**Acute Lymphoblastic Leukemia**

*DUX4r, ZNF384r and PAX5-P80R mutated B-cell precursor acute lymphoblastic leukemia frequently undergo monocytic switch*

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### Table S1. S1a. List of antibodies used for diagnostic immunophenotyping.

| Antibody | Fluorochrome | Clone | Catalogue number | Manufacturer |
|----------|--------------|-------|------------------|--------------|
| CD2      | PE           | 39C1.5 | A07744           | Beckman Coulter |
| CD3      | FITC         | UCHT1 | 1F-202-T100      | Exbio        |
| CD4      | PE-Cy7       | MEM-241 | T7-359-T100     | Exbio        |
| CD5      | PerCP-Cy5.5  | L17F12 | T9-691-T100      | Exbio        |
| CD7      | APC          | 124-1D1 | 1A-183-T100      | Exbio        |
| CD8      | APC-Cy7      | MEM-31 | T4-207-T100      | Exbio        |
| CD10     | PE           | SS2/36 | R084801          | Dako         |
| CD11b    | PE           | ICRF44 | 347557           | BD Biosciences |
| CD11c    | PerCP-Cy5.5  | B-ly6  | 646784           | BD Biosciences |
| CD13     | PE           | SJ1D1  | A07762           | Beckman Coulter |
| CD14     | Pacific Blue | MEM-15 | PB-293-T100      | Exbio        |
| CD15     | FITC         | MMA    | 332778           | BD Biosciences |
| CD16     | Alexa Fluor 700 | 3G8 | A7-646-T100   | Exbio        |
| CD19     | APC          | LT19   | 1A-305-T100      | Exbio        |
| CD19     | PE-Cy7       | J3119  | IM3628           | Beckman Coulter |
| CD20     | FITC         | L27    | 345792           | BD Biosciences |
| CD22     | FITC         | SJ10.1H11 | IM0779U      | Beckman Coulter |
| CD24     | PE           | ALB9   | IM1428U          | Beckman Coulter |
| CD26     | PE           | M-T271 | 560609           | BD Biosciences |
| CD33     | PE           | D3HL60.251 | A07775        | Beckman Coulter |
| CD34     | APC          | S81    | IM2472           | Beckman Coulter |
| CD38     | PE           | T16    | IM1832U          | Beckman Coulter |
| CD44     | FITC         | G44-26 | 555478           | BD Biosciences |
| CD45     | PerCP        | 2D1    | PC-222-T100      | Exbio        |
| CD56     | PE           | NCAM16.2 | 345812        | BD Biosciences |
| CD64     | FITC         | 22     | B49185           | Beckman Coulter |
| CD65     | FITC         | 88H7   | B36299           | Beckman Coulter |
| CD66c    | FITC         | KOR-SA3544 | IM2039U     | Beckman Coulter |
| CD71     | Alexa Fluor 700 | MEM-75 | A7-235-T100      | Exbio        |
| CD79a    | Alexa Fluor 647 | 2L7-4 | MCA1298A647      | Exbio        |
| CD99     | PE           | 3B2/TA8 | 1P-658-T100     | Exbio        |
| CD117    | PE           | 95C3   | IM1360U          | Beckman Coulter |
| CD371    | APC          | 50C1   | 353606           | BioLegend    |
| IgM      | FITC         | G20-127 | 555782          | BD Biosciences |
| HLA DR   | PE           | L243   | 1P-690-T100      | Exbio        |
| NG2      | PE           | 7.1    | B92429           | Beckman Coulter |
| TSLPR    | PE           | 1D3    | 322906           | BioLegend    |
| Kappa    | PE           | TB28-2 | 1P-674-T100      | Exbio        |
| Lambda   | FITC         | 1-155-2 | 1F-673-T100     | Exbio        |
| CD3      | APC          | UCHT1  | IM2467           | Beckman Coulter |
| CD22     | APC          | S-HCL-1 | 333145        | BD Biosciences |
| cycCD79a | PE           | HM57   | R715901          | Dako         |
| TdT      | FITC         | HT-6   | F713950          | Dako         |
| Lysozyme | PE           | LZ-2   | GM-4133          | Nordic Mubio |
| MPO      | FITC         | CLB-MPO-1 | IM1874U     | Beckman Coulter |
**S1b. Diagnostic antibody combinations.** B1: FITC, B2: PE, B3: PerCP/PerCP-Cy5.5, B4: PE-Cy7, R1: APC/Alexa Fluor 647, R2: Alexa Fluor 700, R3: APC-Cy7, V1: Syto-41/Pacific Blue, V2: Pacific Orange.

