**Supplementary Table S1: Fusion transcript predictions in KM-H2 and L428**

| Gene 1 in the fusion pair | Gene 2 in the fusion pair | Chromosome 1 | Strand 1 | Chromosome 2 | Strand 2 | Number of paired end reads spanning the breakpoint | Number of reads split by the breakpoint | Breakpoint sequence | Fusion between adjacent genes | Inter-chromosomal | Genomic inversion | Genomic eversion |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **KM-H2** | | | | | | | | | | | | |
| CIITA | FLJ27352 | 16 | + | 15 | + | 13 | 275 | GACCAGATGGACCTGGCTGGAGAAGAAGAGATTGAGCTCTACTCAGAACCCGACACAGACACCATCAACTGCGACCAGTTCAGCAGGCTGTTGTGTGACATGGAAGGTGATGAAGAGACCAGGGAGGCTTATGCCAATATCGCGGAACTGGACCAGTATGTCTTCCAGGACTCCCAGCTGGAGGGCCTGAGCAAGGACATTTTCA\|GATAAGAAAAGTACTTCACCTTCAAATTCAGACACAGAAATGAAATCTGAACAACTGCCTCCTTGTGTGAACCCTGGCAATCCTGTGTTTTCATGTATGTTGGATCCAAAGACACTCCAGACAGCCACCTCACTATCAAAACCTCAAATGATTATGTATAAAACC | N | Y | N | N |
| CIITA | FLJ27352 | 16 | + | 15 | + | 417 | 273 | ATTGAGCTCTACTCAGAACCCGACACAGACACCATCAACTGCGACCAGTTCAGCAGGCTGTTGTGTGACATGGAAGGTGATGAAGAGACCAGGGAGGCTTATGCCAATATCGCGGAACTGGACCAGTATGTCTTCCAGGACTCCCAGCTGGAGGGCCTGAGCAAGGACATTTTCA\|GATAAGAAAAGTACTTCACCTTCAAATTCAGACACAGAAATGAAATCTGAACAACTGCCTCCTTGTGTGAACCCTGGCAATCCTGTGTTTTCATGTATGTTGGATCCAAAGACACTCCAGACAGCCACCTCACTATCAAAACCTCAAATGATTATGTATAA | N | Y | N | N |
| CIITA | FLJ27352 | 16 | + | 15 | + | 35 | 56 | ATTGAGCTCTACTCAGAACCCGACACAGACACCATCAACTGCGACCAGTTCAGCAGGCTGTTGTGTGACATGGAAGGTGATGAAGAGACCAGGGAGGCTTATGCCAATATCGCGGAACTGGACCAGTATGTCTTCCAGGACTCCCAGCTGGAGGGCCTGAGCAAGGACATTTTCA\|GTGTATGTGATTTTAAGGGTAGTCTTCAACGTCAAGAGAAGAGACCACCAAACAGGCTTTGTGTGA | N | Y | N | N |
| BAT2L | MGMT | 9 | + | 10 | + | 55 | 34 | CGAGCGGCGAGACAGGCGCCGAGGCTCCACCGCGCAGCGACGAGCGAGCCCGGGAGGAGGGAGGGAGCGAGCGAGCGAGCAGCCCGCGCCGCCGCCTCGCAATCCGCCGCCATCCCGCCGCCCCCGTGCCCGACCGCCGCCCGACTGCCATCGCCCGGCCCGGCCGCGCCCGCGGAACCAGACCAGGT\|ACTTGGAAAAATGGACAAGGATTGTGAAATGAAACGCACCACACTGGACAGCCCTTTGGGGAAGCTGGAGCTGTCTGGTTGTGAGCAGGGTCTGCACGAAATAAAGCTCCTGGGCAAGGGGACGTCTGCAGCTGATGCCGTGGAGGTCCCAGCCCCCGCTGCGGTTCTCGGAGGTCCGGAG | N | Y | N | N |
| TP53BP1 | HISPPD2A | 15 | - | 15 | - | 62 | 29 | AAAAATGGCTAATGCAAAGCAGCTAAGCTCAGATGCAGAGGCCCAGAAGCTGGGGAAGCCCTCTGCCCATGCCTCACAAAGCTTCTGTGAAAGTTCTAGTGGTGAGTGTGATTGTAGATTATTCTTGTCTCCACCTAAATTATAATCTGGAATGGAAAGTTGGCGAGAACTGCATGCTT\|ATATCATTGTGTCTGAGGGCCAGATATGATTATGAAGCTTTTTCCAAAGATCCAGGGATGGGAATGGGAGTGGGTAGGAGGGGTAATGCGGTCATTGGAGTCGGGGGCTGGAACATTATGAGTGCTCAATAAATATAAACTAATGAGAAT | Y | N | N | Y |
| DYNLT3 | CYBB | X | - | X | + | 12 | 15 | CATATAAAATATGCAACTCTTAGTTAAAGGCCTTATTATCAGTCTTACCTATACAAGTAGTAAATTTTGTCATTGCTTTAGTTACAACCATCTGTAAATAACTTAAAAGACTTATTATGTGGGGTTCAAATTGAGTGGAATAAAGTATAGATTAAAAGTATA\|GATCAAAAGGTTCAGTAACTTCCCTAAGATTATGAAACTGTGACCAGATCTAGCCCATCTTACTCCAGGTTTGATACTCTTTCCACAATACTGAGCTGCCTCAGAATCCTCAAAATCAGTTTTTATATTCCCCAAAAGAAGAAGGAAACCAAGGAGT | Y | N | Y | N |
| AC008993.3 | VPS18 | 19 | - | 15 | + | 18 | 12 | CGGGAGCTTCCGGGAGGGCGGCTCGCAGGCACCATGACTCCTGTGAGGATGCAGCACTCCCTGGCAGGTCAGACCTATGCCGTGCCCTTCATCCAGCCAGACCTGCGGCGAGAGGAGGCCGTCCAGCAGATGGCGGATGCCCTGCAGTACCTGCAGAAGGTCTCTGGAGACATCTTCAGCAG\|CTTGTAGATGCCTGGATTGAGATGGGCAGCCGGCTGGATGCTCGTCAGCTCATTCCTGCCCTGGTGAACTACAGCCAGGGTGGTGAGGTCCAGCAGGTGAGCCAGGCCATCCGCTACATGGAGTTCTGCGTGAACGTGCTGGGGGAGACTGAGCAGGCCATCCACAACTACCTGCTGTCA | N | Y | N | N |
| CIITA | FLJ27352 | 16 | + | 15 | + | 8 | 11 | TGGGGGGTGCCCTAATACCTGACGACCATTCATTGATGGGCAGTCAGACCCCTCTCCCCAAGGTGGGTACAATAGAGACTCACCTTGGGCTTTCATTGATTGTGTGAGTTGGTCTCTGGTTTTTCTCAAAGTAGAGCACATAGGACCAGATGA\|AGTGCCTCAAAATTAGACCTTTTTTATTTTTTATTTTTGCTTTTCTATTAACTATATTCAACATCAACAGTGACATCAAAAAATCTTAATTTTATAATTACAGCTTCTGCGATGGGCATTATTAATCAATGGCTTGTTTTCATTTATCTTTTTAAATGTATATGTAT | N | Y | N | N |
| PACS1 | TSGA10IP | 11 | + | 11 | + | 12 | 11 | CACCTCGGCGGCGGCTGCCTCCTCCTCGTCCTCGTCTACCTCCACCTCCATGGCCGTGGCGGTGGCCTCGGGCTCCGCGCCTCCCGGTGGCCCGGGGCCAGGCCGCACCCCCGCCCCGGTGCAGATGAACCTGTACGCCACCTGGGAGGTGGACCGGAGCTCGTCCAGCTGCGTGCCTAGG\|CGCCAGGAGCGACAGCGCTTTGCTGAGTACCAGGCGGAGCTGCAAGGCATCCAGCACAGGGTGCAGGCCCGGCCCTTCCTGTTCCAGCAGGCTATGCAGGCCAATGCCCGGCTCACCGTCACTCGGCGCTTCTCCCAGGTGCTGTCAGCACTGGGGCTGGATGAGGAGCAGCT | N | N | N | Y |
