Patient ID	Response[1]	Cycles on Treatment[1]	CTNNB1 Mutation	Predicted Effect	Allelic Frequency	Gene Panel
105-023	PR (-73%)	16+ cycles (on going)	Exon 2-4 deletion	Stabilizing	Unknown	Foundation One
104-004	PR (-67%)	13+ cycles (on going)	Not detected	NA	NA	Archer VariantPlex Solid Tumor
108-003	PR (-40%)	10 cycles (off treatment)	C-term truncation: Q27Ter	Unknown	6%	Archer VariantPlex Solid Tumor
109-008	PR (-35%)	3+ cycles (on going)	S45F	Stabilizing	2%	Archer VariantPlex Solid Tumor
109-003	SD (-7%)	9+ cycles (on going)	I35N T41I	Most likely stabilizing Stabilizing	3% 4%	Archer VariantPlex Solid Tumor
104-014	SD (-6%)	4+ cycles (on going)	Not detected	NA	NA	Solid Tumor Hotspot NGS
109-001	SD (-2%)	3 cycles (off treatment)	Not detected	NA	NA	Archer VariantPlex Solid Tumor
104-016	PD (13%)	2 cycles (off treatment)	Not detected	NA	NA	Guardant 360
104-017	PD (8%)	2 cycles (off treatment)	Not detected	NA	NA	Foundation One
104-020	PD (69%)	2 cycles (off treatment)	Not detected	NA	NA	Archer VariantPlex Solid Tumor
104-018	PD (90%)	2 cycles (off treatment)	D6N	Most likely no effect	11%	Archer VariantPlex Solid Tumor
104-023	PD (260%)	2 cycles (off treatment)	Not detected	NA	NA	Archer VariantPlex Solid Tumor

[1] Response as of 8/3/16, best response. Cycles are 28 day periods – treatment delays may prolong or adjust these durations.
Legend: Partial response (PR). Stable disease (SD). Progressive disease (PD).
[2]For the Archer VariantPlex Solid Tumor Gene Panel, the Archer Analysis (version 4.1.0.5) default parameters were used to identify CTNNB1 mutations