| B1  | B2  | B3  | B4  | R1   | R2     | R3   | V1   | V2   |
|-----|-----|-----|-----|------|--------|------|------|------|
| CD4 | CD99| CD5 | CD3 | CD7  | CD16+CD56 | CD8  | Syto-41 | CD45 |
| CD10| CD13| CD45| CD19|      |         |      |      |      |
| CD10| CD33| CD45| CD19|      |         |      |      |      |
| CD15| CD117| CD45| CD19| CD33 | CD71   |      |      |      |
| CD20| CD10| CD45| CD19| CD34 | CD38   |      | Syto-41 |      |
| CD22| CD24| CD45| CD19|      | CD79a  |      |      |      |
| CD34| CD38| CD45| CD19|      |        |      |      |      |
| CD44| CD27| CD34| CD19| CD10 | CD38   | CD20 | CD45 |      |
| CD64| CD45| CD19|      |      |        |      |      |      |
| CD65| CD2  | CD45| CD19|      |        |      |      |      |
| CD66c| CD56 | CD45| CD19|      |        |      |      |      |
| CD19| NG2  | CD45|      |      |        |      |      |      |
| CD19| TSLPR| CD45|      |      |        |      |      |      |
| CD33| VNN2 | CD34| CD19| CD371|        | CD14 | CD45 |      |
| IgM | CD19 | CD45|      |      |        |      |      |      |
| Lambda| Kappa| CD20| CD19| CD5  |        | CD45 |      |      |
| CD45| intra-Lysozyme| CD11c| CD34| CD33 |        | CD14 |      |      |
| intra-TdT| CD7  | CD45| CD3  |      | intra-CD3|      |      |      |
| CD7  | CD11b| CD45| CD19|      | intra-CD22|      |      |      |
| intra-MPO| intra-CD79a| CD45| CD19|      | intra-CD3|      |      |      |
| intra-IgM| CD19 | CD45|      |      |        |      |      |      |
Table S2. Association of switch with the most frequent recurrent genetic alterations within DUX4r subtype.

|                | Total (n=56) | Switch No (n=11) | Switch Yes (n=45) | p-Value |
|----------------|--------------|------------------|-------------------|---------|
|                |              | Switch no versus yes |                   |         |
| ERG deletion   |              |                   |                   |         |
| No             | 16           | 4                 | 12                | 0.46    |
| Yes            | 38           | 6                 | 32                |         |
| No data        | 2            | 1                 | 1                 |         |
| IKZF1 deletion |              |                   |                   |         |
| No             | 35           | 8                 | 27                | 0.17    |
| Yes            | 10           | 0                 | 10                |         |
| No data        | 11           | 3                 | 8                 |         |
| CDKN2A deletion|              |                   |                   |         |
| No             | 26           | 6                 | 20                | 0.44    |
| Yes            | 19           | 2                 | 17                |         |
| No data        | 11           | 3                 | 8                 |         |
| CDKN2B deletion|              |                   |                   |         |
| No             | 26           | 6                 | 20                | 0.44    |
| Yes            | 19           | 2                 | 17                |         |
| No data        | 11           | 3                 | 8                 |         |
| PAX5 deletion  |              |                   |                   |         |
| No             | 36           | 7                 | 29                | 0.67    |
| Yes            | 9            | 1                 | 8                 |         |
| No data        | 11           | 3                 | 8                 |         |
| NRAS mutation  |              |                   |                   |         |
| No             | 36           | 9                 | 27                | 0.25    |
| Yes            | 14           | 1                 | 13                |         |
| No data        | 6            | 1                 | 5                 |         |
| KMT2D mutation |              |                   |                   |         |
| No             | 39           | 9                 | 30                |         |
| Yes            | 11           | 1                 | 10                | 0.42    |
| No data        | 6            | 1                 | 5                 |         |
Table S3. Top ranking differentially expressed genes (n = 50) between switching and non-switching cases. Only protein-coding genes with absolute fold change ≥ 2.5 were considered. Genes with Cluster of Differentiation nomenclature IDs are highlighted.

