This document provides a general product overview of the HemeScreen CLL Assay. Additional information can be found on Precipio's website at www.precipiodx.com, and the associated IFU (Instructions For Use), available upon request.

Technology Overview	HemeScreen® is a proprietary set of RUO (Research Use Only) reagents used to screen wild type (Negative) from Mutated (Positive) genes in a simple workflow relative to alternative molecular testing technologies (RT-PCR or NGS).
CLL	Chronic Lymphocytic Leukemia (CLL) is a cancer of the blood and bone marrow affecting the white blood cells.

Genes Tested	Coverage
MYD88 Exon 3	c.649G>T; p.V217F, c.656C>G; p.S219C
MYD88 Exon 4	c.649G>T; p.V217F, c.656C>G; p.S219C
MYD88 Exon 5	c.794T>C; p.L265P
CXCR4 Exon 2	c.598C>T; p.Q200*, c.952dup; p.T318Nfs*26, c.959_960del; p.V320Efs*23, c.993dup; p.G332Rfs*12, c.997A>T; p.K333*, c.1000C>T; p.R334*, c.1005dup; p.G336Wfs*8, c.1012_1015del; p.S338Lfs*27, c.1012dup; p.S338Ffs*6, c.1013C>A; p.S338*, c.1013C>G; p.S338*, c.1014_1017del; p.S339Ffs*26, c.1021del; p.S341Pfs*25
SF3B1 Exon 15	c.1866G>T; p.E622D, c.1866G>C; p.E622D, c.1873C>T; p.R625C, c.1874G>T; p.R625L, c.1984C>G; p.H662D, c.1986C>G; p.H662Q, c.1986C>A; p.H662Q, c.1996A>C; p.K666Q, c.1996A>G; p.K666E, c.1997A>C; p.K666T, c.1997A>G; p.K666R, c.1998G>T; p.K666N, c.1998G>C; p.K666N
SF3B1 Exon 16	c.2098A>G; p.K700E
SF3B1 Exon 17	c.2225G>A; p.G742D
NOTCH1 Exon 34	c.7541_7542delCT; p.P2514Rfs*4

Results	The results from HemeScreen® CLL are qualitative.
Associated WHO/NCCN Guidelines[1]	*Per the WHO:* The genomic landscape of CLL/SLL is very heterogeneous, lacking a unifying genetic lesion. The most frequent chromosomal aberrations are deletions of 13q [del(13q)], 11q [del(11q)], 17p [(del(17p)] and trisomy 12. Occurring in 50-60% of patients, del(13q) removes the *DLEU2*-mir-15-16 cluster, which regulates expression of anti-apoptotic and cell cycle regulatory proteins { 20060366 ; 16166262 }. del(11q), detected in 10-20% patients, removes *ATM*, while del(17p) (5-10% of patients) results in loss of *TP53*. Trisomy 12 occurs in 15-20% of patients, although the genes involved remain unknown { 26466571 ; 28584254 ; 26200345 }. The most frequently mutated genes in CLL/SLL at the time of first treatment are *NOTCH1* (10-15%), *ATM* (10-15%), *SF3B1* (10%), *TP53* (5-10%), and *BIRC3* (5%) { 26466571 ; 26200345 }. Genetic aberrations commonly involve *TP53* mutations and/or del(17p) (60-70% of cases), *NOTCH1* mutations (30%), activation of *MYC* by translocation, amplification or mutation (30%), and 9p21 deletion affecting *CDKN2A* (20%). One or more of these abnormalities is present in 90% of RT cases, typically acquired at transformation { 24127483 ; 22077063 ; 21266718 ; 24004666 }.

	Specificity	Sensitivity	LOD	Storage
Assay Specifications	>99%	98%	2%	-20 °C

SKU	Product Configuration	Assay Contents			
HS-3P-CLL	3 sample pre-plated plate	Primers/MasterMix Mix	Positive controls	NTC	Wild Type

Instrument Required	HRM-enabled RT-PCR (example ThermoFisher Quantstudio 3 or higher)
Contact	For questions, contact our technical support team at techsupport@precipiodx.com or call 203-787-7888
Disclaimer	*The information in this document represents the company's best understanding of the technical and regulatory landscape; however, it should not serve as any guidance to any laboratory seeking to implement HemeScreen. Laboratory managers and medical directors should seek their own information independently through their CLIA inspector and any other state and federal regulatory body available.*

1 World Health Organization. Available at: https://tumourclassification.iarc.who.int/chaptercontent/63/116 (Accessed: November 22, 2022).