

## Panel Design

Gen	Transkript	Genomische Lokalisation	Abdeckung (Exon)	Hotspot Mutationen
ASXL1	NM_015338	chr20:30946146-31027122	1-13	
CALR	NM_004343	chr19:13049413-13055304	8,9	52bp-Deletion (Typ 1) / 5bp-Insertion in Exon 9 (Typ 2)
CSF3R	NM_000760	chr1:36931643-36948915	14,15,16	Kodon 618
	NM_156039	chr1:36931643-36948915	17	
	NM_172313	chr1:36931643-36948915	10,18	
EZH2	NM_004456	chr7:148504463-148581441	2-20	
IDH1	NM_005896	chr2:209100952-209118910	3,4	Kodon 132
IDH2	NM_002168	chr15:90627211-90645708	4,6	Kodon 140 und 172
JAK2	NM_004972	chr9:4985244-5128183	Alle Exone	Kodon 617
MPL	NM_015559	chr18:42260862-42648475	Alle Exone	Kodon 515
SETBP1	NM_003016	chr17:74730196-74733493	4	Kodon 868
SF3B1	NM_012433	chr2:198256697-198299771	13-21	Kodon 666 und 700
SRSF2	NM_006758	chr21:44513065-44527688	1	Kodon 95
TET2	NM_017628	chr4:106067031-106163928	3	
	NM_001127208	chr4:106067841-106200960	4-11	
U2AF1	NM_006758	chr21:44513065-44527688	2, 6	Kodon 34 und 157

## Beschreibung der untersuchten Gene

Gen	Funktion	TSG/Onkogen*	Ref.
ASXL1 (Additional Sex Combs Like 1)	Epigenetische Modifikation (Histon-Methylierung)	TSG	[1, 2]
CALR	ER Chaperon	Onkogen	[3] [4, 5]
CSF3R	Signaltransduktion (Regulation von Zellproliferation und Differenzierung von Granulozyten)	Onkogen	[6] [7, 8]
EZH2	Epigenetische Modifikation (Methylierung)	TSG / Onkogen	[9, 10]
IDH1 (Isocitrat-Dehydrogenase 1)	Epigenetische Modifikation (Methylierung)	Onkogen	[6] [7, 8]
IDH2 (Isocitrat-Dehydrogenase 1)	Epigenetische Modifikation (Methylierung)	Onkogen	[6] [7, 8]
JAK2 (Janus Kinase 2)	Signaltransduktion (JAK-STAT-Signalweg)	Onkogen	[11-14]
MPL	Thrombopoetinrezeptor des JAK-STAT- Signalwegs	Onkogen	[15, 16]
SETBP1	Epigenetische Modifikation (Teil eines Proteinkomplexes involviert in der Histon-Methylierung)	Onkogen	[17, 18]
SF3B1 (Splicing Factor 3B Subunit 1)	Spleiss-Faktor	Onkogen	[19, 20] [21, 22]
SRSF2 (Serine and Arginine Rich Splice Factor 2)	Spleiss-Faktor	TSG / Onkogen	[19] [21, 22]

\* Gemäss OncoKB Cancer Gene List, TSG=Tumor Suppressor Gen

## Literatur

1. Abdel-Wahab, O., et al., *ASXL1 mutations promote myeloid transformation through loss of PRC2-mediated gene repression*. *Cancer Cell*, 2012. **22**(2): p. 180-93.
2. Alvarez Argote, J. and C.A. Dasanu, *ASXL1 mutations in myeloid neoplasms: pathogenetic considerations, impact on clinical outcomes and survival*. *Curr Med Res Opin*, 2017: p. 1-7.
3. Koschmieder, S., et al., *Dysregulation of the C/EBPalpha differentiation pathway in human cancer*. *J Clin Oncol*, 2009. **27**(4): p. 619-28.
4. Pabst, T. and B.U. Mueller, *Transcriptional dysregulation during myeloid transformation in AML*. *Oncogene*, 2007. **26**(47): p. 6829-37.
5. Pabst, T., et al., *Somatic CEBPA mutations are a frequent second event in families with germline CEBPA mutations and familial acute myeloid leukemia*. *J Clin Oncol*, 2008. **26**(31): p. 5088-93.
6. Figueroa, M.E., et al., *Leukemic IDH1 and IDH2 mutations result in a hypermethylation phenotype, disrupt TET2 function, and impair hematopoietic differentiation*. *Cancer Cell*, 2010. **18**(6): p. 553-67.
7. Amatangelo, M.D., et al., *Enasidenib induces acute myeloid leukemia cell differentiation to promote clinical response*. *Blood*, 2017.
8. Stein, E.M., et al., *Enasidenib in mutant-IDH2 relapsed or refractory acute myeloid leukemia*. *Blood*, 2017.
9. Falini, B., et al., *Cytoplasmic nucleophosmin in acute myelogenous leukemia with a normal karyotype*. *N Engl J Med*, 2005. **352**(3): p. 254-66.
10. Ivey, A., et al., *Assessment of Minimal Residual Disease in Standard-Risk AML*. *N Engl J Med*, 2016. **374**(5): p. 422-33.
11. Grinfeld, J., et al., *Classification and Personalized Prognosis in Myeloproliferative Neoplasms*. *N Engl J Med*, 2018. **379**(15): p. 1416-1430.
12. Baxter, E.J., et al., *Acquired mutation of the tyrosine kinase JAK2 in human myeloproliferative disorders*. *Lancet*, 2005. **365**(9464): p. 1054-61.
13. Levine, R.L., et al., *Activating mutation in the tyrosine kinase JAK2 in polycythemia vera, essential thrombocythemia, and myeloid metaplasia with myelofibrosis*. *Cancer Cell*, 2005. **7**(4): p. 387-97.
14. James, C., et al., *A unique clonal JAK2 mutation leading to constitutive signalling causes polycythaemia vera*. *Nature*, 2005. **434**(7037): p. 1144-8.
15. Pardanani, A.D., et al., *MPL515 mutations in myeloproliferative and other myeloid disorders: a study of 1182 patients*. *Blood*, 2006. **108**(10): p. 3472-6.
16. Pikman, Y., et al., *MPLW515L is a novel somatic activating mutation in myelofibrosis with myeloid metaplasia*. *PLoS Med*, 2006. **3**(7): p. e270.
17. Trimarchi, T., P. Ntziachristos, and I. Aifantis, *A new player SETs in myeloid malignancy*. *Nat Genet*, 2013. **45**(8): p. 846-7.
18. Makishima, H., et al., *Somatic SETBP1 mutations in myeloid malignancies*. *Nat Genet*, 2013. **45**(8): p. 942-6.
19. Yoshida, K., et al., *Frequent pathway mutations of splicing machinery in myelodysplasia*. *Nature*, 2011. **478**(7367): p. 64-9.
20. Malcovati, L., et al., *SF3B1 mutation identifies a distinct subset of myelodysplastic syndrome with ring sideroblasts*. *Blood*, 2015. **126**(2): p. 233-41.
21. Abelson, S., et al., *Prediction of acute myeloid leukaemia risk in healthy individuals*. *Nature*, 2018. **559**(7714): p. 400-404.
22. Desai, P., et al., *Somatic mutations precede acute myeloid leukemia years before diagnosis*. *Nat Med*, 2018. **24**(7): p. 1015-1023.