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DATA SHEET

Tapestri Single-Cell DNA AML Panel

Advance your understanding of the genetic heterogeneity underpinning acute myeloid leukemia (AML) by targeting **20 genes with 127 amplicons** for single-cell sequencing. Covering a combination of oncogenes and tumor suppressor genes, this panel is designed to cover some of the most commonly mutated genes associated with AML.

Panel Specifications

Metric	Value
Number of genes	20
Number of targets	529
Target type possible	SNVs. Indels, CNVs, LOH
Number of amplicons	127
Coverage	100%
Panel size	~24 kb
Amplicon length	175 - 275 bp
Panel uniformity: % of amplicons >0.2x mean	>=90%
Amplicon completeness: % of amplicons in >80% of cells	>=80%
Cell completeness: % of cells with >80% amplicons above 10 reads	>=80%
Verified NGS systems	MiSeq, NextSeq, HiSeq, NovaSeq
Recommended number of reads per sample	~77 M

Table 1: Panel specifications.

20-GENE AML PANEL

ASXL1	GATA2	KIT	PTPN11	TET2
DNMT3A	IDH1	KRAS	RUNX1	TP53
EZH2	IDH2	NPM1	SF3B1	U2AF1
FLT3	JAK2	NRAS	SRSF2	WT1

Table 2: Panel gene targets.

Panel Performance

Metric	Value
Panel uniformity	97.6%
Amplicon completeness	85.6%
Cell completeness	89.0%
Cells recovered	4718
% reads mapped to genome	96.4%
% reads mapped to targets	94.1%
% reads mapped to cells	70.8%

Table 3: Panel performance. Data generated from a pure Raji cell line.

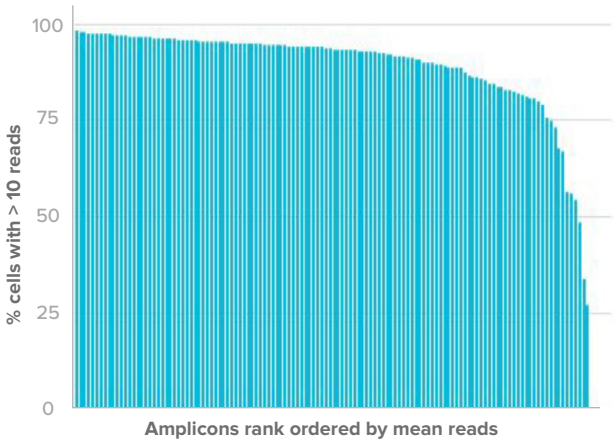

Figure 1: Cell completeness per amplicon.

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Panel Targets

Gene	Exon	Protein-level Variants	cDNA Variants
ASXL1	3	G67	
	4	K85	
	11	R417; Q428; Q491; P511; A530	
	12	W583; Q588; R606; A611; K618; A772; L775; Q778; R786; T787; E797; A809; W898; G927; W960; K982; V1060	
DNMT3A	7	D268	
	8	P307; S312; W313; R320; W327	
	9	L344; L347; R366	
	10	W409; L422	
	11	K429; Y436; E444; A447	
	13	C494; C497; G511; M513	
	14	Q527; C540; G543; L547; G550; C554; C555	
	15	E561; W581; L595; R598; Q606; D614	
	16	R635; L637	
	17	L653; Y660; A662; S669; I681; D686; R688; V690	
	18	G699; D702; I705; G707; N711; L713; S714; V716; P718	
	19	F732; R736; R749; F751; F752; A760; S770; R771; L773; E774	
	20	P777; R792; W795; G796; N797; M801; R803	
	21	E817; H821	
	22	K829; T835; N838; Q842; P849; M852; E863	
	23	F868; D876; N879; M880; S881; R882; Q886; W893; I898; R899; P904	
	Intron		c.640-1437G>A; c.1429+2T>C; c.1667+1G>A; c.2408+5G>A; c.2479-1G>T
EZH2	2	M1; V13; Q28	
	3	N57	
	4	M121	
	5	H129; I131; Y133; Y153; G155	
	6	R207	
	8	E249; G266	
	10	T374	
	14	C548	
	15	K568; T573	