| ensembl_gene_id         | gene                  | CD | log2FoldChange | padj       | description                                                                 |
|-------------------------|-----------------------|----|----------------|------------|-----------------------------------------------------------------------------|
| ENSG00000154188         | ANGPT1                | 4.32| 1.40E-60       |            | angiopoietin 1                                                              |
| ENSG00000169083         | AR                    | 8.16| 7.60E-57       |            | androgen receptor                                                           |
| ENSG00000133687         | TMTC1                 | 4.3 | 1.10E-35       |            | transmembrane O-mannosyltransferase                                         |
| ENSG00000171855         | IFNB1                 | 7.52| 3.20E-35       |            | targeting cadherins 1                                                      |
| ENSG00000203727         | SAMD5                 | 5.2 | 3.20E-35       |            | interferon beta 1                                                          |
| ENSG00000196989         | PPP4R4                | 4.62| 1.40E-33       |            | protein phosphatase 4 regulatory subunit 4                                 |
| ENSG00000119922         | IFIT2                 | 3.25| 1.40E-33       |            | interferon induced protein with tetratricopeptide repeats 2                |
| ENSG00000145794         | MEGF10                | 4.57| 2.50E-32       |            | multiple EGF like domains 10                                               |
| ENSG00000178662         | CSRPNP3               | 7.07| 3.70E-32       |            | cysteine and serine rich nuclear protein 3                                 |
| ENSG00000170421         | KRT8                  | 3.21| 8.70E-28       |            | keratin 8                                                                   |
| ENSG00000088538         | DOCK3                 | 3.12| 1.80E-25       |            | dedicator of cytokinesis 3                                                  |
| ENSG00000144369         | FAM171B               | 4.76| 3.20E-25       |            | family with sequence similarity 171 member B                               |
| ENSG00000145685         | LHFP2                 | 2.71| 3.40E-25       |            | LHFPL tetraspan subfamily member 2                                         |
| ENSG00000159674         | SPON2                 | 2.57| 3.60E-25       |            | spondin 2                                                                  |
| ENSG00000182853         | VMO1                  | 2.79| 9.70E-25       |            | vitelline membrane outer layer 1 homolog                                   |
| ENSG00000172322         | CLEC12A               | 3.83| 4.90E-24       |            | C-type lectin domain family 12 member A                                    |
| ENSG00000091129         | NRCAM                 | 3.49| 6.30E-24       |            | neuronal cell adhesion molecule                                             |
| ENSG00000165509         | MAGEC3                | 6.84| 4.40E-23       |            | MAGE family member C3                                                       |
| ENSG00000180767         | CHST13                | 3.57| 4.90E-23       |            | carbohydrate sulfotransferase 13                                           |
| ENSG00000205755         | CRLF2                 | -4.09| 5.60E-23       |            | cytokine receptor like factor 2                                             |
| ENSG00000256660         | CLEC12B               | 4.06| 8.90E-23       |            | C-type lectin domain family 12 member B                                    |
| ENSG00000169855         | ROBO1                 | -3.7 | 1.30E-22       |            | roundabout guidance receptor 1                                              |
| ENSG00000103139         | SLC6A13               | 3.21| 1.30E-22       |            | solute carrier family 6 member 13                                            |
| ENSG00000134207         | SYT6                  | 6.83| 1.30E-22       |            | synaptotagmin 6                                                             |
| ENSG00000133101         | CCNA1                 | 3.96| 1.80E-22       |            | cyclin A1                                                                  |
