# REQUEST FORM: ONCOGENOMIC ANALYSIS


**Centre hospitalier universitaire vaudois**

**Service d'hématologie**
**Laboratoire d'oncogénomique**
Réception des laboratoires BH18-100
1011 Lausanne
Tel. : 021 314 33 93
http://www.chuv.ch/log
e-mail : log@chuv.ch
Laboratory opening hours : Monday-Friday 8am-5pm


## PATIENT

Surname :
Name :
Adress :
Date of birth :
Sex : ☐ Male ☐ Female

**Sample date :**

## BILLING

☐ Patient
☐ Requester

## PROVENANCE

**Clinician :**
Tel./BIP :
Hospital :
Departement :

COPY(IES) of results to be sent (IF ANY) :

## CONSENT FOR BIOLOGICAL ANALYSES

**Following any biological analysis performed in our laboratory, any sample or analysis product:**

☐ can be stored in the laboratory in order to be able to respond to a request to add analyses by the requesting doctor (by default)

☐ can be used for development and research (by default)

☐ must be destroyed

Every constitutional genetic test must be accompanied by genetic counseling (Federal Act on Human Genetic Testing – HGTA). By his signature, the requesting doctor certifies having informed the person concerned according to the legal obligations in force for constitutional genetics and having received his consent for genetic analyses and all other biological analyses.

**Signature of the requesting doctor required :**

## MATERIAL

Lithium Heparin, to stock at room temperature

If < 2ml justify the reason for the small volume please :
☐ Bone marrow
☐ Biopsy
☐ Peripheral blood, blasts proportion (%) :……..
☐ Autre :……..

## STATUS

Date of initial diagnosis :
☐ Initial diagnosi ☐ Follow up ……..
Comments :

## THERAPY / OTHER PATHOLOGY

☐ No
☐ Yes
Comments :

## TRANSPLANT

☐ No ☐ Yes
Date : ……
O Autologous
O Allogenic
Sex of the donor: O Male O Female

## DIAGNOSIS

☐ Preliminary ☐ Definitive

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ☐ AML | ☐ MDS | ☐ CMML | ☐ MDS-MPN | ☐ MPN | ☐ PV | ☐ ET | ☐ PMF |
| ☐ Eosinophilia | ☐ AA/SAA | ☐ Mastocytosis | ☐ CML | ☐ B-ALL | ☐ T-ALL | ☐ Myeloma | ☐ MGUS |
| ☐ CLL | ☐ Waldenström | ☐ Lymphoma (Type :……..) | | | ☐ VEXAS Syndr. | ☐ Other : …… | |

Comments :

## METHODES

☐ **Standard analyses according to diagnosis** ☐ **Standard analyses without NGS/ddPCR** according to diagnosis

*(If no method is selected, the laboratory will perform the most appropriate oncogemic analyses according to the diagnosis/indication)*

Apart from the standard analyses, the analyses below may be performed :

☐ **Conventional cytogenetics (CC)**
☐ **SNP array**
☐ **Next generation sequencing (NGS DNA, mutation analysis)**
- ☐ **Myeloid Panel** (see below for gene details*)
- ☐ **Myeloma Panel** ( *BRAF,GPRC5D, KRAS, NRAS, TNFRSF17, TP53*)
- ☐ ***TP53* only**
- ☐ ***UBA1*** (VEXAS, Syndr. Full gene sequencing)

☐ **Digital PCR (ddPCR)**
- ☐ ***KIT*** c.2447A>T p.D816V
- ☐ ***MYD88*** c.794T>C p.L265P
- ☐ ***BRAF*** c.1799T>A p.V600E

☐ **Fluorescence in situ hybridization (FISH):** ……..

**Standard analyses according to diagnosis**

- **AML Panel** (CC, SNP array, OGM***, NGS myeloid panel*)
- **MDS/AA Panel** (SNP array, NGS myeloid panel*)
- **Eosinphilia Panel** (CC, OGM***)
- **MDS-MPN/CMML Panel** (CC, SNP array, NGS myeloid panel*)
- **CML Panel** (CC + NGS/Fragments analysis *ASXL1*)
- **MPN Panel** (CC, NGS myeloid panel* reduced** including *JAK2* ex12+14, *MPL, CALR*)
- **ALL Panel** (CC, SNP array, OGM***)
- **CLL Panel** (SNP array, NGS *TP53*)
- **Myeloma Panel** (SNP array ; Panel NGS Myeloma & FISH *IGH*)
  *If IGH positive:analysis of IGH::CCND1, IGH::FGFR3, IGH::MAF*
- **Mastocytosis Panel** (CC, ddPCR *KIT*)
- **Waldenström Panel** (CC, ddPCR *MYD88*)

* NGS - Standard large myeloid panel genes: ***ABL1,*** *ANKRD26, ARID1A,* ***ASXL1****, ASXL2, ATRX,* ***BCOR, BCORL1, BRAF,*** *BRCC3,* ***CALR, CBL, CEBPA, CSF3R, CUX1,*** *CXCR4,* ***DDX41, DNMT3A,*** *EP300,* ***ETNK1, ETV6, EZH2,*** *FBXW7,* ***FLT3,*** *GATA1,* ***GATA2,*** *GNAS,* ***GNB1, HRAS, IDH1, IDH2, IKZF1, JAK2,*** *JAK3, KDM6A,* ***KIT, KRAS, MPL, MYD88, NF1,*** *NOTCH1,* ***NPM1, NRAS,*** *PDGFRA,* ***PHF6, PPM1D, PRPF8,*** *PTEN,* ***PTPN11, RB1,*** *RAD21,* ***RUNX1, SETBP1, SF3B1, SH2B3,*** *SMC1A, SMC3,* ***SRSF2, STAG2, TET2, TP53, U2AF1, UBA1,*** *WAS,* ***WT1,*** *ZBTB7A,* ***ZRSR2 + Fragments analysis FLT3-ITD, ASXL1***

** genes in bold, ***analysis carried out outside the scope of accreditation

canton de vaud

**Comments :**