

Description of Supplementary Files

File Name: Supplementary Information

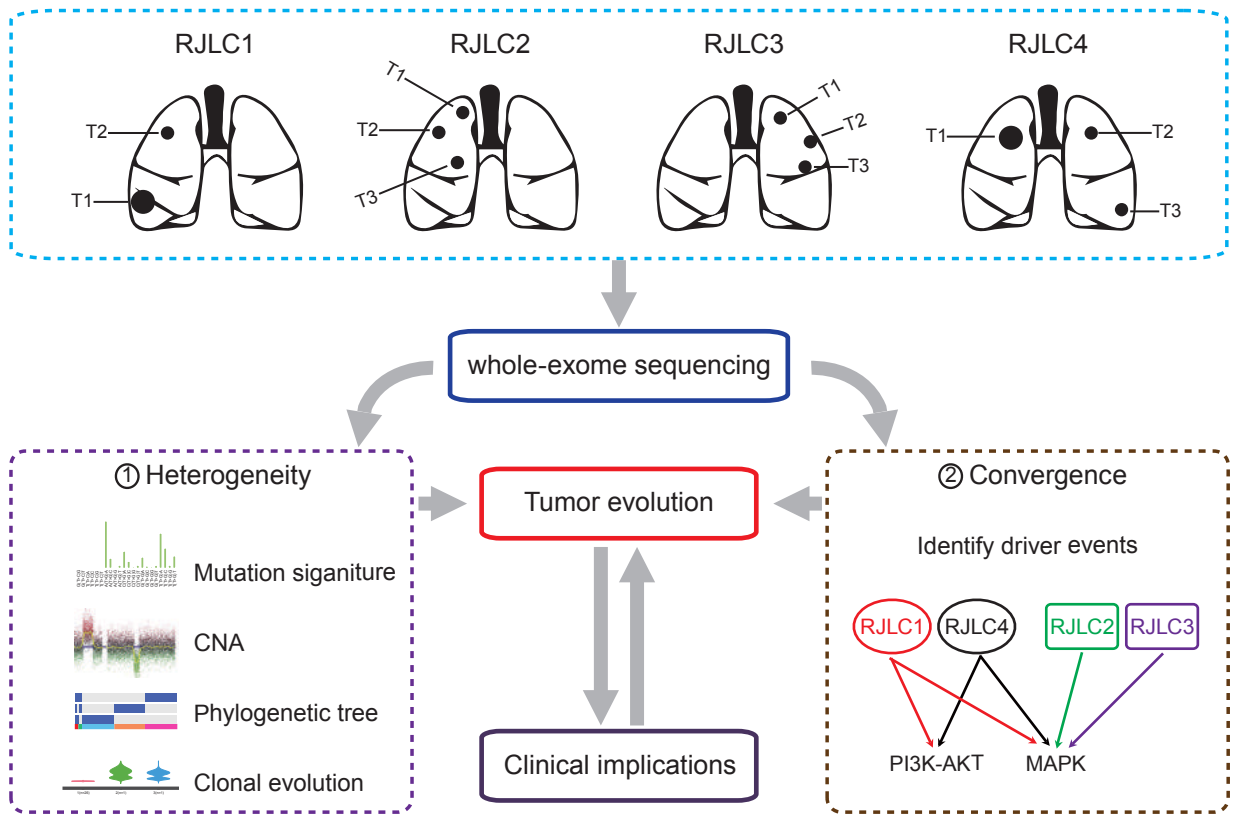
Description: Supplementary Figures and Supplementary Tables

File Name: Supplementary Data 1

Description: Identification of 167-679 somatic alterations per tumor, including a total of 373 non-synonymous exonic mutations present in at least one tumor region.

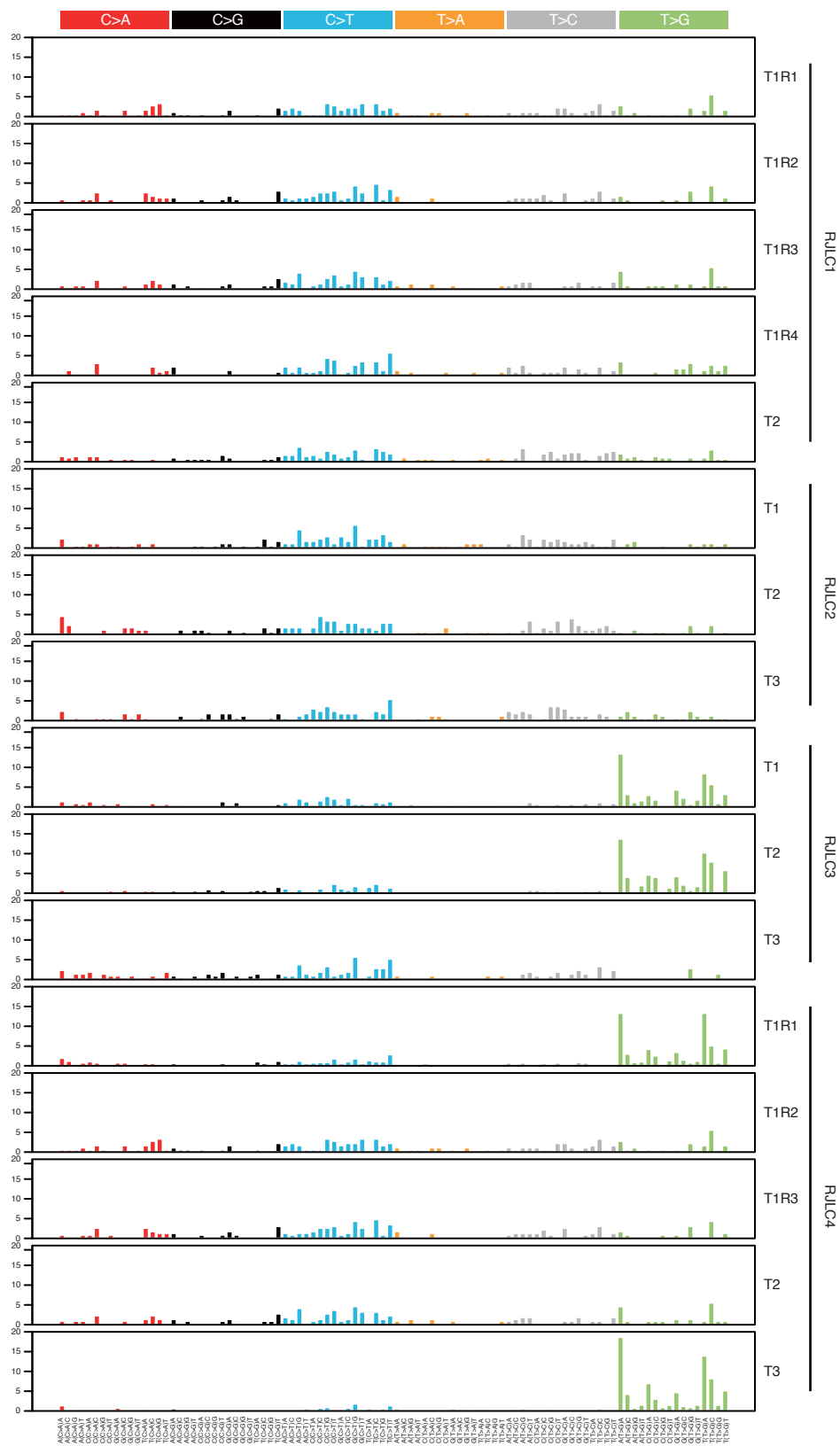
File Name: Peer Review File

Supplementary Figure 1.



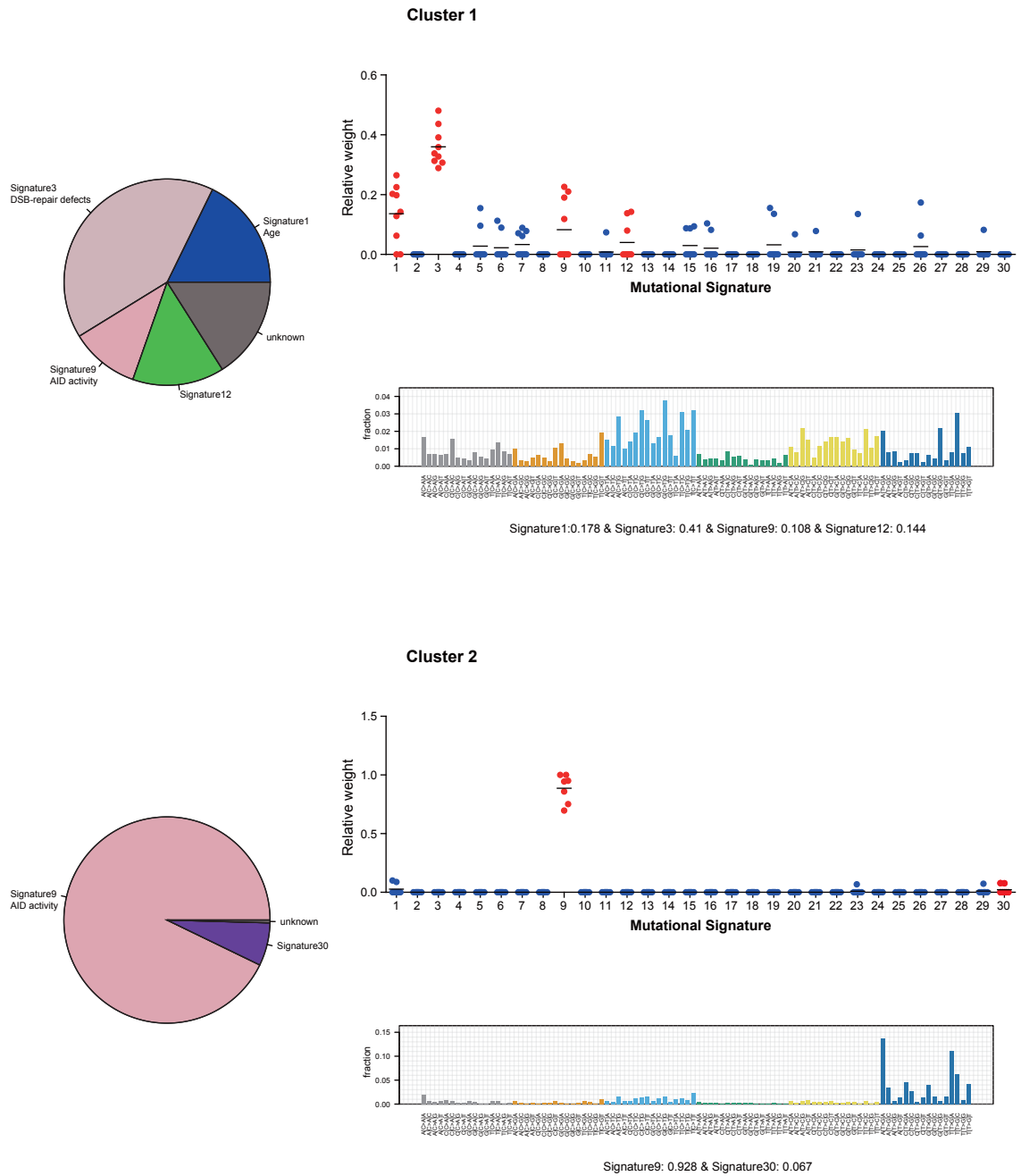
Supplementary Figure 1. A schematic overview of the study design.

Supplementary Figure 2.



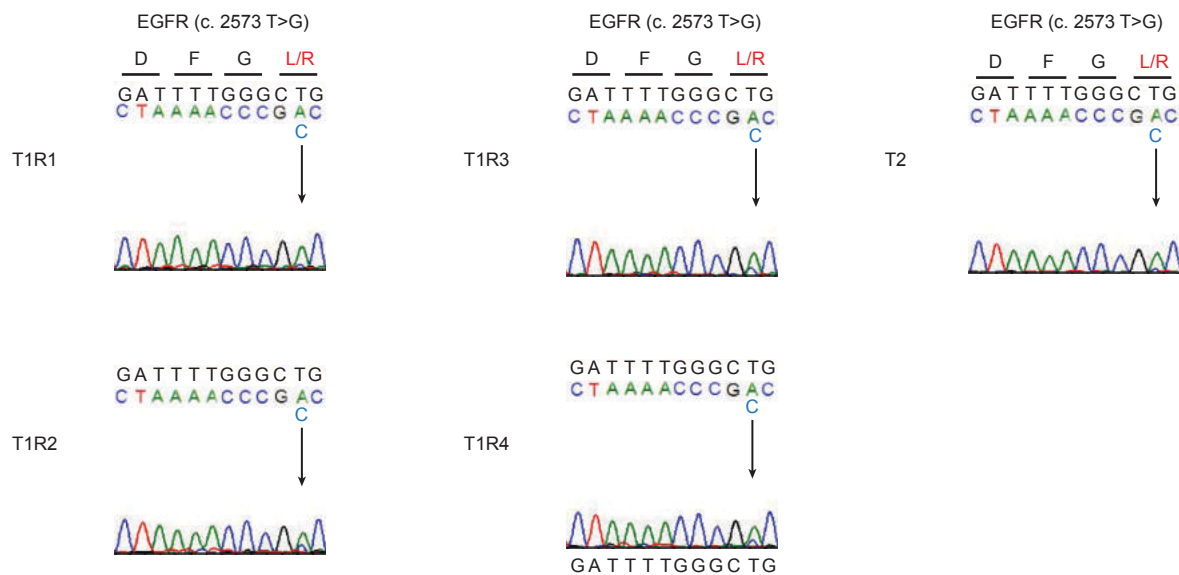
Supplementary Figure 2. Mutational signatures of sequenced tumor samples.

Supplementary Figure 3.



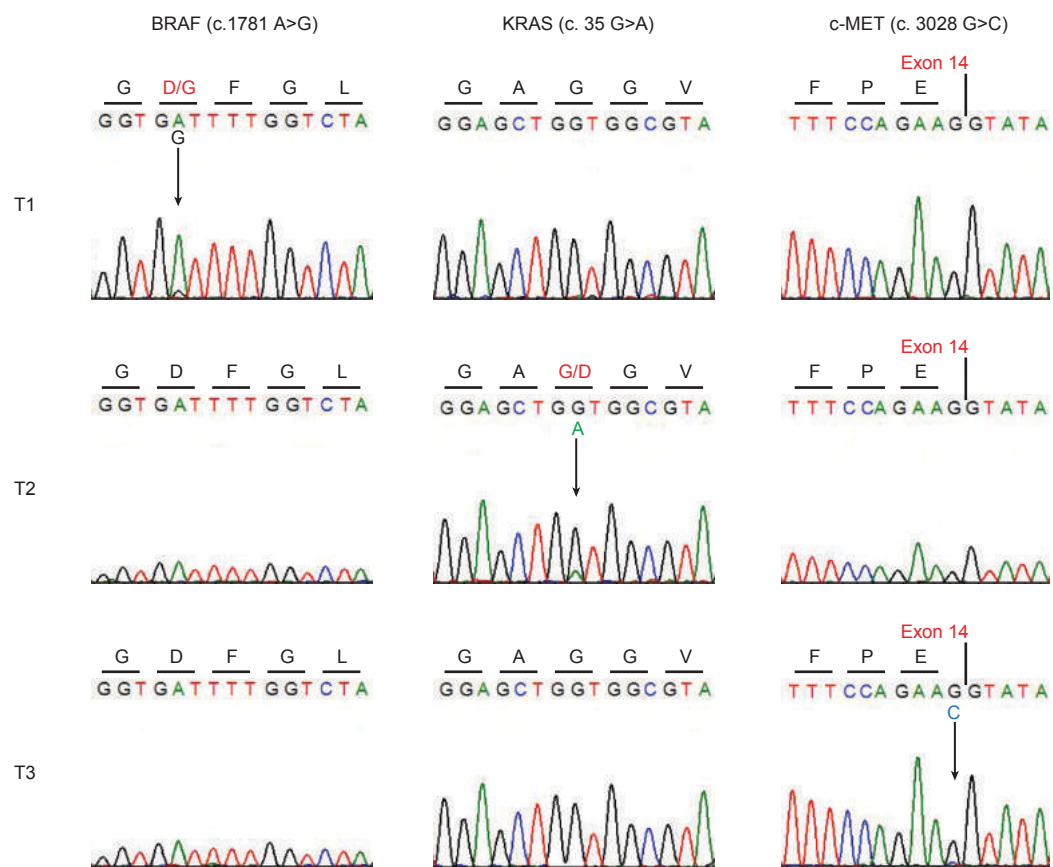
Supplementary Figure 3. A multiple regression approach, deconstructSigs, was used to extract known signatures based on the Wellcome Trust Sanger Institute Mutational Signature Framework and to statistically quantify the contribution of each signature for each cluster.

