

## HAEMATOLOGY – CLINICAL DATASET COLLECTION GUIDANCE

Clinical Dataset	SITE SPECIFIC DATA ITEM																										
<b>AML</b>	<p><b>WHITE BLOOD CELL COUNT (HIGHEST PRE TREATMENT)</b> - Highest White blood cell count pre-treatment (x 10<sup>9</sup> per litre). Normally provided by Haematology lab before transfusion, before treatment. <b>Range 0.0 to 999.9 (to 1dp)</b></p> <p><b>EUROPEAN LEUKAEMIA NET (ELN) GENETIC RISK</b> - Cytogenetic and Molecular analysis of bone marrow (preferably) or blood sample. Classify genetics abnormalities as:</p> <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="text-align: center; width: 5%;"><b>F</b></td> <td style="width: 45%;">Favourable - t(8;21)(q22;q22.1); RUNX1-RUNX1T1, inv(16)(p13.1q22) or t(16;16)(p13.1;q22); CFBF-MYH11, Mutated NPM1 without FLT3-ITD or with FLT3-ITDlow†, Biallelic mutated CEBPA</td> <td style="text-align: center; width: 5%;"><b>A</b></td> <td style="width: 45%;">Adverse - t(6;9)(p23;q34.1); DEK-NUP214, t(v;11q23.3); KMT2A rearranged, t(9;22)(q34.1;q11.2); BCR-ABL1, inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); GATA2,MECOM(EVI1), -5 or del(5q); -7; -17/abn(17p), Complex karyotype,§ monosomal karyotype   , Wild-type NPM1 and FLT3-ITDhigh†, Mutated RUNX1¶, Mutated ASXL1¶, Mutated TP53#</td> </tr> <tr> <td style="text-align: center;"><b>I</b></td> <td>Intermediate - Mutated NPM1 and FLT3-ITDhigh†, Wild-type NPM1 without FLT3-ITD or with FLT3-ITDlow† (without adverse-risk genetic lesions), t(9;11)(p21.3;q23.3); MLLT3-KMT2A‡, Cytogenetic abnormalities not classified as favourable or adverse</td> <td style="text-align: center;"><b>N</b></td> <td>No result <i>includes "Test not done"</i></td> </tr> </table> <p><b>CYTOGENETICS SUBSIDIARY COMMENT</b> – Description of cytogenetic findings.</p>	<b>F</b>	Favourable - t(8;21)(q22;q22.1); RUNX1-RUNX1T1, inv(16)(p13.1q22) or t(16;16)(p13.1;q22); CFBF-MYH11, Mutated NPM1 without FLT3-ITD or with FLT3-ITDlow†, Biallelic mutated CEBPA	<b>A</b>	Adverse - t(6;9)(p23;q34.1); DEK-NUP214, t(v;11q23.3); KMT2A rearranged, t(9;22)(q34.1;q11.2); BCR-ABL1, inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); GATA2,MECOM(EVI1), -5 or del(5q); -7; -17/abn(17p), Complex karyotype,§ monosomal karyotype   , Wild-type NPM1 and FLT3-ITDhigh†, Mutated RUNX1¶, Mutated ASXL1¶, Mutated TP53#	<b>I</b>	Intermediate - Mutated NPM1 and FLT3-ITDhigh†, Wild-type NPM1 without FLT3-ITD or with FLT3-ITDlow† (without adverse-risk genetic lesions), t(9;11)(p21.3;q23.3); MLLT3-KMT2A‡, Cytogenetic abnormalities not classified as favourable or adverse	<b>N</b>	No result <i>includes "Test not done"</i>																		