| NFAT5 | CYB5B | 16 | + | 16 | + | 36 | 9 | CCCCTCCCGCTGCCCTCGGGCCGGGCTGGGTCGAGCTGCGATGCCCTCGGACTTCATCTCATTGCTCAGCGCGGACCTAGACCTGGAATCGCCCAAGTCCCTCTACTCGCGAGATTCTCTGAAGTTACACCCATCACAGAATTTTCATAGAGCTGGACTATTGG\|AAGGACCCTTCAAAAAATGATACATGCAAAAGTTGCTGGGCATATTGGATTTTACCCATCATAGGCGCTGTTCTCTTAGGTTTCCTGTACCGCTACTACACATCGGAAAGCAAATCCTCCTGAGGAGGCCTTGCTGAAGTTAGAAAGTGCATCCACTTTGGGGCGAAAACTAGAGACTTGCTTGGGGGCT | Y | N | N | Y |
| CIITA | FLJ27352 | 16 | + | 15 | + | 16 | 8 | CTGTCAGAGCCCCAAGGCAGCTCACAGTGTGCCACCATGGAGTTGGGGCCCCTAGAAGGTGGCTACCTGGAGCTTCTTAACAGCGATGCTGACCCCCTGTGCCTCTACCACTTCTATGACCAGATGGACCTGGCTGGAGAAGAAGAGATTGAGCTCTACTCAG\|GATAAGAAAAGTACTTCACCTTCAAATTCAGACACAGAAATGAAATCTGAACAACTGCCTCCTTGTGTGAACCCTGGCAATCCTGTGTTTTCATGTATGTTGGATCCAAAGACACTCCAGACAGCCACCTCACTATCAAAACCTCAAATG | N | Y | N | N |
| IARS | ECM2 | 9 | - | 9 | - | 12 | 8 | AACGATTTGGAAATTGGCTGAAAGATGCACGTGACTGGACAATTTCCAGAAACAGATACTGGGGCACCCCCATCCCACTGTGGGTCAGCGATGACTTTGAGG\|AGAAATTGGCTGGTGGAAAAAAATCAAACATGAAGATTGCAGTTTTGTTTTGTTTTTTTCTGCTTATCATTTTTCAAACTGACTTTGGAAAAAATGAAGAAATTCCTAGGAAGCAAAGGAGGAAGATCTACCACAGAAGGTTGAGGAAAAGTTCAACCTCACACAAG | Y | N | N | Y |
| AC008993.3 | VPS18 | 19 | - | 15 | + | 14 | 7 | CCGGGAGGGCGGCTCGCAGGCACCATGACTCCTGTGAGGATGCAGCACTCCCTGGCAGGTCAGACCTATGCCGTGCCCTTCATCCAGCCAGACCTGCGGCGAGAGGAGGCCGTCCAGCAGATGGCGGATGCCCTGCAGTACCTGCAGAAGGTCTCTGGAGACATCTTCAGCAGGTGG\|ATGTGGACCTGGCCAAGCAGTGTGCAGACCTGCCTGAGGAGGATGAGGAATTGCGCAAGAAGCTGTGGCTGAAGATCGCACGGCACGTGGTGCAGGAAGAGGAAGATGTACAGACAGCCATGGCTTGCCTGGCTAGCTGCCCCTTGCTCAAGATTGAGGATGTGCT | N | Y | N | N |
| MLL3 | TPTE | 7 | - | 21 | - | 21 | 6 | GGGAGTGGAAGGAACAGATGGTGTCAAAAAGAGAAAAAGGAAACCATACAGACCAGGTATTGGTGGATTTATGGTGCGGCAAAGAAGTCGAACTGGGCAAGGGAAAACCAAAAGATCTGTGATCAGAAAAGATTCCTCAGGCTCTATTTCCGAGCAGTTACCTTGCAGAGATGATG\|AGAATGTTGGACCGACGACACAAGACCTCAGACTTGTGTTATTCTAGCAGCTGAACACACCCCAGGCTCTTCTGCCCGGCAGTGGCTCTGGAAGCAGTCTGGTGTATAGAGTTATGGATTCACTACCAGATTCTACTGTATGCTCTTGACAACTATGACCACAATGGTCCA | N | Y | N | N |
| **L428** | | | | | | | | | | | | |
| TNRC18B | MYLPF | 7 | - | 16 | + | 20 | 21 | TCCAGATCGCATCCCAGGCGCGCGATGCCCGGGCCCGCGAGCGCGAGGCTGGCAGGCCAGGGGTCCTGCAGGCGCCCCCCGGCTCCCCGCGGCCTCTGGACCGGCCCGAGGGCCTGCGCGAGAAGAACTCGGTCATCCGCTCGCTCAAGCGGCCGCCCCCCGCGGATGCCCCCACGGTGCGGGCCACACGCGCCTC\|CGCCCAGCACATCTGCTCCTCCACCTGCACCTGACTCCCTGGCCCTCGTGAAGCCACTCCCATACTCCTAGACAGGGCTGCTGCGCCCTCCACTTCTGGGCTCCTGACCAGCTCTGGTATGTCAGTTTCTGCATTCATTCCTGTCTCTATTAGTTATAAGGCAAGTTCTGTGGGATGGGAACTACATC | N | Y | N | N |
| ELMO1 | SLCO3A1 | 7 | - | 15 | + | 8 | 6 | GGTATAGACACGTGTGGCCGTTTACGCTGTAGGATCCTCATTCCCACTGGCTTTGAACATTTTGGGGACTTACAATGCCGCCACCCGCGGACATCGTCAAGGTGGCCATAGAATGGCCGGGCGCCTACCCCAAACTCATGGAAATTGATC\|AGGCTAGATCGTAAAAGATGTTGCTGTTTCTACCCTGCTCTCTTGGATCGCTTGCTCTGGAGGGAAGCTGGTCACCATGTTGTGAGGACACCTAAGCAGGCTGTGGAAAGGACCGCATGGAGAGCTGAGCCTTCCTGCCAACAACCAGC | N | Y | N | N |
| ELMO1 | SLCO3A1 | 7 | - | 15 | + | 17 | 5 | CTTTTTCTGTCATTCCTCATTAGGTATAGACACGTGTGGCCGTTTACGCTGTAGGATCCTCATTCCCACTGGCTTTGAACATTTTGGGGACTTACAATGCCGCCACCCGCGGACATCGTCAAGGTGGCCATAGAATGGCCGGGCGCCTACCCCAAACTCATGGAAATTGAT\|CAGACCATTAGAATGTGACCTCTGTGAAGACAACAGAAATGGAGGAGGCGATCCATGGGCATCTTCTGAAGCTGTTTTGGTTAACTTTGATTTGGAAGTCCTGGTTCCAGGTTCTCCTGTTTCCTGGGACCAGCTCCAGAAGTTCATTATTTTCATAAATAATAAATGAATGCATACTAG | N | Y | N | N |
| ELMO1 | SLCO3A1 | 7 | - | 15 | + | 15 | 5 | CACGTGTGGCCGTTTACGCTGTAGGATCCTCATTCCCACTGGCTTTGAACATTTTGGGGACTTACAATGCCGCCACCCGCGGACATCGTCAAGGTGGCCATAGAATGGCCGGGCGCCTACCCCAAACTCATGGAAATTGATCAGG\|AATCCTGTTCACGATGCTGGTATTTGGACCAGCCTGCGGGTTTATCCTGGGCTCTTTCTGTACCAAAATCTACGTGGATGCGGTCTTCATTGACACAAGTAACCTGGACATCACTCCGGACGACCCCCGCTGGAT | N | Y | N | N |
| | | | | | | | | ATTGACATGGCGGGTCAGGGTTAGAGCCAGGTTTCAGATTCTTCTTCCCCCACCCCCCTTTTTTTTTCCCCCTCAGAAATCCTTGTTTGGACAGATTCTTCTTTTGGAACCACATCGAGTTGACAGACCTGAGCCTTTGGTTTTCTCTTCTTCTTGCTTCACTTCCTTTTGGTCATTCAGCATCAATACT\|CTTTGTTGGTGATTGGAATGGACAGGAAATAGTTGGGTTGATAATCTTTTCTCTTTTTTTTCCTCTTCTTTACTTGATCACTCTTGACCCATTCA | | | | |

**Supplementary Table S2: Differentially expressed genes between KMH2 CIITA-FLJ27352 knockdown cultures and non-silencing controls**

NS-1: non-silencing control, baseline replicate 1; NS-2: non-silencing control, baseline replicate 2; H5-1: fusion gene knockdown, experiment replicate 1 (clone H5); H5-2, fusion gene knockdown, experiment replicate 2 (clone 5). Fold change (FC): negative values indicate lower expression in knockdown cells, positive values higher expression knockdown cells.