Supplementary Figure 4.



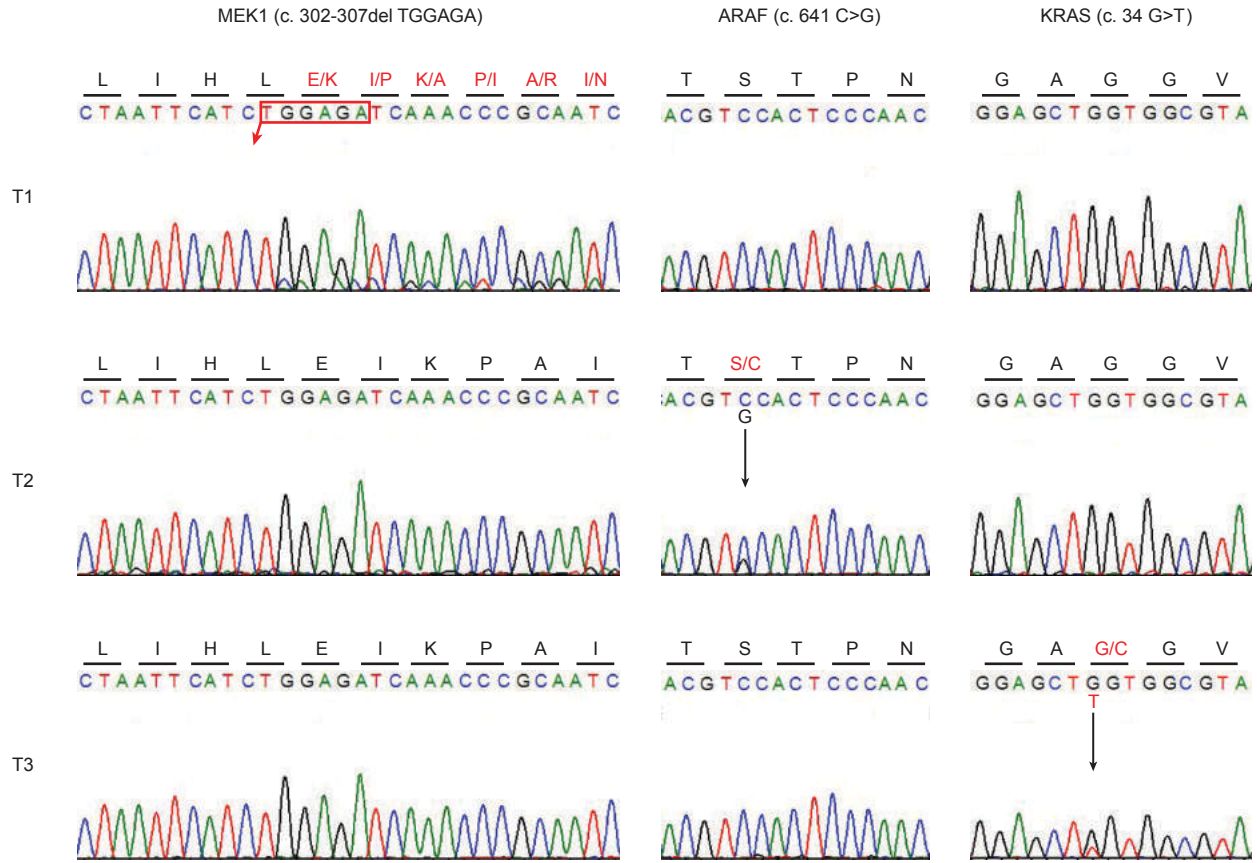
Supplementary Figure 4. Sanger sequencing validation of EGFR mutation in RJLC1.

Supplementary Figure 5.



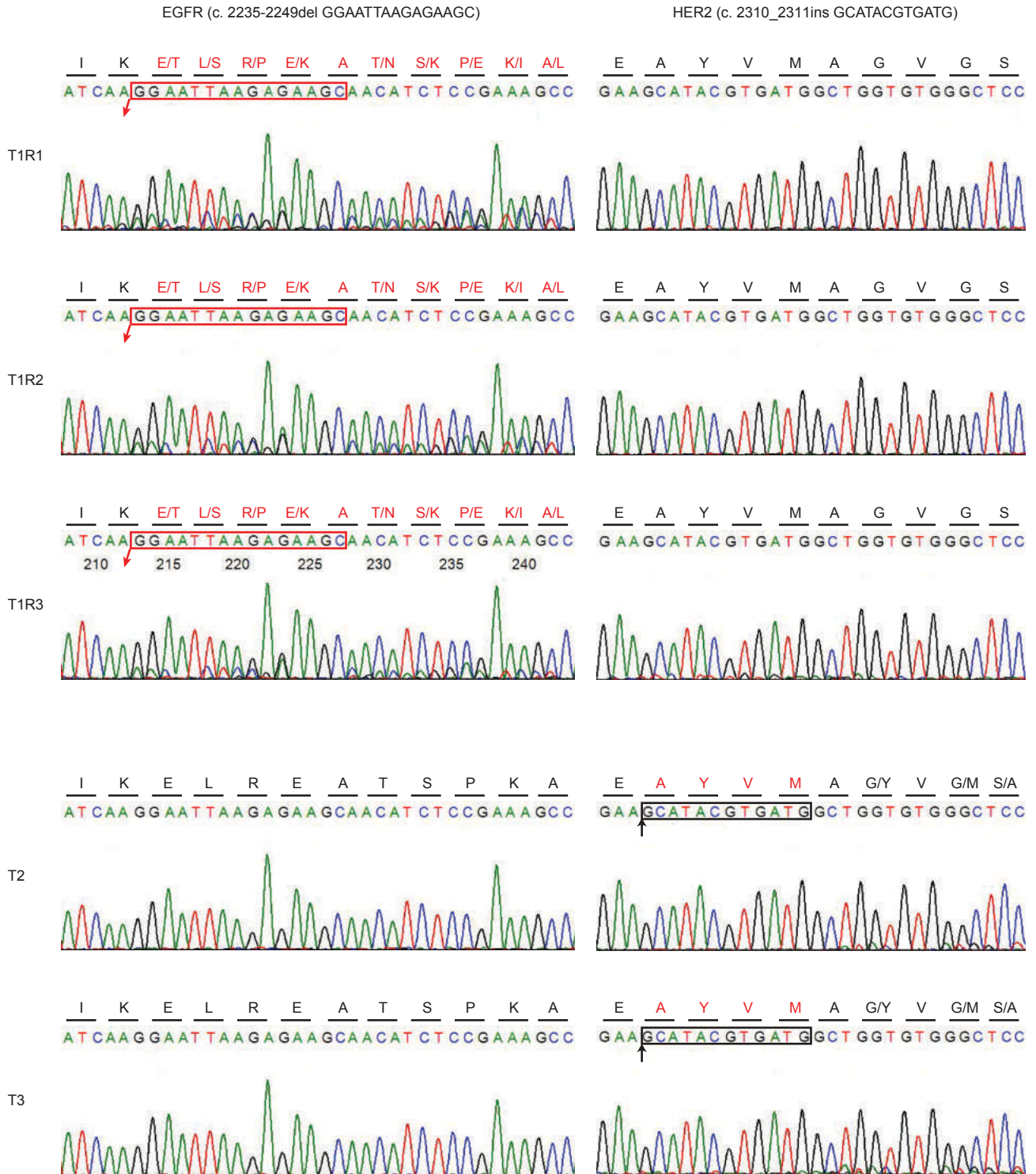
Supplementary Figure 5. Sanger sequencing validation of BRAF, KRAS and c-MET mutations in RJLC2.

Supplementary Figure 6.



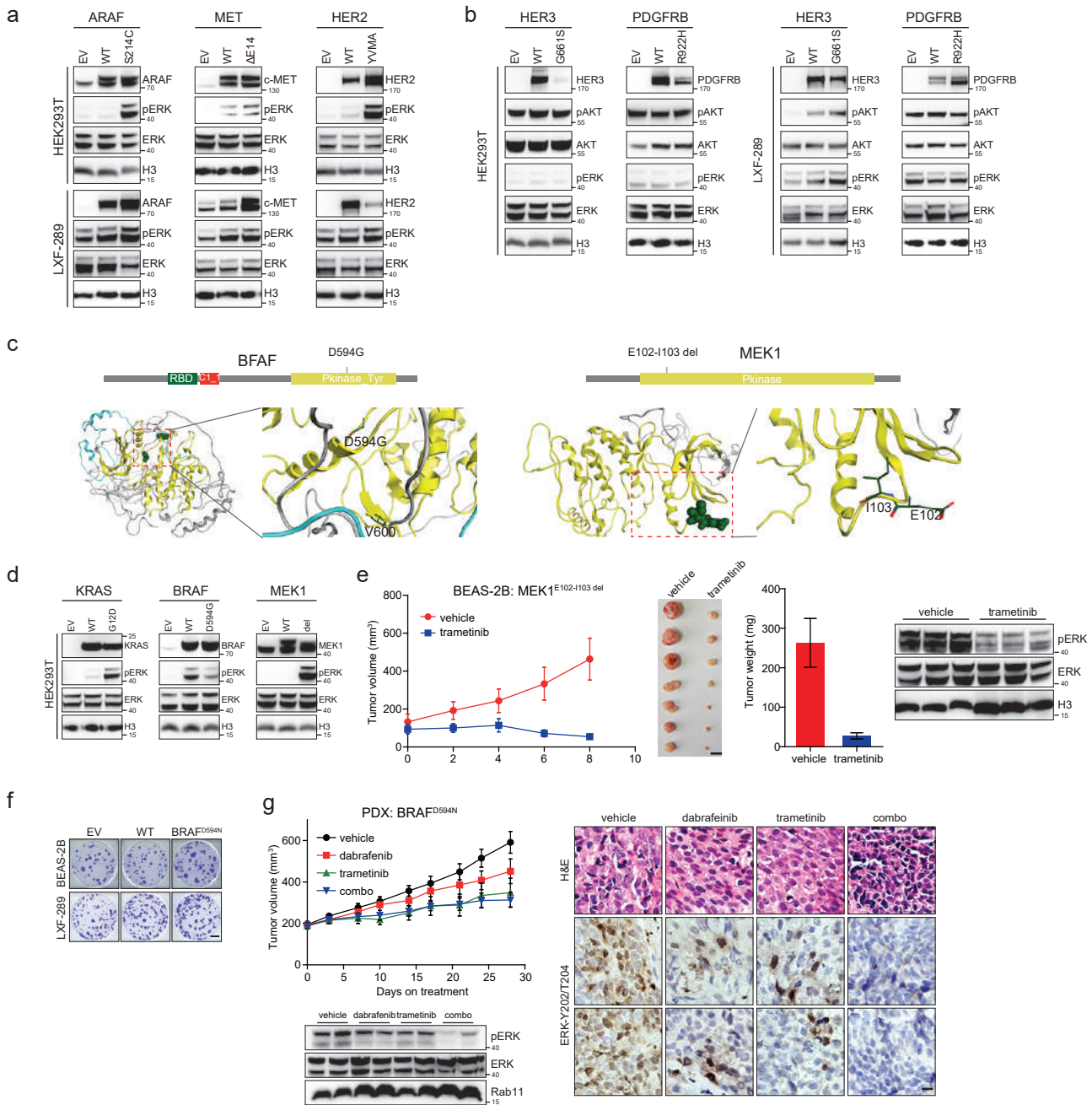
Supplementary Figure 6. Sanger sequencing validation of MEK1, ARAF and KRAS mutations in RJLC3.

Supplementary Figure 7.



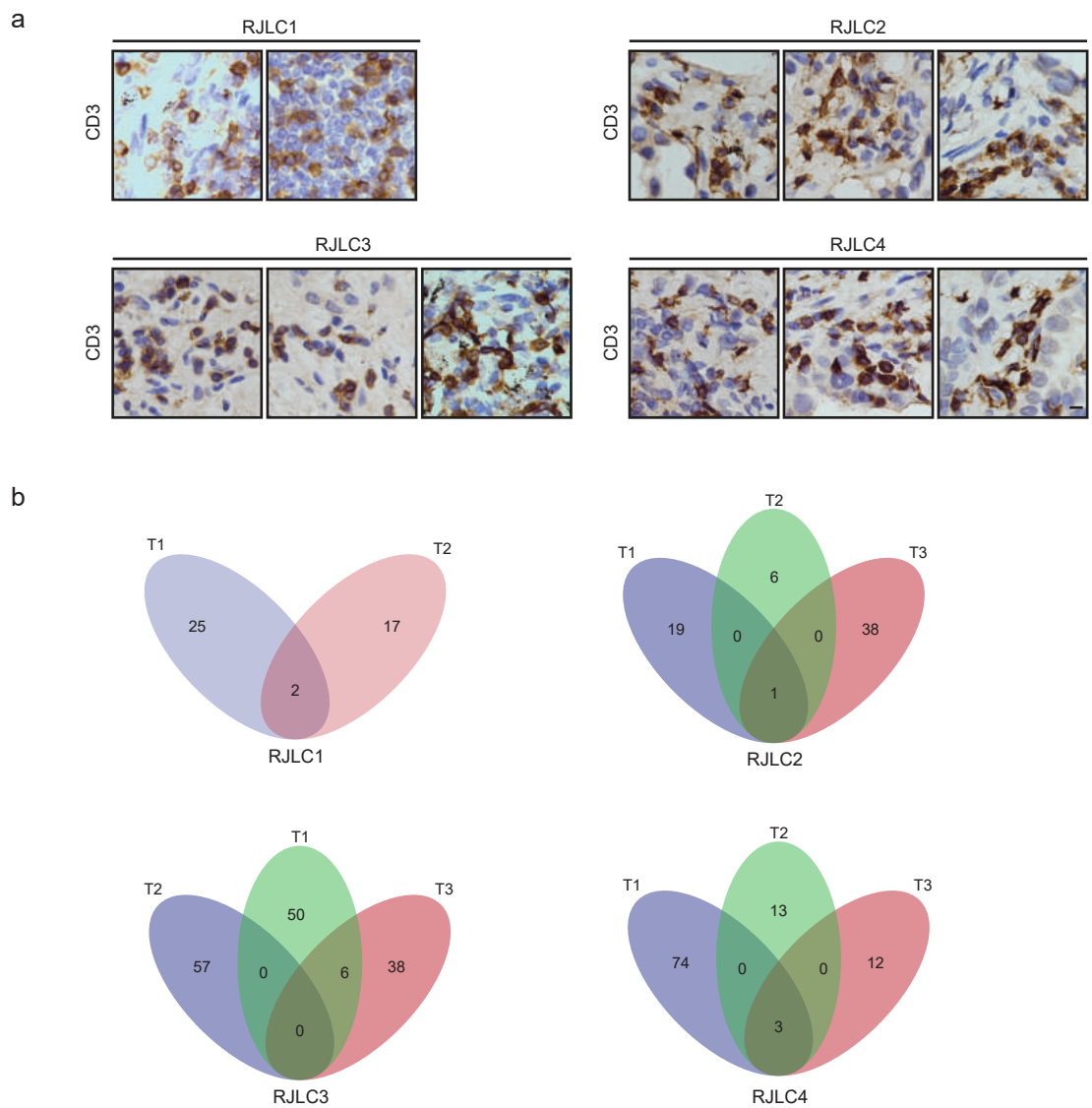
Supplementary Figure 7. Sanger sequencing validation of EGFR and HER2 mutations in RJLC4.

Supplementary Figure 8.



