

Tapestri Single-Cell DNA CML Panel

Advance your understanding of the genetic heterogeneity underpinning chronic myeloid leukemia (CML) by targeting **13 genes with 52 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 CML

Panel Specifications

Metric	Value
Number of genes	13
Number of targets	195
Target type	SNVs, indels
Number of amplicons	52
Coverage	99.57%
Panel size	9.5 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	~31 M

Table 1: Panel specifications.

13-GENE CML PANEL

DNMT3A	CDKN2A	TP53	U2AF1
KIT	ABL1	SETBP1	-
TET2	ETV6	ASXL1	-
EZH2	FLT3	RUNX1	-

Table 2: Panel gene targets.

Panel Targets

Gene	Exon	Protein-level Variants	cDNA Variants
DNMT3A	18	I705	
KIT	2	D52	
	17	D816	
TET2	3	E796; Q913; C1135	c.2079delA; c.2198_2199insT; c.3340dupA
	11	Y1631; G1719; H1817	c.5041_5048delC- CAAGGTT

Gene	Exon	Protein-level Variants	cDNA Variants
EZH2	3		c.188_189insA
	8	L252; A255; R288	c.786_787insC
	9	Q328	
	10		c.1200_1203delAGAA
	17	D664; F670	
	18	R690; N693	
CDKN2A	1	S43	
	2	R138	

Table 3: Panel content. Exon numbers are based on canonical isoform provided by NCBI's Reference Sequence database

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Panel Targets (cont'd)

Gene	Exon	Protein-level Variants	cDNA Variants
ABL1	3	K84	
	4	R220; G227; M237; M244; K247; L248; G250; G251; Q252; Y253; E255; V256; E258; S265; T267; V268	c.742_822del
	5	E275; D276; T277; E279; E282; V289; K291; E292; L298; V299	c.908_909insCAGG
	6	T315; M351; E352; Y353; E355; F359; I360	c.1068_1069insGAA
	7	D363; L364; N368; L370; V371; E373; N374; K378; V379; A399; F382; L384; L387; M388; T389; H396; A397; G398; K419	
	8	A433; S438; D444; S446; E450; E453; E459; P480	c.1423_1424ins- ACTTTGATAAC- CGTGAAGAAAGAA- CAAGATAGAAG
	9	D482; F486; F493; E494; T495; F497	
	11	P1108	
	ETV6	1	C8
2		Q12	
3		F102; R105	c.197delTinsGCCG- GGC; c.215delG; c.283_285delCTG; c.303_304insT; R103G; c.308_309insCTAT; c.309_310insCT; c.311_323delATC- GATCTCCTCA
5		R191; R211	c.450_451insA
6		R339; R353; R369; A377	
7		Y401; K403; F417	
8		R433	
Intron			c.329-2A>G
FLT3	20	D835	
TP53	5	C141; H179	c.404_405insC
	8	C275; P278; R280; R283	
	7	Y234; G244	
SETBP1	4	E858; D868; S869; G870; I871; D874	
	7	T232	

Gene	Exon	Protein-level Variants	cDNA Variants
ASXL1	11	K427	
	12	Y591; Q708; V751; L866	c.2498_2501del- GTCA; c.2580_2581delAG
RUNX1	5	S141; R166	
	6	D198; R201	
	8	R320	
U2AF1	2	S34; R35	
	6	G137; R156	

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