| Probe set | Gene | Accession | EntrezGene | NS-1 | NS-2 | Baseline mean | H5-1 | H5-2 | Experiment mean | Fold change | Lower bound of FC |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 1558407_at | CDNA FLJ38638 fis, clone HHDPC2003381 | AK095957 | | 139.7 | 131.03 | 135.65 | 33.87 | 30.31 | 32.02 | -4.24 | -3.14 |
| 230093_at | testis specific A2 homolog (mouse) | AI683428 | 89765 | 125.96 | 134.11 | 129.6 | 58.98 | 60.8 | 59.8 | -2.17 | -1.88 |
| 204430_s_at | solute carrier family 2 (facilitated glucose/fructose transporter), member 5 | NM_003039 | 6518 | 51.94 | 50.29 | 51.12 | 25.86 | 26.18 | 26.08 | -1.96 | -1.68 |
| 1569372_at | Tubulin, beta 2B | AV723391 | 347733 | 53.88 | 53.49 | 53.63 | 26.53 | 28.15 | 27.6 | -1.94 | -1.67 |
| 210182_at | cortistatin | AB000263 | 1325 | 53.71 | 57.29 | 55.34 | 31.44 | 22.5 | 26.94 | -2.05 | -1.52 |
| 214135_at | claudin 18 | BE551219 | 51208 | 50.94 | 47 | 48.76 | 26.92 | 24.28 | 25.76 | -1.89 | -1.47 |
| 215450_at | gb:W87901 /DB_XREF=gi:1401985 /DB_XREF=zh66f04.r1 /CLONE=IMAGE:417055 /FEA=mRNA /CNT=4 /TID=Hs.1066.2 /TIER=ConsEnd /STK=0 /UG=Hs.1066 /LL=6635 /UG_GENE=SNRPE /UG_TITLE=small nuclear ribonucleoprotein polypeptide E | W87901 | | 207.66 | 227.58 | 218.38 | 139.04 | 128.19 | 133.63 | -1.63 | -1.43 |
| 222201_s_at | CASP8 associated protein 2 | AB037736 | 9994 | 56.64 | 57.7 | 57.28 | 33.18 | 28.98 | 31.08 | -1.84 | -1.42 |
| 214677_x_at | coagulation factor XIII, B polypeptide /// immunoglobulin lambda locus /// immunoglobulin lambda variable 4-3 /// immunoglobulin lambda variable 3-25 /// immunoglobulin lambda variable 2-14 /// immunoglobulin lambda joining 3 | X57812 | 2165 /// 28786 ///<br>28793 /// 28815 ///<br>28831 /// 3535 | 94.11 | 100.6 | 96.86 | 52.62 | 61.89 | 56.47 | -1.72 | -1.39 |
| 212261_at | trinucleotide repeat containing 15 | AB014542 | 26058 | 93.26 | 88.34 | 90.94 | 59.07 | 47.78 | 53.78 | -1.69 | -1.38 |
| 78047_s_at | Cluster Incl. AW001777:ws04f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2496233 /clone_end=3' /gb=AW001777 /gi=5848693 /ug=Hs.233641 /len=485 | AW001777 | | 176.79 | 168.26 | 172.51 | 119.76 | 119.38 | 119.61 | -1.44 | -1.36 |
| 239084_at | Transcribed locus | BE896490 | | 59.91 | 66.56 | 63.26 | 35.58 | 35.81 | 35.69 | -1.77 | -1.35 |
| 1552912_a_at | interleukin 23 receptor | NM_144701 | 149233 | 51.64 | 55.86 | 54.05 | 27.2 | 35.58 | 31.56 | -1.71 | -1.35 |
| 224851_at | cyclin-dependent kinase 6 | AW274756 | 1021 | 178.61 | 153.32 | 165.89 | 100.31 | 109.21 | 104.83 | -1.58 | -1.35 |
| 202403_s_at | collagen, type I, alpha 2 | AA788711 | 1278 | 56.38 | 53.28 | 54.68 | 37.27 | 32.9 | 35.14 | -1.56 | -1.35 |
| 243309_at | hypothetical LOC145788 | AA398658 | 145788 | 879.78 | 947.45 | 914.53 | 620.59 | 590.34 | 605.96 | -1.51 | -1.35 |
| 223839_s_at | PRO1933 | AF132203 | | 172.71 | 151.81 | 162.92 | 95.43 | 103.98 | 98.97 | -1.65 | -1.34 |
| 203685_at | B-cell CLL/lymphoma 2 | NM_000633 | 596 | 122.4 | 148.7 | 135.97 | 81.1 | 85.9 | 83.49 | -1.63 | -1.34 |
| 226959_at | gb:AL137430.1 /DB_XREF=gi:6807987 /FEA=mRNA /CNT=36 /TID=Hs.8087.2 /TIER=Stack /STK=16 /UG=Hs.8087 /LL=51754 /UG_GENE=LOC51754 /UG_TITLE=NAG-5 protein /DEF=Homo sapiens mRNA; cDNA DKFZp761D1624 | AL137430 | | 97.41 | 97.5 | 97.45 | 64.61 | 52.57 | 58.74 | -1.66 | -1.33 |
| 201626_at | insulin induced gene 1 | BG292233 | 3638 | 958.63 | 835.33 | 898.32 | 597.01 | 580.89 | 589.06 | -1.53 | -1.33 |
| 203592_s_at | follistatin-like 3 (secreted glycoprotein) | NM_005860 | 10272 | 102.11 | 170.94 | 136.29 | 62.61 | 58.03 | 60.12 | -2.27 | -1.31 |
| 31837_at | transmembrane protein 153 | U62317 | 91289 | 64.98 | 61.66 | 63.71 | 42.19 | 30.08 | 36.34 | -1.75 | -1.31 |
| 201951_at | activated leukocyte cell adhesion molecule | BF242905 | 214 | 238.11 | 224.71 | 231.28 | 166.2 | 149.72 | 158.1 | -1.46 | -1.31 |
| 207963_at | chromosome 6 open reading frame 54 | NM_014354 | 26236 | 43.24 | 50.26 | 46.36 | 29.03 | 13.81 | 21.32 | -2.17 | -1.3 |
| 234675_x_at | CDNA: FLJ23566 fis, clone LNG10880 | AK027219 | | 90.28 | 88.6 | 89.54 | 62.17 | 52.68 | 57.28 | -1.56 | -1.3 |
| 228468_at | microtubule associated serine/threonine kinase-like | BF108964 | 84930 | 82.02 | 85.22 | 83.41 | 55.64 | 58.26 | 56.65 | -1.47 | -1.3 |
| 228171_s_at | pleckstrin homology domain containing, family G (with RhoGef domain) member 4 | AI056683 | 25894 | 85.16 | 87.25 | 86.18 | 62.41 | 58.91 | 60.64 | -1.42 | -1.29 |
| 203020_at | RAB GTPase activating protein 1-like | NM_014857 | 9910 | 56.68 | 51.73 | 53.79 | 34.89 | 30.36 | 32.53 | -1.65 | -1.28 |
| 205089_at | zinc finger protein 7 | NM_003416 | 7553 | 88.73 | 81.57 | 84.82 | 56.57 | 55.95 | 56.22 | -1.51 | -1.28 |
| 201296_s_at | WD repeat and SOCS box-containing 1 | NM_015626 | 26118 | 336.23 | 328.19 | 332.87 | 248.65 | 220.39 | 234.51 | -1.42 | -1.28 |
| 202048_s_at | chromobox homolog 6 | NM_014292 | 23466 | 212.98 | 216.81 | 214.73 | 154.68 | 156.21 | 155.56 | -1.38 | -1.28 |
| 217814_at | coiled-coil domain containing 47 | NM_020198 | 57003 | 270.49 | 271.1 | 270.76 | 198.12 | 192.21 | 195.58 | -1.38 | -1.28 |
| 1556385_at | Cardiotrophin-like cytokine factor 1 | BQ028191 | 23529 | 80.13 | 60.76 | 70.37 | 44.76 | 36.02 | 40.34 | -1.74 | -1.27 |
| 212500_at | chromosome 10 open reading frame 22 | AL049319 | 84890 | 78.17 | 84.87 | 80.68 | 50.11 | 56.23 | 52.77 | -1.53 | -1.27 |
| 215716_s_at | ATPase, Ca++ transporting, plasma membrane 1 | L14561 | 490 | 96.9 | 91.94 | 94.59 | 67.28 | 56.96 | 62.25 | -1.52 | -1.27 |
| 231992_x_at | RAB guanine nucleotide exchange factor (GEF) 1 pseudogene | AK024371 | 493754 | 72.13 | 67.25 | 69.7 | 42.62 | 49.43 | 46.14 | -1.51 | -1.27 |