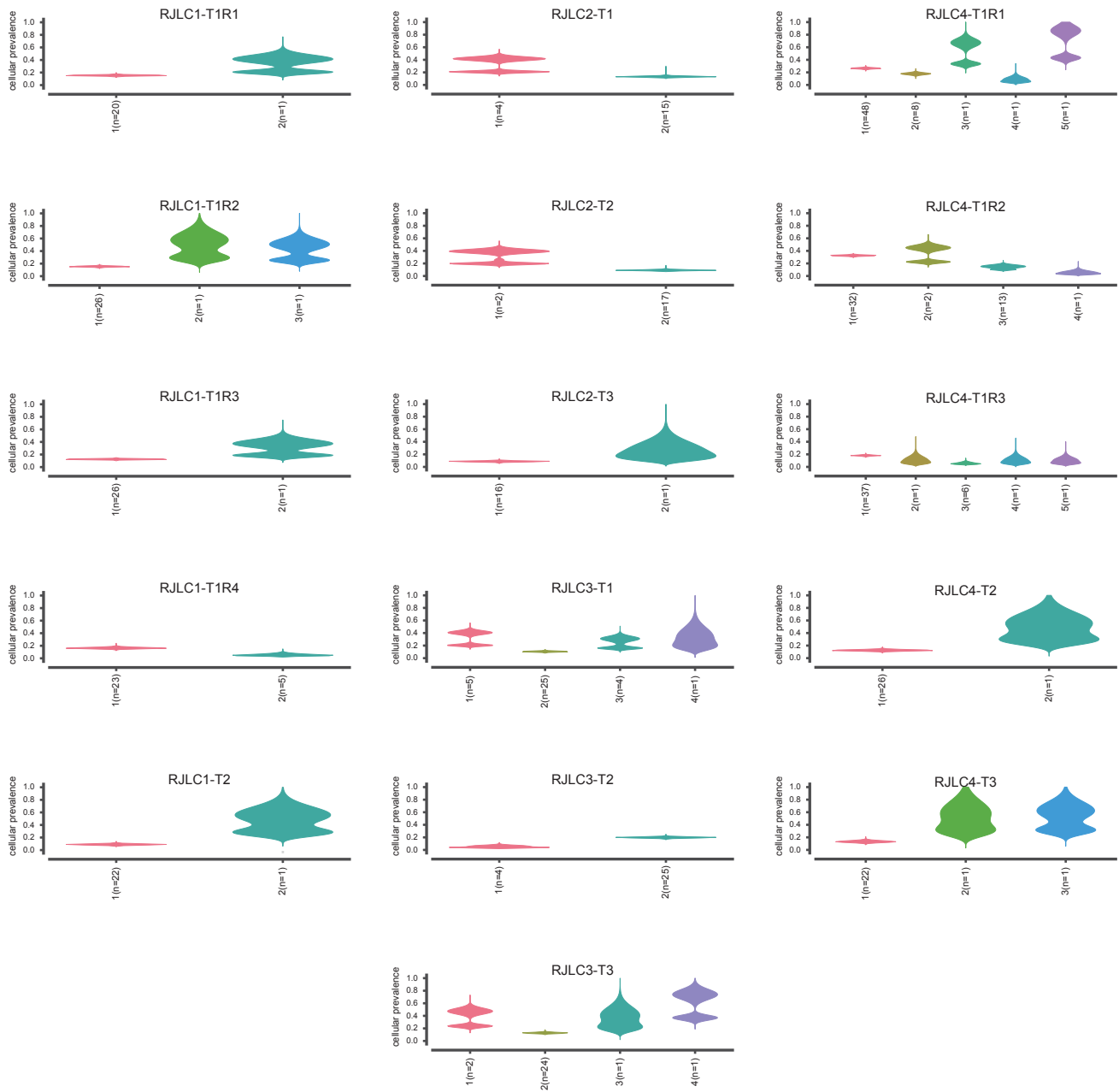
Supplementary Figure 8. (a) Overexpression of indicated wild-type or mutant genes in HEK293T or LXF-289 cells. Gene expression and ERK phosphorylation were measured by immunoblotting. (b) Overexpression of indicated wild-type or mutant genes in HEK293T or LXF-289 cells. AKT and ERK phosphorylation was measured by immunoblotting. (c) The mutated protein structures were generated by Phyre2 web portal and figures were prepared by using PyMOL. (d) Overexpression of indicated wild-type or mutant genes in HEK293T cells. Gene expression and ERK phosphorylation were measured by immunoblotting. (e) Tumor growth of BEAS-2B xenografts treated with trametinib or vehicle control. Each line represented mean tumor volume of the respective group, and error bars indicated standard deviation (10 mice per group). ERK phosphorylation was measured by immunoblotting. Scale bar, 10 mm. (f) Indicated wild-type or mutant genes were lentivirally introduced into BEAS-2B or LXF-289 cells. Cells were cultured for two weeks and stained with crystal violet. Scale bar, 5 mm. (g) Tumor growth of BRAF^{D594N} PDX treated with indicated drugs. Each line represented mean tumor volume of the respective group, and error bars indicated standard deviation (10 mice per group). ERK phosphorylation was measured by immunoblotting or IHC. Scale bar, 5 μ m.

Supplementary Figure 9.



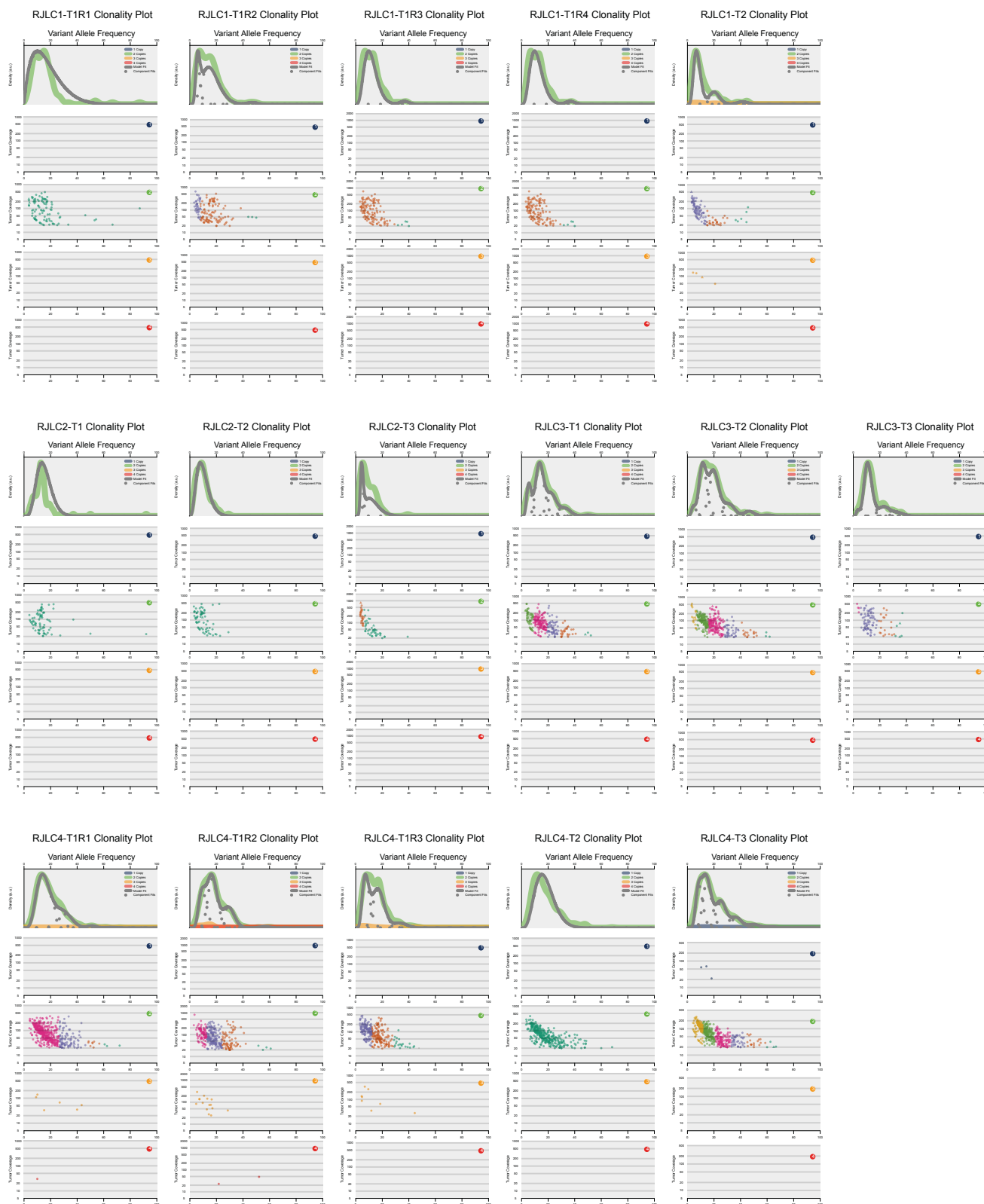
Supplementary Figure 9. (a) IHC of CD3 in different MSLC tumors. Scale bar, 5 μ m. (b) Load and overlap of predicted neoantigens in each MSLC case using NetMHCpan algorithm.

Supplementary Figure 10.



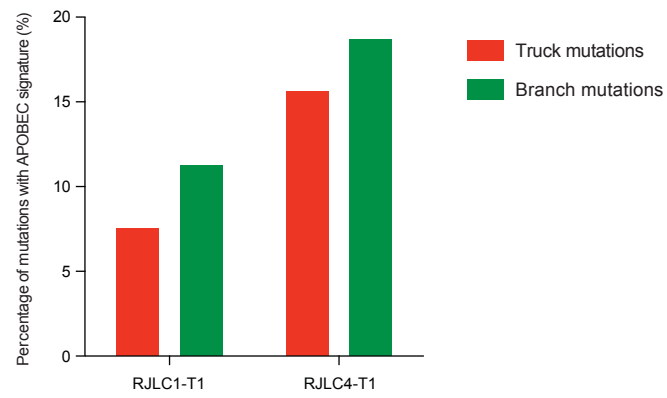
Supplementary Figure 10. PyClone analysis of sequenced tumor samples.

Supplementary Figure 11.



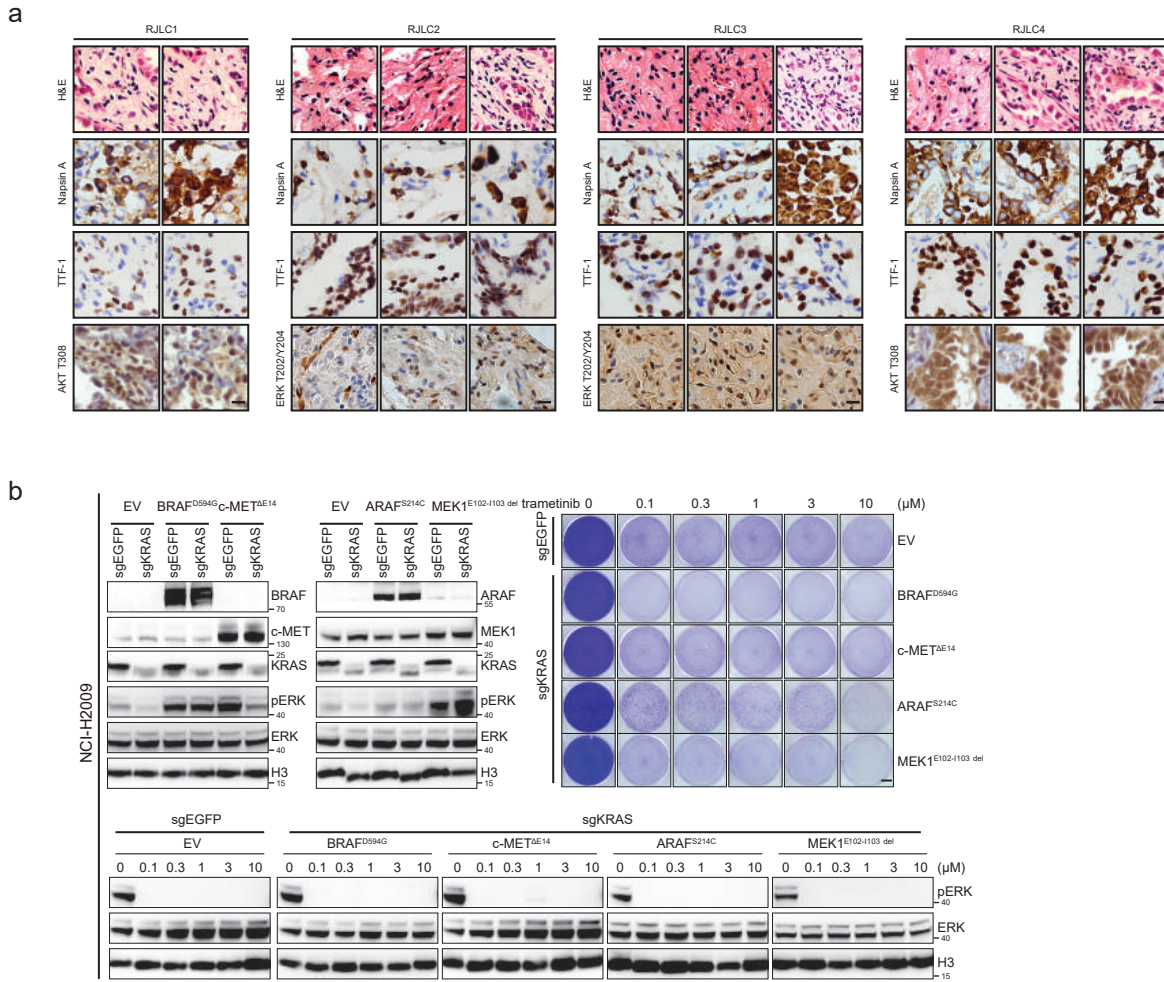
Supplementary Figure 11. SciClone analysis of sequenced tumor samples.

Supplementary Figure 12.



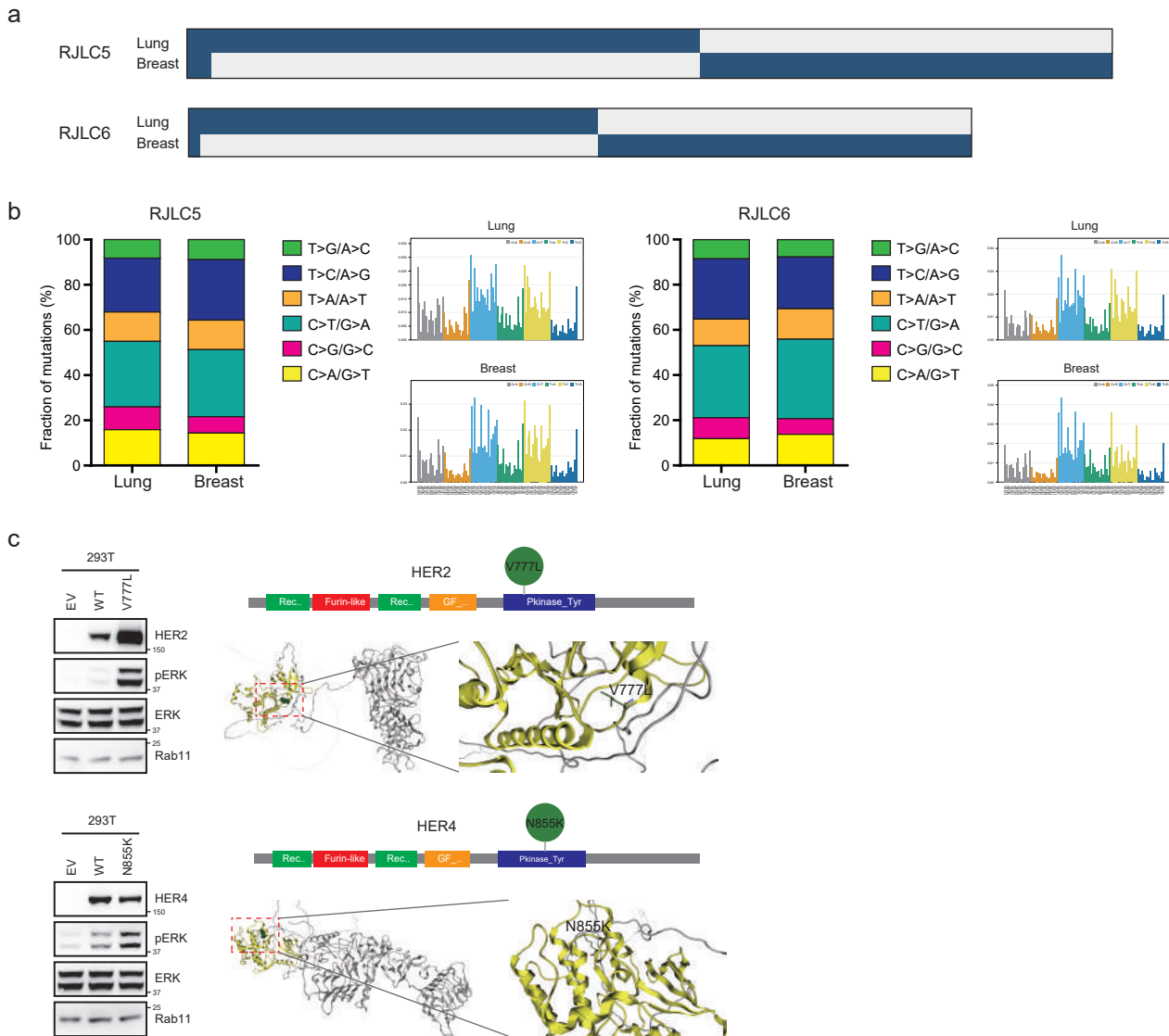
Supplementary Figure 12. Percentage of mutations with APOBEC signature for trunk and branch mutations in two M-seq tumors.

Supplementary Figure 13.