| ENSG00000129654         | FOXJ1                 | 4.03| 2.60E-22       |            | forkhead box J1                                                             |
| ENSG00000187783         | TMEM72                | -4.72| 6.80E-22       |            | transmembrane protein 72                                                    |
| ENSG00000144824         | PHLDB2                | -2.61| 7.50E-22       |            | pleckstrin homology domain family member 2                                  |
| ENSG00000240403         | KIR3DL2               | -4.01| 1.70E-21       |            | killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 2 |
| ENSG00000156738         | MS4A1                 | -2.74| 3.40E-21       |            | membrane spanning 4-domains A1                                              |
| ENSG00000132514         | CLEC10A               | 3.67| 7.90E-21       |            | C-type lectin domain containing 10A                                         |
| ENSG00000164023         | SGMS2                 | 3.18| 8.20E-21       |            | sphingomyelin synthase 2                                                    |
| ENSG00000100867         | DHR2S                 | 4.53| 1.80E-20       |            | dehydrogenase/reductase 2                                                  |
| ENSG00000157510         | AFAP1L1               | -3.1 | 9.40E-20       |            | actin filament associated protein 1 like 1                                 |
| ENSG00000011145         | DCN                   | 3.17| 7.50E-19       |            | decorin                                                                    |
| ENSG00000158488         | CD1E                  | 4.23| 9.40E-19       |            | CD1e molecule                                                               |
| ENSG00000137962         | ARHGAP29              | -3.38| 3.20E-18       |            | Rho GTPase activating protein 29                                              |
| ENSG00000143850         | PLEKHA6               | 2.56| 3.20E-18       |            | pleckstrin homology domain containing A6                                    |
| ENSG00000182676         | PPP1R27               | 3.24| 3.30E-18       |            | protein phosphatase 1 regulatory subunit 27                                 |
| ENSG00000184507         | NUTM1                 | -7.31| 7.70E-18       |            | NUT midline carcinoma family member 1                                       |
| ENSG00000091181         | IL5RA                 | 3    | 7.70E-18       |            | interleukin 5 receptor subunit alpha                                         |
| ENSG00000183775         | KCTD16                | 2.6  | 8.40E-18       |            | potassium channel tetramerization domain containing 16                      |
| ENSG00000183421         | RIPK4                 | -4.15| 2.60E-17       |            | receptor interacting serine/threonine kinase 4                             |
| ENSG00000198576         | ARC                   | 3.24| 3.40E-17       |            | activity regulated cytoskeleton associated protein                          |
| ENSG00000185028         | LRRC14B               | -2.67| 4.40E-17       |            | leucine rich repeat containing 14B                                          |
| ENSG00000129595         | EPB41L4A              | 2.51| 5.90E-17       |            | erythrocyte membrane protein band 4.1 like 4A                               |
| ENSG00000165186         | PTCHD1                | 3.03| 7.10E-17       |            | patched domain containing 1                                                |
| ENSG00000074590         | NUAK1                 | 3   | 7.90E-17       |            | NUAK family kinase 1                                                       |
| ENSG00000147655         | RSPO2                 | 4.18| 8.00E-17       |            | R-spondin 2                                                                |
| ENSG00000178882         | RFLNA                 | 2.99| 1.10E-16       |            | refilin A                                                                  |
Table S4. Top ranking differentially expressed genes (n = 50) between switching and non-switching cases inside DUX4 rearranged cases. Only protein-coding genes with absolute fold change ≥ 2.5 were considered. Genes with Cluster of Differentiation nomenclature IDs are highlighted.