FIG. 1

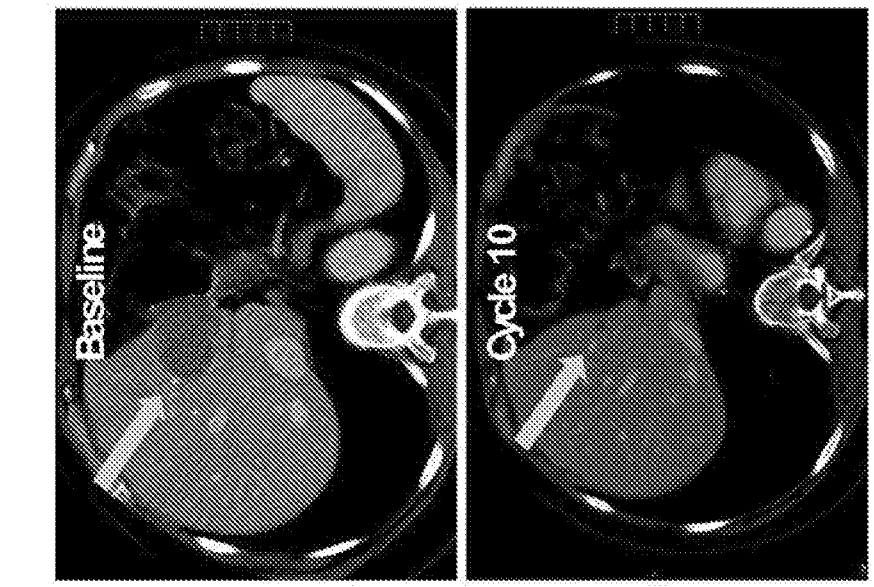
B)
Baseline
Cycle 10

FIG. 2B

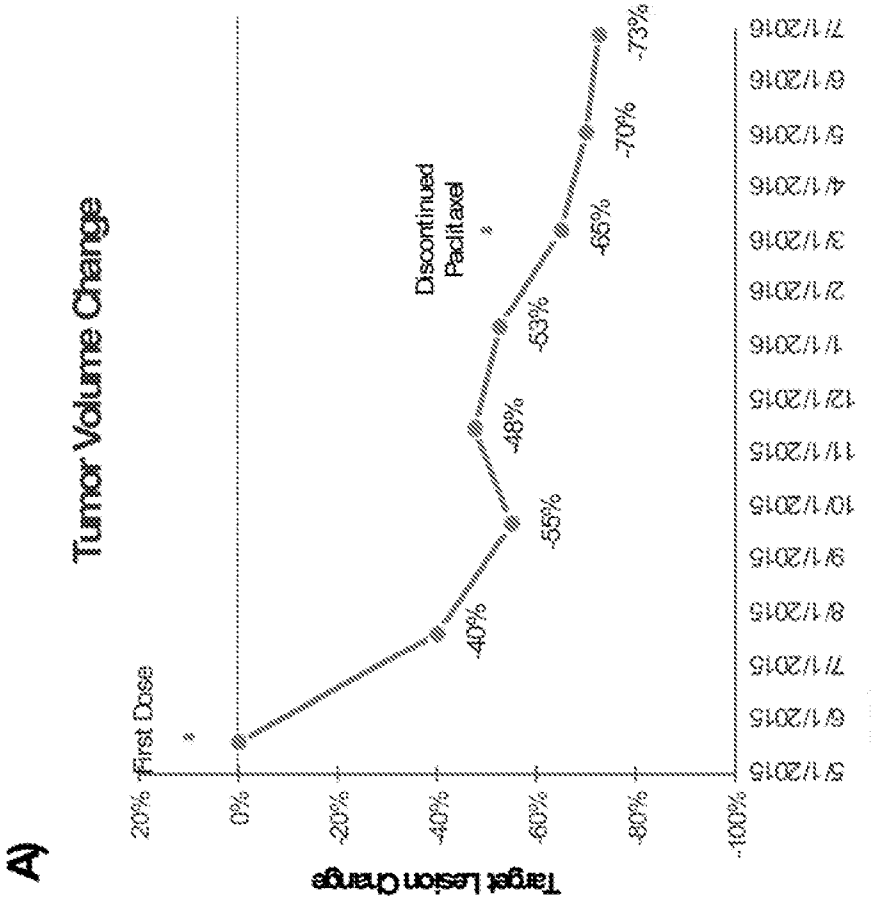
A)
Tumor Volume Change
Target Lesion Change
20%
0%
-20%
-40%
-60%
-80%
-100%
First Dose
-40%
-55%
-48%
-53%
-65%
-70%
-73%
Discontinued Paclitaxel
5/1/2015
6/1/2015
7/1/2015
8/1/2015
9/1/2015
10/1/2015
11/1/2015
12/1/2015
1/1/2016
2/1/2016
3/1/2016
4/1/2016
5/1/2016
6/1/2016
7/1/2016

FIG. 2A

CTNNB1 genomic DNA sequence (includes introns)
(SEQ ID NO: 1)