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<b>ALL</b>	<p><b>WHITE BLOOD CELL COUNT (HIGHEST PRE TREATMENT)</b> - Highest White blood cell count pre-treatment (x 10<sup>9</sup> per litre). Normally provided by Haematology lab before transfusion, before treatment. <b>Range 0.0 to 999.9 (to 1dp)</b></p> <p><b>CYTOGENETICS SUBSIDIARY COMMENT</b> – Description of cytogenetic findings.</p> <p><b>POST INDUCTION MRD</b> – Percentage of leukaemic cells present at the end of Minimal Residual Disease induction</p> <table border="1" style="width: 100%; border-collapse: collapse; text-align: center;"> <tr> <td style="width: 25%;"><b>1</b></td> <td style="width: 25%;">0%</td> <td style="width: 25%;"><b>5</b></td> <td style="width: 25%;">&lt;5%</td> </tr> <tr> <td><b>2</b></td> <td>&lt;0.01%</td> <td><b>6</b></td> <td>&gt;=5%</td> </tr> <tr> <td><b>3</b></td> <td>&lt;0.1%</td> <td></td> <td></td> </tr> <tr> <td><b>4</b></td> <td>&lt;1%</td> <td><b>9</b></td> <td>Unknown</td> </tr> </table> <p><b>EXTRAMEDULLARY DISEASE</b> - Sites of disease identified outside bone marrow, including presence of blasts within CFS.</p> <table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="width: 10%; text-align: center;"><b>1</b></td> <td>CNS1 (without blasts)</td> </tr> <tr> <td style="text-align: center;"><b>2</b></td> <td>CNS2 (&lt; 5 WBC in the CSF with blasts)</td> </tr> <tr> <td style="text-align: center;"><b>3</b></td> <td>CNS3 (≥ 5 WBC in the CSF with blasts)</td> </tr> <tr> <td style="text-align: center;"><b>4</b></td> <td>Testes</td> </tr> <tr> <td style="text-align: center;"><b>9</b></td> <td>Other</td> </tr> </table>	<b>1</b>	0%	<b>5</b>	<5%	<b>2</b>	<0.01%	<b>6</b>	>=5%	<b>3</b>	<0.1%			<b>4</b>	<1%	<b>9</b>	Unknown	<b>1</b>	CNS1 (without blasts)	<b>2</b>	CNS2 (< 5 WBC in the CSF with blasts)	<b>3</b>	CNS3 (≥ 5 WBC in the CSF with blasts)	<b>4</b>	Testes	<b>9</b>	Other
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<b>CML</b>	<p><b><u>SOKAL INDEX (CHRONIC MYELOID LEUKAEMIA)</u></b> Index derived from age, spleen size, platelet count, myeloblasts %.</p>										
<b>CLL</b>	<p><b><u>SPLENOMEGALY INDICATOR</u></b> - Spleen enlargement identified from clinical examination</p> <table border="1" data-bbox="352 389 766 443"> <tr> <td><b>Y</b></td> <td>Yes</td> <td><b>N</b></td> <td>No</td> </tr> </table> <p><b><u>BINET STAGE</u></b> - Prognostic index derived from platelet count, Hb, lymphadenopathy, hepatomegaly and splenomegaly. (Binet Stage “solely rely on physical examination and standard laboratory tests, and do not require ultrasound, computed tomography, or magnetic resonance imaging.” <a href="http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2972576/?tool=pubmed">http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2972576/?tool=pubmed</a> )</p> <table border="1" data-bbox="352 685 1471 873"> <tr> <td><b>A</b></td> <td>Stage A: if Platelet count &gt; 99 and Hb &gt;9.9 and 0, 1 or 2 areas of organ enlargement (number of lymph node groups plus score 1 for hepatomegaly, 1 for splenomegaly)</td> </tr> <tr> <td><b>B</b></td> <td>Stage B: if Platelet count &gt; 99 and Hb &gt;9.9 and 3, 4 or 5 areas of organ enlargement</td> </tr> <tr> <td><b>C</b></td> <td>Stage C: if Hb &lt;10 or platelet count &lt;100</td> </tr> </table> <p><b><u>BINET STAGE DATE</u></b> – The date on which the Binet Stage was recorded.