VariantPlex® Core Myeloid

Part # SK0121

Description

The Archer® VariantPlex Core Myeloid panel is an optimized balance of gene-specific primer (GSP) oligonucleotides that is used in conjunction with VariantPlex HGC Reagents for Illumina® (SK0115) and Molecular Barcode (MBC) Adapters to produce targeted NGS libraries of 37 genes frequently mutated in myeloid malignancies.

Contents

Description	Part Number	Storage Conditions
VariantPlex® Core Myeloid GSP1 - 8 reactions	SA5030081	-20°C ± 10°C
VariantPlex® Core Myeloid GSP2 - 8 reactions	SA5030082	
PreSeq® DNA QC Assay Standard - 32 µL	SA0597	
PreSeq® DNA QC Assay 10X Primer Mix - 120 µL	SA0598	

Required Reagent volumes:

Protocol Reference	Protocol Step	Reagent	Required volume (per reaction)
A	Ligation Step 2 Elution	5mM NaOH	**32µL**
B	First PCR	VariantPlex® Core Myeloid GSP1 (SA5030081)	**8µL**
C	First PCR	10mM Tris-HCl pH 8.0	**34µL**
D	First PCR	Purified PCR1 eluate	**32µL**
E	Second PCR	VariantPlex® Core Myeloid GSP2 (SA5030082)	**8µL**

Recommended PCR Cycling:

	Step	Temperature (°C)	Time	Cycles
First PCR Reaction	**1**	95	3 min	1
	2	95	30 sec	16
	3	63	5 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	22*
	3	65	5 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 Core Myeloid libraries produced should be sequenced to a minimum of **3M** 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

Gene	Accession	Exon
ABL1	NM_005157	4,5,6,7,8,9,10
ANKRD26	NM_014915	1 (c.-113-c.-134)
ASXL1	NM_015338	11,12,13
BCOR	NM_017745	2,3,4,5,6,7,9,10,11,12,13,14,15
BCOR	NM_001123385	8
BRAF	NM_004333	11,15
CALR	NM_004343	8,9
CBL	NM_005188	8,9
CEBPA	NM_004364	1
CSF3R	NM_000760	10,14,15,16
CSF3R	NM_156039	17
CSF3R	NM_172313	18
DDX41	NM_016222	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
DNMT3A	NM_022552	2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
DNMT3A	NM_153759	1,2
DNMT3A	NM_175630	4
ETNK1	NM_018638	3
ETV6	NM_001987	1,2,3,4,5,6,7,8
EZH2	NM_004456	2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20
FLT3	NM_004119	8,9,10,11,12,13,14,15,16,17,19,20,21
GATA1	NM_002049	2
GATA2	NM_032638	2,3,4,5,6
IDH1	NM_005896	3,4
IDH2	NM_002168	4,6
JAK2	NM_004972	12,13,14,15,16

KIT	NM_000222	2,8,9,10,11,12,13,14,15,17,18
KRAS	NM_004985	2,3,4
MPL	NM_005373	10,12
NPM1	NM_002520	11
NRAS	NM_002524	2,3,4
PHF6	NM_032458	9,10
PHF6	NM_032335	2,3,4,5,6,7,8
PTPN11	NM_002834	3,4,7,8,12,13
PTPN11	NM_080601	11
RUNX1	NM_001754	2,3,5,6,7,8,9
RUNX1	NM_001122607	1,5
SETBP1	NM_015559	4 (p.799-p.950)
SF3B1	NM_012433	13,14,15,16,17,18
SRSF2	NM_003016	1,2
STAG2	NM_006603	2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33
STAG2	NM_001042749	32
TET2	NM_001127208	4,5,6,7,8,9,10,11
TET2	NM_017628	3
TP53	NM_000546	1,2,3,4,5,6,7,8,9,10,11
TP53	NM_001276696	10
TP53	NM_001276695	10
U2AF1	NM_006758	2,5,6
WT1	NM_000378	1,2,3,4,5,6,7,9
WT1	NM_001198552	8
ZRSR2	NM_005089	1,2,3,4,5,6,7,8,9,10,11

Genes targeted for CNV detection:

ASXL1	ETV6	RUNX1	U2AF1
BCOR	EZH2	TET2	WT1
CBL	FLT3	TP53	ZRSR2

SNPs targeted for sample tracking:

rs560681	**rs430046**	**rs987640**	**rs10776839**	**rs12393891**
rs740598	rs8078417	rs6444724	rs6530357	chrX 4429309
rs1498553	rs9951171	rs6811238	rs5971553	chrX 11314433
rs10773760	rs576261	rs13182883	rs5953060	chrY 6738552
rs1058083	rs1109037	rs214955	rs6524626	chrY 19490214
rs4530059	rs1523537	rs321198	rs5940270	
rs1821380	rs221956	rs4606077	rs722847	

Note: SNPs may be used in combination to uniquely tag and track samples over time. Contact tech@archerdx.com for further details.

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 Core Myeloid 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 Core Myeloid libraries also require 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 in treatment of animal or human diseases.

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

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