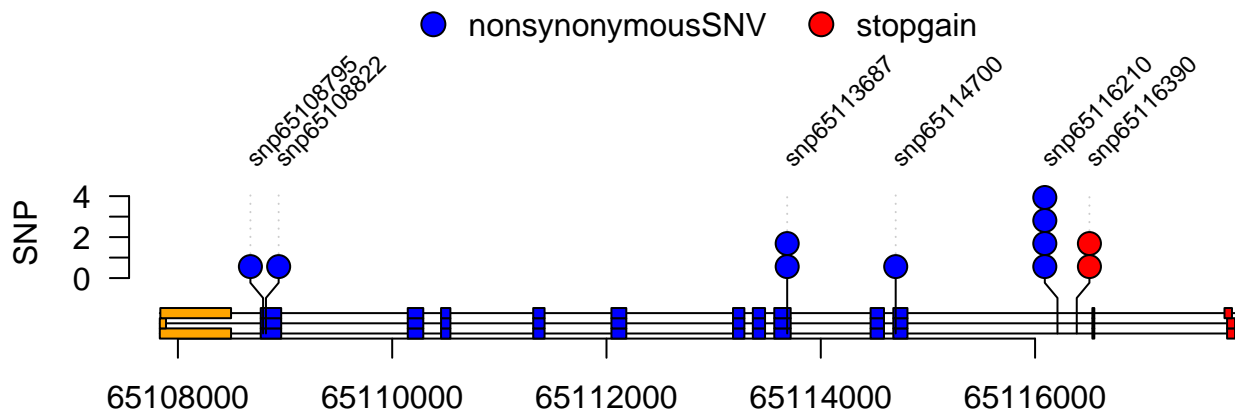
Input data set used for plotting gene MTOR

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	X0.408
MTOR_11308007_C_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_A329T	0.408

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
MTOR_11308007_C_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_A329T	MTOR	nonsynonymousSNV	11308007	1	blue	0	1

Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda



PIF1 - Chr.15

Input data set used for plotting gene PIF1

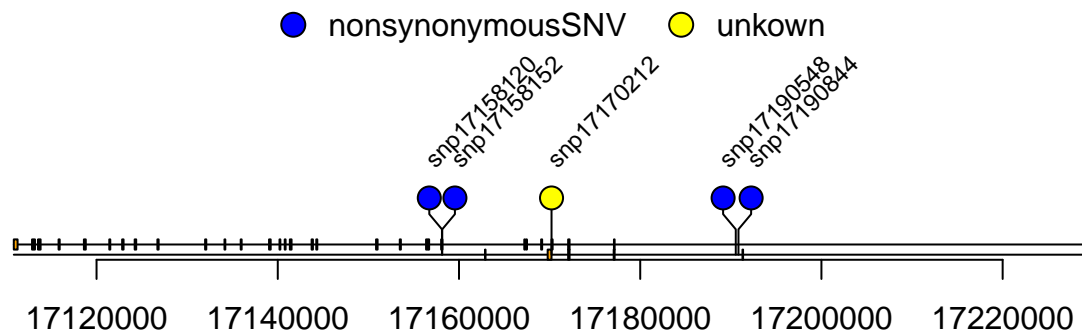
(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	r3t	r5t	b13	b8	ch1	ch19	r17t	b3	b5	r3n	r11t
PIF1_65108795_C_T_nonsynonymousSNV_DOWNSTREAM_.	0	0.2865	0	0	0	0	0	0	0	0	0
PIF1_65108822_C_T_nonsynonymousSNV_DOWNSTREAM_.	0	0	0	0	0	0	0.2704	0	0	0	0
PIF1_65113687_A_G_nonsynonymousSNV_DOWNSTREAM_.	0	0	0	0	0	0.4283	0	0.4347	0	0	0
PIF1_65114700_C_G_nonsynonymousSNV_DOWNSTREAM_.	0	0	0	0	0.4182	0	0	0	0	0	0
PIF1_65116210_G_A_nonsynonymousSNV_NON_SYNONYMOUS_CODING_P109S	0.4102	0	0	0.5007	0	0	0	0	0.4663	0.3184	0
PIF1_65116390_C_A_stopgain_STOP_GAINED_E49*	0	0	0.3172	0	0	0	0	0	0	0	0.2555