| 208072_s_at | diacylglycerol kinase, delta 130kDa | NM_003648 | 8527 | 91 | 86.69 | 88.6 | 62.14 | 57.95 | 59.87 | -1.48 | -1.27 |
| 218381_s_at | U2 small nuclear RNA auxiliary factor 2 | NM_007279 | 11338 | 296.35 | 274.84 | 285.86 | 205.6 | 210.21 | 208.13 | -1.37 | -1.27 |
| 217678_at | solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 | AA488687 | 23657 | 44.06 | 63.24 | 53.52 | 26.91 | 30.65 | 28.47 | -1.88 | -1.26 |
| 241380_at | FLJ41603 protein | BF508325 | 389337 | 52.42 | 41.75 | 47.14 | 28.19 | 30.41 | 29.01 | -1.63 | -1.26 |
| 1569522_at | SLC7A5 pseudogene | BC015443 | 81893 | 100.94 | 91.27 | 96.24 | 68.24 | 50.96 | 59.69 | -1.61 | -1.26 |
| 214149_s_at | ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e | AI252582 | 8992 | 92.85 | 100.65 | 97.25 | 68.84 | 63.02 | 65.88 | -1.48 | -1.26 |
| 219805_at | chromosome X open reading frame 56 | NM_022101 | 63932 | 47.14 | 47.23 | 47.19 | 34.22 | 29.7 | 32.11 | -1.47 | -1.26 |
| 224847_at | cyclin-dependent kinase 6 | AW051349 | 1021 | 115.92 | 112.74 | 114.31 | 81.63 | 82.1 | 81.81 | -1.4 | -1.26 |
| 227728_at | CDNA FLJ42306 fis, clone TRACH2001646 | AA886888 | | 134.77 | 133.79 | 134.32 | 95.41 | 101.41 | 98.14 | -1.37 | -1.26 |
| 200832_s_at | stearoyl-CoA desaturase (delta-9-desaturase) | AB032261 | 6319 | 1048.81 | 1085.85 | 1067.28 | 814.68 | 814.75 | 814.73 | -1.31 | -1.26 |
| 215623_x_at | structural maintenance of chromosomes 4 | AK002200 | 10051 | 98.42 | 69.52 | 84.1 | 49.34 | 42.83 | 46.46 | -1.81 | -1.25 |
| 213275_x_at | cathepsin B | W47179 | 1508 | 70.02 | 57.73 | 63.46 | 39.93 | 41.42 | 40.61 | -1.56 | -1.25 |
| 224791_at | development and differentiation enhancing factor 1 | AW513835 | 50807 | 105.27 | 100.42 | 103.25 | 73.08 | 74.83 | 74.1 | -1.39 | -1.25 |
| 205890_s_at | ubiquitin D | NM_006398 | 10537 | 231.7 | 231.51 | 231.63 | 173.47 | 176.07 | 174.78 | -1.33 | -1.25 |
| 206147_x_at | sex comb on midleg-like 2 (Drosophila) | NM_006089 | 10389 | 54.63 | 65.44 | 60 | 41.9 | 30.46 | 36.1 | -1.66 | -1.24 |
| 201887_at | interleukin 13 receptor, alpha 1 | NM_001560 | 3597 | 146.12 | 171.33 | 158.78 | 106.63 | 107.18 | 106.86 | -1.49 | -1.24 |
| 226254_s_at | KIAA1430 | AI912523 | 57587 | 274.08 | 296.35 | 285.95 | 204.37 | 199.07 | 202.05 | -1.42 | -1.24 |
| 212373_at | fem-1 homolog b (C. elegans) | AW139179 | 10116 | 81.47 | 85.41 | 83.49 | 56.97 | 61.67 | 59.18 | -1.41 | -1.24 |
| 211452_x_at | leucine rich repeat (in FLII) interacting protein 1 | AF130054 | 9208 | 152.1 | 148.19 | 150.23 | 107.96 | 112.5 | 110.04 | -1.37 | -1.24 |
| 229419_at | F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila) | BF222826 | 55294 | 178.45 | 171.3 | 174.74 | 131.99 | 125.93 | 129.11 | -1.35 | -1.24 |
| 212930_at | ATPase, Ca++ transporting, plasma membrane 1 | AW576457 | 490 | 33.25 | 33.29 | 33.27 | 22.64 | 20.35 | 21.46 | -1.55 | -1.23 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 213813_x_at | RNA binding protein S1, serine-rich domain | AI345238 | 10921 | 44.21 | 47.49 | 45.86 | 32.58 | 26.63 | 29.76 | -1.54 | -1.23 |
| 201373_at | plectin 1, intermediate filament binding protein 500kDa | NM_000445 | 5339 | 56.21 | 51.07 | 53.6 | 33.62 | 40.16 | 36.86 | -1.45 | -1.23 |
| 212561_at | RAB6 interacting protein 1 | AA349595 | 23258 | 192.87 | 202.88 | 198.77 | 144.41 | 133.19 | 137.71 | -1.44 | -1.23 |
| 203845_at | p300/CBP-associated factor | AV727449 | 8850 | 52.01 | 56.3 | 53.66 | 39.26 | 35.01 | 37.46 | -1.43 | -1.23 |
| 204407_at | transcription termination factor, RNA polymerase II | AF080255 | 8458 | 98.09 | 88.79 | 93.39 | 67.39 | 64.72 | 66.24 | -1.41 | -1.23 |
| 213497_at | ankyrin repeat and BTB (POZ) domain containing 2 | AL050374 | 25841 | 89.14 | 92.26 | 90.74 | 67 | 60.75 | 64.22 | -1.41 | -1.23 |
| 203966_s_at | protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform /// protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform | NM_021003 | 5494 | 235.8 | 228.63 | 231.64 | 177.92 | 160.15 | 169.21 | -1.37 | -1.23 |
| 213225_at | protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform | AJ271832 | 5495 | 135.99 | 132.1 | 134.12 | 98.29 | 100.57 | 99.45 | -1.35 | -1.23 |
| 227068_at | phosphoglycerate kinase 1 | AA069778 | 5230 | 699.44 | 702.47 | 701.4 | 553.24 | 536.48 | 545.17 | -1.29 | -1.23 |
| 209229_s_at | SAPS domain family, member 1 | BC002799 | 22870 | 76.7 | 86 | 81.26 | 55.37 | 42.76 | 49.13 | -1.65 | -1.22 |
| 213951_s_at | PSMC3 interacting protein | BE964655 | 29893 | 64.92 | 68.86 | 66.42 | 48.05 | 34.7 | 41.32 | -1.61 | -1.22 |
| 1569190_at | sodium channel and clathrin linker 1 | BC014677 | 132320 | 81.64 | 80.18 | 80.73 | 58.9 | 47.14 | 53.47 | -1.51 | -1.22 |
| 65086_at | Yip1 domain family, member 2 | Z78349 | 78992 | 49.41 | 41.72 | 45.77 | 30.57 | 30.57 | 30.57 | -1.5 | -1.22 |
| 230098_at | Transcribed locus | AW612407 | | 66.46 | 70.79 | 68.27 | 49.33 | 45.25 | 47.19 | -1.45 | -1.22 |
| 225445_at | Hypothetical protein FLJ25778 | AI332346 | 254048 | 61.52 | 66.94 | 63.99 | 47.21 | 42.01 | 44.42 | -1.44 | -1.22 |
| 202260_s_at | syntaxin binding protein 1 | NM_003165 | 6812 | 117.97 | 117.83 | 117.92 | 89.65 | 77.64 | 84.1 | -1.4 | -1.22 |
| 203395_s_at | hairy and enhancer of split 1, (Drosophila) | NM_005524 | 3280 | 87.55 | 87.07 | 87.29 | 64.88 | 66.41 | 65.32 | -1.34 | -1.22 |
| 213168_at | Sp3 transcription factor | AU145005 | 6670 | 292.23 | 282.02 | 286.77 | 216.83 | 212.8 | 214.74 | -1.34 | -1.22 |
| 214599_at | involucrin | NM_005547 | 3713 | 14.58 | 21.04 | 17.55 | 7.66 | 8.86 | 8.06 | -2.18 | -1.21 |