Supplementary Figure 13. (a) H&E and IHC of indicated markers in different MSLC tumors. Scale bar, 5 μm . (b) KRAS was knocked out using CRISPR-Cas9 system in NCI-H2009 cells and replaced with BRAF^{D594G}, c-MET ^{Δ E14}, ARAF^{S214C} or MEK1^{E102-1103 del}. ERK phosphorylation was measured by Western blot analysis. Indicated cells were treated with a serial dilution of trametinib for a week and stained with crystal violet. Scale bar, 5 mm. The corresponding cell lysates were analyzed by immunoblotting.

Supplementary Figure 14.



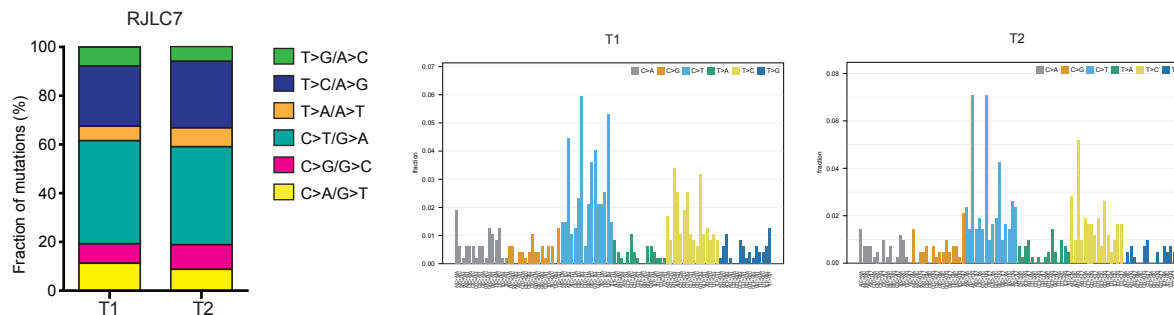
Supplementary Figure 14. (a) Heat maps showed the presence (blue) or absence (gray) of all non-silent somatic mutations in lung and breast tumors. (b) Mutation spectra and mutational signatures of lung and breast tumors in RJLC5 and RJLC6. (c) Overexpression of indicated wild-type or mutant genes in HEK293T cells. Gene expression and ERK phosphorylation were measured by immunoblotting. The mutated protein structures were generated by Phyre2 web portal and figures were prepared by using PyMOL.

Supplementary Figure 15.

a



b



Supplementary Figure 15. (a) Heat maps showed the presence (blue) or absence (gray) of all non-silent somatic mutations in two tumors of RJLC7. (b) Mutation spectra and mutational signatures of two tumors in RJLC7.

Supplementary Figure 16.

Figure 2c

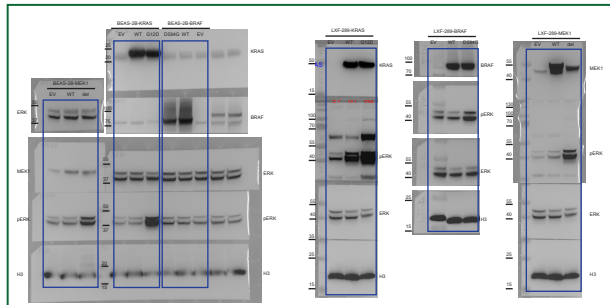


Figure 3d

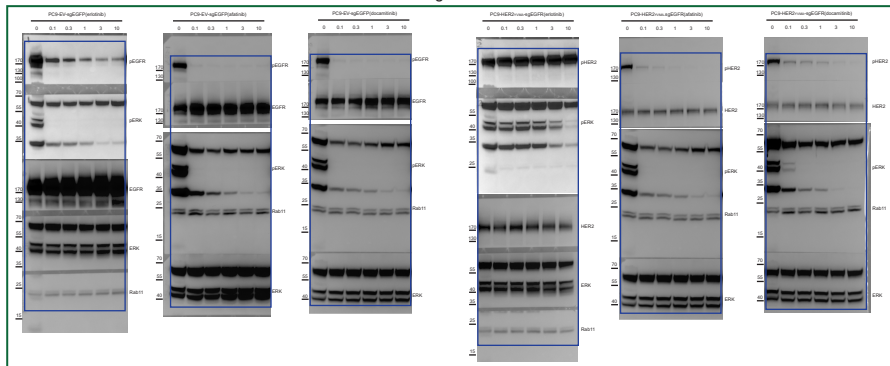


Figure 3c

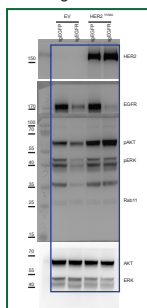
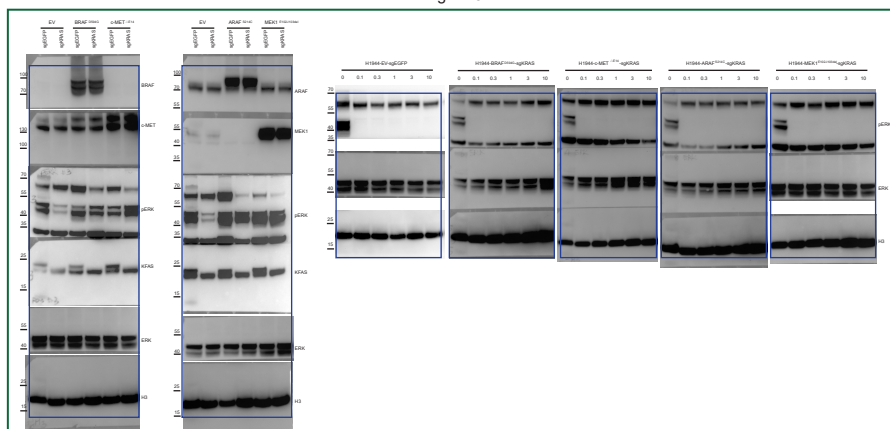
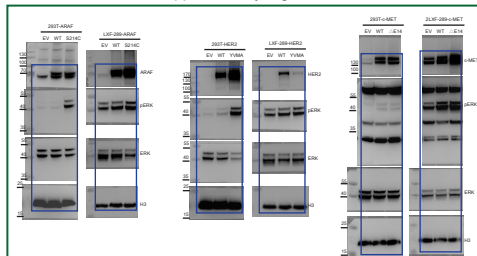


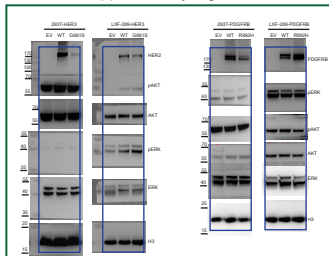
Figure 3e



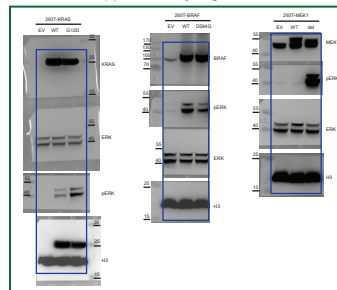
Supplementary Figure 8a



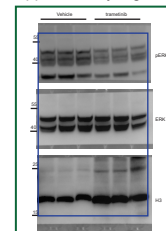
Supplementary Figure 8b



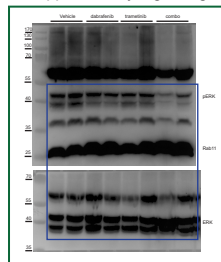
Supplementary Figure 8d



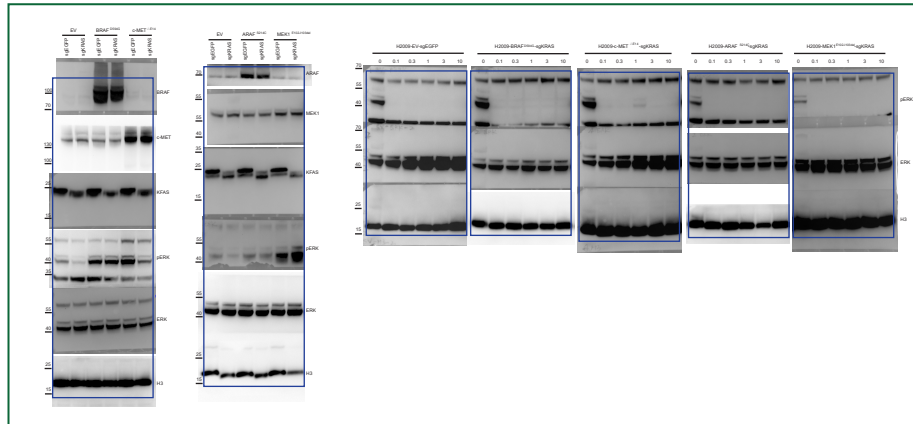
Supplementary Figure 8e



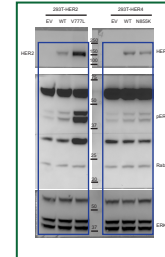
Supplementary Figure 8g



Supplementary Figure 13b



Supplementary Figure 14c



Supplementary Table 1: Sequencing statistics

Sample ID	Description	Tissue	Coverage	>20X Coverage	Somatic SNVs	Mutation Rate	Protein-altering SNVs	Somatic Indels	Somatic CNVs	CNV gain	CNV loss
RJLC1-N	Normal	Frozen	236.22	99.30%	NA	NA	NA	NA	NA	NA	NA
RJLC1-T1R1	Tumor	Frozen	262.55	99.30%	180	0.658	28	1	48	36	12
RJLC1-T1R2	Tumor	Frozen	295.77	99.40%	232	0.897	35	5	15	14	1
RJLC1-T1R3	Tumor	Frozen	281.14	99.40%	219	0.877	33	3	25	23	2
RJLC1-T1R4	Tumor	Frozen	281.36	99.40%	229	0.797	32	3	25	25	0
RJLC1-T2	Tumor	Frozen	249.27	99.30%	296	0.758	26	2	199	199	0
RJLC2-N	Normal	Frozen	249.33	99.40%	NA	NA	NA	NA	NA	NA	NA
RJLC2-T1	Tumor	Frozen	256.62	99.40%	173	0.578	21	2	26	26	0
RJLC2-T2	Tumor	Frozen	265.06	99.40%	177	0.458	20	3	34	32	2
RJLC2-T3	Tumor	Frozen	263.22	99.40%	167	0.538	20	2	49	47	2
RJLC3-N	Normal	Frozen	243.74	99.40%	NA	NA	NA	NA	NA	NA	NA
RJLC3-T1	Tumor	Frozen	234.68	99.50%	443	0.857	35	4	88	88	0
RJLC3-T2	Tumor	Frozen	211.45	99.10%	525	0.818	30	9	58	44	14
RJLC3-T3	Tumor	Frozen	225.54	99.30%	224	0.797	31	13	73	72	1
RJLC4-N	Normal	Frozen	243.43	99.40%	NA	NA	NA	NA	NA	NA	NA
RJLC4-T1R1	Tumor	Frozen	221.46	99.30%	679	1.500	59	11	311	308	3
RJLC4-T1R2	Tumor	Frozen	235.33	99.40%	531	1.375	51	10	747	714	33
RJLC4-T1R3	Tumor	Frozen	214.65	99.30%	441	1.356	52	8	282	279	3
RJLC4-T2	Tumor	Frozen	204.98	99.20%	495	0.619	28	1	32	30	2
RJLC4-T3	Tumor	Frozen	212.78	99.30%	662	0.638	26	3	130	102	28