Gene	Exon	Protein-level Variants	cDNA Variants
EZH2 (cont'd)	16	G628; E645; Y646; C647; G648	
	17	A656; D664; N675	
	18	R684; R690; N693; H694; S695	
	19	Y731	
	20	D737; I744; E745	
FLT3	11	E444; S451	
	12	V491; Q494; A506; I507; S519; S531	
	13	I548	
	14	Y572; L576; V592; F594	
	16	M659; K663; M664; N676; A680	
	17	Q730	
	19	N781; T784	
	20	A814; V819; R834; D835; M837; S838; D839; N841; Y842	
	21	A856; T866	
GATA2	4	P304; N317; A318; G320; L321; R330	
	5	T358; L359; R361; R362; A372	
	6	R398	
IDH1	4	R132	
IDH2	4	R140; R172	
JAK2	14	V617	
KIT	2	P34; D52	
	5	G265	
	9	G487; G498	
	11	M552; W557; L576	
	12	T594; A617; M618; P627	
	17	D816; D820; N822; Y823	
	18	A837	
KRAS	2	G12; G13; H27	
	3	T58; Q61	
	4	K117; A146	

Table 4: Panel content. Exon numbers are curated from UCSC Genome Browser by collapsing the exons in the forward strand by start and stop site and then numbering the exons from 5' -> 3' end with the first exon at 5' end representing Exon 1.

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Panel Targets (cont'd)

Gene	Exon	Protein-level Variants	cDNA Variants
NPM1	11	L287; W290	c.860_861in-sCTGC; c.861_862in-sTGCA; c.863_864in-sCATG; c.867_868in-sAGGA
NRAS	2	G12; G13	
	3	Q61	
PTPN11	3	N58; G60; D61; E69; F71; A72; T73; E76; Q79	
	4	E139	
	7	F285	
	8	M311	
	11	D437	
	12	A461; G464	
	13	P491; S502; G503; T507; Q510	
RUNX1	5	G127; E138; S141; A142; R145; R157; D160; R162; G165; R166; S167; G168R; R169; K171	
	6	V197; D198; S200; R201; R204	
	7	R207; G217; S226; E229; R250; N260; M267	
	8	Y281; P298; E316	
	Intron		c.805+1G>A
SF3B1	14	G605; S611; R625; H662; K666; A672	
	15	K700; V701; I704	
	16	G742; A749; R775; E776; D781	
	17	D799	
	Intron		c.2224-1G>A
SRSF2	2	R167	
TET2	3	V9; E10; T27; L34; P46; Q80; G92; R96; D143; S145; S152; P174; E283; N312; Q325; Q414; Q417; Q481; R544; Q574; S588; Q591; Q622; Q635; H682; S714; Q734; Q810; S794; R814; S825; G898; Q913; Q916; P941; Q966; P989; W1003; Q1020; Q1053; Q1083; E1106; L1119	
	4	E1144; Y1148; N1156; R1167	
	5	Q1170; E1178; Q1191; C1193; W1198	
	6	s1203; S1204; R1214; R1216; D1242; Y1245; Y1255; R1261; R1262	

Gene	Exon	Protein-level Variants	cDNA Variants
TET2 (cont'd)	7	C1271; F1287; G1288; C1289; Y1294; C1298; E1318	
	8	L1322; E1323; L1340	
	9	R1359; H1366; C1378; H1380	
	10	C1396; E1401; R1404; R1440; R1452; R1465; S1486; L1511; A1512	
	11	R1516; Q1532; Q1539; Q1542; Q1548; Q1624; Q1652; V1718; L1721; P1723S; R1739; L1740; H1757; I1762; C1811; L1819; Q1828; G1861; S1898; V1900; H1904; H1912; A1919; R1926; P1941; P1962; R1966; P1988; Y1998; R2000; I2002	
	Intron		c.3409+70G>A
TP53	2		c.-87G>C; c.-93A>G
	5	L91; K93; F95; T101; V104; W107; V108; G115; R119; Y124; K125; Q126; H129; V134; R136; C137	
	6	H154; I156; R157; V164; Y166; R174; S176; Y181; P184	
	7	Y195; M198; C199; N200; S202; C203; G206; R209; I215; E219	
	8	G223; L226; G227; R228; V233; R234; C236; A237; P239; D242; R244; R251	
	10	F302; R303	
	11	F346	
	Intron		c.259-2A>G; c.259-1G>A; c.443-1G>A; c.876+1G>A; c.877-1G>A
U2AF1	2	R28; S34; R35	
	6	R156; Q157	
	7	R188	
WT1	4	L299; M302; K321	
	6	G356	
	7	R374; R375; S386	
	8	R435; R436; R439; Q442	
	9	R463; R467; D469; H470	
	Intron		c.1115_1264+1del; c.1264+3_1264 +4insT

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