| 201928_at | plakophilin 4 | AA194254 | 8502 | 112.79 | 113.83 | 113.27 | 82.67 | 72.46 | 77.5 | -1.46 | -1.21 |
| 225569_at | Eukaryotic translation initiation factor 2C, 2 | AI813489 | 27161 | 63.23 | 71.41 | 67.94 | 47.92 | 45.24 | 46.97 | -1.45 | -1.21 |
| 213017_at | abhydrolase domain containing 3 | AL534702 | 171586 | 153.13 | 139.71 | 146.25 | 110.22 | 103.35 | 106.39 | -1.37 | -1.21 |
| 207663_x_at | G antigen 3 | NM_001473 | 2575 | 471.99 | 458.17 | 466.15 | 361.94 | 365.07 | 363.19 | -1.28 | -1.21 |
| 215127_s_at | RNA binding motif, single stranded interacting protein 1 /// chromosome 2 open reading frame 12 /// region containing chromosome 2 open reading frame 12; RNA binding motif, single stranded interacting protein 1 | AL517946 | 192137 /// 5937 /// 648293 | 397.07 | 386.49 | 391.98 | 312.49 | 302.04 | 307.64 | -1.27 | -1.21 |
| 204970_s_at | v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian) | NM_002359 | 4097 | 111.68 | 125.73 | 118.28 | 72.61 | 88.86 | 80.82 | -1.46 | -1.2 |
| 204003_s_at | nucleoporin like 2 | NM_007342 | 11097 | 63.32 | 62.81 | 63.07 | 44.15 | 46.07 | 45.32 | -1.39 | -1.2 |
| 1569973_at | Similar to cell division cycle 10 homolog | BC015774 | 441220 | 76.8 | 81.96 | 78.99 | 59.57 | 55.23 | 57.69 | -1.37 | -1.2 |
| 224984_at | nuclear factor of activated T-cells 5, tonicity-responsive | W61007 | 10725 | 129.53 | 126.37 | 128.1 | 94.2 | 99.23 | 96.61 | -1.33 | -1.2 |
| 217788_s_at | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) | NM_004481 | 2590 | 248.53 | 243.38 | 246.39 | 308.31 | 314.91 | 312.41 | 1.27 | 1.2 |
| 202564_x_at | ADP-ribosylation factor-like 2 | NM_001667 | 402 | 131.55 | 132.32 | 132.01 | 169.44 | 173.66 | 171.9 | 1.3 | 1.2 |
| 203708_at | phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) | NM_002600 | 5142 | 126.08 | 127.26 | 126.58 | 171.38 | 163.16 | 167.49 | 1.32 | 1.2 |
| 208692_at | ribosomal protein S3 /// structural maintenance of chromosomes 1B | U14990 | 27127 /// 6188 | 1145.96 | 1245.69 | 1195.37 | 1570.41 | 1580.59 | 1574.63 | 1.32 | 1.2 |
| 217140_s_at | voltage-dependent anion channel 1 | AJ002428 | 7416 | 129.94 | 122.98 | 126.57 | 169.08 | 165.64 | 167.25 | 1.32 | 1.2 |
| 229113_s_at | chromosome 1 open reading frame 86 | W16779 | 199990 | 107.72 | 109.12 | 108.48 | 143.45 | 142.2 | 142.93 | 1.32 | 1.2 |
| 200011_s_at | ADP-ribosylation factor 3 /// ADP-ribosylation factor 3 | NM_001659 | 377 | 139.9 | 142.39 | 140.92 | 187.05 | 189.11 | 187.98 | 1.33 | 1.2 |
| 210982_s_at | major histocompatibility complex, class II, DR alpha | M60333 | 3122 | 322.76 | 323.94 | 323.3 | 422.97 | 437.19 | 430.13 | 1.33 | 1.2 |
| 214473_x_at | postmeiotic segregation increased 2-like 3 | NM_005395 | 5387 | 90.72 | 86.37 | 88.72 | 113.86 | 120.66 | 117.64 | 1.33 | 1.2 |
| 226400_at | Cell division cycle 42 (GTP binding protein, 25kDa) | N92917 | 998 | 220.44 | 223.26 | 221.84 | 284.2 | 307.35 | 296.03 | 1.33 | 1.2 |
| 209344_at | tropomyosin 4 | BC002827 | 7171 | 43.08 | 41.25 | 42.04 | 57.45 | 58.34 | 57.93 | 1.38 | 1.2 |
| 210178_x_at | FUS interacting protein (serine/arginine-rich) 1 /// similar to FUS interacting protein (serine-arginine rich) 1 | AF047448 | 10772 /// 642558 | 121.5 | 105.7 | 114.24 | 159.54 | 156.81 | 158.1 | 1.38 | 1.2 |
| 205967_at | histone 1, H4c | NM_003542 | 8364 | 230.89 | 226.03 | 228.19 | 294.69 | 343.83 | 318.71 | 1.4 | 1.2 |
| 202915_s_at | family with sequence similarity 20, member B | BF115776 | 9917 | 64.73 | 63.81 | 64.29 | 84.14 | 97.31 | 90.43 | 1.41 | 1.2 |
| 219336_s_at | activating signal cointegrator 1 complex subunit 1 | NM_015947 | 51008 | 47.62 | 55.23 | 52.35 | 71.62 | 75.49 | 73.95 | 1.41 | 1.2 |
| 223591_at | ring finger protein 135 | BC005084 | 84282 | 46.93 | 44.38 | 45.64 | 64.72 | 66.59 | 65.58 | 1.44 | 1.2 |
| 223917_s_at | solute carrier family 39 (zinc transporter), member 3 | BC000085 | 29985 | 69.2 | 58.43 | 63.39 | 87.69 | 94.34 | 91.1 | 1.44 | 1.2 |
| 218206_x_at | SCAN domain containing 1 | NM_016558 | 51282 | 38.36 | 45.95 | 42.12 | 58.85 | 63.05 | 61.44 | 1.46 | 1.2 |
| 226436_at | Ras association (RalGDS/AF-6) domain family 4 | N49935 | 83937 | 150.92 | 120.87 | 136.01 | 195.68 | 200.78 | 197.94 | 1.46 | 1.2 |
| 234947_s_at | chromosome 10 open reading frame 84 | AK026630 | 63877 | 31.62 | 31.79 | 31.69 | 42.87 | 51.18 | 46.87 | 1.48 | 1.2 |
| 225320_at | coiled-coil domain containing 109A | AA579630 | 90550 | 143.65 | 139.16 | 141.49 | 176.56 | 184.6 | 180.42 | 1.28 | 1.21 |
| 224932_at | chromosome 22 open reading frame 16 | AI814909 | 400916 | 471.53 | 476.2 | 474 | 598.58 | 631.4 | 614.19 | 1.3 | 1.21 |
| 212305_s_at | melanoma inhibitory activity family, member 3 | AK025122 | 375056 | 90.39 | 86.49 | 88.52 | 117.7 | 116.65 | 117.2 | 1.32 | 1.21 |
| 215952_s_at | ornithine decarboxylase antizyme 1 | AF090094 | 4946 | 952.5 | 964.19 | 958.43 | 1315.2 | 1224.1 | 1268.46 | 1.32 | 1.21 |
| 37966_at | parvin, beta | AA187563 | 29780 | 57.97 | 56.65 | 57.24 | 74.77 | 77.62 | 76.29 | 1.33 | 1.21 |
| 218118_s_at | translocase of inner mitochondrial membrane 23 homolog (yeast) | NM_006327 | 10431 | 55.61 | 54.67 | 55.27 | 74.05 | 74.17 | 74.11 | 1.34 | 1.21 |
| 224981_at | hypothetical protein BC017488 | AL520900 | 124446 | 75.69 | 77.95 | 76.76 | 101.77 | 103.2 | 102.6 | 1.34 | 1.21 |
| 226319_s_at | THO complex 4 | AF047002 | 10189 | 167.7 | 162.75 | 165.43 | 229.91 | 212.28 | 221.03 | 1.34 | 1.21 |
| 219971_at | interleukin 21 receptor | NM_021798 | 50615 | 210.76 | 188.04 | 199.5 | 264.82 | 273.68 | 269.21 | 1.35 | 1.21 |
| 202513_s_at | protein phosphatase 2, regulatory subunit B (B56), delta isoform | NM_006245 | 5528 | 63.29 | 59.07 | 60.96 | 82.45 | 83.46 | 82.97 | 1.36 | 1.21 |