Supplementary Table 2: Driver mutation analysis

Human_Symbol	Chromosome	Position	Ref_Allele	Alt_Allele	Variant_Classification	ACChange	dbSNP_RS	COSMIC	CGC	BerVogelstein125	Comprehensive4v35	SMG127	Tumor_Sample_Name	U2B3_u23t	U2B3_u23twr	U2B3_u23hdv	U2B3_u23t
EGFR	7	5525915	T	G	Missense_Mutation	DSTFM_017723:exon4:c.5252A>G;G178R							R4.C11.T1R1	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
EGFR	7	5525915	T	G	Missense_Mutation	EGFR.NM_005228:exon21:c.1257G>G.L858R	rs121434568	COSM224a.NSCLCN		OncoGene	High Confidence Drive	4.60%	R4.C11.T1R1	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
EGFR	7	5525915	T	G	Missense_Mutation	SPEG.NM_005878:exon3:c.G175A>A.A297			OSM140561				R4.C11.T1R1	0.21,0.79,1.0	0.011,0.0	0.166,0.0	1.1,0.0
RECQL4	8	145738379	C	T	Missense_Mutation	RECQL4.NM_004200:exon16:c.G200A>G.G89D			n basal cell				R4.C11.T1R1	-	-	-	-
STAG2	20	39742014	A	T	Missense_Mutation	STAG2.NM_006003:exon29:c.A322T>T.K1074			elanoma.Ev	TSG	High Confidence Drive	2.20%	R4.C11.T1R1	0.01,0.99,0.0	0.921,0.0	0.987,0.0	1.00,1.00,0.0
TOP1	20	39742014	A	T	Missense_Mutation	TOP1.NM_003286:exon15:c.A437A>G.A48V			AML*				R4.C11.T1R1	0.1,0.0	0.99,0.0	1.0	1.1,0.0
PLG1	20	39801264	G	A	Missense_Mutation	PLG1.NM_002680:exon28:c.G319A>A.P1037			ingiosarcom		High Confidence Drive	-	R4.C11.T1R1	0.1,0.0	0.99,0.0	1.0	1.1,0.0
MYH11	18	15841968	C	T	Missense_Mutation	MYH11.NM_002474:exon17:c.G2116A>G.E79K			AML*				R4.C11.T1R2	0.1,0.0	0.98,0.0	1.0	1.1,0.0
DST	6	56505297	C	T	Missense_Mutation	DSTFM_017723:exon4:c.G32A>G.G178R			AML*				R4.C11.T1R2	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
PLG1	20	39801264	G	C	Missense_Mutation	PLG1.NM_002680:exon28:c.G292T>C.P578S			ingiosarcom		High Confidence Drive	4.60%	R4.C11.T1R2	0.75,0.25,1.0	0.03,0.0	0.073,0.0	1.1,0.0
EGFR	7	5525915	T	G	Missense_Mutation	EGFR.NM_005228:exon21:c.1257G>G.L858R	rs121434568	COSM224a.NSCLCN		OncoGene	High Confidence Drive	4.60%	R4.C11.T1R2	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
SPEG	2	220209843	A	T	Missense_Mutation	SPEG.NM_005878:exon3:c.G175A>A.A297			OSM140561				R4.C11.T1R2	0.21,0.79,1.0	0.011,0.0	0.166,0.0	1.1,0.0
RECQL4	8	145738379	C	T	Missense_Mutation	RECQL4.NM_004200:exon16:c.G200A>G.G89D			n basal cell				R4.C11.T1R2	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
STAG2	20	39742014	A	T	Missense_Mutation	STAG2.NM_006003:exon29:c.A322T>T.K1074			elanoma.Ev	TSG	High Confidence Drive	2.20%	R4.C11.T1R2	0.01,0.99,0.0	0.921,0.0	0.987,0.0	1.00,1.00,0.0
TOP1	20	39742014	A	T	Missense_Mutation	TOP1.NM_003286:exon15:c.A437T>G.A48V			AML*				R4.C11.T1R2	0.1,0.0	0.99,0.0	1.0	1.1,0.0
DST	6	56505297	C	T	Missense_Mutation	DSTFM_017723:exon4:c.G32A>G.G178R			AML*				R4.C11.T1R2	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
PTPRC	1	198717250	T	G	Missense_Mutation	PTPRC.NM_009021:exon24:c.T227T>G.Y79D			TALL				R4.C11.T1R2	0.1,0.0	0.99,0.0	1.0	1.1,0.0
EGFR	7	5525915	T	G	Missense_Mutation	EGFR.NM_005228:exon21:c.1257G>G.L858R	rs121434568	COSM224a.NSCLCN		OncoGene	High Confidence Drive	4.60%	R4.C11.T1R3	0.01,0.99,0.0	0.99,0.0	1.0	1.00,1.00,0.0
SPEG	2	220209843	A	T	Missense_Mutation	SPEG.NM_005878:exon3:c.G175A>A.A297			OSM140561				R4.C11.T1R3	0.21,0.79,1.0	0.011,0.0	0.166,0.0	1.1,0.0
RECQL4	8	145738379	C	T	Missense_Mutation	RECQL4.NM_004200:exon16:c.G200A>G.G89D			n basal cell				R4.C11.T1R3	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
STAG2	20	39742014	A	T	Missense_Mutation	STAG2.NM_006003:exon29:c.A322T>T.K1074			elanoma.Ev	TSG	High Confidence Drive	2.20%	R4.C11.T1R3	0.01,0.99,0.0	0.921,0.0	0.987,0.0	1.00,1.00,0.0
TOP1	20	39742014	A	T	Missense_Mutation	TOP1.NM_003286:exon15:c.A437T>G.A48V			AML*				R4.C11.T1R3	0.1,0.0	0.99,0.0	1.0	1.1,0.0
DST	6	56505297	C	T	Missense_Mutation	DSTFM_017723:exon4:c.G32A>G.G178R			AML*				R4.C11.T1R3	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
EGFR	7	5525915	T	G	Missense_Mutation	EGFR.NM_005228:exon21:c.1257G>G.L858R	rs121434568	COSM224a.NSCLCN		OncoGene	High Confidence Drive	4.60%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
SPEG	2	220209843	A	T	Missense_Mutation	SPEG.NM_005878:exon3:c.G175A>A.A297			OSM140561				R4.C11.T1R4	0.21,0.79,1.0	0.011,0.0	0.166,0.0	1.1,0.0
RECQL4	8	145738379	C	T	Missense_Mutation	RECQL4.NM_004200:exon16:c.G200A>G.G89D			n basal cell				R4.C11.T1R4	0.01,0.99,0.0	0.921,0.0	0.987,0.0	1.00,1.00,0.0
STAG2	20	39742014	A	T	Missense_Mutation	STAG2.NM_006003:exon29:c.A322T>T.K1074			elanoma.Ev	TSG	High Confidence Drive	2.20%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
TOP1	20	39742014	A	T	Missense_Mutation	TOP1.NM_003286:exon15:c.A437T>G.A48V			AML*				R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
DST	6	56505297	C	T	Missense_Mutation	DSTFM_017723:exon4:c.G32A>G.G178R			AML*				R4.C11.T1R4	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
EGFR	7	5525915	T	G	Missense_Mutation	EGFR.NM_005228:exon21:c.1257G>G.L858R	rs121434568	COSM224a.NSCLCN		OncoGene	High Confidence Drive	4.60%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
SPEG	2	220209843	A	T	Missense_Mutation	SPEG.NM_005878:exon3:c.G175A>A.A297			OSM140561				R4.C11.T1R4	0.21,0.79,1.0	0.011,0.0	0.166,0.0	1.1,0.0
RECQL4	8	145738379	C	T	Missense_Mutation	RECQL4.NM_004200:exon16:c.G200A>G.G89D			n basal cell				R4.C11.T1R4	0.01,0.99,0.0	0.921,0.0	0.987,0.0	1.00,1.00,0.0
STAG2	20	39742014	A	T	Missense_Mutation	STAG2.NM_006003:exon29:c.A322T>T.K1074			elanoma.Ev	TSG	High Confidence Drive	2.20%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
TOP1	20	39742014	A	T	Missense_Mutation	TOP1.NM_003286:exon15:c.A437T>G.A48V			AML*				R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
DST	6	56505297	C	T	Missense_Mutation	DSTFM_017723:exon4:c.G32A>G.G178R			AML*				R4.C11.T1R4	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
EGFR	7	5525915	T	G	Missense_Mutation	EGFR.NM_005228:exon21:c.1257G>G.L858R	rs121434568	COSM224a.NSCLCN		OncoGene	High Confidence Drive	4.60%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
SPEG	2	220209843	A	T	Missense_Mutation	SPEG.NM_005878:exon3:c.G175A>A.A297			OSM140561				R4.C11.T1R4	0.21,0.79,1.0	0.011,0.0	0.166,0.0	1.1,0.0
RECQL4	8	145738379	C	T	Missense_Mutation	RECQL4.NM_004200:exon16:c.G200A>G.G89D			n basal cell				R4.C11.T1R4	0.01,0.99,0.0	0.921,0.0	0.987,0.0	1.00,1.00,0.0
STAG2	20	39742014	A	T	Missense_Mutation	STAG2.NM_006003:exon29:c.A322T>T.K1074			elanoma.Ev	TSG	High Confidence Drive	2.20%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
TOP1	20	39742014	A	T	Missense_Mutation	TOP1.NM_003286:exon15:c.A437T>G.A48V			AML*				R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
DST	6	56505297	C	T	Missense_Mutation	DSTFM_017723:exon4:c.G32A>G.G178R			AML*				R4.C11.T1R4	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
EGFR	7	5525915	T	G	Missense_Mutation	EGFR.NM_005228:exon21:c.1257G>G.L858R	rs121434568	COSM224a.NSCLCN		OncoGene	High Confidence Drive	4.60%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
SPEG	2	220209843	A	T	Missense_Mutation	SPEG.NM_005878:exon3:c.G175A>A.A297			OSM140561				R4.C11.T1R4	0.21,0.79,1.0	0.011,0.0	0.166,0.0	1.1,0.0
RECQL4	8	145738379	C	T	Missense_Mutation	RECQL4.NM_004200:exon16:c.G200A>G.G89D			n basal cell				R4.C11.T1R4	0.01,0.99,0.0	0.921,0.0	0.987,0.0	1.00,1.00,0.0
STAG2	20	39742014	A	T	Missense_Mutation	STAG2.NM_006003:exon29:c.A322T>T.K1074			elanoma.Ev	TSG	High Confidence Drive	2.20%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
TOP1	20	39742014	A	T	Missense_Mutation	TOP1.NM_003286:exon15:c.A437T>G.A48V			AML*				R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
DST	6	56505297	C	T	Missense_Mutation	DSTFM_017723:exon4:c.G32A>G.G178R			AML*				R4.C11.T1R4	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
EGFR	7	5525915	T	G	Missense_Mutation	EGFR.NM_005228:exon21:c.1257G>G.L858R	rs121434568	COSM224a.NSCLCN		OncoGene	High Confidence Drive	4.60%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
SPEG	2	220209843	A	T	Missense_Mutation	SPEG.NM_005878:exon3:c.G175A>A.A297			OSM140561				R4.C11.T1R4	0.21,0.79,1.0	0.011,0.0	0.166,0.0	1.1,0.0
RECQL4	8	145738379	C	T	Missense_Mutation	RECQL4.NM_004200:exon16:c.G200A>G.G89D			n basal cell				R4.C11.T1R4	0.01,0.99,0.0	0.921,0.0	0.987,0.0	1.00,1.00,0.0
STAG2	20	39742014	A	T	Missense_Mutation	STAG2.NM_006003:exon29:c.A322T>T.K1074			elanoma.Ev	TSG	High Confidence Drive	2.20%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
TOP1	20	39742014	A	T	Missense_Mutation	TOP1.NM_003286:exon15:c.A437T>G.A48V			AML*				R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
DST	6	56505297	C	T	Missense_Mutation	DSTFM_017723:exon4:c.G32A>G.G178R			AML*				R4.C11.T1R4	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
EGFR	7	5525915	T	G	Missense_Mutation	EGFR.NM_005228:exon21:c.1257G>G.L858R	rs121434568	COSM224a.NSCLCN		OncoGene	High Confidence Drive	4.60%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.00,1.00,0.0
SPEG	2	220209843	A	T	Missense_Mutation	SPEG.NM_005878:exon3:c.G175A>A.A297			OSM140561				R4.C11.T1R4	0.21,0.79,1.0	0.011,0.0	0.166,0.0	1.1,0.0
RECQL4	8	145738379	C	T	Missense_Mutation	RECQL4.NM_004200:exon16:c.G200A>G.G89D			n basal cell				R4.C11.T1R4	0.01,0.99,0.0	0.921,0.0	0.987,0.0	1.00,1.00,0.0
STAG2	20	39742014	A	T	Missense_Mutation	STAG2.NM_006003:exon29:c.A322T>T.K1074			elanoma.Ev	TSG	High Confidence Drive	2.20%	R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
TOP1	20	39742014	A	T	Missense_Mutation	TOP1.NM_003286:exon15:c.A437T>G.A48V			AML*				R4.C11.T1R4	0.1,0.0	0.99,0.0	1.0	1.1,0.0
DST	6	56505297	C	T	Missense_Mutation	DSTFM_017723:exon4:c.G32A>G.G178R			AML*				R4.C11.T1R4	0.58,0.42,1.0	1.0	1.0	0.83,0.83,3.0
EGFR	7	5525915															

Supplementary Table 3: Driver mutation prevalence in lung cancer samples

Driver genes	Prevalence in pan-lung cancer of TCGA (n=1144 samples)	Prevalence in LUAC of TCGA (n=230 samples)	Mutations identified in this study	Mutated tumors	Mutations functionally implicated in lung tumorigenesis
KRAS	23.0%	36.0%	G12C; G12D	RJLC2-T2; RJLC3-T3	Yes
EGFR	14.0%	17.0%	L858R; E746-A750 deletion	RJLC1-T1; RJLC1-T2; RJLC4-T1	Yes
ERBB2	4.0%	5.0%	Y772-A775 duplication	RJLC4-T2; RJLC4-T3	Yes
MET	5.0%	12.0%	Exon 14 splice site	RJLC2-T3	Yes
ARAF	2.7%	2.6%	S214C	RJLC3-T2	Yes
BRAF	7.0%	11.0%	D594G	RJLC2-T1	No
MAP2K1	1.7%	1.7%	E102-I103 deletion	RJLC3-T1	No

Supplementary Table 4: Neoantigen repertoires predicted by NetMHCpan algorithm

Sample	MutatedGene	Mutation information	Chr	Position	ref	alt	T_val	T(DV/DN)	N(DV/DN)	HLA	wildPeptide	Neoantigens	wildPeptide-Aff(nM)	Neoantigens-Aff(nM)
RJLC1-1	NBPF10	NM_01039703:exon6:c.7836G>A.L279W	1	145299787	G	A	0.12	3.22	0.17	HLA-A*11:01	SAGPLSSEK	SAGPWSSEK	135.7	73.8
RJLC1-1	SPEG	NM_005876:exon3:c.G775A>p.A259T	2	220309843	T	G	0.171	0.855555556	0.084027778	HLA-A*11:01	SAFSLYRGR	STFSLYRGR	309.5	42.5
RJLC1-1	PRR21	NM_01080835:exon1:c.C847T.p.P283S	2	240981553	G	A	0.167	3.15	1.21	HLA-A*11:01	GPSSMPLHPR	GPSSMPLHPR	134.5	76.5
RJLC1-1	PK2	NM_138733:exon1:c.A676T.p.M227L	6	49754222	T	A	0.08	26.300	0.157638889	HLA-A*11:01	OLIKMLDK	OLIKMLDK	1123.5	27
RJLC1-1	RSFH3	NM_031924:exon6:c.C1273A>p.P425I	6	158401816	G	T	0.118	0.984027778	0.088888889	HLA-A*11:01	SGYFYDPIR	SGYFYDPIR	556.2	313.4
RJLC1-1	RECQ4	NM_004260:exon16:c.G2606A>p.G869D	8	145738379	C	T	0.175	37.14	0.122222222	HLA-A*11:01	AVGGERVPVK	AVGGERVPVK	135.2	90.8
RJLC1-1	SERPIN5	NM_00624:exon3:c.C452T.p.T151M	14	95054151	C	T	0.151	50.281	0.289583333	HLA-A*11:01	FVFSAMKTYL	FVFSAMKTYL	1622.6	249.1
RJLC1-1	SERPIN5	NM_00624:exon3:c.C452T.p.T151M	14	95054151	C	T	0.151	50.281	0.289583333	HLA-A*11:01	FVFSAMKTYL	FVFSAMKTYL	1495	275.2
RJLC1-1	PLA2G4D	NM_178034:exon3:c.G160A>p.A54T	15	42379593	C	T	0.036	0.6	0.154861111	HLA-A*11:01	LQLSTAPGMK	LQLSTAPGMK	402.1	354.6
RJLC1-1	PLA2G4D	NM_178034:exon3:c.G160A>p.A54T	15	42379593	C	T	0.036	0.6	0.154861111	HLA-A*11:01	TAPGMKFKTK	TAPGMKFKTK	1452.9	244
RJLC1-1	TOP1	NM_003286:exon15:c.C1457T.p.A486V	20	39742614	C	T	0.118	0.65625	0.051388889	HLA-A*11:01	KLALRAGNEK	KLVRAGNEK	326.3	251.8
RJLC1-1	TOP1	NM_003286:exon15:c.C1457T.p.A486V	20	39742614	C	T	0.118	0.65625	0.051388889	HLA-A*11:01	LALRAGNEK	LVLRAGNEK	453	101.2
RJLC1-1	CHM	NM_000390:exon13:c.G1570C.p.V524L	X	85134009	C	G	0.064	0.311111111	0.045138889	HLA-A*11:01	SVVQKLFVPY	SVLQKLFVPY	97.4	88.7
RJLC1-1	STAG2	NM_006603:exon29:c.A3221T.p.K1074I	X	123220564	A	T	0.156	35.189	0.113944444	HLA-A*11:01	SKKSPKSTGK	SKKSPKSTGK	2400.8	112
RJLC1-1	STAG2	NM_006603:exon29:c.A3221T.p.K1074I	X	123220564	A	T	0.156	35.189	0.113944444	HLA-A*11:01	SKKSPKSTGK	SKKSPKSTGK	18407.8	118.9
RJLC1-1	STAG2	NM_006603:exon29:c.A3221T.p.K1074I	X	123220564	A	T	0.156	35.189	0.113944444	HLA-A*11:01	STVRSKSKK	STVRSKSKK	239.6	18.3
RJLC1-1	STAG2	NM_006603:exon29:c.A3221T.p.K1074I	X	123220564	A	T	0.156	35.189	0.113944444	HLA-A*11:01	SKKSPKSTGK	SKKSPKSTGK	11479.2	44.9
RJLC1-1	CYBRD1	NM_01256909:exon4:c.C413T.p.P138L	2	172411063	C	T	0.032	0.438888889	0.129166667	HLA-B*40:01	AYSTFFLEGVGF	AYSTFFLEGVGF	891	380.5
RJLC1-1	SERPIN5	NM_00624:exon3:c.C452T.p.T151M	14	95054151	C	T	0.151	50.281	0.289583333	HLA-A*11:01	KMLYLADTF	KMLYLADTF	1044.4	147.1
RJLC1-1	RALGAP2	NM_020343:exon10:c.G1222T.p.V408L	20	20610018	C	A	0.043	0.343055556	0.063194444	HLA-A*11:01	RGYVNFNEV	RGYVNFNEV	383.8	180.3
RJLC1-1	RALGAP2	NM_020343:exon10:c.G1222T.p.V408L	20	20610018	C	A	0.043	0.343055556	0.063194444	HLA-A*11:01	RGYVNFNEV	RGYVNFNEV	78.7	36.7
RJLC1-1	RALGAP2	NM_020343:exon10:c.G1222T.p.V408L	20	20610018	C	A	0.043	0.343055556	0.063194444	HLA-A*11:01	RGYVNFNEV	RGYVNFNEV	667.6	342.8
RJLC1-1	CYBRD1	NM_01256909:exon4:c.C413T.p.P138L	2	172411063	C	T	0.032	0.438888889	0.129166667	HLA-B*40:01	PEGVFNVL	LEGVFNVL	1314.5	32.8
RJLC1-1	WNT9B	NM_003396:exon3:c.C446T.p.P149L	17	44952578	C	T	0.038	0.652777778	0.185416667	HLA-B*40:01	MERCCTDDSP	MERCCTDDSL	19257.5	155.1
RJLC1-1	CHM	NM_000390:exon13:c.G1570C.p.V524L	X	85134009	C	G	0.064	0.311111111	0.045138889	HLA-A*11:01	REDESIV	REDESIV	1546.7	284.2
RJLC1-1	EPMZAI1P	NM_014805:exon3:c.C1024T.p.L342F	3	37033545	G	A	0.184	99.438	0.311805556	HLA-C*07:02	LRRGKTLK	FRRGKTLK	158	31
RJLC1-1	NBPF10	NM_01039703:exon6:c.7836G>A.L279W	1	145299787	T	G	0.19	0.784722222	0.101805556	HLA-A*11:01	SAGPLSSEK	SAGPWSSEK	135.7	73.8
RJLC1-1	TAF1B	NM_005680:exon13:c.C1317A>p.D439E	2	10059215	C	A	0.036	0.6	0.203472222	HLA-A*11:01	KPLYSFVDK	KPLYSFVDK	232.4	22.5
RJLC1-1	TAF1B	NM_005680:exon13:c.C1317A>p.D439E	2	10059215	C	A	0.036	0.6	0.203472222	HLA-A*11:01	KPLYSFVDK	KPLYSFVDK	764.6	76.7
RJLC1-1	MANEA	NM_024641:exon5:c.G1283T.p.R428L	6	96054175	G	T	0.034	0.733333333	0.214583333	HLA-A*11:01	NTVYLDYRPHK	NTVYLDYRPHK	1243.7	300.6
RJLC1-1	MANEA	NM_024641:exon5:c.G1283T.p.R428L	6	96054175	G	T	0.034	0.733333333	0.214583333	HLA-A*11:01	NTVYLDYRPHK	NTVYLDYRPHK	63.8	19.4
RJLC1-1	ERCC6L2	NM_01010895:exon6:c.G1099T.p.A367S	9	98678624	G	T	0.079	0.397916667	0.063888889	HLA-A*11:01	RKAMQRLAKK	RKAMQRLAKK	121.6	53.1
RJLC1-1	ERCC6L2	NM_01010895:exon6:c.G1099T.p.A367S	9	98678624	G	T	0.079	0.397916667	0.063888889	HLA-A*11:01	ATGRKSMQR	ATGRKSMQR	266.2	217.4
RJLC1-1	ERCC6L2	NM_01010895:exon6:c.G1099T.p.A367S	9	98678624	G	T	0.079	0.397916667	0.063888889	HLA-A*11:01	KVAFRKAARK	KVAFRKAARK	29.5	14
RJLC1-1	TF1	NM_032225:exon2:c.C140T.p.T47M	21	43783462	A	G	0.091	0.486111111	0.077083333	HLA-A*11:01	GYPISQCAK	GYPISQCAK	187.9	30.4
RJLC1-1	F9	NM_000133:exon8:c.G1012C.p.D338H	X	138643856	C	G	0.03	0.966666667	0.333333333	HLA-A*11:01	VTPICADK	VTPICIAHK	137	92
RJLC1-1	F9	NM_000133:exon8:c.G1012C.p.D338H	X	138643856	C	G	0.03	0.966666667	0.333333333	HLA-A*11:01	VTPICADK	VTPICIAHK	410.7	179.6
RJLC1-1	DGAT2	NM_010253891:exon2:c.T143G>p.L48R	11	75501254	T	G	0.106	0.332638889	0.044444444	HLA-A*11:01	LMYIFCTDCW	LMYIFCTDCW	226.1	83.2
RJLC1-1	SLC9A7	NM_001257291:exon15:c.G1790T.p.W597L	X	46480445	C	A	0.038	0.413888889	0.139583333	HLA-A*11:01	WIFRLWYSF	LIFRLWYSF	424.4	208.6
RJLC1-1	F9	NM_000133:exon8:c.G1012C.p.D338H	X	138643856	C	G	0.03	0.966666667	0.333333333	HLA-A*11:01	DEKYNIFLKF	DEKYNIFLKF	550.5	256.5
RJLC1-1	ADD3	NM_001121:exon2:c.A119C.p.N40S	10	111860530	A	G	0.046	0.504861111	0.11875	HLA-B*40:01	RERNMSPLD	RERNMSPLD	196.6	138.1
RJLC1-1	SLC9A7	NM_001257291:exon15:c.G1790T.p.W597L	X	46480445	C	A	0.038	0.413888889	0.139583333	HLA-A*11:01	KQESAWIFRL	KQESAWIFRL	506.2	314.5
RJLC1-1	SLC9A7	NM_001257291:exon15:c.G1790T.p.W597L	X	46480445	C	A	0.038	0.413888889	0.139583333	HLA-A*11:01	QESAWIFRL	QESAWIFRL	91.4	21.9
RJLC1-1	KIF26B	NM_018012:exon10:c.G2107C.p.G703R	1	245809431	C	G	0.101	0.430555556	0.069444444	HLA-C*07:02	GRRSLHLI	GRRSLHLI	3981.9	419.2
RJLC1-1	DLK1	NM_003836:exon5:c.G779A.p.S260N	14	101200860	A	C	0.032	0.377083333	0.138888889	HLA-C*07:02	TRLPSGYL	TRLPSGYL	3732.6	420.6
RJLC1-1	BRAF	NM_004333:exon15:c.A1781G.p.D594G	7	140453154	T	C	0.075	0.301388889	0.065277778	HLA-A*11:01	GDFGLATVK	GDFGLATVK	7382.2	396.7
RJLC1-1	CSMD3	NM_052900:exon3:c.G481T.p.V161F	8	114290854	C	A	0.219	61.217	0.147222222	HLA-A*11:01	SDFVSAHGFK	SDFVSAHGFK	1022.9	272.7
RJLC1-1	CSMD3	NM_052900:exon3:c.G481T.p.V161F	8	114290854	C	A	0.219	61.217	0.147222222	HLA-A*11:01	DFVSAHGFK	DFVSAHGFK	1152	290
RJLC1-1	CSMD3	NM_052900:exon3:c.G481T.p.V161F	8	114290854	C	A	0.219	61.217	0.147222222	HLA-A*11:01	FVSAHGFK	FVSAHGFK	112	28.7
RJLC1-1	F7	NM_01267554:exon6:c.G871T.p.R291W	13	117373044	C	T	0.127	59.199	0.193055556	HLA-A*11:01	MTQDCLQOSRK	MTQDCLQOSWK	680.1	340.9
RJLC1-1	RYR1	NM_01042723:exon9:c.A1286S>p.T4289A	19	39055854	A	G	0.286	0.173611111	0.008333333	HLA-A*11:01	ATAAGATAR	ATAAGATAR	184.8	184.6
RJLC1-1	SLC5A1	NM_001256314:exon7:c.G310A>p.A104T	22	32480452	A	G	0.106	25.211	0.180555556	HLA-A*11:01	EVGGYDAFMEK	EVGGYDAFMEK	512.8	298.3
RJLC1-1	SLC5A1	NM_001256314:exon7:c.G310A>p.A104T	22	32480452	A	G	0.106	25.211	0.180555556	HLA-A*11:01	YDAFMEKYMK	YDAFMEKYMK	1500	266.1
RJLC1-1	SLC5A1	NM_001256314:exon7:c.G310A>p.A104T	22	32480452	A	G	0.106	25.211	0.180555556	HLA-A*11:01	VGVDYDAFMEK	VGVDYDAFMEK	221.7	202.2
RJLC1-1	SLC5A1	NM_001256314:exon7:c.G310A>p.A104T	22	32480452	A	G	0.106	25.211	0.180555556	HLA-A*11:01	YDAFMEKYMK	YDAFMEKYMK	166.8	43.2
RJLC1-1	SLC5A1	NM_001256314:exon7:c.G310A>p.A104T	22	32480452	A	G	0.106	25.211	0.180555556	HLA-A*11:01	DAFMEKYMK	DFMEKYMK	2400.8	398.1
RJLC1-1	IL13RA2	NM_000640:exon9:c.C1090T.p.R364C	X	114239786	A	G	0.12	65.4861111	0.08125	HLA-A*11:01	LLRKPNTYK	LLRKPNTYK	326.5	286.4
RJLC1-1	IL13RA2	NM_000640:exon9:c.C1090T.p.R364C	X	114239786	A	G	0.12	65.4861111	0.08125	HLA-A*11:01	LLRKPNTYK	LLRKPNTYK	210.9	72.5
RJLC1-1	CSMD3	NM_052900:exon3:c.G481T.p.V161F	8	114290854	C	A	0.219	61.217	0.147222222	HLA-B*15:02	SDFVSAHGFK	SDFVSAHGFK	763.2	60.8
RJLC1-1	CSMD3	NM_052900:exon3:c.G481T.p.V161F	8	114290854	C	A	0.219	61.217	0.147222222	HLA-B*15:02	FVSAHGFKVY	FVSAHGFKVY	271	135.8
RJLC1-1	CSMD3	NM_052900:exon3:c.G481T.p.V161F	8	114290854	C	A	0.219	61.217	0.147222222	HLA-B*15:02	SLRLTDFVAF	SLRLTDFVAF	11626.4	116.6
RJLC1-1	CSMD3	NM_052900:exon3:c.G481T.p.V161F	8	114290854	C	A	0.219	61.217	0.147222222	HLA-B*15:02	VSAHGFKVY	VSAHGFKVY	776.1	190.9
RJLC1-1	CSMD3	NM_052900:exon3:c.G481T.p.V161F	8	114290854	C	A	0.219	61.217	0.147222222	HLA-B*				

