

VariantPlex® Solid Tumor

Part # SK0111

Description

The VariantPlex Solid Tumor panel is an optimized balance of gene-specific primer (GSP) oligonucleotides that is used in conjunction with VariantPlex HS Reagents for Illumina® (SK0117) and Molecular Barcode (MBC) Adapters to produce targeted NGS libraries of 660 regions of interest across 67 genes frequently mutated in a broad spectrum of solid tumor-type malignancies.

Contents

Description	Part Number	Storage Conditions
VariantPlex® Solid Tumor GSP1 - 8 reactions	SA0192	-20°C ± 10°C
VariantPlex® Solid Tumor GSP2 - 8 reactions	SA0193	
Archer® PreSeq™ DNA QC Assay Standard	SA0597	
Archer® PreSeq™ DNA QC Assay 10x Primer Mix	SA0598	

Required Reagent volumes:

Protocol Reference	Protocol Step*	Reagent	Required volume (per reaction)
A	Ligation Step 2 Elution	5mM NaOH	36µL
B	First PCR	VariantPlex® Solid Tumor GSP1 (SA0192)	4µL
C	First PCR	10mM Tris-HCl pH 8.0	38µL
D	First PCR	Purified PCR1 eluate	36µL
E	Second PCR	VariantPlex® Solid Tumor GSP2 (SA0193)	4µL

*Refers to steps within LA560

Recommended PCR Cycling:

	Step	Temperature (°C)	Time	Cycles
First PCR Reaction	1	95	3 min	1
	2	95	30 sec	18
	3	65	3 min (100% ramp rate)	
	4	72	3 min	1
	5	4	Hold	1
Second PCR Reaction	1	95	3 min	1
	2	95	30 sec	20*
	3	65	3 min (100% ramp rate)	
	4	72	3 min	1
	5	4	Hold	1

*The number of PCR2 cycles may be decreased if you regularly experience library yields greater than 200nM.

Recommended Reads and Multiplexing

VariantPlex Solid Tumor libraries produced should be sequenced to a minimum of **2.5M** reads per sample. Based on end-user experience, fewer reads may be sufficient for libraries prepared using limited input masses. For more information, visit our frequently asked questions resource page at: www.archerdx.com/faqs

Assay Targets

* red asterisk denotes partial coverage of that exon for SNV/Indel detection

Gene	Association Number	Exon Number	SNV & Indel	CNV
ABL1	NM_005157	4,5,6,7	yes	yes
AKT1	NM_005163	3,6	yes	no
ALK	NM_004304	21,22,23,25	yes	yes
APC	NM_000038	16	yes	yes
ATM	NM_000051	8,9,12,17,26,34,35,36,39,50,54,55,56,59,61,63	yes	yes
AURKA	NM_003600	2,5,6,7,8	yes	yes
BRAF	NM_004333	11,15	yes	no
CCND1	NM_053056	na	no	yes
CCNE1	NM_001238	3,4,5,6,7,8,10,12	yes	yes
CDH1	NM_004360	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16	yes	yes
CDK4	NM_000075	2,3,4,5,6,7	yes	yes
CDKN2A	NM_000077	1,2,3	yes	yes
CSF1R	NM_005211	7,22	yes	no
CTNNB1	NM_001904	3	yes	no
DDR2	NM_006182	12,13,14,15,16,17,18	yes	yes
EGFR	NM_005228	3,7,15,18,19,20,21	yes	yes
ERBB2	NM_004448	10,19,20,21,24	yes	yes
ERBB3	NM_001982	2,3,7,8	yes	yes
ERBB4	NM_005235	3,4,6,7,8,9,15,23	yes	yes
ESR1	NM_000125	8	yes	no
EZH2	NM_004456	16	yes	no
FBXW7	NM_018315	1,2,3,4,5,6,7,8,9,10,11	yes	yes
FGFR1	NM_015850	4,7,8,13,15,17	yes	yes
FGFR2	NM_000141	7,9,12,14	yes	yes
FGFR3	NM_000142	7,8,9,14,15,16,18	yes	yes
FLT3	NM_004119	11,14,16,20	yes	yes
FOXL2	NM_023067	1	yes	no
GNA11	NM_002067	5	yes	no
GNAQ	NM_002072	4,5	yes	no
GNAS	NM_000516	6,7,8,9	yes	yes
H3F3A	NM_002107	2	yes	no
HNF1A	NM_000545	3,4	yes	no
HRAS	NM_005343	2,3	yes	no
IDH1	NM_005896	3,4	yes	no