</p> <p><b><u>STAGING ORGANISATION CODE</u></b> – The organisation who carried out the stage.</p>	<b>Y</b>	Yes	<b>N</b>	No	<b>A</b>	Stage A: if Platelet count > 99 and Hb >9.9 and 0, 1 or 2 areas of organ enlargement (number of lymph node groups plus score 1 for hepatomegaly, 1 for splenomegaly)	<b>B</b>	Stage B: if Platelet count > 99 and Hb >9.9 and 3, 4 or 5 areas of organ enlargement	<b>C</b>	Stage C: if Hb <10 or platelet count <100
<b>Y</b>	Yes	<b>N</b>	No								
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<b>Myelodysplasia (MDS)</b>	<p><b><u>BONE MARROW BLASTS PERCENTAGE:</u></b> Blast cells in bone marrow aspirate as percentage of all nucleated cells. Normally taken from laboratory report on diagnostic bone marrow. (% ) Range 0 – 100</p> <p><b><u>IPSS- R (MYELODYSPLASIA)</u></b> - REVISED INTERNATIONAL PROGNOSTIC SCORING SYSTEM for myelodysplasia. Index derived from BM blasts %, Platelet count, Hb, Absolute Neutrophil Count, Cytogenetic Category.</p> <ul style="list-style-type: none"> <li>• Score 0 for BM Blasts % less than 2, 1 for &gt;2 to 5, 2 for &gt;5 to 10 and 3 for &gt;10.</li> <li>• Score 0 for Cytogenetics Very Good, 1 for Good, 2 for Intermediate, 3 for Poor and 4 for Very Poor.</li> <li>• Score 0 for Haemoglobin =&gt;10, 1 for 8 to &lt;10 and 1.5 for &lt;8.</li> <li>• Score 0 for Platelets =&gt;100, 0.5 for 50 to &lt;100 and 1 for &lt;50.</li> <li>• Score 0 for ANC =&gt;0.8 and 0.5 for &lt;0.8.</li> </ul>										
<b>Myeloma</b>	<p><b><u>R-ISS STAGE for MYELOMA</u></b> – The Revised International Staging System (R-ISS) includes variables included in the original ISS (serum beta-2 microglobulin and serum albumin), while also including the additional prognostic information obtained from serum LDH and high-risk chromosomal abnormalities detected by interphase fluorescent in situ hybridization (iFISH) after CD138 plasma cell purification.</p> <table border="1" data-bbox="352 1783 1383 1946"> <tr> <td>1</td> <td>Stage 1: ISS stage 1 and standard risk CA by iFISH and normal LDH</td> </tr> <tr> <td>2</td> <td>Stage 2: Not R-ISS stage 1 or 3</td> </tr> <tr> <td>3</td> <td>Stage 3: ISS stage 3 and either high risk CA by iFISH or high LDH</td> </tr> </table> <p><b><u>R-ISS STAGE for MYELOMA DATE</u></b> – The date on which the ISS Stage was recorded.</p> <p><b><u>STAGING ORGANISATION CODE</u></b> – The organisation who carried out the stage.</p>	1	Stage 1: ISS stage 1 and standard risk CA by iFISH and normal LDH	2	Stage 2: Not R-ISS stage 1 or 3	3	Stage 3: ISS stage 3 and either high risk CA by iFISH or high LDH				
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**ANN ARBOR STAGE:** Staging based on location of detected disease.