RJLC2-T3	DPY19L2	NM_173812:exon5:c.T610C;p.C204R	12	64041124	A	G	0.053	0.215972222		0-59	HLA-C*14:02	CTFMGIMNL	RTFMGIMNL	1170.1	350.4
RJLC3-T1	LRR0C6	NM_001024611:exon1:c.A355G;p.N119D	4	52883425	T	C	0.156	25.135	0.159027778	HLA-A*02:01	LNLSNAIHL	LNLSNAIHL	1655.2	433.7	
RJLC3-T1	VPS13B	NM_017890:exon4:c.G8148T;p.Q2716H	8	100821734	G	T	0.041	0.077508333	0.201388889	HLA-A*02:01	SLIIVQVQL	SLIIVQVQL	392.5	103.3	
RJLC3-T1	MROH6	NM_001100878:exon3:c.C583G;p.R195G	8	144653856	G	C	0.062	0.3125	0.065277778	HLA-A*02:01	LPLRSLPADRV	LPLRSLPADRV	884.9	30.2	
RJLC3-T1	MROH6	NM_001100878:exon3:c.C583G;p.R195G	8	144653856	G	C	0.062	0.3125	0.065277778	HLA-A*02:01	CALLPRSLPA	CALLPRSLPA	529.9	379.4	
RJLC3-T1	MROH6	NM_001100878:exon3:c.C583G;p.R195G	8	144653856	G	C	0.062	0.3125	0.065277778	HLA-A*02:01	ALLPRSLPA	ALLPRSLPA	92.1	51.1	
RJLC3-T1	GOLGA2	NM_004486:exon19:c.G1939A;p.V647M	9	131021523	C	T	0.226	14.48	0.047222222	HLA-A*02:01	LQITQLVDQL	LQITQLVDQL	539.3	493.7	
RJLC3-T1	OR10G4	NM_001004462:exon1:c.G319A;p.G107R	11	123886600	G	A	0.048	0.777777778	0.292361111	HLA-A*02:01	GSTECFLYTV	GSTECFLYTV	571.3	431.3	
RJLC3-T1	TRAPP1	NM_0012120:exon4:c.C395G;p.S132C	17	7833967	G	C	0.13	0.972916667	0.115277778	HLA-B*27:05	RLDSYVRS	RLDSYVRS	104.1	66.7	
RJLC3-T1	PAGE2	NM_207339:exon4:c.C286G;p.P96A	X	55117857	C	G	0.029	0.456944444	0.243055556	HLA-A*02:01	GIMPTFDLTKV	GIMPTFDLTKV	798.4	314.8	
RJLC3-T1	PAGE2	NM_207339:exon4:c.C286G;p.P96A	X	55117857	C	G	0.029	0.456944444	0.243055556	HLA-A*02:01	IMPTFDLTKV	IMPTFDLTKV	1678.2	448.4	
RJLC3-T1	PAGE2	NM_207339:exon4:c.C286G;p.P96A	X	55117857	C	G	0.029	0.456944444	0.243055556	HLA-A*02:01	IMPTFDLTKV	IMPTFDLTKV	88.8	18.9	
RJLC3-T1	GLR4	NM_001024452:exon7:c.C757T;p.R253W	X	102974161	G	A	0.154	26.143	0.136805556	HLA-A*02:01	HLERQMYYL	HLERQMYYL	1389.5	51.8	
RJLC3-T1	GLR4	NM_001024452:exon7:c.C757T;p.R253W	X	102974161	G	A	0.154	26.143	0.136805556	HLA-A*02:01	RMQGYLIQM	RMQGYLIQM	208.3	144.8	
RJLC3-T1	GLR4	NM_001024452:exon7:c.C757T;p.R253W	X	102974161	G	A	0.154	26.143	0.136805556	HLA-A*02:01	RMQGYLI	RMQGYLI	1163.1	393.9	
RJLC3-T1	ZRANB2	NM_005455:exon1:c.A332C;p.D12A	1	71546644	T	G	0.134	32.207	0.229166667	HLA-A*11:01	GDWICPKDK	GDWICPKDK	16072.8	219.8	
RJLC3-T1	PITX1	NM_002653:exon2:c.A332C;p.N111S	5	134367036	T	G	0.202	65.256	0.200694444	HLA-A*11:01	RNRYPDMSMR	RNRYPDMSMR	6817.8	309.3	
RJLC3-T1	TNIP1	NM_001252386:exon13:c.C1348G;p.L450V	5	150415157	G	C	0.134	26.168	0.111111111	HLA-A*11:01	TLNSAQLKAFK	TLNSAQLKAFK	108.2	91.2	
RJLC3-T1	TNIP1	NM_001252386:exon13:c.C1348G;p.L450V	5	150415157	G	C	0.134	26.168	0.111111111	HLA-A*11:01	LSNAQLKAFK	LSNAQLKAFK	46.9	38.8	
RJLC3-T1	WNK2	NM_0069648:exon25:c.C6137A;p.T2046K	9	96062354	C	A	0.045	0.45	0.029166667	HLA-A*11:01	GGQWTVYHPT	GGQWTVYHPT	31424	128.4	
RJLC3-T1	WNK2	NM_0069648:exon25:c.C6137A;p.T2046K	9	96062354	C	A	0.045	0.45	0.029166667	HLA-A*11:01	GGWTVYHPT	GGWTVYHPT	33924.4	238.2	
RJLC3-T1	OR10G4	NM_001004462:exon1:c.G319A;p.G107R	11	123886600	A	G	0.048	0.777777778	0.292361111	HLA-A*11:01	QLVFHFLR	QLVFHFLR	17004.4	44.2	
RJLC3-T1	OR10G4	NM_001004462:exon1:c.G319A;p.G107R	11	123886600	G	A	0.048	0.777777778	0.292361111	HLA-A*11:01	QLVFHFLG	QLVFHFLR	15706.7	42.7	
RJLC3-T1	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.111	5.40	1.47	HLA-A*11:01	SFSWALDFCK	SFSWALDFCK	35.6	28.5	
RJLC3-T1	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.111	5.40	1.47	HLA-A*11:01	SFSWALDFCK	SFSWALDFCK	37.6	13.5	
RJLC3-T1	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.111	5.40	1.47	HLA-A*11:01	ALDFCKACWK	ALDFCKACWK	146.7	64.1	
RJLC3-T1	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.111	5.40	1.47	HLA-A*11:01	SFSWALDF	SFSWALDF	1138.2	486.1	
RJLC3-T1	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.111	5.40	1.47	HLA-A*11:01	SFSWALDFCK	SFSWALDFCK	52.7	23.7	
RJLC3-T1	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.111	5.40	1.47	HLA-A*11:01	LDFCKACWK	LDFCKACWK	3242.2	72.4	
RJLC3-T1	PAGE2	NM_207339:exon4:c.C286G;p.P96A	X	55117857	C	G	0.029	0.456944444	0.243055556	HLA-A*11:01	IMPTFDLTK	IMPTFDLTK	93.2	17.9	
RJLC3-T1	ARMCX2	NM_014782:exon5:c.G1531A;p.A511T	X	100911044	C	T	0.168	32.159	0.184027778	HLA-A*11:01	LVNSINFFR	LVNSINFFR	57.9	48.2	
RJLC3-T1	RNF17	NM_001184993:exon3:c.G1234T;p.V412L	13	25367478	G	T	0.172	36.173	0.225	HLA-B*13:01	VESSALVF	VESSALVF	377	258.6	
RJLC3-T1	PAGE2	NM_207339:exon4:c.C286G;p.P96A	X	55117857	C	G	0.029	0.456944444	0.243055556	HLA-B*13:01	REGIMPTFDL	REGIMPTFDL	799.5	490.4	
RJLC3-T1	GLR4	NM_001024452:exon7:c.C757T;p.R253W	X	102974161	G	A	0.154	26.143	0.136805556	HLA-B*13:01	LERQMYYLI	LERQMYYLI	832	81.0	
RJLC3-T1	GLR4	NM_001024452:exon7:c.C757T;p.R253W	X	102974161	G	A	0.154	26.143	0.136805556	HLA-B*13:01	LERQMYYLI	LERQMYYLI	569	47.3	
RJLC3-T1	VVAAS1	NM_001039500:exon5:c.G622A;p.A208T	1	20644081	G	A	0.052	0.868055556	0.214563333	HLA-B*27:05	WNKGLATLL	WNKGLATLL	508.2	461.4	
RJLC3-T1	GARS	NM_002047:exon13:c.A1697C;p.Y566S	7	30665933	A	C	0.167	8.40	0.042361111	HLA-B*27:05	KRFKQTLVY	KRFKQTLVY	347.6	156.2	
RJLC3-T1	GARS	NM_002047:exon13:c.A1697C;p.Y566S	7	30665933	A	C	0.167	8.40	0.042361111	HLA-B*27:05	KRFKQTLVY	KRFKQTLVY	253.9	222.9	
RJLC3-T1	GARS	NM_002047:exon13:c.A1697C;p.Y566S	7	30665933	A	C	0.167	8.40	0.042361111	HLA-B*27:05	KRFKQTLVY	KRFKQTLVY	44.1	23.4	
RJLC3-T1	OR10G4	NM_001004462:exon1:c.G319A;p.G107R	11	123886600	G	A	0.048	0.777777778	0.292361111	HLA-B*27:05	FLGSTEFLY	FLRSTECFLY	16946	366.9	
RJLC3-T1	OR10G4	NM_001004462:exon1:c.G319A;p.G107R	11	123886600	G	A	0.048	0.777777778	0.292361111	HLA-B*27:05	LGSTECFLY	LGSTECFLY	26717.9	331.1	
RJLC3-T1	TRAPP1	NM_0012120:exon4:c.C395G;p.S132C	17	7833967	G	C	0.13	0.972916667	0.115277778	HLA-B*27:05	RSRLDSYVRS	RSRLDSYVRS	635.8	326.4	
RJLC3-T1	TRAPP1	NM_0012120:exon4:c.C395G;p.S132C	17	7833967	G	C	0.13	0.972916667	0.115277778	HLA-B*27:05	FRSLDSYVR	FRSLDSYVR	146.2	139.3	
RJLC3-T1	TRAPP1	NM_0012120:exon4:c.C395G;p.S132C	17	7833967	G	C	0.13	0.972916667	0.115277778	HLA-B*27:05	RSRLDSYVRS	RSRLDSYVRS	870.3	397.3	
RJLC3-T1	TRAPP1	NM_0012120:exon4:c.C395G;p.S132C	17	7833967	G	C	0.13	0.972916667	0.115277778	HLA-B*27:05	RSRLDSYVRS	RSRLDSYVRS	45.6	26.7	
RJLC3-T1	TRAPP1	NM_0012120:exon4:c.C395G;p.S132C	17	7833967	G	C	0.13	0.972916667	0.115277778	HLA-B*27:05	FRSLDSYV	FRSLDSYV	551.3	493.7	
RJLC3-T1	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.111	5.40	1.47	HLA-B*27:05	RPRSFSWALD	RPRSFSWALD	2184	279.1	
RJLC3-T1	FCRL4	NM_031282:exon7:c.G1165A;p.A389T	1	157551405	C	T	0.086	3.32	1.44	HLA-C*03:04	AAGATGGLL	TAGATGGLL	561	462.6	
RJLC3-T1	LRR0C6	NM_001024611:exon1:c.A355G;p.N119D	4	52883425	T	C	0.156	25.135	0.159027778	HLA-C*03:04	LNLSNAIHL	LNLSNAIHL	33.2	26.1	
RJLC3-T1	PITX1	NM_002653:exon2:c.A332C;p.N111S	5	134367036	T	G	0.202	65.256	0.200694444	HLA-C*03:04	RNRYPDMSM	RNRYPDMSM	6887.4	312.8	
RJLC3-T1	C2CD0A	NM_207322:exon2:c.C125T;p.T421	15	62359937	C	T	0.149	24.137	0.131944444	HLA-C*03:04	TAACANVTL	TAACANVTL	10969.2	276.5	
RJLC3-T1	CAS3	NM_007359:exon7:c.A1779T;p.N300S	17	38319847	A	G	0.073	0.353472222	0.081944444	HLA-C*03:04	RSAACTGRM	RSAACTGRM	6128.7	165.6	
RJLC3-T1	MUC16	NM_0024890:exon3:c.C1771T;p.T5924I	19	9069675	A	G	0.105	0.713888889	0.134027778	HLA-C*03:04	TSSPSPVPL	ISSPSPVPL	1299.1	430.3	
RJLC3-T1	PAGE2	NM_207339:exon4:c.C286G;p.P96A	X	55117857	C	G	0.029	0.456944444	0.243055556	HLA-C*03:04	MPTFDLTKV	MPTFDLTKV	1228.5	186.5	
RJLC3-T1	PAGE2	NM_207339:exon4:c.C286G;p.P96A	X	55117857	C	G	0.029	0.456944444	0.243055556	HLA-C*03:04	MPTFDLTKV	MPTFDLTKV	3392.7	254.7	
RJLC3-T1	PAGE2	NM_207339:exon4:c.C286G;p.P96A	X	55117857	C	G	0.029	0.456944444	0.243055556	HLA-C*03:04	PTFDLTKV	ATFDLTKV	5463.4	113.2	
RJLC3-T1	VVAAS1	NM_001039500:exon5:c.G622A;p.A208T	1	20644081	G	A	0.052	0.868055556	0.214563333	HLA-C*15:02	LATLNTVE	LTLTNTVE	663	335.8	
RJLC3-T1	NASP	NM_001195193:exon8:c.G1658C;p.R553T	1	46080868	G	C	0.186	59.258	0.207638889	HLA-A*02:01	EVENRMAV	EVIENTMAV	1765.3	167.0	
RJLC3-T1	NASP	NM_001195193:exon8:c.G1658C;p.R553T	1	46080868	G	C	0.186	59.258	0.207638889	HLA-A*02:01	NRMVNLNEQV	NRMVNLNEQV	1495.6	369.3	
RJLC3-T1	PIK3CA	NM_006218:exon8:c.G1357C;p.E453Q	3	178928079	G	C	0.195	57.235	0.2125	HLA-A*02:01	GLEDLNPVIG	GLEDLNPVIG	888.8	147.0	
RJLC3-T1	PIK3CA	NM_006218:exon8:c.G1357C;p.E453Q	3	178928079	G	C	0.195	57.235	0.2125	HLA-A*02:01	GLEDLNPVIG	GLEDLNPVIG	1026.7	246.4	
RJLC3-T1	PIK3CA	NM_006218:exon8:c.G1357C;p.E453Q	3	178928079	G	C	0.195	57.235	0.2125	HLA-A*02:01	GLEDLNPVIG	GLEDLNPVIG	16812.7	489.3	
RJLC3-T1	PIK3CA	NM_006218:exon8:c.G1357C;p.E453Q	3	178928079	G	C	0.195	57.235	0.2125	HLA-A*02:01	GLEDLNPVIG	GLEDLNPVIG	53	14.5	
RJLC3-T1	SLC9B1	NM_001100874:exon6:c.A651C;p.L217F	4	103866352	T	G	0.153	0.864583333	0.088194444	HLA-A*02:01	WAFLLGFLVGA	WAFLLGFLVGA	623.6	332.9	
RJLC3-T1	SLC9B1	NM_001100874:exon6:c.A651C;p.L217F	4	103866352	T										