| ensembl_gene_id | gene | CD | log2FoldChange | padj     | description                                      |
|-----------------|------|----|----------------|---------|--------------------------------------------------|
| ENSG00000169083 | AR   |    | 9.91           | 6.60E-15| androgen receptor                                |
| ENSG00000133101 | CCNA1|    | 5.42           | 5.00E-13| cyclin A1                                        |
| ENSG00000133104 | SPART|    | 2.87           | 2.50E-10| NA                                               |
| ENSG00000179388 | EGR3 |    | 5.24           | 1.00E-09| NA                                               |
| ENSG00000245848 | CEBPA|    | 5.12           | 8.90E-09| NA                                               |
| ENSG00000164283 | ESM1 |    | -6.7           | 2.80E-08| endothelial cell specific molecule 1             |
| ENSG00000164023 | SGMS2|    | 4.28           | 4.70E-08| sphingomyelin synthase 2                         |
| ENSG00000159217 | IGF2BP1 |    | -6.64          | 8.00E-08| insulin like growth factor 2 mRNA binding protein 1 |
| ENSG00000138798 | EGF  |    | 4.6            | 8.30E-08| NA                                               |
| ENSG00000133101 | CCNA1|    | 5.42           | 5.00E-13| NA                                               |
| ENSG00000133104 | SPART|    | 2.87           | 2.50E-10| NA                                               |
| ENSG00000179388 | EGR3 |    | 5.24           | 1.00E-09| NA                                               |
| ENSG00000245848 | CEBPA|    | 5.12           | 8.90E-09| NA                                               |
| ENSG00000164283 | ESM1 |    | -6.7           | 2.80E-08| endothelial cell specific molecule 1             |
| ENSG00000164023 | SGMS2|    | 4.28           | 4.70E-08| sphingomyelin synthase 2                         |
| ENSG00000159217 | IGF2BP1 |    | -6.64          | 8.00E-08| insulin like growth factor 2 mRNA binding protein 1 |
| ENSG00000138798 | EGF  |    | 4.6            | 8.30E-08| NA                                               |
| ENSG00000133101 | CCNA1|    | 5.42           | 5.00E-13| NA                                               |
| ENSG00000133104 | SPART|    | 2.87           | 2.50E-10| NA                                               |
| ENSG00000179388 | EGR3 |    | 5.24           | 1.00E-09| NA                                               |
| ENSG00000245848 | CEBPA|    | 5.12           | 8.90E-09| NA                                               |
| ENSG00000164283 | ESM1 |    | -6.7           | 2.80E-08| endothelial cell specific molecule 1             |
| ENSG00000164023 | SGMS2|    | 4.28           | 4.70E-08| sphingomyelin synthase 2                         |
| ENSG00000159217 | IGF2BP1 |    | -6.64          | 8.00E-08| insulin like growth factor 2 mRNA binding protein 1 |
| ENSG00000138798 | EGF  |    | 4.6            | 8.30E-08| NA                                               |
| ENSG00000133101 | CCNA1|    | 5.42           | 5.00E-13| NA                                               |
| ENSG00000133104 | SPART|    | 2.87           | 2.50E-10| NA                                               |
| ENSG00000179388 | EGR3 |    | 5.24           | 1.00E-09| NA                                               |
| ENSG00000245848 | CEBPA|    | 5.12           | 8.90E-09| NA                                               |
| ENSG00000164283 | ESM1 |    | -6.7           | 2.80E-08| endothelial cell specific molecule 1             |
| ENSG00000164023 | SGMS2|    | 4.28           | 4.70E-08| sphingomyelin synthase 2                         |
| ENSG00000159217 | IGF2BP1 |    | -6.64          | 8.00E-08| insulin like growth factor 2 mRNA binding protein 1 |
| ENSG00000138798 | EGF  |    | 4.6            | 8.30E-08| NA                                               |
| ENSG00000133101 | CCNA1|    | 5.42           | 5.00E-13| NA                                               |
| ENSG00000133104 | SPART|    | 2.87           | 2.50E-10| NA                                               |
| ENSG00000179388 | EGR3 |    | 5.24           | 1.00E-09| NA                                               |
| ENSG00000245848 | CEBPA|    | 5.12           | 8.90E-09| NA                                               |
| ENSG00000164283 | ESM1 |    | -6.7           | 2.80E-08| endothelial cell specific molecule 1             |
| ENSG00000164023 | SGMS2|    | 4.28           | 4.70E-08| sphingomyelin synthase 2                         |
| ENSG00000159217 | IGF2BP1 |    | -6.64          | 8.00E-08| insulin like growth factor 2 mRNA binding protein 1 |
| ENSG00000138798 | EGF  |    | 4.6            | 8.30E-08| NA                                               |
| ENSG00000133101 | CCNA1|    | 5.42           | 5.00E-13| NA                                               |
| ENSG00000133104 | SPART|    | 2.87           | 2.50E-10| NA                                               |
| ENSG00000179388 | EGR3 |    | 5.24           | 1.00E-09| NA                                               |
| ENSG00000245848 | CEBPA|    | 5.12           | 8.90E-09| NA                                               |
| ENSG00000164283 | ESM1 |    | -6.7           | 2.80E-08| endothelial cell specific molecule 1             |
| ENSG00000164023 | SGMS2|    | 4.28           | 4.70E-08| sphingomyelin synthase 2                         |
| ENSG00000159217 | IGF2BP1 |    | -6.64          | 8.00E-08| insulin like growth factor 2 mRNA binding protein 1 |
| ENSG00000138798 | EGF  |    | 4.6            | 8.30E-08| NA                                               |
| ENSG00000133101 | CCNA1|    | 5.42           | 5.00E-13| NA                                               |
| ENSG00000133104 | SPART|    | 2.87           | 2.50E-10| NA                                               |
| ENSG00000179388 | EGR3 |    | 5.24           | 1.00E-09| NA                                               |
| ENSG00000245848 | CEBPA|    | 5.12           | 8.90E-09| NA                                               |
| ENSG00000164283 | ESM1 |    | -6.7           | 2.80E-08| endothelial cell specific molecule 1             |
| ENSG00000164023 | SGMS2|    | 4.28           | 4.70E-08| sphingomyelin synthase 2                         |
| ENSG00000159217 | IGF2BP1 |    | -6.64          | 8.00E-08| insulin like growth factor 2 mRNA binding protein 1 |
| ENSG00000138798 | EGF  |    | 4.6            | 8.30E-08| NA                                               |
**Figure S1.** Flow chart showing the number of patients.

