SUPPLEMENTALS

Supplemental Table 1. 54 gene panel (N = 1 patient (1 sample)): identifies potential tumor-related genomic alterations within 54 cancer-related genes including amplifications in *ERBB2, EGFR*, and *MET*. Only non-synonymous alterations were analyzed.

GENES WITH COMPLETE EXON COVERAGE					
ALK	*APC*	*AR*	*BRAF*	18 GENES **3 Copy Number Variations in BOLD**	
CDKN2A	***EGFR***	***ERBB2***	*FBXW7*		
KRAS	***MET***	*MYC*	*NOTCH1*		
NRAS	*PIK3CA*	*PTEN*	*PROC*		
RB1	*TP53*				
GENES WITH CRITICAL EXON COVERAGE 36 GENES					
ABL1	*AKT1*	*ATM*	*CDH1*	*CSF1R*	*CTNNB1*
ERBB4	*EZH2*	*FGFR1*	*FGFR2*	*FGFR3*	*FLT3*
GNA11	*GNAQ*	*GNAS*	*HNF1A*	*HRAS*	*IDH1*
IDH2	*JAK2*	*JAK3*	*KDR*	*KIT*	*MLH1*
MPL	*NPM1*	*PDGFRA*	*PTPN11*	*RET*	*SMAD4*
SMARCB1	***SMO***	***SRC***	***STK11***	***TERT***	***VHL***

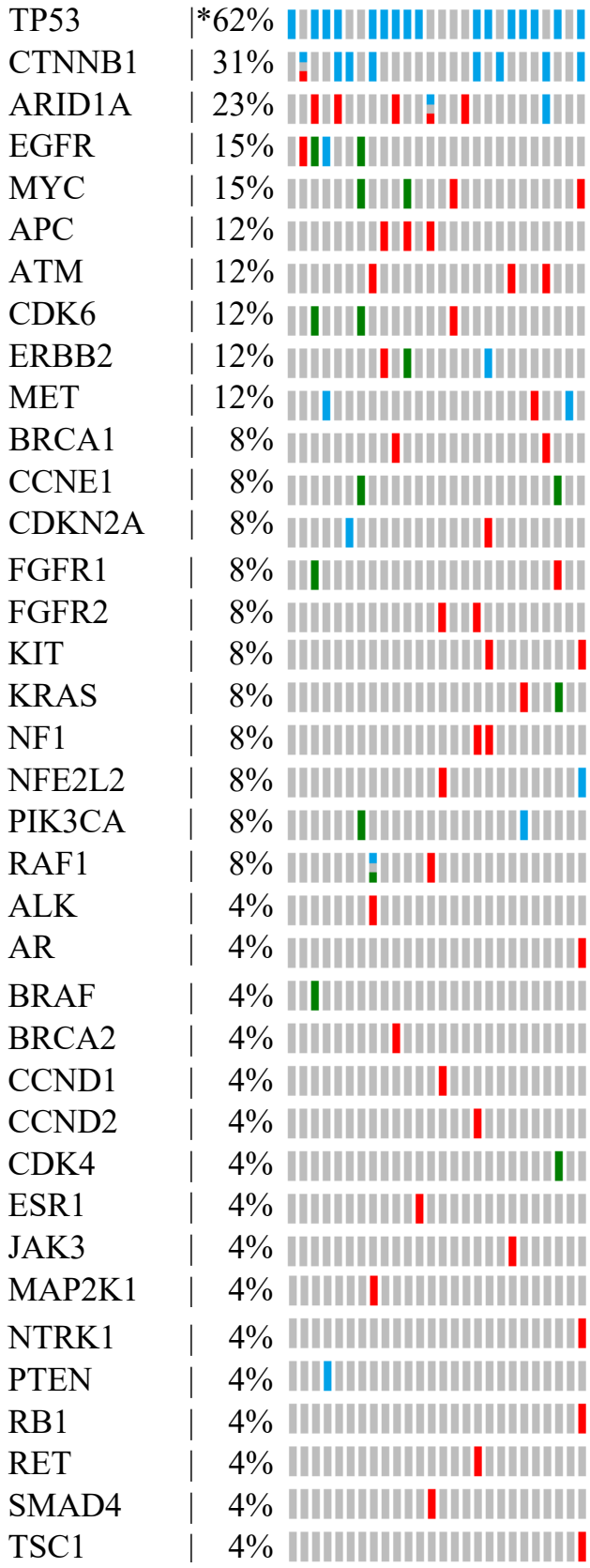
Supplemental Table 2. 68 gene panel (N = 23 patients (28 samples)), comprising amplifications in 16 genes as well as some fusions and indels. Only non-synonymous alterations were analyzed.