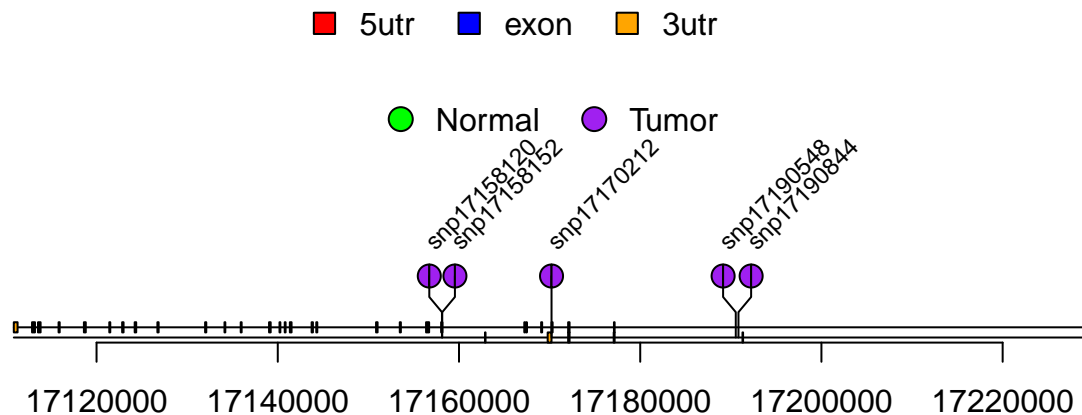
	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
PIF1_65108795_C_T_nonsynonymousSNV_DOWNSTREAM_.	PIF1	nonsynonymousSNV	65108795	1	blue	0	1
PIF1_65108822_C_T_nonsynonymousSNV_DOWNSTREAM_.	PIF1	nonsynonymousSNV	65108822	1	blue	0	1
PIF1_65113687_A_G_nonsynonymousSNV_DOWNSTREAM_.	PIF1	nonsynonymousSNV	65113687	2	blue	0	2
PIF1_65114700_C_G_nonsynonymousSNV_DOWNSTREAM_.	PIF1	nonsynonymousSNV	65114700	1	blue	0	1
PIF1_65116210_G_A_nonsynonymousSNV_NON_SYNONYMOUS_CODING_P109S	PIF1	nonsynonymousSNV	65116210	4	blue	1	3
PIF1_65116390_C_A_stopgain_STOP_GAINED_E49*	PIF1	stopgain	65116390	2	red	0	2

Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda

SNP



normal & tumor amount



PIK3C2A – Chr.11

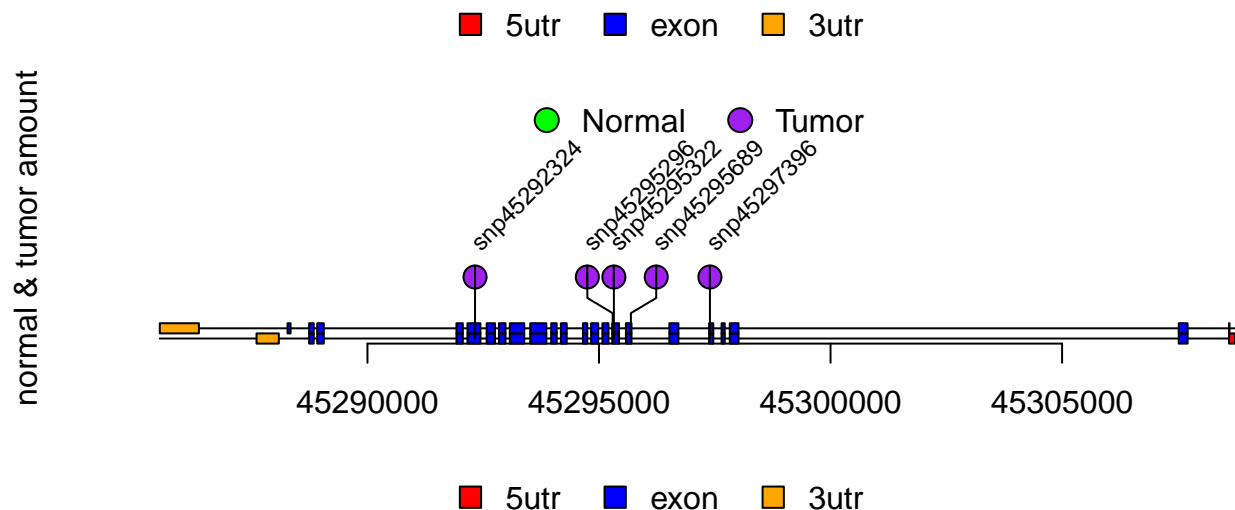
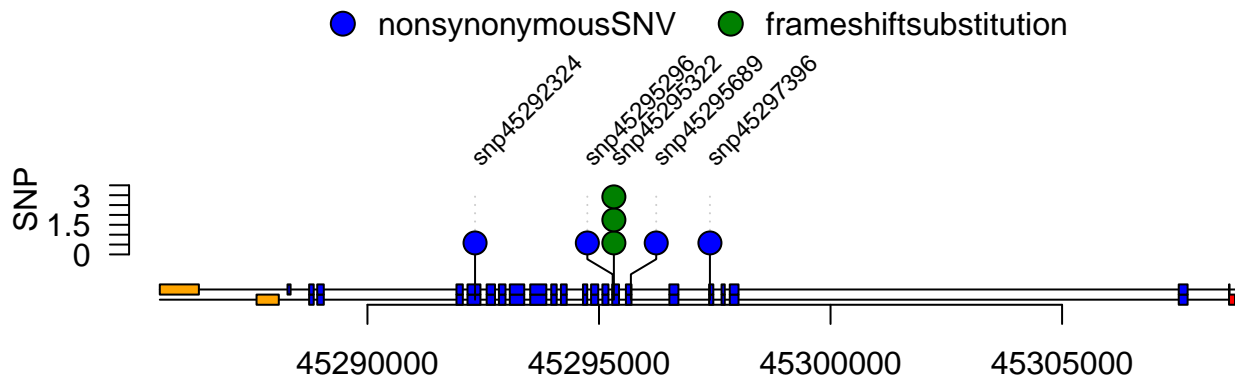
Input data set used for plotting gene PIK3C2A

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	r20t	ch7	ch17
PIK3C2A_17158120_C_T_nonsynonymousSNV_DOWNSTREAM_.	0	0.1188	0
PIK3C2A_17158152_A_C_nonsynonymousSNV_DOWNSTREAM_.	0	0	0.0541
PIK3C2A_17170212_AC_A_...EXON_.	0.063	0	0
PIK3C2A_17190548_C_A_nonsynonymousSNV_DOWNSTREAM_.	0	0	0.086
PIK3C2A_17190844_G_T_nonsynonymousSNV_DOWNSTREAM_.	0.0766	0	0

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
PIK3C2A_17158120_C_T_nonsynonymousSNV_DOWNSTREAM_.	PIK3C2A	nonsynonymousSNV	17158120	1	blue	0	1
PIK3C2A_17158152_A_C_nonsynonymousSNV_DOWNSTREAM_.	PIK3C2A	nonsynonymousSNV	17158152	1	blue	0	1
PIK3C2A_17170212_AC_A_...EXON_.	PIK3C2A	unkown	17170212	1	yellow	0	1
PIK3C2A_17190548_C_A_nonsynonymousSNV_DOWNSTREAM_.	PIK3C2A	nonsynonymousSNV	17190548	1	blue	0	1
PIK3C2A_17190844_G_T_nonsynonymousSNV_DOWNSTREAM_.	PIK3C2A	nonsynonymousSNV	17190844	1	blue	0	1

Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda



PTCH2 – Chr.1

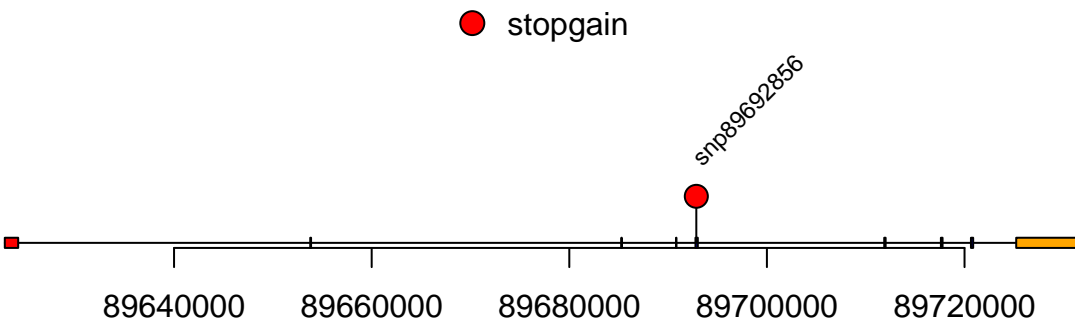
Input data set used for plotting gene PTCH2

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	r20t	r1t	b8	ch17	b25	b11
PTCH2_45292324_C_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_G938S	0	0	0	0	0.4688	0
PTCH2_45295296_C_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_R358H	0	0	0.4828	0	0	0
PTCH2_45295322_GC_G_frameshiftsubstitution_FRAME_SHIFT_S349	0.0645	0.0613	0	0.0538	0	0
PTCH2_45295689_G_A_nonsynonymousSNV_NON_SYNONYMOUS_CODING_A276V	0	0	0	0	0	0.3608
PTCH2_45297396_C_G_nonsynonymousSNV_NON_SYNONYMOUS_CODING_G200A	0	0	0.3067	0	0	0

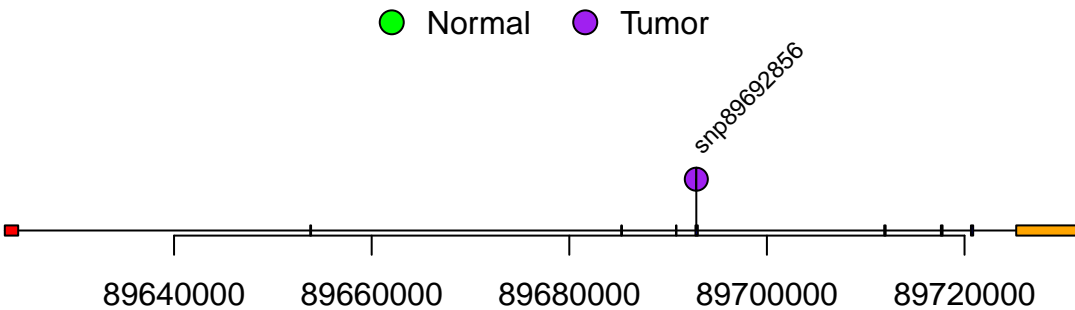
	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
PTCH2_45292324_C_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_G938S	PTCH2	nonsynonymousSNV	45292324	1	blue	0	1
PTCH2_45295296_C_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_R358H	PTCH2	nonsynonymousSNV	45295296	1	blue	0	1
PTCH2_45295322_GC_G_frameshiftsubstitution_FRAME_SHIFT_S349	PTCH2	frameshiftsubstitution	45295322	3	#008000	0	3
PTCH2_45295689_G_A_nonsynonymousSNV_NON_SYNONYMOUS_CODING_A276V	PTCH2	nonsynonymousSNV	45295689	1	blue	0	1
PTCH2_45297396_C_G_nonsynonymousSNV_NON_SYNONYMOUS_CODING_G200A	PTCH2	nonsynonymousSNV	45297396	1	blue	0	1