IDH2	NM_002168	4	yes	no
JAK2	NM_004972	11,13,14,16,19	yes	yes
JAK3	NM_000215	4,13,16	yes	yes
KDR	NM_002253	6,7,11,19,21,26,27,30	yes	yes
KIT	NM_000222	2,8,9,10,11,13,14,15,17,18	yes	yes
KRAS	NM_004985	2,3,4,5	yes	yes
MAP2K1	NM_002755	2,3	yes	no
MDM2	NM_002392	2,3,4,6,8*,10	no	yes
MET	NM_000245	2,11,14,16,19,21	yes	yes
MYC	NM_002467	na	no	yes
MYCN	NM_005378	na	no	yes
MLH1	NM_000249	12	yes	no
MPL	NM_005373	10	yes	no
NOTCH1	NM_017617	25,26,27,34	yes	yes
NPM1	NM_002520	11	yes	no
NRAS	NM_002524	2,3,4,5	yes	yes
PDGFRA	NM_006206	12,14,15,18,23	yes	yes
PIK3CA	NM_006218	2,5,7,8,10,14,19,21	yes	yes
PIK3R1	NM_181504	1,2,3,4,5,6,7,8,9,10	yes	yes
PTEN	NM_000314	1,2,3,4,5,6,7,8,9	yes	yes
PTPN11	NM_002834	3,13	yes	no
RB1	NM_000321	4,6,10,11,14,17,18,20,21,22*	yes	yes
RET	NM_020630	10,11,13,14,15,16	yes	yes
RHOA	NM_001664	2,3	yes	no
ROS1	NM_002944	38	yes	no
SMAD4	NM_005359	2,3,4,5,6,7,8,9,10,11,12	yes	yes
SMARCB1	NM_003073	2,4,5,9	yes	yes
SMO	NM_005631	3,5,6,9,11	yes	yes
SRC	NM_005417	14	yes	no
STK11	NM_000455	1,2,3,4,5,6,7,8,9	yes	yes
TERT	NM_198253	Promoter, 1	yes	no
TP53	NM_000546	1,2,3,4,5,6,7,8,9,10,11	yes	yes
VHL	NM_000551	1,2,3	yes	yes

Archer Analysis Settings

Sequencing data produced by this method must be converted to de-multiplexed FASTQ's, and then processed using [Archer Analysis](#) (v5.1 or greater). This provides all secondary analysis (read trimming/cleaning, de-duplication, error correction, alignment, and mutation calling), as well as some tertiary analysis (e.g., annotations and protein effect predictions). Analysis will produce detailed mutation reporting via graphical user interface, as well as raw text and BAM outputs.

The VariantPlex Solid Tumor libraries supports the following DNA Analysis Types: **DNA Copy Number Variation, DNA SNP/InDel, and DNA Structural Variation** in Archer Analysis (see the software user manual for further details on setting up analyses).

The Archer Analysis software is available as a separate download, which can be requested via a webform on the product webpage: [Archer Analysis](#). VariantPlex Solid Tumor also requires a one-time upload of a Target Region file (a text file, in GTF format, which directs the software on how to analyze data from the panel) which can be obtained by contacting tech@archerdx.com.

Limitations of Use

For Research Use Only. Not for use in diagnostic procedures. Not intended to be used for treatment of human or animal diseases.

Safety data sheets pertaining to this product are available upon request.

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