

Supplementary information for:

## **Label-free imaging and identification of typical cells of acute myeloid leukaemia and myelodysplastic syndrome by Raman microspectroscopy**

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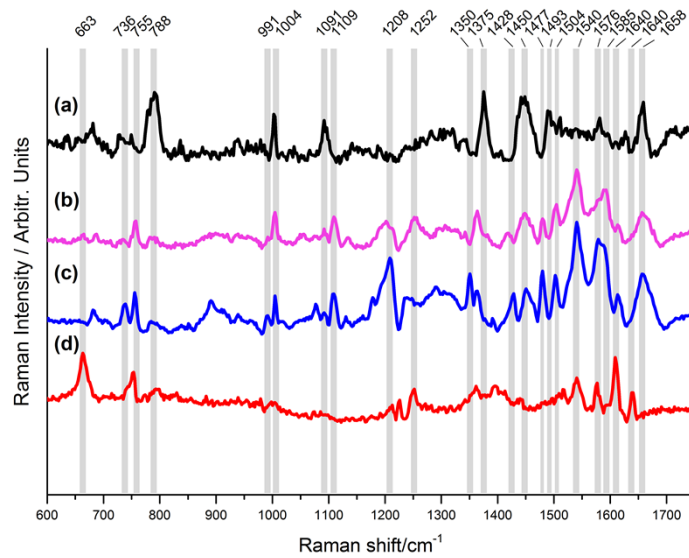
**Supplementary Table S1. Patients' characteristics.** Abbreviations: FAB, French-American-British classification; AML, acute myeloid leukaemia; APL, acute promyelocytic leukaemia; MPO, myeloperoxidase; NEC, nonerythroid cells; NSE, non-specific esterase.

	Patient #1	Patient #2	Patient #3	Patient #4	Patient #5	Patient #6	Patient #7
<b>Age (at diagnosis)</b>	83	70	65	60	23	35	64
<b>Gender</b>	F	M	M	M	M	M	M
<b>WHO classification</b>	AML with minimal differentiation	AML with minimal differentiation	AML with t(8;21)(q22;q22); <i>RUNX1-RUNX1T1</i>	AML with t(8;21)(q22;q22); <i>RUNX1-RUNX1T1</i>	APL with t(15;17)(q22;q12); <i>PML-RARA</i>	APL with t(15;17)(q22;q12); <i>PML-RARA</i>	Acute erythroid leukaemia (in clinical remission)
<b>FAB classification</b>	AML M0	AML M0	AML M2	AML M2	AML M3	AML M3	AML M6
<b>BM Abnormal promyelocytes</b>	-	-	-	-	++ (with Auer rods)	++ (with Auer rods)	-
<b>Immunophenotype</b>	CD34+ CD117+	CD34+ CD117+	CD34+ CD117+	CD34+ CD117+	CD34- CD117+ DR-	CD34- CD117+ DR-	n.d
<b>Cytochemistry</b>	MPO + (2% of NEC) NSE neg	MPO neg NSE neg	MPO + (54% of NEC) NSE + (4% of NEC)	n.d	n.d	n.d	n.d
<b>Cytogenetic</b>	no common abnormalities	no common abnormalities	t(8;21)	t(8;21)	t(15;17)	t(15;17)	no common abnormalities
<b>Mutations</b>	no common mutations	no common mutations	<i>RUNX1T1</i>	<i>RUNX1T1</i>	<i>PML/RARA</i> : <i>BCR1</i>	<i>PML/RARA</i> : <i>BCR1</i>	no common abnormalities

**Supplementary Table S2.** Raman bands position assignments. \* M0: myeloblasts from patients affected by “AML with minimal differentiation”; M2: promyelocytes from patients affected by “AML with t(8;21) ; *RUNX1-RUNX1T1*”; M3: abnormal promyelocytes from patients affected by “APL with t(15;17); *PML-RARA*”; M6: erythroblasts from a patient affected by “Acute erythroid leukaemia”. Symbols +/- indicate the relative band intensity relatively to the local baseline. The peak positions were mainly selected from subpopulation average fingerprints.

Peak Position (cm <sup>-1</sup> )	Assignment	Ref.	AML Subpopulations*			
			M0	M2	M3	M6
665	Hb; porphyrin; pyr. def.	(Wood & McNaughton, 2002)	-	-	-	+++
734	MPO; porphyrin (?)	(Puppels <i>et al</i> , 1991)	-	+	++	-
752	MPO; porphyrin	(Puppels <i>et al</i> , 1991)	+	++	++	-
755	Hb; porphyrin; pyr. breath.	(Wood & McNaughton, 2002)	-	-	-	+++
783-788	DNA; T,C, ring breath./OPO str.	(Puppels <i>et al</i> , 1990; Pully <i>et al</i> , 2011)	+++	+	+	+
991	MPO; phorphyrin	(Puppels <i>et al</i> , 1991)	-	+	++	-
1004	proteins; phenylalanine	(Pully <i>et al</i> , 2011)	+++	++	++	+
1091	DNA; OPO str.	(Puppels <i>et al</i> , 1990)	+++	+	+	-
~1107	MPO; porphyrin	(Puppels <i>et al</i> , 1991)	-	+++	+++	-
~1208	MPO; phorphyrin	(Puppels <i>et al</i> , 1991)	+	++	++	+
1249	Hb; porphyrin; CH methane	(Wood & McNaughton, 2002)	-	-	-	+++
1250	proteins; Amide III, C-N, N-H str.	(Puppels <i>et al</i> , 1990)	+++	+	+	-
1302	DNA; A, ring breath.	(Puppels <i>et al</i> , 1991)	+++	++	+	-
1341	DNA; G, / Prot. Charb; CH def	(Puppels <i>et al</i> , 1990)	+++	++	++	+
1361	MPO; phorphyrin	(Puppels <i>et al</i> , 1991)	-	+	+	-
1366	Hb; porphyrin; pyr. str.	(Wood & McNaughton, 2002)	-	+	+	++
1375	DNA; T,G,A, ring breath.	(Puppels <i>et al</i> , 1990)	++	-	-	-
1397	Hb; porphyrin; pyr. str.	(Wood & McNaughton, 2002)	-	-	+	++
1450	proteins/lipids; CH <sub>2</sub> bending	(Uzunbajakava <i>et al</i> , 2003)	+++	+++	++	+
1493	DNA; G,A, ring breath.	(Puppels <i>et al</i> , 1990)	++	+	+	-
1540	Hb; porphyrin; C <sub>β</sub> -C <sub>β</sub>	(Wood & McNaughton, 2002)	-	+	+	+++
~1579	MPO; porphyrin	(Puppels <i>et al</i> , 1991)	+	++	+++	+
1610	Hb; porphyrin; C <sub>α</sub> -C <sub>m</sub>	(Wood & McNaughton, 2002)	-	+	+	+++
1658	Proteins; Amide I, C=O str.	(Uzunbajakava <i>et al</i> , 2003)	+++	++	+	-

**Supplementary Figure S1.** Subpopulation fingerprint standard deviations. Standard deviation of each overall mean Raman spectra (see Fig.3) related to the four subpopulation analyzed: (a) myeloblasts from patients affected by “AML with minimal differentiation” (M0); (b) promyelocytes from patients affected by “AML with t(8;21) ; *RUNX1-RUNX1T1*” (M2); (c) abnormal promyelocytes from patients affected by “APL with t(15;17); *PML-RARA*” (M3); (d) erythroblasts from a patient affected by “Acute erythroid leukaemia” (M6). All spectra were multiplied, normalized and shifted for better showing the spectral features.



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