SNP



5utr exon 3utr

normal & tumor amount



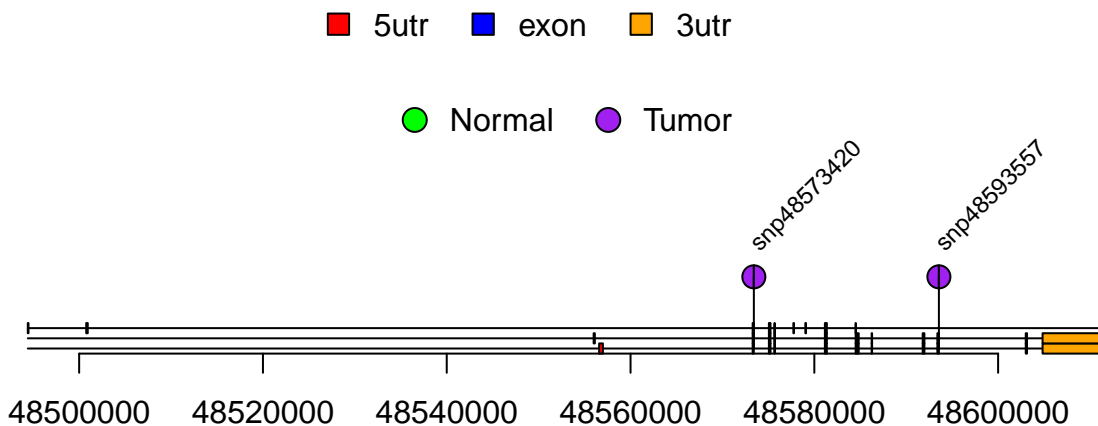
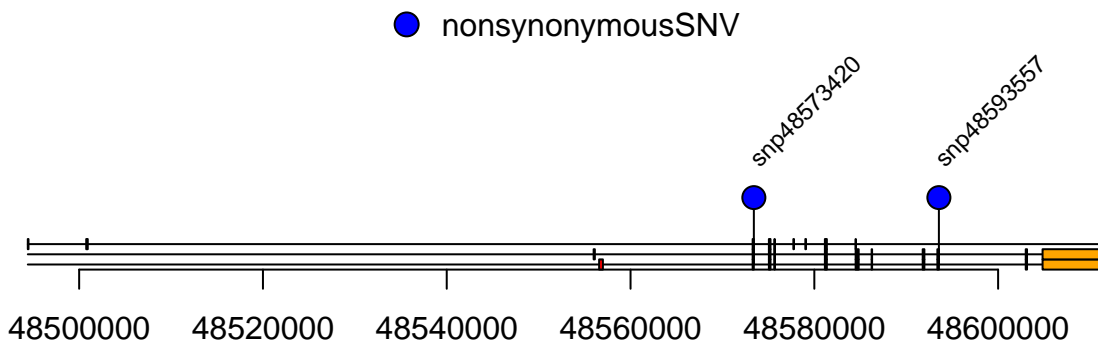
5utr exon 3utr

PTEN – Chr.10

Input data set used for plotting gene PTEN
(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	X0.105
PTEN_89692856_G_T_stopgain_EXON_.	0.105

	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
PTEN_89692856_G_T_stopgain_EXON_.	PTEN	stopgain	89692856	1	red	0	1