![Flow chart showing the number of patients](image1.png)

**Figure S2.** Monocytic switch in a typical patient with the DUX4r subtype, d+8 PB sample. Changes in expression of the precursor, B lineage and monocytic markers and side scatter (SSC) are depicted.

![Monocytic switch in a typical patient](image2.png)
**Figure S3.** Intermediate B-monocytoid cells and monocytes in patients with monocytic switch. **S3a.** Absolute monocyte count by morphology in switching patients. Separately are shown data from randomly selected 122 patients without switch. Subtypes are marked with asterisk if significantly different from non-switching patient values by Mann-Whitney test. HYPO, hypodiploid; HHD, hyperdiploid. **S3b.** Dynamics of diagnostic blast count in PB compared to d+8 monocyte count in PB in patients with monocytic switch. HYPO, hypodiploid; HHD, hyperdiploid. **S3c.** The maximum proportion of intermediate B-monocytoid cells defined as CD19*CD14* at time-points d0 (BM, PB), d+8 (PB), d+15 (BM, PB), and d+33 (BM) are shown. Each dot represents the maximum value of a single patient. HYPO, hypodiploid; HHD, hyperdiploid; B-other unknown, B-other without performed RNA-seq.

**S3a.**

**S3b.**
Figure S4. Unsupervised Hierarchical Clustering Analysis of all cases (n = 197) based on most variable genes (only genes with SD higher than 0.4 times maximum SD, n = 271).

Figure S5. Unsupervised Hierarchical Clustering of DUX4r cases (n = 55) based on most variable genes (only genes with SD higher than 0.4 times maximum SD).
Figure S6. Correlation of FC and PCR MRD on d+8 and w+12 in DUX4r, PAX5-P80R and ZNF384r. Spearman’s rank correlation coefficient indicated if p value<0.05.

Figure S7. Correlation of FC and PCR MRD in DUX4r\textsuperscript{neg}PAX5-P80R\textsuperscript{neg}ZNF384r\textsuperscript{neg} cases with monocytic switch in different time points. Spearman’s rank correlation coefficient indicated if p value<0.05.
Figure S8. Immunophenotype of genetic subtypes. Expressions are positive if present on ≥10% blasts, dim expressions as being positive on ≤50% of blasts. CD10\textsuperscript{bright} is defined as CD10 overexpression on ≥20% of blasts; CD10\textsuperscript{low} as being positive (≥10% of blasts) but not fulfilling definition for CD10\textsuperscript{high}; CD2\textsuperscript{4 high} as expressed on ≥60% of blasts; CD66c\textsuperscript{high} as expressed on ≥75% of blasts. Typical phenotype of DUX4r is defined as CD10\textsuperscript{low} CD20\textsuperscript{neg} CD34\textsuperscript{pos} CD2\textsuperscript{pos} CD371\textsuperscript{pos} (sensitivity 60%, specificity 100%), typical phenotype of ZNF384r as CD10\textsuperscript{neg/low} CD13\textsuperscript{pos} CD66c\textsuperscript{neg} CD34\textsuperscript{pos} CD135\textsuperscript{pos} CD24\textsuperscript{low} (sensitivity 50%, specificity 99.7%) and PAX5-P80R as CD10\textsuperscript{neg/low} CD66c\textsuperscript{high} CD2\textsuperscript{dim/neg} CD4\textsuperscript{neg} CD34\textsuperscript{pos} CD33\textsuperscript{neg/dim} or CD10\textsuperscript{neg/low} CD66c\textsuperscript{high} CD2\textsuperscript{pos} CD4\textsuperscript{pos} CD34\textsuperscript{neg} CD33\textsuperscript{pos} (sensitivity 100%, specificity 98.5%).
Figure S9. Comparison of EFS in patients with (n=18) or without (n=23) monocytic switch belonging to slow early response (SER) or high risk (HR) prognostic group using PCR MRD data at day 33 and week 12. 5-year EFS of patients with monocytic switch was 75± 13%, 5-year EFS of patients without monocytic switch was 50±9.5%.