

REQUEST FORM: ONCOGENOMIC ANALYSIS



Centre hospitalier
universitaire vaudois



Service d'hématologie

Laboratoire d'oncogénomique

Réception des laboratoires BH18-100

1011 Lausanne

<http://www.chuv.ch/log>

Tel. : 021 314 33 93

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Laboratory opening hours : Monday-Friday 8am-5pm

PATIENT

Surname :

Name :

Address :

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 diagnosis
- Follow up : Remission
- Relapse/Progression
- Transformation

THERAPY / OTHER PATHOLOGY

No

Yes

Comments :

TRANSPLANT

- | | | | |
|-----------------------------|------------------------------|--------------|--|
| <input type="checkbox"/> No | <input type="checkbox"/> Yes | Date : | Sex of the donor: <input type="radio"/> Male |
| | | | <input type="radio"/> Female |
| | | | <input type="radio"/> Autologous |
| | | | <input type="radio"/> Allogenic |

DIAGNOSIS Preliminary Definitive

- | | | | | | | | |
|---------------------------------------|--------------------------------------|---|----------------------------------|--------------------------------|---------------------------------------|--|-------------------------------|
| <input type="checkbox"/> AML | <input type="checkbox"/> MDS | <input type="checkbox"/> CMML | <input type="checkbox"/> MDS-MPN | <input type="checkbox"/> MPN | <input type="checkbox"/> PV | <input type="checkbox"/> ET | <input type="checkbox"/> PMF |
| <input type="checkbox"/> Eosinophilia | <input type="checkbox"/> AA/SAA | <input type="checkbox"/> Mastocytosis | <input type="checkbox"/> CML | <input type="checkbox"/> B-ALL | <input type="checkbox"/> T-ALL | <input type="checkbox"/> Myeloma | <input type="checkbox"/> MGUS |
| <input type="checkbox"/> CLL | <input type="checkbox"/> Waldenström | <input type="checkbox"/> Lymphoma (Type : | | | <input type="checkbox"/> VEXAS Syndr. | <input type="checkbox"/> Other : | |

Comments :

METHODES

□ Standard analyses according to diagnosis

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

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

- | | |
|--|--|
| <input type="checkbox"/> Conventional cytogenetics (CC) | <input type="checkbox"/> Digital PCR (ddPCR) |
| <input type="checkbox"/> SNP array | <input type="checkbox"/> KIT c.2447A>T p.D816V |
| <input type="checkbox"/> Fluorescence in situ hybridization (FISH): | <input type="checkbox"/> MYD88 c.794T>C p.L265P |
| <input type="checkbox"/> Next generation sequencing (NGS DNA, mutation analysis) | <input type="checkbox"/> BRAF c.1799T>C p.V600E |
| <input type="checkbox"/> Standard Myeloid Panel (see below for gene details*) | <input type="checkbox"/> NOTCH1 c.7541_7542delCT p.P2514Rfs*4 |
| <input type="checkbox"/> Additional available genes (see below for gene details**) : | |
| <input type="checkbox"/> Myeloma Panel (TP53, BRAF, NRAS, KRAS) | <input type="checkbox"/> Next generation sequencing (NGS RNA, 687 Fusions) |
| <input type="checkbox"/> TP53 only | <input type="checkbox"/> UBA1 (VEXAS, Syndr. Full gene sequencing) |

Standard analyses according to diagnosis

- AML Panel (CC, SNP array, FISH KMT2A, MECOM and RUNX1, NGS standard myeloid panel*)
- MDS/AA Panel (SNP array, NGS standard myeloid panel*)
- Eosinophilia Panel (CC, FISH FIP1L1::PDGFRA, PDGFRB, FGFR1, JAK2)
- MDS-MPN/CMMI Panel (CC, SNP array, NGS standard myeloid panel*)
- CML Panel (CC)
- MPN Panel (CC, NGS standard myeloid panel* including JAK2 ex12+14, MPL, CALR)
- ALL Panel (CC, SNP array, test for KMT2A, TCF3, ETV6::RUNX1, BCR::ABL1 rearrangements)
- CLL Panel (SNP array, NGS TP53)
- Myeloma Panel (SNP array & 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 myeloid panel genes: ASXL1, BCOR, BCORL1, BRAF, CALR, CBL, CEBPA, CSF3R, CUX1, DDX41, DNMT3A, ETNK1, ETV6, EZH2, FLT3, GATA2, GNB1, HRAS, IDH1, IDH2, JAK2, KIT, KRAS, MPL, NPM1, NF1, NRAS, PHF6, PPM1D, PRPF8, PTPN11, RUNX1, SETBP1, SF3B1, SH2B3, SRSF2, STAG2, TET2, TP53, UBA1, U2AF1, WT1, ZRSR2 + Fragment analysis FLT3-ITD, ASXL1

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



Comments :