5utr exon 3utr

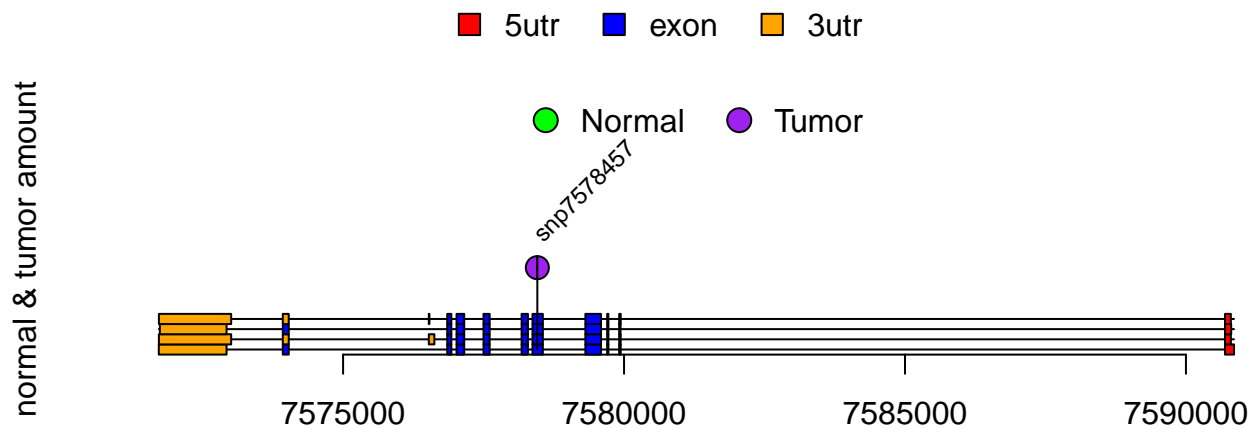
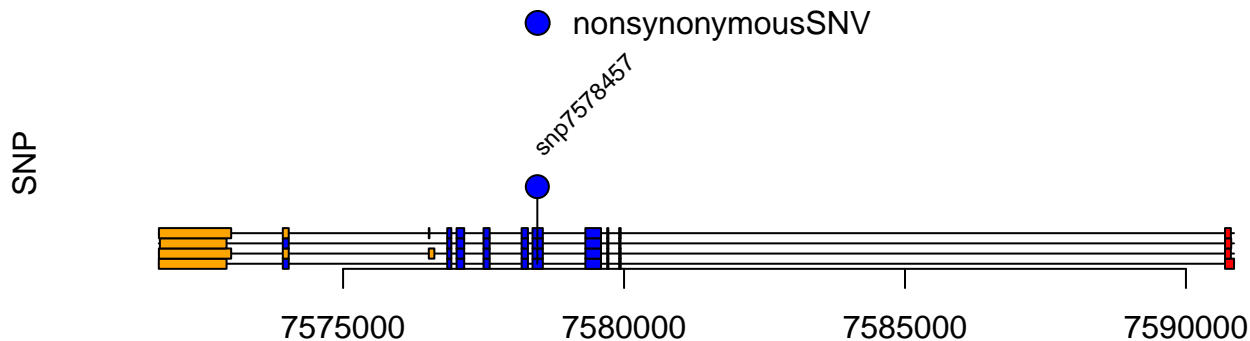
SMAD4 – Chr.18

Input data set used for plotting gene SMAD4

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	ch15	ch17
SMAD4_48573420_G_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_D2Y	0	0.0865
SMAD4_48593557_G_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_K436N	0.6267	0

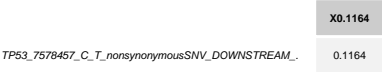
	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
SMAD4_48573420_G_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_D2Y	SMAD4	nonsynonymousSNV	48573420	1	blue	0	1
SMAD4_48593557_G_T_nonsynonymousSNV_NON_SYNONYMOUS_CODING_K436N	SMAD4	nonsynonymousSNV	48593557	1	blue	0	1