Exon 2
ATGGCTACTCAAGgtttgtgtcattaaatctttagttactgaattggggc 50
tctgcttcgttgccattaagccagtctggctgagatccccctgctttcct
ctctccctgcttacttgtcaggctacctttttgctccatttttctgctcact
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tgagctaaccctggctatcattctgcttttcttggctgtctttcagattt
gactttatttctaaaaatatttcaatgggtcatatcacagattcttttttt
tttaaattaaagtaacatttccaatctactaatgctaatactgtttcgta 400
Exon 3
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AGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGACTCTGGAATCC 500
ATTCTGGTGCCACTACCACAGCTCCTTCTCTGAGTGGTAAAGGCAATCCT
GAGGAAGAGGATGTGGATACCTCCCAAGTCCTGTATGAGTGGGAACAGGG
ATTTTCTCAGTCCTTCACTCAAGAACAAGTAGCTGgtaagagtattattt
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gtgtataatagtttaaataaaatgttgtggtgaagaaaagagagtaatag
caatgtcacttttaccatttaggatagcaaatacttaggtaaatgctgaa
Exon 4
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FIG. 3A

```
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gaaacgaaggaaggagatggaaagttttgggaatttaagaaatactaata
gtaaggaggaagaaaggtttgaggtgaggctattgagatagacttagcag 2500
atctcatagggctttgtagagcatgtttaaaagcacaatgggaaatttca
gcagaagcctgaaatgatgaaatttgtttttagaaaattggggcagtgtt
gaaagggaagatatacagggaatgaaaggacaagcatgaatgatcatttt
atggtatctgtttttaaggtggatataattaggaaaattaaagggccaaa
tgatgaggagttaagtgccagttctggttcaaattttcagtgaatcagtt
ttgatataactttcatcttagggcattactcttgcctaccaacatagttt
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```

FIG. 3B

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```

FIG. 3C

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AACCTCACTTGCAATAATTATAAGAACAAGATGATGGTCTGCCAAGTGGG
TGGTATAGAGGCTCTTGTGCGTACTGTCCTTCGGGCTGGTGACAGGGAAG 9500
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tctctagctgttggatggctgtctaagcatagtgatcaataagtaggaat
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FIG. 3D

```
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CTTTGTCCCGCAAATCATGCACCTTTGCGTGAGCAGGGTGCCATTCCACG 10000
ACTAGTTCAGTTGCTTGTTCGTGCACATCAGGATACCCAGCGCCGTACGT
CCATGGGTGGGACACAGCAGCAATTTGTGGtaggtaaattcttacagtga
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agcctttagcagatgtgtacattgaagtctcagtttttcctcaagggcct
ttttctccttgtctcttagCGACATATGCAGCTGCTGTTTTGTTCCGAAT
GTCTGAGGACAAGCCACAAGATTACAAGAAACGGCTTTCAGTTGAGCTGA
CCAGCTCTCTCTTCAGAACAGAGCCAATGGCTTGGAATGAGgtagggaaa 12500
```

FIG. 3E