RJLC3-T3	PRAMEF11	NM_001146344:exon3:c.G683A;p.R228H	1	12887174	C	T	0.061	3.46	1:41 HLA-A*02:01	KLRLCLQKLYM	KLHCLQKLYM	2109.3	383.6
RJLC3-T3	FBOXA1	NM_001080410:exon2:c.C1003T;p.R335W	2	73493713	G	A	2.008	10.38	0.04375 HLA-A*02:01	FEIELLERA	FIEELLEWA	503.7	133.6
RJLC3-T3	HRH1	NM_001098211:exon2:c.T446C;p.L149P	3	11301169	T	C	0.125	35.244	0.217361111 HLA-A*02:01	ATILGAWFL	ATIPGAWFL	257.7	61.5
RJLC3-T3	CSN1S1	NM_001025104:exon11:c.C307A;p.L103I	4	70806707	C	A	0.095	0.338194444	0.58 HLA-A*02:01	RLNEYNQLQL	RLNEYNQIQL	98.5	67.9
RJLC3-T3	PLEC	NM_201378:exon25:c.C3200A;p.S1067Y	8	145003289	G	T	0.091	4.40	0.47 HLA-A*02:01	SLSAIYLELK	SLVAIYLELK	104.1	49.1
RJLC3-T3	TMEM245	NM_032012:exon15:c.T2210C;p.V737A	9	111800311	A	G	0.043	0.797916667	0.272222222 HLA-A*02:01	TMFGINIVFI	TMFGINIAFI	39.1	38.6
RJLC3-T3	TMEM245	NM_032012:exon15:c.T2210C;p.V737A	9	111800311	A	G	0.043	0.797916667	0.272222222 HLA-A*02:01	GINVIFPSA	GINVIFPSA	1059.6	251.7
RJLC3-T3	TMEM245	NM_032012:exon15:c.T2210C;p.V737A	9	111800311	A	G	0.043	0.797916667	0.272222222 HLA-A*02:01	RMFGINIVF	RMFGINIVF	659.2	457.8
RJLC3-T3	KRAS	NM_004985:exon2:c.G34T;p.G12C	12	25398285	C	A	0.37	74.126	0.140277778 HLA-A*11:01	VVVGAGGVGK	LVVVGAGGVGK	392.9	203.6
RJLC3-T3	DCT	NM_001922:exon8:c.A1498G;p.K500E	13	95092214	T	C	0.08	1.041666667	0.206944444 HLA-A*02:01	RLRKYGTPL	RLREYGTPL	1051.2	138.6
RJLC3-T3	ALDH1A3	NM_000693:exon13:c.G1477A;p.A493T	15	101454916	G	A	0.036	0.725	0.252777778 HLA-A*11:01	YLALEYTEVK	YTLALEYTEV	84.9	26.7
RJLC3-T3	MC2R	NM_000529:exon2:c.T184A;p.F62I	18	13885334	A	T	0.23	73.244	0.255555556 HLA-A*02:01	KNLOQPMYFF	KNLOQPMYFI	7092.3	149.4
RJLC3-T3	MC2R	NM_000529:exon2:c.T184A;p.F62I	18	13885334	A	T	0.23	73.244	0.255555556 HLA-A*02:01	NLQAPMYFF	NLQAPMYFI	3530.4	46.9
RJLC3-T3	C18orf63	NM_001174123:exon3:c.G221C;p.A71P	18	71987824	G	C	0.11	0.425694444	0.073611111 HLA-A*02:01	ILNQIWWVMAI	ILNQIWWVMPI	817.6	301.3
RJLC3-T3	C18orf63	NM_001174123:exon3:c.G221C;p.A71P	18	71987824	G	C	0.11	0.425694444	0.073611111 HLA-A*02:01	LNQIWWVMAI	LNQIWWVMPI	409.5	147.0
RJLC3-T3	C18orf63	NM_001174123:exon3:c.G221C;p.A71P	18	71987824	G	C	0.11	0.425694444	0.073611111 HLA-A*02:01	NQIWWVMAI	NQIWWVMPI	105.7	33.6
RJLC3-T3	MPP1	NM_00116640:exon1:c.C43A;p.H15N	X	154033606	G	T	0.134	0.784722222	0.110416667 HLA-A*02:01	SMHTALS DL	SMHTALS DL	96.4	47.1
RJLC3-T3	FSTL1	NM_007085:exon10:c.G806A;p.G269E	3	120118806	C	T	0.127	0.743055556	0.099305556 HLA-A*11:01	VTAMTCDGK	VTAMTCDCK	306.4	258.2
RJLC3-T3	PCDH13	NM_018933:exon1:c.C889T;p.P297S	5	140594584	C	T	0.082	26.292	0.2375 HLA-A*11:01	NPLTGEIELK	NLSLGEIELK	9636.1	264
RJLC3-T3	PCDH13	NM_018933:exon1:c.C889T;p.P297S	5	140594584	C	T	0.082	26.292	0.2375 HLA-A*11:01	PLTGEIELKK	PLTGEIELKK	2531.3	173.7
RJLC3-T3	PCDH13	NM_018933:exon1:c.C889T;p.P297S	5	140594584	C	T	0.082	26.292	0.2375 HLA-A*11:01	PLTGEIELK	SLTGEIELK	10884.2	272.1
RJLC3-T3	PLEC	NM_201378:exon25:c.C3200A;p.S1067Y	8	145003289	G	T	0.091	4.40	0.47 HLA-A*11:01	SLSAIYLELK	SLVAIYLELK	15.9	74.8
RJLC3-T3	PLEC	NM_201378:exon25:c.C3200A;p.S1067Y	8	145003289	G	T	0.091	4.40	0.47 HLA-A*11:01	SLSAIYLELK	SLVAIYLELK	8.2	7.6
RJLC3-T3	KRAS	NM_004985:exon2:c.G34T;p.G12C	12	25398285	C	A	0.37	74.126	0.140277778 HLA-A*11:01	VVVGAGGVGK	VVVGAGGVGK	271.4	165.8
RJLC3-T3	KRAS	NM_004985:exon2:c.G34T;p.G12C	12	25398285	C	A	0.37	74.126	0.140277778 HLA-A*11:01	VVVGAGGVGK	VVVGAGGVGK	139.3	90.6
RJLC3-T3	ALDH1A3	NM_000693:exon13:c.G1477A;p.A493T	15	101454916	G	A	0.036	0.725	0.252777778 HLA-A*11:01	YLALEYTEVK	YTLALEYTEV	416.4	74.3
RJLC3-T3	C18orf63	NM_001174123:exon3:c.G221C;p.A71P	18	71987824	G	C	0.11	0.425694444	0.073611111 HLA-A*11:01	VVWMAIPFYKA	VVWMAIPFYKY	11.1	10.1
RJLC3-T3	C18orf63	NM_001174123:exon3:c.G221C;p.A71P	18	71987824	G	C	0.11	0.425694444	0.073611111 HLA-A*11:01	VVWMAIPFYKA	VVWMAIPFYKY	197.1	152.6
RJLC3-T3	C18orf63	NM_001174123:exon3:c.G221C;p.A71P	18	71987824	G	C	0.11	0.425694444	0.073611111 HLA-A*11:01	VVWMAIPFYKA	VVWMAIPFYKY	6.2	5.8
RJLC3-T3	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.06	3.47	1:47 HLA-A*11:01	SFSWALDFCK	SFSWALDFCK	35.6	28.5
RJLC3-T3	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.06	3.47	1:47 HLA-A*11:01	SFSWALDFCK	SFSWALDFCK	37.6	13.5
RJLC3-T3	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.06	3.47	1:47 HLA-A*11:01	ALDFCKACWK	ALDFCKACWK	146.7	64.0
RJLC3-T3	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.06	3.47	1:47 HLA-A*11:01	SFSWALDF	SFSWALDF	1138.2	486.1
RJLC3-T3	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.06	3.47	1:47 HLA-A*11:01	SFSWALDFCK	SFSWALDFCK	52.7	23.7
RJLC3-T3	FUT3	NM_001097641:exon2:c.A1007C;p.D336A	19	5843844	T	G	0.06	3.47	1:47 HLA-A*11:01	LDFCKACWK	LDFCKACWK	3242.2	724.4
RJLC3-T3	MPP1	NM_00116640:exon1:c.C43A;p.H15N	X	154033606	G	T	0.134	0.784722222	0.110416667 HLA-A*11:01	GSMHTALS DL	GSMHTALS DL	370.9	314.3
RJLC3-T3	MPP1	NM_00116640:exon1:c.C43A;p.H15N	X	154033606	G	T	0.134	0.784722222	0.110416667 HLA-A*11:01	SMHTALS DL	SMHTALS DL	683.2	452.8
RJLC3-T3	LAMB2	NM_002292:exon17:c.C2281T;p.P761S	3	49163463	A	G	0.15	30.170	0.135416667 HLA-B*13:01	PSEACAPL	PSEACAPLI	1142.7	328.5
RJLC3-T3	PLEC	NM_201378:exon25:c.C3200A;p.S1067Y	8	145003289	G	T	0.091	4.40	0.47 HLA-B*13:01	LEQVRSLSAI	LEQVRSLSAI	953	317.6
RJLC3-T3	PLEC	NM_201378:exon25:c.C3200A;p.S1067Y	8	145003289	G	T	0.091	4.40	0.47 HLA-B*13:01	EQVRSLSAI	EQVRSLSAI	1165.5	194
RJLC3-T3	LAMB2	NM_002292:exon17:c.C2281T;p.P761S	3	49163463	A	G	0.15	30.170	0.135416667 HLA-C*03:04	SPSEACAPL	SSSEACAPL	638.8	33.9
RJLC3-T3	TMEM245	NM_032012:exon15:c.T2210C;p.V737A	9	111800311	A	G	0.043	0.797916667	0.272222222 HLA-C*03:04	NIAPFISAL	NIAPFISAL	671	419.2
RJLC3-T3	TMEM245	NM_032012:exon15:c.T2210C;p.V737A	9	111800311	A	G	0.043	0.797916667	0.272222222 HLA-C*03:04	IVFISAL	IFAPISAL	2381.1	494.5
RJLC4-T1	RSG1	NM_003907:exon4:c.G505A;p.V169I	1	16599207	C	T	0.122	0.420138889	0.046527778 HLA-A*11:01	GVVRMVGSK	GVVRMVGSK	81.5	46
RJLC4-T1	SRSF11	NM_001190987:exon7:c.T597G;p.N199K	1	70703114	T	G	0.194	12.50	0.04375 HLA-A*11:01	KLMSTVDPKLN	KLMSTVDPKLN	8648.5	336.3
RJLC4-T1	SRSF11	NM_001190987:exon7:c.T597G;p.N199K	1	70703114	T	G	0.194	12.50	0.04375 HLA-A*11:01	LMSTVDPKLN	LMSTVDPKLN	33738.4	240.6
RJLC4-T1	LRIG2	NM_014813:exon12:c.C1421C;p.P474R	1	113650323	C	G	0.216	61.222	0.145138889 HLA-A*11:01	SVNVSCHAP	SVNVSCHAP	28463.9	363
RJLC4-T1	NBPF8	NM_001037501:exon12:c.T1121G;p.M574R	1	148017582	A	C	0.25	3.09	1:13 HLA-A*11:01	STLSIPPER	STLSIPPER	6287.6	80.2
RJLC4-T1	SULT1C3	NM_001008743:exon1:c.C297T;p.T10M	2	108863679	C	T	0.152	48.267	0.281944444 HLA-A*11:01	KIEKNAPTMEK	KIEKNAPMMEK	134	118.1
RJLC4-T1	ZFP62	NM_001172638:exon2:c.T2399G;p.L80R	5	160276096	A	C	0.328	79.162	0.154861111 HLA-A*11:01	KAYISHSSL	KAYISHSSR	22978.2	256.4
RJLC4-T1	RP1-257A7.4	NM_001242698:exon4:c.G186C;p.M62I	6	13281740	G	C	0.19	0.713888889	0.045138889 HLA-A*11:01	AMISAHCNLR	AISAHCNLR	415.6	254.1
RJLC4-T1	VPS13B	NM_017890:exon48:c.A8849C;p.N2950T	8	100831792	A	C	0.08	0.645833333	0.122222222 HLA-A*11:01	SLOPIWPYK	SLOPIWPYK	148.3	141.5
RJLC4-T1	VPS13B	NM_017890:exon48:c.A8849C;p.N2950T	8	100831792	A	C	0.08	0.645833333	0.122222222 HLA-A*11:01	SLOPIWPYK	SLOPIWPYK	25.7	21.9
RJLC4-T1	VPS13B	NM_017890:exon48:c.A8849C;p.N2950T	8	100831792	A	C	0.08	0.645833333	0.122222222 HLA-A*11:01	SLOPIWPYK	SLOPIWPYK	494.4	35.3
RJLC4-T1	HHLA1	NM_001145095:exon8:c.C561G;p.I187M	8	133100120	G	C	0.341	72.139	0.152777778 HLA-A*11:01	IFICVMTGK	MFICVMTGK	701.1	317.4
RJLC4-T1	C9orf3	NM_001193329:exon1:c.T41G;p.L14R	9	97522106	T	G	0.108	0.852777778	0.127777778 HLA-A*11:01	LMAMTSHLVK	RMAMTSHLVK	333.4	189.8
RJLC4-T1	COQ4	NM_016035:exon2:c.A188G;p.N63S	9	131085412	A	G	0.123	0.652777778	0.045138889 HLA-A*11:01	SAAMALYNPYR	SAAMALYSPYR	495.7	396.9
RJLC4-T1	COQ4	NM_016035:exon2:c.A188G;p.N63S	9	131085412	A	G	0.123	0.652777778	0.045138889 HLA-A*11:01	SAAMALYNPYR	SAAMALYSPYR	242.3	161.6
RJLC4-T1	COQ4	NM_016035:exon2:c.A188G;p.N63S	9	131085412	A	G	0.123	0.652777778	0.045138889 HLA-A*11:01	SAAMALYNPYR	SAAMALYSPYR	36.9	25.2
RJLC4-T1	COQ4	NM_016035:exon2:c.A188G;p.N63S	9	131085412	A	G	0.123	0.652777778	0.045138889 HLA-A*11:01	SAAMALYNPYR	SAAMALYSPYR	78.1	49.4
RJLC4-T1	COQ4	NM_016035:exon2:c.A188G;p.N63S	9	131085412	A	G	0.123	0.652777778	0.045138889 HLA-A*11:01	AMALYNPYR	AMALYSPYR	83	54.9
RJLC4-T1	MED27	NM_004269:exon5:c.G607T;p.V203F	9	134769346	C	A	0.1	0.622916667	0.095833333 HLA-A*11:01	IVMRSFLDR	IVMRSFLDR	1601	314.8
RJLC4-T1	MED27	NM_004269:exon5:c.G607T;p.V203F	9	134769346	C	A	0.1	0.622916667	0.095833333 HLA-A*11:01	KVLRVIVMR	KVLRVIVMR	661.6	186.3
RJLC4-T1	SCUBE2	NM_001170690:exon18:c.G2411C;p.R804T	11	9042605	C	G	0.148	31.178	0.176388889 HLA-A*11:01	SKVSRFLRPYK	SKVSRFLRPYK	198	97.8
RJLC4-T1	SCUBE2	NM_001170690:exon18:c.G2411C;p.R804T	11	9042605	C	G	0.148	31.178	0.176388889 HLA-A*11:01	SKVSRFLRPYK	SKVSRFLRPYK	292.5	106.8
RJLC4-T1	SCUBE2	NM_001170690:exon18:c.G2411C;p.R804T	11	9042605	C	G	0.148	31.178	0.176388889 HLA-A*11:01	SKVSRFLRPYK	SKVSRFLTPYK	11.7	8.7
RJLC4-T1	SCUBE2	NM_001170690:exon18:c.G2411C;p.R804T	11	9042605	C	G	0.148	31.178	0.17				