| 226467_at | hypothetical protein FLJ12688 | AK022750 | 79613 | 41.35 | 44.32 | 42.9 | 57.24 | 59.5 | 58.5 | 1.36 | 1.21 |
| 201316_at | proteasome (prosome, macropain) subunit, alpha type, 2 | AL523904 | 5683 | 52.28 | 51.52 | 51.8 | 68.7 | 73.2 | 70.83 | 1.37 | 1.21 |
| 203460_s_at | presenilin 1 (Alzheimer disease 3) | NM_007318 | 5663 | 62.69 | 60.52 | 61.69 | 83.02 | 90.36 | 86.56 | 1.4 | 1.21 |
| 204331_s_at | mitochondrial ribosomal protein S12 | NM_021107 | 6183 | 151.39 | 139.24 | 144.46 | 212.38 | 193.5 | 202.4 | 1.4 | 1.21 |
| 202658_at | peroxisomal biogenesis factor 11B | NM_003846 | 8799 | 43.3 | 45.87 | 44.33 | 62.32 | 62.25 | 62.29 | 1.41 | 1.21 |
| 203388_at | arrestin, beta 2 | NM_004313 | 409 | 53.12 | 48.15 | 51.13 | 73.65 | 70.18 | 72.18 | 1.41 | 1.21 |
| 225003_at | hypothetical protein MGC3205 /// MBC3205 | BF343862 | 374882 /// 90585 | 41.42 | 40.04 | 40.8 | 56.07 | 59.86 | 57.78 | 1.42 | 1.21 |
| 228899_at | Cullin 1 | AI870903 | 8454 | 68.61 | 80.16 | 74.09 | 107 | 102.75 | 104.97 | 1.42 | 1.21 |
| 202387_at | BCL2-associated athanogene /// BCL2-associated athanogene | NM_004323 | 573 | 99.67 | 86.26 | 93.98 | 128.73 | 138.27 | 134.1 | 1.43 | 1.21 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 1555193_a_at | zinc finger protein 277 | BC020626 | 11179 | 36.01 | 38.62 | 37.34 | 51.47 | 55.39 | 53.34 | 1.43 | 1.21 |
| 201233_at | proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 | NM_002817 | 5719 | 62.86 | 56.07 | 59.81 | 85.58 | 86.18 | 85.82 | 1.44 | 1.21 |
| 204610_s_at | coiled-coil domain containing 85B | NM_006848 | 11007 | 82 | 72.97 | 78.06 | 106.64 | 120.62 | 113.98 | 1.46 | 1.21 |
| 206919_at | ELK4, ETS-domain protein (SRF accessory protein 1) | NM_021795 | 2005 | 36.93 | 33.36 | 35.14 | 49.03 | 54.31 | 51.57 | 1.47 | 1.21 |
| 32032_at | DiGeorge syndrome critical region gene 14 | L77566 | 8220 | 43.5 | 38.27 | 40.47 | 57.72 | 61.56 | 59.91 | 1.48 | 1.21 |
| 227864_s_at | family with sequence similarity 125, member A | AI091713 | 93343 | 70.17 | 61.72 | 65.79 | 104.51 | 90.54 | 97.49 | 1.48 | 1.21 |
| 204044_at | quinolinate phosphoribosyltransferase (nicotinate-nucleotide pyrophosphorylase (carboxylating)) | NM_014298 | 23475 | 24.33 | 25.13 | 24.73 | 37.89 | 36.05 | 36.92 | 1.49 | 1.21 |
| 201940_at | carboxypeptidase D | AA897514 | 1362 | 43.7 | 50.65 | 47.95 | 66.42 | 78.59 | 72.68 | 1.52 | 1.21 |
| 211530_x_at | HLA-G histocompatibility antigen, class I, G | M90686 | 3135 | 36.94 | 53.98 | 45.35 | 72.79 | 73.44 | 73.05 | 1.61 | 1.21 |
| 208447_s_at | phosphoribosyl pyrophosphate synthetase 1 | NM_002764 | 5631 | 66.16 | 46.77 | 56.28 | 98.14 | 86.46 | 92.23 | 1.64 | 1.21 |
| 210664_s_at | tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor) | AF021834 | 7035 | 27.45 | 40.87 | 34.28 | 56.29 | 58.93 | 57.63 | 1.68 | 1.21 |
| 215193_x_at | major histocompatibility complex, class II, DR beta 1 | AJ297586 | 3123 | 701.38 | 700 | 700.78 | 914.14 | 911.65 | 912.89 | 1.3 | 1.22 |
| 223040_at | N-acetyltransferase 5 | BC005181 | 51126 | 168.93 | 165.83 | 167.43 | 216.65 | 222.61 | 219.24 | 1.31 | 1.22 |
| 200975_at | palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile) | NM_000310 | 5538 | 449.51 | 421.99 | 435.65 | 585.54 | 564.65 | 573.81 | 1.32 | 1.22 |
| 225161_at | G elongation factor, mitochondrial 1 | AI659020 | 85476 | 167.47 | 160.28 | 163.88 | 219.61 | 211.15 | 215.62 | 1.32 | 1.22 |
| 203650_at | protein C receptor, endothelial (EPCR) | NM_006404 | 10544 | 44.84 | 45.29 | 45.05 | 59.53 | 60.59 | 60 | 1.33 | 1.22 |
| 200746_s_at | guanine nucleotide binding protein (G protein), beta polypeptide 1 | NM_002074 | 2782 | 350.35 | 324.98 | 340.82 | 467.2 | 454.62 | 460.63 | 1.35 | 1.22 |
| 217979_at | Tetraspanin 13 | NM_014399 | 27075 | 159.22 | 178.93 | 169.06 | 224.46 | 232.67 | 228.52 | 1.35 | 1.22 |
| 207809_s_at | ATPase, H+ transporting, lysosomal accessory protein 1 | NM_001183 | 537 | 127.11 | 129.23 | 128.17 | 195.63 | 170.23 | 182.21 | 1.42 | 1.22 |
| 37226_at | BCL2/adenovirus E1B 19kDa interacting protein 1 | U15172 | 662 | 36.94 | 42.85 | 40.38 | 59.24 | 57.18 | 58.26 | 1.44 | 1.22 |
| 200751_s_at | heterogeneous nuclear ribonucleoprotein C (C1/C2) | BE898861 | 3183 | 142.39 | 119.3 | 130.17 | 183.34 | 196.69 | 189.32 | 1.45 | 1.22 |
| 211475_s_at | BCL2-associated athanogene | AF116273 | 573 | 196.4 | 159.97 | 177.77 | 262.42 | 253.12 | 257.15 | 1.45 | 1.22 |
| 201875_s_at | myelin protein zero-like 1 | NM_024569 | 9019 | 66.41 | 71.85 | 69.24 | 93.79 | 108.44 | 100.88 | 1.46 | 1.22 |
| 225954_s_at | midnolin | AL512725 | 90007 | 55.89 | 42.13 | 48.74 | 75.1 | 77.39 | 76.02 | 1.56 | 1.22 |
| 200712_s_at | microtubule-associated protein, RP/EB family, member 1 | AI633566 | 22919 | 42.27 | 60.92 | 52.14 | 82.67 | 85.27 | 83.77 | 1.61 | 1.22 |
| 211998_at | H3 histone, family 3B (H3.3B) | AW138159 | 3021 | 53.42 | 37.46 | 46.04 | 85.22 | 72.92 | 79.09 | 1.72 | 1.22 |
| 202552_s_at | cysteine rich transmembrane BMP regulator 1 (chordin-like) | NM_016441 | 51232 | 66.92 | 65.41 | 66.05 | 90.57 | 85.27 | 88.06 | 1.33 | 1.23 |
| 215719_x_at | Fas (TNF receptor superfamily, member 6) | X83493 | 355 | 129.07 | 125.34 | 127.14 | 171.22 | 170.58 | 170.8 | 1.34 | 1.23 |
| 200607_s_at | RAD21 homolog (S. pombe) | BG289967 | 5885 | 208.78 | 205.92 | 207.48 | 278.94 | 282.63 | 280.74 | 1.35 | 1.23 |
| 204670_x_at | major histocompatibility complex, class II, DR beta 1 | NM_002125 | 3123 | 819.73 | 911.79 | 865.93 | 1170.24 | 1188.96 | 1177.36 | 1.36 | 1.23 |