■ 5utr ■ exon ■ 3utr

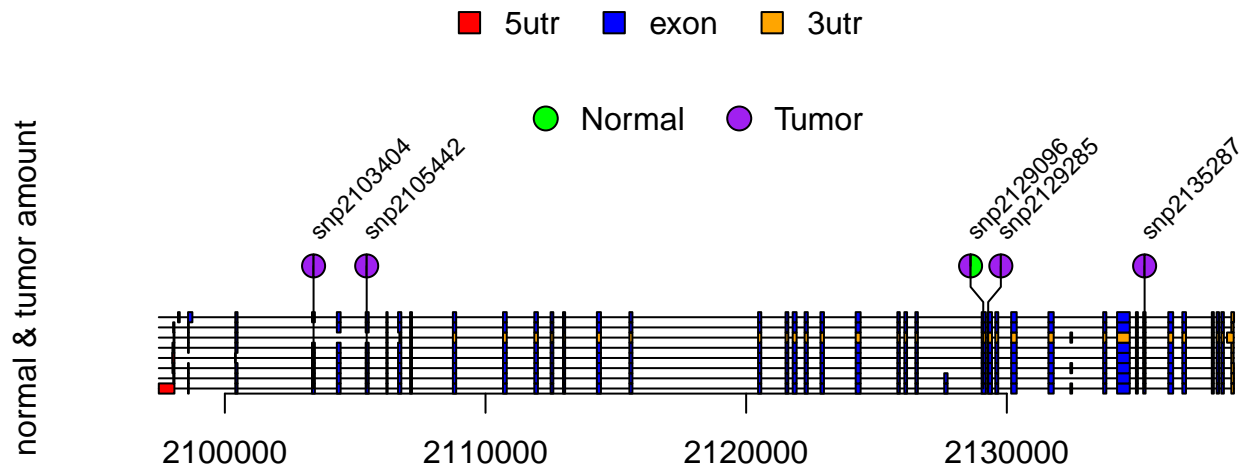
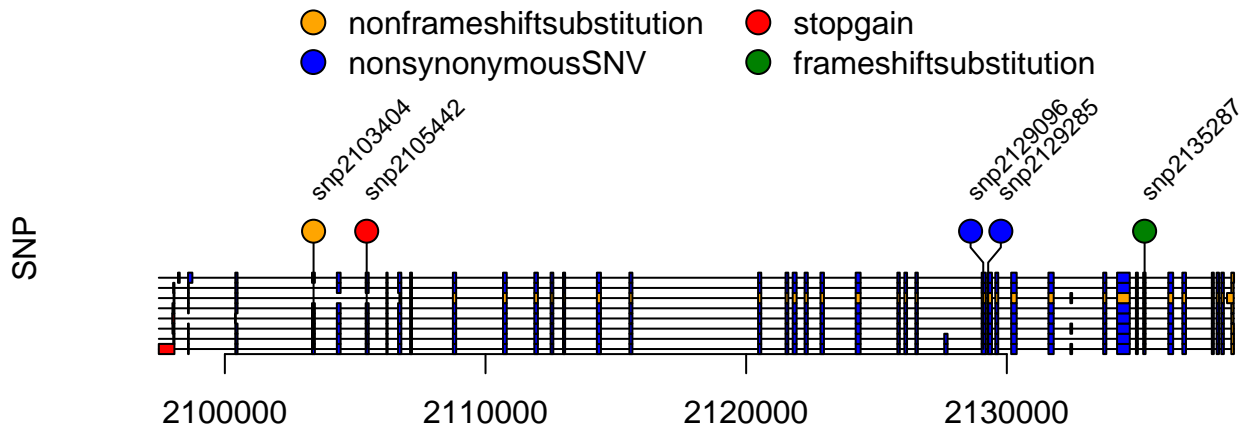
TP53 – Chr.17

Input data set used for plotting gene TP53
(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)



	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
<i>TP53_7578457_C_T_nonsynonymousSNV_DOWNSTREAM_</i>	TP53	nonsynonymousSNV	7578457	1	blue	0	1

Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda



TSC2 – Chr.16

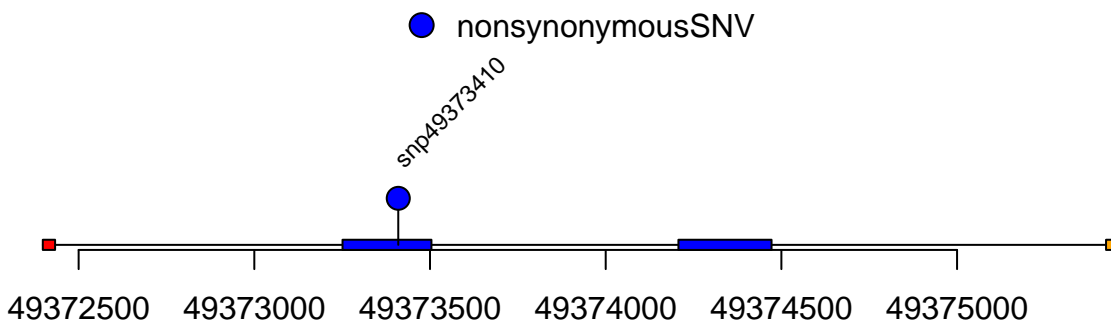
Input data set used for plotting gene TSC2