RJLC4-T1	MED27	NM_004269:exon5:c.G607T.p.V203F	9	134769346	C	A	0.1	0.622916667	0.095833333	HLA-C*03:04	IVVMRSLFI	IVFMRSLFI	1310.5	488.4
RJLC4-T1	GPRC5A	NM_003979:exon2:c.T133A.p.F45I	12	13061316	T	A	0.24	56.177	0.284027778	HLA-C*03:04	VAFMLTLPI	VAIMLTLPI	15.6	13.5
RJLC4-T1	TMC3	NM_001080532:exon14:c.C1535A.p.S512Y	15	81636370	G	T	0.193	37.155	0.101388889	HLA-C*03:04	SIIDMLFTV	YIIDMLFTV	886.7	156
RJLC4-T1	S1PR5	NM_001166215:exon2:c.A298G.p.T100A	19	10625390	T	C	0.151	34.191	0.2125	HLA-C*03:04	ILLSGPLTL	ILLSGPLAL	89.9	52.6
RJLC4-T1	S1PR5	NM_001166215:exon2:c.A298G.p.T100A	19	10625390	T	C	0.151	34.191	0.2125	HLA-C*03:04	LTLKSPAL	LALKSPAL	71.5	15.9
RJLC4-T2	SRSF11	NM_001190987:exon7:c.T597G.p.N199K	1	70703114	T	G	0.141	9.55	0.04375	HLA-A*11:01	KLMSTVDPKLN	KLMSTVDPKLN	8648.5	336.3
RJLC4-T2	SRSF11	NM_001190987:exon7:c.T597G.p.N199K	1	70703114	T	G	0.141	9.55	0.04375	HLA-A*11:01	LMSTVDPKLN	LMSTVDPKLN	33738.4	240.6
RJLC4-T2	ADCY10	NM_018417:exon4:c.G2611T.p.L87F	1	167871285	C	A	0.145	9.53	0.102083333	HLA-A*11:01	KVLFSGDILK	KVIFSGDILK	201.3	116.6
RJLC4-T2	CCDC132	NM_017667:exon25:c.A2460C.p.L820F	7	92979342	A	C	0.076	0.551388889	0.132638889	HLA-A*11:01	QHNIYVDALLK	QHNIYVDALFK	810.7	375.5
RJLC4-T2	CCDC132	NM_017667:exon25:c.A2460C.p.L820F	7	92979342	A	C	0.076	0.551388889	0.132638889	HLA-A*11:01	HNIYVDALLK	HNIYVDALFK	73	32.4
RJLC4-T2	CCDC132	NM_017667:exon25:c.A2460C.p.L820F	7	92979342	A	C	0.076	0.551388889	0.132638889	HLA-A*11:01	NIYVDALLK	NIYVDALFK	51.9	24.4
RJLC4-T2	MYOF	NM_133337:exon34:c.A3833C.p.Y1278S	10	95111003	T	G	0.085	0.736805556	0.139583333	HLA-A*11:01	LYMVPQGIT	LSMVPQGIT	9937.8	479.3
RJLC4-T2	UBL7	NM_001286740:exon5:c.A397G.p.M133V	15	74743852	T	C	0.034	0.36875	0.144444444	HLA-A*11:01	AVFKMLSNKE	AVFKVLSNKE	224.9	221.9
RJLC4-T2	KCNQ5	NM_001160134:exon10:c.T1260G.p.F420L	6	73900308	T	G	0.115	0.422916667	0.067361111	HLA-B*40:01	GEASSRIMKF	GEASSRIMKL	508.4	93.2
RJLC4-T2	C5	NM_001735:exon8:c.T765G.p.F255L	9	123789546	A	C	0.111	0.425	0.055555556	HLA-B*40:01	FEITIKARYF	FEITIKARYL	1198.4	112.4
RJLC4-T2	UBL7	NM_001286740:exon5:c.A397G.p.M133V	15	74743852	T	C	0.034	0.36875	0.144444444	HLA-B*40:01	REAVFKML	REAVFKVL	720.9	326.3
RJLC4-T2	LMO7	NM_015842:exon1:c.A1887T.p.E1224V	13	76427233	A	T	0.055	0.804166667	0.224305556	HLA-B*55:02	LPGIMRRGE	YVLMRRGE	9281.9	355.4
RJLC4-T2	NAA11	NM_032693:exon1:c.A1887T.p.E63V	4	80246844	T	A	0.035	0.605555556	0.220833333	HLA-C*03:04	YVLAKMEEE	YVLAKMEEV	18273.4	248
RJLC4-T2	SLC9B1	NM_001100874:exon6:c.A651C.p.L217F	4	103866352	T	G	0.168	0.811805556	0.127083333	HLA-C*03:04	WAFLLGFVL	WAFLLGFVL	103	94.9
RJLC4-T2	CCDC132	NM_017667:exon25:c.A2460C.p.L820F	7	92979342	A	C	0.076	0.551388889	0.132638889	HLA-C*03:04	YVDALLKEF	YVDALFKEF	383.6	227.9
RJLC4-T2	PAK6	NM_001276717:exon3:c.C224T.p.A75V	15	40558062	C	T	0.066	0.669444444	0.151388889	HLA-C*03:04	VVRGSAIMPV	VVRGSAIMPV	435	419.9
RJLC4-T3	MROH7	NM_001039464:exon19:c.C3214T.p.R1072W	1	55166924	C	T	0.103	0.381944444	0.063888889	HLA-A*11:01	KAVFKGRDQK	KAVFKGVDQK	243.9	129.5
RJLC4-T3	MROH7	NM_001039464:exon19:c.C3214T.p.R1072W	1	55166924	C	T	0.103	0.381944444	0.063888889	HLA-A*11:01	AVFKGRDQK	AVFKGVDQK	23.3	15.7
RJLC4-T3	SRSF11	NM_001190987:exon7:c.T597G.p.N199K	1	70703114	T	G	0.167	8.40	0.04375	HLA-A*11:01	KLMSTVDPKLN	KLMSTVDPKLN	8648.5	336.3
RJLC4-T3	SRSF11	NM_001190987:exon7:c.T597G.p.N199K	1	70703114	T	G	0.167	8.40	0.04375	HLA-A*11:01	LMSTVDPKLN	LMSTVDPKLN	33738.4	240.6
RJLC4-T3	HSD3B1	NM_000862:exon4:c.C689T.p.A230V	1	120056835	C	T	0.042	0.402083333	0.114583333	HLA-A*11:01	VVAHALALR	VVAHALALR	322.8	204.6
RJLC4-T3	MRS2	NM_001286266:exon3:c.A266T.p.Y89F	6	24412451	A	T	0.296	8.19	1.28	HLA-A*11:01	SVAPVFTVYK	SVAPVFTVFK	17.2	13.2
RJLC4-T3	MRS2	NM_001286266:exon3:c.A266T.p.Y89F	6	24412451	A	T	0.296	8.19	1.28	HLA-A*11:01	VAPVFTVYK	VAPVFTVFK	55.6	37.9
RJLC4-T3	ALDH1A3	NM_000693:exon9:c.C997T.p.R333W	15	101440893	C	T	0.05	0.439583333	0.120833333	HLA-A*11:01	FVRSVVEYAK	FVRSVVEYAK	267.8	127.3
RJLC4-T3	MRS2	NM_001286266:exon3:c.A266T.p.Y89F	6	24412451	A	T	0.296	8.19	1.28	HLA-B*55:02	APVFTVYKA	APVFTVYKA	203.9	112.7
RJLC4-T3	TTC21B	NM_024753:exon18:c.A2456C.p.E819A	2	166767842	T	G	0.128	0.463888889	0.109722222	HLA-C*03:04	LAHEPVNEL	LAHAPVNEL	11.9	10.2
RJLC4-T3	MUC4	NM_018406:exon2:c.C6506T.p.A2169V	3	195511945	G	A	0.333	2.04	0.10	HLA-C*03:04	ASTGHATSL	VSTGHATSL	51.7	25.6
RJLC4-T3	SLC9B1	NM_001100874:exon6:c.A651C.p.L217F	4	103866352	T	G	0.167	0.8125	0.127083333	HLA-C*03:04	WAFLLGFVL	WAFLLGFVL	103	94.9
RJLC4-T3	MRS2	NM_001286266:exon3:c.A266T.p.Y89F	6	24412451	A	T	0.296	8.19	1.28	HLA-C*03:04	SVAPVFTVY	SVAPVFTVY	757.8	47.8
RJLC4-T3	EML3	NM_153265:exon19:c.A2246C.p.E749A	11	62371212	T	G	0.093	0.532638889	0.060416667	HLA-C*03:04	MSNSGDYEI	MSNSGDYAI	150	53.8
RJLC4-T3	MGA	NM_001164273:exon15:c.A5167C.p.I1723L	15	42035325	A	C	0.096	0.675	0.13125	HLA-C*03:04	SSLGSPVPI	SSLGSPVPI	246.1	75.9

Supplementary Table 5: Clonal numbers inferred by PyClone or SciClone analyses

Sample ID	PyClone	SciClone
RJLC1-T1R1	2	1
RJLC1-T1R2	3	3
RJLC1-T1R3	2	2
RJLC1-T1R4	2	3
RJLC1-T2	2	3
RJLC2-T1	2	1
RJLC2-T2	2	1
RJLC2-T3	2	2
RJLC3-T1	4	5
RJLC3-T2	2	6
RJLC3-T3	4	4
RJLC4-T1R1	5	4
RJLC4-T1R2	4	4
RJLC4-T1R3	5	3
RJLC4-T2	2	1
RJLC4-T3	3	6

Supplementary Table 6: Branch:trunk indices (ITB) from WES for MSLCs

Patient ID	Age	Sex	TNM stage	Smoking status	branch/trunk	ITB
RJLC1-T1	64	Female	pTisN0M0	Never	30/23	1.304
RJLC4-T1	60	Female	pT1N0M0	Never	60/35	1.714
L001	59	Female	pT2aN1M0	Former	4/15	0.267
L002	78	Male	pT3N2M0	Current	16/12	1.333
L004	73	Male	pT3N0M0	Current	7/23	0.304
L011	49	Female	pT2aN0M0	Current	3/29	0.103
LS01	69	Male	pT2aN0M0	Former	3/24	0.125
317	55	Male	N0	Former	16/1424	0.011
499	73	Female	N0	Former	2/98	0.02
292	57	Female	N0	Never	2/20	0.1
324	68	Female	N0	Current	23/147	0.156
283	50	Male	N2	Former	2/11	0.182
339	73	Male	N0	Never	13/40	0.325
472	74	Female	N0	Former	16/41	0.39
330	59	Female	N0	Former	116/223	0.52
4990	75	Male	N1	Former	107/138	0.775
270	62	Female	N1	Former	71/72	0.986
356	69	Female	N0	Never	27/27	1

Supplementary Table 7: Mutation co-occurrence in the same cancer gene of MSLC

	Pa1		Pa4		Pa5		Pa6			L003	
	T1	T3	T1	T2	T1	T2	T1	T2	T3	R2	R4
EGFR			L858R	S229C	L858R	L858R	L858R	L858R	L858R	L858R	L858R
KRAS	G12A	G12V									

Pa1,4,5,6 (Liu, Y. et al. Genomic heterogeneity of multiple synchronous lung cancer. *Nat Commun* 7, 13200 (2016))

L003 (de Bruin, E.C. et al. Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. *Science* 346, 251-256 (2014))