| 202246_s_at | cyclin-dependent kinase 4 | NM_000075 | 1019 | 374.04 | 330.3 | 351.63 | 481.16 | 484.82 | 483.15 | 1.37 | 1.23 |
| 206332_s_at | interferon, gamma-inducible protein 16 | NM_005531 | 3428 | 411.54 | 463.93 | 438.89 | 631.51 | 584.38 | 608.61 | 1.39 | 1.23 |
| 202637_s_at | intercellular adhesion molecule 1 (CD54), human rhinovirus receptor | AI608725 | 3383 | 319.79 | 350.47 | 335.6 | 490.37 | 449.98 | 470.31 | 1.4 | 1.23 |
| 221090_s_at | 2-oxoglutarate and iron-dependent oxygenase domain containing 1 | NM_018233 | 55239 | 63 | 62.18 | 62.62 | 84 | 92.28 | 88.03 | 1.41 | 1.23 |
| 210978_s_at | transgelin 2 | BC002616 | 8407 | 205.28 | 238.19 | 222.19 | 319.42 | 311.4 | 315.78 | 1.42 | 1.23 |
| 218105_s_at | mitochondrial ribosomal protein L4 | NM_015956 | 51073 | 59.87 | 58.46 | 59.17 | 83.8 | 84.03 | 83.9 | 1.42 | 1.23 |
| 201523_x_at | ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast) | BE262760 | 7334 | 95.53 | 89.12 | 91.96 | 138.68 | 125.72 | 131.56 | 1.43 | 1.23 |
| 218229_s_at | pogo transposable element with KRAB domain | NM_017542 | 57645 | 73.04 | 68.24 | 70.59 | 97.83 | 102.85 | 100.7 | 1.43 | 1.23 |
| 216252_x_at | Fas (TNF receptor superfamily, member 6) | Z70519 | 355 | 90 | 105.01 | 96.56 | 143.22 | 137.56 | 140.13 | 1.45 | 1.23 |
| 218119_at | translocase of inner mitochondrial membrane 23 homolog (yeast) /// similar to Mitochondrial import inner membrane translocase subunit Tim23 | NM_006327 | 10431 /// 653252 | 42.02 | 43.14 | 42.68 | 61.57 | 63.18 | 62.53 | 1.46 | 1.23 |
| 208629_s_at | hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit | BG472176 | 3030 | 69.95 | 69.96 | 69.96 | 95.66 | 112.16 | 103.38 | 1.48 | 1.23 |
| 212432_at | GrpE-like 1, mitochondrial (E. coli) | AL542571 | 80273 | 68.35 | 66.75 | 67.71 | 109.21 | 96.61 | 102.14 | 1.51 | 1.23 |
| 209270_at | laminin, beta 3 | L25541 | 3914 | 29.29 | 29.76 | 29.51 | 42.17 | 47.71 | 44.84 | 1.52 | 1.23 |
| 208750_s_at | ADP-ribosylation factor 1 | AA580004 | 375 | 50.76 | 40.25 | 46.03 | 70.08 | 75.22 | 72.42 | 1.57 | 1.23 |
| 209222_s_at | oxysterol binding protein-like 2 | BC000296 | 9885 | 46.71 | 46.8 | 46.75 | 63.74 | 62.79 | 63.21 | 1.35 | 1.24 |
| 202424_at | mitogen-activated protein kinase kinase 2 | NM_030662 | 5605 | 206.91 | 195.11 | 201.33 | 275.51 | 275.95 | 275.71 | 1.37 | 1.24 |
| 221267_s_at | family with sequence similarity 108, member A1 /// family with sequence similarity 108, member A1 | NM_031213 | 81926 | 122.88 | 111.27 | 117.24 | 160.73 | 166.23 | 163.52 | 1.39 | 1.24 |
| 238010_at | chromosome 1 open reading frame 174 | BF970340 | 339448 | 47.45 | 43.73 | 45.8 | 65.43 | 64.35 | 64.77 | 1.41 | 1.24 |
| 221770_at | ribulose-5-phosphate-3-epimerase | BE964473 | 6120 | 46.58 | 40.26 | 43.38 | 63.28 | 63.77 | 63.48 | 1.46 | 1.24 |
| 1555812_a_at | Rho GDP dissociation inhibitor (GDI) beta | AF498927 | 397 | 58.41 | 52.74 | 55.83 | 83.52 | 79.22 | 81.48 | 1.46 | 1.24 |
| 202706_s_at | uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) | D86227 | 7372 | 35.17 | 42.81 | 39.31 | 57.37 | 60.48 | 59.01 | 1.5 | 1.24 |
| 211012_s_at | promyelocytic leukemia /// hypothetical protein LOC161527 /// similar to promyelocytic leukemia protein isoform 9 | BC000080 | 161527 /// 5371 /// 652671 | 31.72 | 36.63 | 34.11 | 52.35 | 51.7 | 51.96 | 1.52 | 1.24 |
| 201571_s_at | dCMP deaminase | AI656493 | 1635 | 164.35 | 160.79 | 162.74 | 217.09 | 217.9 | 217.58 | 1.34 | 1.25 |
| 202284_s_at | cyclin-dependent kinase inhibitor 1A (p21, Cip1) | NM_000389 | 1026 | 135.58 | 139.34 | 137.26 | 179.85 | 189.17 | 184.41 | 1.34 | 1.25 |
| 220230_s_at | cytochrome b5 reductase 2 | NM_016229 | 51700 | 380.91 | 363.71 | 371.08 | 500.81 | 493.82 | 496.53 | 1.34 | 1.25 |
| 224903_at | cirrhosis, autosomal recessive 1A (cirhin) | AL519818 | 84916 | 471.22 | 508.74 | 491.37 | 679.42 | 652.69 | 666.18 | 1.36 | 1.25 |
| 201720_s_at | lysosomal associated multispanning membrane protein 5 | AI589086 | 7805 | 181.36 | 171.43 | 176.05 | 239.58 | 242.25 | 240.91 | 1.37 | 1.25 |
| 209893_s_at | fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific) | M58596 | 2526 | 76.61 | 73.92 | 75.5 | 101.97 | 105.42 | 103.66 | 1.37 | 1.25 |
| 228204_at | Proteasome (prosome, macropain) subunit, beta type, 4 | AA630330 | 5692 | 219.05 | 239.59 | 228.47 | 309.52 | 317.28 | 313.76 | 1.37 | 1.25 |
| 209995_s_at | T-cell leukemia/lymphoma 1A /// T-cell leukemia/lymphoma 1A | BC003574 | 8115 | 231.22 | 235.22 | 233.36 | 310.29 | 334.46 | 321.55 | 1.38 | 1.25 |
| 202361_at | SEC24 related gene family, member C (S. cerevisiae) | NM_004922 | 9632 | 86.31 | 83.69 | 84.85 | 119.06 | 117.22 | 117.93 | 1.39 | 1.25 |
| 210222_s_at | reticulon 1 | BC000314 | 6252 | 85.75 | 96.77 | 91.05 | 130.05 | 127.26 | 128.33 | 1.41 | 1.25 |
| 223666_at | Sorting nexin 5 | BC002724 | 27131 | 101.21 | 98.72 | 99.94 | 147.48 | 136.17 | 141.14 | 1.41 | 1.25 |
| 205621_at | alkB, alkylation repair homolog 1 (E. coli) | NM_006020 | 8846 | 48.63 | 54.44 | 51.44 | 72.54 | 74.6 | 73.59 | 1.43 | 1.25 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 223709_s_at | wingless-type MMTV integration site family, member 10A | AY009400 | 80326 | 73.47 | 68.37 | 70.73 | 107.26 | 100.44 | 103.63 | 1.47 | 1.25 |
| 226911_at | EGF-like, fibronectin type III and laminin G domains | BF114725 | 133584 | 47.95 | 54.17 | 50.64 | 72.98 | 76.3 | 74.52 | 1.47 | 1.25 |
| 233878_s_at | 5'-3' exoribonuclease 2 | BE536170 | 22803 | 54.39 | 50.28 | 52.18 | 81.14 | 72.62 | 76.96 | 1.47 | 1.25 |
| 228867_at | TatD DNase domain containing 3 | BE541548 | 128387 | 50.93 | 51.52 | 51.23 | 70.41 | 80.93 | 75.97 | 1.48 | 1.25 |
