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 Fax : 021 314 34 44
e-mail : log@chuv.ch
http://www.chuv.ch/log
Laboratory opening hours : Monday-Friday 8am-5pm

PATIENT

Surname :
Name :
Adress :
Date of birth :

Sex : ☐ Male ☐ Female

Ref. :

Sample date :

BILLING

☐ Patient
☐ Requester

PROVENANCE

Clinician :

Tel./BIP :

Hospital :

Departement :

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

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 (%) :……..
☐ Other : ……

STATUS

Date of initial diagnosis :……..

☐ Initial diagnosis
☐ Follow up : O Remission
O Relapse/Progression
O Transformation

THERAPY

☐ No
☐ Yes
Type :

TRANSPLANT

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

OTHER PATHOLOGY

☐ Previous
☐ Associated
Type :

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 :……..)			☐ Other : ……		

Comments :

METHODES

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

(please see below for details on the methods)

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

☐ **Conventional cytogenetics (CC)**
☐ **SNP array**
☐ **Fluorescence in situ hybridization (FISH):** ……
☐ **Next generation sequencing (NGS RNA, 687 Fusions)**
☐ **Next generation sequencing (NGS DNA, mutation analysis)**
- ☐ **Standard Myeloid Panel** (see below for gene details*)
- ☐ **Additional available genes** (see below for gene details**) : ……..……..
- ☐ **Myeloma Panel** (*TP53*, *BRAF*, *NRAS*, *KRAS)*
- ☐ ***TP53* only**

☐ **Digital PCR (ddPCR)**
- ☐ ***KIT*** c.2447A>T p.D816V
- ☐ ***MYD88*** c.794T>C p.L265P
- ☐ ***BRAF*** c.1799T>C p.V600E
- ☐ ***NOTCH1*** c.7541_7542delCT p.P2514Rfs*4

Standard analyses according to diagnosis

- **AML Panel** (CC, FISH *MECOM+KMT2A*, NGS standard myeloid panel*)
- **MDS/CMML/AA Panel** (SNP array, NGS standard myeloid panel*)
- **Eosinphilia Panel** (CC, FISH *FIP1L1-PDGFRA, PDGFRB, FGFR1, JAK2*)
- **MDS-MPN Panel** (CC, NGS standard myeloid panel*)
- **CML Panel** (CC)
- **Mastocytosis Panel** (CC, ddPCR *KIT*)
- **ALL Panel** (CC, SNP array, FISH *BCR-ABL1 +KMT2A +TCF3 +ETV6-RUNX1* , NGS RNA Fusion)
- **CLL Panel** (SNP array, NGS *TP53*)
- **Myeloma Panel** (SNP array & FISH *IGH*) If IGH positive : analysis of *IGH-CCND1, IGH-FGFR3, IGH-MAF*
- **Waldenström Panel** (CC, ddPCR *MYD88*)

* NGS - Standard myeloid panel genes: *ASXL1, BCOR, BRAF, CALR ,CBL, CEBPA, CSF3R, DNMT3A, ETV6, EZH2, FLT3, GATA2, HRAS, IDH1, IDH2, JAK2, KIT, KRAS, MPL, NPM1, NRAS, PHF6, PRPF8, PTPN11, RUNX1, SETBP1, SF3B1, SH2B3, SRSF2, STAG2, TET2, TP53, U2AF1, WT1, ZRSR2 + Fragment analysis FLT3-ITD, ASXL1*

**NGS - Additional available genes : *CXCR4, ARID1A, CUX1, SMC3, RAD21, GATA1, SETD1B, BCORL1, KMT2D, XPO1, CSF3R (full gene)*

canton de vaud

Comments :

***METHODES : You can find additional information on our website www.chuv.ch/log. There is no requirement to select the method to be used. If no method is selected, the laboratory will perform the most appropriate oncogemic analyses according to the diagnosis/indication.**