POINT MUTATIONS			AMPLIFICATIONS	FUSIONS		INDELS
AKT1	*ALK*	***APC***	***AR***	*AR*	*ALK*	*EGFR* exon 19 deletions
AFAR	***ARID1A***	*ATM*	***BRAF***	*BRAF*	*RET*	*EGFR* exon 20 insertions
BRCA1	***BRCA2***	***CCND1***	***CCDN2***	*CCNE1*	*ROS1*	
CCNE1	*CDH1*	***CDK4***	***CDK6***	*CDK4*	*NTRK1*	
CDKN2A	***CDKN2B***	*CTNNB1*	***EGFR***	*CDK6*		
ERBB2	*ESR1*	*EZH2*	*FBXW7*	*EGFR*		
FGFR1	***FGFR2***	*FGFR3*	*GATA3*	*ERBB2*		
GNA11	*GNAQ*	*GNAS*	*HNF1A*	*FGFR1*		
HRAS	*IDH1*	*IDH2*	*JAK2*	*FGFR2*		
JAK3	***KIT***	***KRAS***	*MAP2K1*	*KIT*		
MAP2K2	***MET***	*MLH1*	*MPL*	*KRAS*		
MYC	***NF1***	*NFE2L2*	*NOTCH1*	*MET*		
NPM1	***NRAS***	*NTRK1*	***PDGFRA***	*MYC*		
PIK3CA	***PTEN***	*PTPN11*	***RAF1***	*PDGFRA*		
RET	*RHEB*	*RHOA*	*RIT1*	*PIK3CA*		
ROS1	*SMAD4*	*SMO*	*SRC*	*RAF1*		
STK11	*TERT*	***TP53***	*VHL*	*Complete exon coverage for genes in **bold**		

Supplemental Table 3: 70 gene panel (N = 3 patients (3 samples))

Complete Exon Sequencing									
Point Mutations (SNVs) (70 Genes)						**Amplifications (CNVs)** (18 Genes)		**Fusions** (6 Genes)	**Indels** (3 Genes)
AKT1	*ALK*	*APC*	*AR*	*ARAF*	*ARID1A*	*AR*	*BRAF*	*ALK*	*EGFR**
ATM	*BRAF*	*BRCA1*	*BRCA2*	*CCND1*	*CCND2*	*CCND1*	*CCND2*	*FGFR2*	*ERBB2**
CCNE1	*CDH1*	*CDK4*	*CDK6*	*CDKN2A*	*CDKN2B*	*CCNE1*	*CDK4*	*FGFR3*	*MET***
CTNNB1	*EGFR*	*ERBB2*	*ESR1*	*EZH2*	*FBXW7*	*CDK6*	*EGFR*	*NTRK1*	
FGFR1	*FGFR2*	*FGFR3*	*GATA3*	*GNA11*	*GNAQ*	*ERBB2*	*FGFR1*	*RET*	
GNAS	*HNF1A*	*HRAS*	*IDH1*	*IDH2*	*JAK2*	*FGFR2*	*KIT*	*ROS1*	
JAK3	*KIT*	*KRAS*	*MAP2K1*	*MAP2K2*	*MET*	*KRAS*	*MET*		
MLH1	*MPL*	*MYC*	*NF1*	*NFE2L2*	*NOTCH1*	*MYC*	*PDGFRA*		
NPM1	*NRAS*	*NTRK1*	*PDGFRA*	*PIK3CA*	*PTEN*	*PIK3CA*	*RAF1*		
PTPN11	*RAF1*	*RB1*	*RET*	*RHEB*	*RHOA*				*exons 19 & 20
RIT1	*ROS1*	*SMAD4*	*SMO*	*SRC*	*STK11*				**exon 14 skipping
TERT	*TP53*	*TSC1*	*VHL*						

Supplemental Figure 1: Oncoprint of genomic alterations at the molecular level in 26 HCC patients



*Percentages represent the number of patients that exhibited at least one of the respective mutation out of 26 patients with HCC.

Genetic Alteration Characterized Mutation VUS Amplification