Table S2. Somatic mutations identified by whole-exome sequencing of a metastatic lung nodule* from Patient 3737

Gene Symbol	Gene Description	Transcript Accession	Mutation Position		Mutation Type	Consequence	% Mutant Reads*
			Nucleotide (genomic)	Amino Acid (protein)			
ALK	anaplastic lymphoma receptor tyrosine kinase	CCDS33172.1	chr2_29996620-29996620_C_T	137R>H	Substitution	Nonsynonymous coding	30%
AR	androgen receptor	CCDS14387.1	chrX_66858483-66858483__C	NA	Insertion	Frameshift	31%
CD93	CD93 molecule	CCDS13149.1	chr20_23012929-23012929_C_T	634R>Q	Substitution	Nonsynonymous coding	26%
DIP2C	DIP2 disco-interacting protein 2 homolog C (Drosophila)	CCDS7054.1	chr10_365545-365545_C_T	NA	Substitution	Splice site acceptor	25%
ERBB2IP	erbb2 interacting protein	CCDS3990.1	chr5_65385316-65385316_A_G	805E>G	Substitution	Nonsynonymous coding	59%
FCER1A	Fc fragment of IgE; high affinity I; receptor for; alpha polypeptide	CCDS1184.1	chr1_157544227-157544227_G_C	219D>H	Substitution	Nonsynonymous coding	30%
GRXCR1	glutaredoxin; cysteine rich 1	CCDS43225.1	chr4_42590102-42590102_C_T	21A>V	Substitution	Nonsynonymous coding	18%
HLA-DOA	HLA class II histocompatibility antigen, DO alpha chain precursor	CCDS4763.1	chr6_33085209-33085209_C_T	NA	Substitution	Splice site donor	36%
KIF9	kinesin family member 9	CCDS2752.1	chr3_47287859-47287859_T_C	155T>A	Substitution	Nonsynonymous coding	20%
KLHL6	kelch-like 6 (Drosophila)	CCDS3245.2	chr3_184692410-184692413_CAGA_	NA	Deletion	Frameshift	20%
LHX9	LIM homeobox 9	CCDS1393.1	chr1_196164923-196164923_A_	NA	Deletion	Frameshift	21%
LONRF3	LON peptidase N-terminal domain and ring finger 3	CCDS35374.1	chrX_118007666-118007666_A_C	NA	Substitution	Splice site donor	10%
NAGS	N-acetylglutamate synthase	CCDS11473.1	chr17_39440355-39440355_G_A	412R>H	Substitution	Nonsynonymous coding	29%
NLRP2	NLR family; pyrin domain containing 2	CCDS12913.1	chr19_60186650-60186650_G_T	591S>I	Substitution	Nonsynonymous coding	32%
PDZD2	PDZ domain containing 2	CCDS34137.1	chr5_32124833-32124833_A_	NA	Deletion	Frameshift	30%
POU5F2	POU domain, class 5, transcription factor 2	NM_153216	chr5_93102847-93102847_A_C	60V>G	Substitution	Nonsynonymous coding	34%
RAC3	ras-related C3 botulinum toxin substrate 3 (rho family; small GTP binding protein Rac3)	CCDS11798.1	chr17_77584690-77584690_C_A	125T>N	Substitution	Nonsynonymous coding	27%
RAP1GDS1	RAP1; GTP-GDP dissociation stimulator 1	CCDS43253.1	chr4_99532209-99532209_C_A	198L>I	Substitution	Nonsynonymous coding	19%
RASA1	RAS p21 protein activator (GTPase activating protein) 1	CCDS34200.1	chr5_86703757-86703757_C_T	589R>C	Substitution	Nonsynonymous coding	63%
RETSAT	retinol saturase (all-trans-retinol 13;14-reductase)	CCDS1972.1	chr2_85424308-85424308_C_T	553R>K	Substitution	Nonsynonymous coding	11%
SEC24D	SEC24 family; member D (S. cerevisiae)	CCDS3710.1	chr4_119872085-119872085_A_G	901M>T	Substitution	Nonsynonymous coding	18%
SENP3	SUMO1/sentrin/SMT3 specific peptidase 3	ENST00000321337	chr17_7408824-7408824_A_G	292M>V	Substitution	Nonsynonymous coding	33%
SLIT1	slit homolog 1 (Drosophila)	CCDS7453.1	chr10_98753840-98753840_G_C	1280N>K	Substitution	Nonsynonymous coding	45%

TARBP1	TAR (HIV-1) RNA binding protein 1	CCDS1601.1	chr1_232649342-232649342_C_A	655G>V	Substitution	Nonsynonymous coding	18%
TGM6	transglutaminase 6	CCDS13025.1	chr20_2332325-2332325_G_A	398D>N	Substitution	Nonsynonymous coding	51%
TTC39C	tetratricopeptide repeat domain 39C	CCDS32804.1	chr18_19966475-19966475_A_C	503N>T	Substitution	Nonsynonymous coding	24%

* The tumor nodule was estimated to be approximately 70% tumor by pathological analysis of an H&E stained section.