# Single nucleotide polymorphism microarray analysis of karyotypically normal acute myeloid leukemia reveals frequent copy number neutral loss of heterozygosity

*Anne Tyybäkinoja,* Erkki Elonen,° Hanna Vauhkonen,* Janna Saarela,¶ Sakari Knuutila**

**Department of Pathology, Haartman Institute and HUSLAB, University of Helsinki and Helsinki University Central Hospital, Helsinki, Finland; °Department of Medicine, Division of Hematology, Helsinki University Central Hospital, Helsinki, Finland; ¶Department of Molecular Medicine, National Public Health Institute, Helsinki, Finland*

Citation: Tyybäkinoja A, Elonen E, Vauhkonen H, Saarela J, Knuutila S. Single nucleotide polymorphism microarray analysis of karyotypically normal acute myeloid leukemia reveals frequent copy number neutral loss of heterozygosity. Haematologica 2008 Apr; 93:(4)xxx-xxx. doi: 10.3324/haematol.12232

## *Supplementary Table 1*

**Table 1.** LOH, aCGH and FLT3 mutation results.

| *Case*[a] | *Sex/age* | *AML subtype* | *LOH detected by SNP arrays* | | | *Agilent 44K* | *Size (Mb) aCGHb cytoband* | *FLT3*[b] |
|---|---|---|---|---|---|---|---|---|
| | | | *Cytoband* | *Location (Mb from pter)* | *Size (Mb)* | | | |
| 1 (2) | M/69 | M2 | 4q31.1-q31.21 | 134.0-145.1 | 5.1 | -8q24.11 | 0.7 | normal |
| | | | 4q32.1-q34.1 | 158.0-175.6 | 17.6 | | | |
| | | | 16q13-q21 | 56.6-61.3 | 4.7 | | | |
| 2 (3) | F/43 | M2 | 12p12.1-p11.22 | 25.0-30.6 | 5.6 | n.d | | ITD |
| | | | 13q | 18.3-114.0 | 95.7 | | | |
| | | | 14q22.1-q22.3 | 50.5-55.6 | 5.1 | | | |
| 3 (4) | F/70 | M2 | n.d | | | n.d | | ITD |
| 4 (5) | M/56 | M2 | 2q21.2-q22.1 | 134.3-138.6 | 4.4 | n.d | | normal |
| | | | 7q21.11 | 81.7-85.7 | 4.0 | | | |
| | | | 7q21.12-q21.2 | 87.3-90.9 | 3.6 | | | |
| 5 (6) | F/48 | M5b | n.d | | | -12p12.3 | 3.6 | D835 |
| 6 (7) | M/47 | M5b | 13q22.1-q31.1 | 73.3-79.3 | 6.0 | n.d | | ITD |
| 7 (8) | M/57 | M5b | n.d | | | n.d | | normal |
| 8 (9) | M/35 | M1 | 18q12.1-q12.2 | 27.6-32.0 | 4.4 | n.d | | D835 |
| 9 (11) | F/43 | M5b | n.d | | | n.d | | ITD |
| 10 (12) | M/47 | M2 | 3q12.1-q13.3 | 99.5-115.6 | 16.1 | n.d | | ITD |
| | | | 4q12-q13.1 | 56.0-64.5 | 8.5 | | | |
| | | | 4q21.1-q21.21 | 76.6-79.6 | 3.0 | | | |
| | | | 8p11.21-q11.23 | 40.3-54.3 | 14.0 | | | |
| | | | 12q14.1-q14.2 | 57.6-62.0 | 4.4 | | | |
| 11 (13) | M/21 | M2 | 2q14.2-q14.3 | 119.6-124.9 | 5.3 | n.d | | normal |
| 12 (14) | F/43 | M5b | 17q12-q21.32 | 34.2-43.6 | 9.4 | n.d | | D835 |
| 13 (15) | F/44 | M5b | n.d | | | n.d | | ITD |
| 14 (16) | M/70 | M2 | 1p21.2-p13.3 | 101.6-107.3 | 5.7 | -1q41, | 1.7 | normal |
| | | | 1q23.2-q23.3 | 157.0-161.4 | 4.4 | -8q21.32, | 0.4 | |
| | | | 7q21.11-q21.12 | 83.6-87.7 | 4.1 | +3p21.3, | 0.7 | |
| | | | 8q24.13-q24.22 | 126.9-131.6 | 4.7 | +8q24.13-q24.21 | 4.1 | |
| 15 (17) | M/49 | M1 | n.d | | | n.d | | D835 |
| 16 (18) | M/74 | M1 | 13q21.1-q21.31 | 58.0-63.0 | 5.0 | n.d | | normal |
| 17 (24) | M/62 | M2 | n.d | | | -12p13.2 | 1.4 | normal |
| 18 (25) | F/70 | M1 | 1p32.2-p31.3 | 56.2-61.2 | 5.0 | n.d | | ITD |
| | | | 4q28.2-q28.3 | 130.0-135.1 | 5.1 | | | |
| 19 (26) | M/68 | MDS | 1q22-q23.2 | 151.6-156.0 | 5.4 | n.d | | D835 |
| | | AML | 10p11.21-q11.22 | 36.0-49.3 | 13.3 | | | |

*[a]Patient numbers in brackets from Tyybäkinoja et al.[5] [b]FLT3 and mutation data from Tyybäkinoja et al.5; ITD: internal tandem duplication; D835: point mutation at aspartic acid residue D835.*