```
tgtgagcagttatttatctggtagtttcctagagcaggtatggcagcttg 12550
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aactataatacaagctttaaagagtctgttcagaatcattacaaataagt
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ctgcttctctcctctctcttttgccttccttcttgcctattttgttgaca
ccctgactcttctagATCCTAGCTATCGTTCTTTTCACTCTGGTGGATAT
GGCCAGGATGCCTTGGGTATGGACCCCATGATGGAACATGAGATGGGTGG 15000
CCACCACCCTGGTGCTGACTATCCAGTTGATGGGCTGCCAGATCTGGGGC
ATGCCCAGGACCTCATGGATGGGCTGCCTCCAGGTGACAGCAATCAGCTG 15100
GCCTGGTTTGATACTGACCTGTAA                             15124
```

FIG. 3F

Uterine Tumor ID	CTNNB1 Mutation
TCGA-AP-A0LV-01	D32G
TCGA-BK-A0CB-01	D32G
TCGA-AX-A05U-01	D32N
TCGA-A5-A0GV-01	D32N
TCGA-BG-A0VX-01	D32N
TCGA-B5-A0T9-01	D32N
TCGA-A5-A0GX-01	D32Y
TCGA-B5-A0K6-01	D32Y
TCGA-BG-A0W2-01	D32Y
TCGA-D1-A17S-01	D32Y
TCGA-AX-A05W-01	G34E
TCGA-A5-A0VQ-01	G34E
TCGA-A5-A0GN-01	G34R
TCGA-AP-A0LL-01	G34R
TCGA-BG-A0MU-01	G34R
TCGA-B5-A11F-01	G34R
TCGA-D1-A102-01	G34R
TCGA-D1-A17N-01	G34R
TCGA-B5-A0WQ-01	G34V
TCGA-D1-A17M-01	G34V,D32N
TCGA-AX-A0J0-01	M553V,S37F
TCGA-D1-A16R-01	Q623E,I35S
TCGA-B5-A0JY-01	R453Q,D32N
TCGA-AX-A062-01	S33C
TCGA-BG-A0MO-01	S33C
TCGA-A5-A0R9-01	S33C
TCGA-B5-A0UT-01	S33C
TCGA-D1-A0ZN-01	S33C
TCGA-AP-A05N-01	S33F
TCGA-AX-A05T-01	S33F
TCGA-A5-A0GU-01	S33F

Esophageal Tumor ID	CTNNB1 Mutation
TCGA-R6-A6XQ-01	S33A
TCGA-R6-A8WG-01	S37F
TCGA-LN-A7HX-01	R90L
TCGA-L5-A4OJ-01	V136A
TCGA-L5-A8NM-01	X561_splice
TCGA-L5-A8NR-01	Q68* (nonsense/truncating)
TCGA-R6-A8W5-01	E571* (nonsense/truncating)
TCGA-VR-AA4G-01	S681F
TCGA-V5-A7RB-01	K335T

Liver Tumor ID	CTNNB1 Mutation
TCGA-DD-AACP-01	D32A,S33Y
TCGA-EP-A2KC-01	D32G
TCGA-G3-A5SL-01	D32G
TCGA-DD-A73D-01	D32G
TCGA-ED-A7PZ-01	D32G
TCGA-G3-AAV1-01	D32G
TCGA-DD-AACB-01	D32G
TCGA-DD-AAW1-01	D32G
TCGA-UB-A7MD-01	D32N
TCGA-G3-AAV5-01	D32N
TCGA-DD-AAVY-01	D32N
TCGA-DD-A73E-01	D32V
TCGA-MI-A75H-01	D32V
TCGA-RC-A6M4-01	D32V
TCGA-CC-A7IK-01	D32V
TCGA-CC-A7IL-01	D32V
TCGA-DD-A4NF-01	D32Y
TCGA-G3-AAV3-01	D32Y
TCGA-DD-AAW2-01	E54D,T41A
TCGA-EP-A3RK-01	G34E
TCGA-ZS-A9CG-01	G34R
TCGA-DD-AAC8-01	G34R
TCGA-DD-A119-01	G34V
TCGA-G3-A3CJ-01	G34V
TCGA-CC-A9FW-01	G34V
TCGA-DD-A1EL-01	H36P
TCGA-DD-A4NI-01	H36P
TCGA-DD-AACD-01	H36P
TCGA-G3-A3CK-01	H36P,S33P
TCGA-ZP-A9D4-01	I35S
TCGA-DD-AACX-01	

FIG. 4A

TCGA-A5-A0GW-01	S33F
TCGA-D1-A0ZU-01	S33F