1	I = One region of lymph nodes, or spleen or thymus or Waldeyer's ring enlarged
2	II = 2 regions of lymph nodes enlarged, on same side of diaphragm
3	III = lymph nodes enlarged on both sides of diaphragm
4	IV = disease outside lymph nodes e.g. liver, bone marrow excluding E

**ANN ARBOR STAGE DATE:** The date on which the Ann Arbor Stage was recorded.

**STAGING ORGANISATION CODE** – The organisation who carried out the stage.

**ANN ARBOR SYMPTOMS:** Additional stage designation based on presence / absence of specific symptoms.

A	No Symptoms
B	Presence of any of the following: unexplained persistent or recurrent fever (greater than 38°C / 101.5°F), drenching night sweats, unexplained weight loss of 10% or more within the last 6 months

**ANN ARBOR EXTRANODALITY** [ANN ARBOR EXTRANODALITY INDICATOR]: Additional staging designation based on extranodal involvement. Code "E" if there is involvement of a single extranodal (other than the lymph nodes) site that directly adjoins or is next to the known nodal group.

E	Extranodal involvement
0	No Extranodal involvement

**Follicular**

**ANN ARBOR BULK:** Additional staging designation based on presence of bulky disease. Code "X" if there is presence of "bulky" disease, that is, a nodal mass whose greatest dimension is more than 10 centimetres in size, and/or a widening of the mediastinum (middle chest) by more than one-third.

X	Yes, "bulky" disease present
0	No "bulky" disease present

**ANN ARBOR SPLENIC INVOLVEMENT:** Additional staging designation based on splenomegaly or normal spleen size with confirmed disease involvement. Code 'S' if either is true.

S	Spleen involvement or splenomegaly
0	No Spleen involvement or splenomegaly

**NUMBER OF ABNORMAL NODAL AREAS:** Number of abnormal nodal areas detected clinically and radiologically.

**FLIPI 2 INDEX SCORE** - Follicular Lymphoma International Prognostic Index 2 Score (FLIPI2), derived from age, Serum beta 2 microglobulin, Hb, bone marrow involvement, longest diameter of largest involved node.

Score 1 for age >60 years, Hb < 12 g/dl, serum beta 2 microglobulin raised, bone marrow involvement present, longest diameter of largest involved node 6cm or more.

**Range 0 - 5**

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E	Extranodal involvement
0	No Extranodal involvement

**ANN ARBOR BULK:** Additional staging designation based on presence of bulky disease. Code "X" if there is presence of "bulky" disease, that is, a nodal mass whose greatest dimension is more than 10 centimetres in size, and/or a widening of the mediastinum (middle chest) by more than one-third.

X	Yes, "bulky" disease present
0	No "bulky" disease present

**DLBCL**

**ANN ARBOR SPLENIC INVOLVEMENT:** Additional staging designation based on splenomegaly or normal spleen size with confirmed disease involvement. Code 'S' if either is true.

S	Spleen involvement or splenomegaly
0	No Spleen involvement or splenomegaly

**NUMBER OF EXTRANODAL SITES CODE** - Number of sites with Lymphoma outside lymph nodes (clinical).

0	Zero	1	One	2	More than one
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**PRIMARY EXTRANODAL SITE** - Site of origin of lymphoma if believed to be outside lymph nodes as agreed by MDT based on clinical and radiological findings

01	Blood	02	Bone	03	CNS	04	GIT
05	GU	06	Liver	07	Marrow	08	Muscle
09	Orbit	10	Pericardium	11	Pulmonary	12	Salivary gland
13	Skin	14	Thyroid	15	Other (specify)		

**NUMBER OF ABNORMAL NODAL AREAS:** Number of abnormal nodal areas detected clinically and radiologically.

**(R)IPI INDEX for DLBCL SCORE** - Revised International Prognostic Index Score, derived from Age, performance status, LDH, extranodal sites, Ann Arbor Stage. **Range 0 – 5**

Score 1 for each of age >60, PS ≥ 2, LDH above Normal, >1 extranodal site, stage III or IV.

Either (R)IPI or IPI may currently be used as prognostic indicators. However the scores calculated as above apply to both indices and can be grouped to provide either the IPI or the (R)IPI Groupings.

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E	Extranodal involvement
0	No Extranodal involvement

Other  
Lymphomas

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13	Skin	14	Thyroid	15	Other (specify)		

**NUMBER OF ABNORMAL NODAL AREAS:** Number of abnormal nodal areas detected clinically and radiologically.

**HASENCLEVER INDEX**- Index derived from age, gender, Hb, Albumin, white blood count, Lymphocyte count, Ann Arbor stage. (Score 1 for each of Age >44, Male gender, Hb<10.5, Albumin <40, White blood count >14.9, Lymphocyte count<0.6 (or Lymphocyte percentage of white blood cells <8%), Ann Arbor Stage IV)  
**Range 0-7**

Hodgkin