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

	r5t	b13	r15t	r3n	ch5
TSC2_2103404_AGGCCCGGCACGC_A_nonframeshiftsubstitution_CODON_DELETION_EARHA107E	0	0	0.2222	0	0
TSC2_2105442_C_A_stopgain_DOWNSTREAM_.	0.0571	0	0	0	0
TSC2_2129096_G_T_nonsynonymousSNV_DOWNSTREAM_.	0	0	0	0.0843	0
TSC2_2129285_T_C_nonsynonymousSNV_DOWNSTREAM_.	0	0.4827	0	0	0
TSC2_2135287_CCACAAGATCGCCGTCTGTATG_C_frameshiftsubstitution_DOWNSTREAM_.	0	0	0	0	0.1557

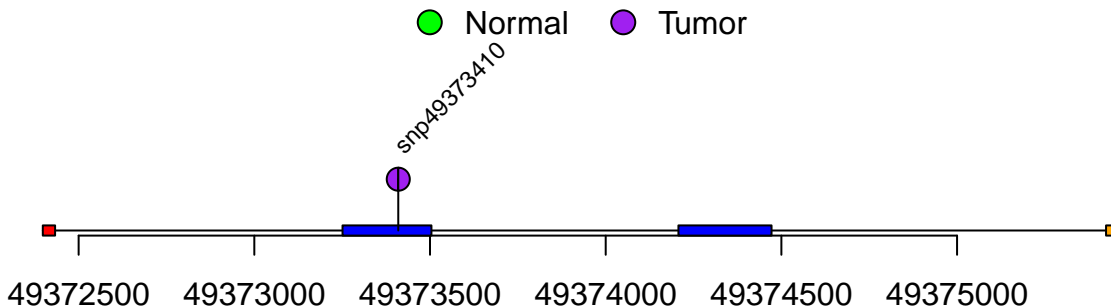
	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
TSC2_2103404_AGGCCCGGCACGC_A_nonframeshiftsubstitution_CODON_DELETION_EARHA107E	TSC2	nonframeshiftsubstitution	2103404	1	orange	0	1
TSC2_2105442_C_A_stopgain_DOWNSTREAM_.	TSC2	stopgain	2105442	1	red	0	1
TSC2_2129096_G_T_nonsynonymousSNV_DOWNSTREAM_.	TSC2	nonsynonymousSNV	2129096	1	blue	1	0
TSC2_2129285_T_C_nonsynonymousSNV_DOWNSTREAM_.	TSC2	nonsynonymousSNV	2129285	1	blue	0	1
TSC2_2135287_CCACAAGATCGCCGTCTGTATG_C_frameshiftsubstitution_DOWNSTREAM_.	TSC2	frameshiftsubstitution	2135287	1	#008000	0	1

SNP



5utr exon 3utr

normal & tumor amount



5utr exon 3utr

WNT1 – Chr.12

Input data set used for plotting gene WNT1

(Matrix_gene_matrix_31052016_pathogenic_noMUC_VAF0.05_TD100.Rda)

WNT1_49373410_T_A_nonsynonymousSNV_DOWNSTREAM_	X0.495
	0.495

WNT1_49373410_T_A_nonsynonymousSNV_DOWNSTREAM_	genes	mutationtype	SNP.start	timesMutated	colorMutationType	countNormals	countTumors
	WNT1	nonsynonymousSNV	49373410	1	blue	0	1