TCGA-D1-A17C-01	S33F
TCGA-AP-A0LN-01	S33Y
TCGA-B5-A0K7-01	S33Y
TCGA-B5-A0JT-01	S33Y
TCGA-D1-A165-01	S33Y
TCGA-AP-A0LG-01	S37A
TCGA-B5-A11V-01	S37A
TCGA-BS-A0V7-01	S37A
TCGA-AP-A0LJ-01	S37C
TCGA-B5-A0K0-01	S37C
TCGA-BG-A0LW-01	S37C
TCGA-AX-A0IS-01	S37C
TCGA-D1-A15Z-01	S37C
TCGA-D1-A17T-01	S37C
TCGA-BG-A0M3-01	S37C,S646F
TCGA-A5-A0GM-01	S37F
TCGA-BG-A0MG-01	S37F
TCGA-BG-A0VT-01	S37F
TCGA-D1-A0ZQ-01	S37F
TCGA-D1-A16B-01	S37F
TCGA-D1-A16Q-01	S37F
TCGA-D1-A17R-01	S37F
TCGA-BG-A0MI-01	S37P
TCGA-AP-A0LE-01	S37P
TCGA-B5-A121-01	S45C
TCGA-BS-A0TG-01	S45F
TCGA-B5-A11Z-01	T41A
TCGA-A5-A0GI-01	T41I
TCGA-BS-A0UJ-01	T41I
TCGA-B5-A11U-01	T41I
TCGA-DD-AAVP-01	I35S
TCGA-EP-A12J-01	S33A
TCGA-FV-A4ZQ-01	S33C
TCGA-ED-A7XP-01	S33C
TCGA-G3-AAV4-01	S33C
TCGA-DD-AAE3-01	S33C
TCGA-DD-AAVX-01	S33C
TCGA-XR-A8TF-01	S33F
TCGA-DD-AACA-01	S33F
TCGA-DD-A116-01	S33P
TCGA-DD-A39V-01	S33P
TCGA-G3-A6UC-01	S33P
TCGA-DD-AADE-01	S33P,S45Y
TCGA-CC-A5UD-01	S33Y
TCGA-DD-AADD-01	S33Y
TCGA-KR-A7K0-01	S37A
TCGA-DD-AAEK-01	S37A
TCGA-UB-A7MC-01	S37C
TCGA-DD-AADG-01	S37C
TCGA-BW-A5NQ-01	S37F
TCGA-5C-A9VG-01	S37F
TCGA-DD-AAD0-01	S37Y
TCGA-4R-AA8I-01	S45F
TCGA-LG-A9QD-01	S45F
TCGA-ZP-A9CV-01	S45F
TCGA-3K-AAZ8-01	S45F
TCGA-BC-A10U-01	S45F,S45Ffs*5
TCGA-O8-A75V-01	S45P
TCGA-RG-A7D4-01	S45P
TCGA-NI-A8LF-01	S45P
TCGA-G3-AAV2-01	S45P
TCGA-G3-AAV6-01	S45P

FIG. 4B

TCGA-2Y-A9H1-01	S45P
TCGA-WX-AA47-01	S45P
TCGA-DD-AAEE-01	S45P
TCGA-DD-AAEH-01	S45P
TCGA-DD-AAVQ-01	S45P
TCGA-DD-AAW3-01	S45P
TCGA-DD-A4NK-01	S45Y
TCGA-5R-AA1C-01	S45Y
TCGA-DD-A11D-01	T41A
TCGA-2Y-A9HB-01	T41A
TCGA-DD-AACJ-01	T41A
TCGA-DD-AADU-01	T41A
TCGA-DD-AAE9-01	T41A
TCGA-EP-A26S-01	T41I
TCGA-2Y-A9HA-01	T41I
TCGA-CC-A7IH-01	T42_K49del
TCGA-DD-A1EA-01	L31_I35del
TCGA-DD-A1ED-01	V136A
TCGA-CC-5262-01	W383C
TCGA-G3-A5SJ-01	Y333F
TCGA-DD-A39Y-01	K181Rfs*28
TCGA-DD-A1EJ-01	K335I
TCGA-DD-A3A4-01	K335I
TCGA-DD-A4NL-01	K335I
TCGA-MI-A75C-01	K335I
TCGA-DD-AACK-01	K335I
TCGA-K7-A6G5-01	K335T
TCGA-DD-A39W-01	L139F
TCGA-G3-A25Z-01	L405F
TCGA-DD-A1EE-01	L405F,K335I
TCGA-DD-A73A-01	N387I
TCGA-EP-A3JL-01	N387K
TCGA-8G-A187-01	T41I
TCGA-AP-A059-01	V199I
TCGA-BS-A0V8-01	K170M
TCGA-B5-A11E-01	K354T
TCGA-AP-A054-01	M688T
TCGA-AP-A0LM-01	R535Q
TCGA-AP-A056-01	R587Q,D712N
TCGA-AX-A0J1-01	R710H
TCGA-D1-A103-01	A215T

FIG. 4C

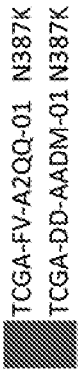

FIG. 4D