| 224410_s_at | limb region 1 homolog (mouse) /// limb region 1 homolog (mouse) | AF348513 | 64327 | 40.57 | 43.96 | 42.33 | 60.68 | 71.63 | 66.18 | 1.56 | 1.25 |
| 206929_s_at | nuclear factor I/C (CCAAT-binding transcription factor) | NM_005597 | 4782 | 43.94 | 27.34 | 35.65 | 65.02 | 63.79 | 64.49 | 1.81 | 1.25 |
| 39318_at | T-cell leukemia/lymphoma 1A | X82240 | 8115 | 447.84 | 443.23 | 445.24 | 575.29 | 602.95 | 589.14 | 1.32 | 1.26 |
| 202736_s_at | LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) | AA112507 | 25804 | 128.58 | 124.02 | 126.35 | 171.33 | 172.65 | 171.98 | 1.36 | 1.26 |
| 224573_at | similar to DNA segment, Chr 11, Brigham & Womens Genetics 0434 expressed | BE744389 | 440400 | 402.13 | 428.76 | 413.96 | 563.67 | 576.95 | 569.8 | 1.38 | 1.26 |
| 201168_x_at | Rho GDP dissociation inhibitor (GDI) alpha | NM_004309 | 396 | 139.23 | 144.91 | 141.86 | 193.05 | 206.91 | 199.43 | 1.41 | 1.26 |
| 215714_s_at | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 | AF254822 | 6597 | 102.47 | 104.38 | 103.34 | 148.56 | 144.92 | 146.8 | 1.42 | 1.26 |
| 222425_s_at | polymerase (DNA-directed), delta interacting protein 2 | AW151250 | 26073 | 49.36 | 49.65 | 49.5 | 75.84 | 71.44 | 73.84 | 1.49 | 1.26 |
| 204118_at | CD48 molecule /// CD48 molecule | NM_001778 | 962 | 148.59 | 179.66 | 163.93 | 252.39 | 246.45 | 248.73 | 1.52 | 1.26 |
| 218220_at | chromosome 12 open reading frame 10 | NM_021640 | 60314 | 48.57 | 49.86 | 49.3 | 77.96 | 71.31 | 74.96 | 1.52 | 1.26 |
| 1557910_at | heat shock protein 90kDa alpha (cytosolic), class B member 1 | BG612458 | 3326 | 324.59 | 266.13 | 294.98 | 422.55 | 491.61 | 457.06 | 1.55 | 1.26 |
| 202357_s_at | complement factor B | NM_001710 | 629 | 71.24 | 79.75 | 75.33 | 131.85 | 106.64 | 119.23 | 1.58 | 1.26 |
| 201234_at | integrin-linked kinase | NM_004517 | 3611 | 235.39 | 241.25 | 238.24 | 325.34 | 320.26 | 322.97 | 1.36 | 1.27 |
| 208887_at | eukaryotic translation initiation factor 3, subunit 4 delta, 44kDa | BC000733 | 8666 | 274.46 | 259.61 | 266.03 | 373.14 | 367.53 | 370.26 | 1.39 | 1.27 |
| 213175_s_at | small nuclear ribonucleoprotein polypeptides B and B1 | AL049650 | 6628 | 615.89 | 576.14 | 593.49 | 819.34 | 841.62 | 827.71 | 1.39 | 1.27 |
| 208687_x_at | heat shock 70kDa protein 8 | AF352832 | 3312 | 1067.69 | 973.61 | 1017.35 | 1378.72 | 1473.68 | 1427.39 | 1.4 | 1.27 |
| 217806_s_at | polymerase (DNA-directed), delta interacting protein 2 | NM_015584 | 26073 | 88.34 | 90.08 | 89.04 | 129.45 | 122.27 | 125.72 | 1.41 | 1.27 |
| 221270_s_at | queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase) /// queuine tRNA-ribosyltransferase 1 (tRNA-guanine transglycosylase) | NM_031209 | 81890 | 86.75 | 87.62 | 87.28 | 127.26 | 121.57 | 124.81 | 1.43 | 1.27 |
| 200927_s_at | RAB14, member RAS oncogene family | AA919115 | 51552 | 143.86 | 129.7 | 136.95 | 204.87 | 188.58 | 196.55 | 1.44 | 1.27 |
| 201562_s_at | sorbitol dehydrogenase | NM_003104 | 6652 | 41.01 | 41.22 | 41.09 | 57.74 | 62.51 | 59.71 | 1.45 | 1.27 |
| 223012_at | UBX domain containing 1 | AF272894 | 80700 | 80.45 | 82.56 | 81.41 | 115.21 | 119.99 | 117.97 | 1.45 | 1.27 |
| 200841_s_at | glutamyl-prolyl-tRNA synthetase | AI142677 | 2058 | 112.4 | 100.24 | 106.17 | 148.53 | 163.42 | 155.87 | 1.47 | 1.27 |
| 204116_at | interleukin 2 receptor, gamma (severe combined immunodeficiency) | NM_000206 | 3561 | 103.72 | 122.95 | 113.87 | 176.84 | 164.34 | 170.22 | 1.49 | 1.27 |
| 219978_s_at | nucleolar and spindle associated protein 1 | NM_018454 | 51203 | 119.92 | 102.22 | 110.86 | 159.04 | 183.09 | 171.11 | 1.54 | 1.27 |
| 202094_at | baculoviral IAP repeat-containing 5 (survivin) | AA648913 | 332 | 42.97 | 34.3 | 38.87 | 61.59 | 63.04 | 62.24 | 1.6 | 1.27 |
| 209953_s_at | CDC37 cell division cycle 37 homolog (S. cerevisiae) | U63131 | 11140 | 109.58 | 82.69 | 96.19 | 155.4 | 152.28 | 154.16 | 1.6 | 1.27 |
| 213887_s_at | polymerase (RNA) II (DNA directed) polypeptide E, 25kDa | AI554759 | 5434 | 58.81 | 48.19 | 53.37 | 87.08 | 83.46 | 85.2 | 1.6 | 1.27 |
| 208894_at | major histocompatibility complex, class II, DR alpha /// major histocompatibility complex, class II, DR alpha | M60334 | 3122 | 290.85 | 288.99 | 289.98 | 394.49 | 415.44 | 405.74 | 1.4 | 1.28 |
| 209312_x_at | major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 1 | U65585 | 3123 | 840.21 | 822.65 | 831.37 | 1127.01 | 1199.25 | 1160.1 | 1.4 | 1.28 |
| 200866_s_at | prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) /// phospholipid scramblase 3 | M32221 | 5660 /// 57048 | 89.88 | 95.62 | 92.71 | 131.22 | 134.24 | 132.65 | 1.43 | 1.28 |
| 203931_s_at | mitochondrial ribosomal protein L12 | NM_002949 | 6182 | 201.01 | 181.63 | 190.55 | 282.12 | 268.13 | 274.8 | 1.44 | 1.28 |
| 229713_at | CDNA FLJ13267 fis, clone OVARC1000964 | AW665227 | | 108.21 | 121.78 | 114.86 | 168.44 | 163.67 | 166.32 | 1.45 | 1.28 |
| 200736_s_at | glutathione peroxidase 1 | NM_000581 | 2876 | 202.55 | 181.09 | 190.83 | 290.67 | 272.43 | 281.76 | 1.48 | 1.28 |
| 207831_x_at | deoxyhypusine synthase | NM_013407 | 1725 | 71.28 | 83.97 | 77.13 | 120.87 | 114.36 | 117.61 | 1.52 | 1.28 |
| 218493_at | chromosome 16 open reading frame 33 | NM_024571 | 79622 | 72.96 | 70.58 | 71.56 | 114.96 | 103.32 | 108.98 | 1.52 | 1.28 |
| 215728_s_at | acyl-CoA thioesterase 7 | AL031848 | 11332 | 43.6 | 37.03 | 40.67 | 62.9 | 63.7 | 63.39 | 1.56 | 1.28 |
| 217786_at | protein arginine methyltransferase 5 | NM_006109 | 10419 | 92.38 | 75.61 | 84.92 | 138.51 | 130.1 | 133.52 | 1.57 | 1.28 |
| 205996_s_at | adenylate kinase 2 | NM_013411 | 204 | 56.87 | 57.34 | 57.12 | 85.51 | 82.35 | 83.9 | 1.47 | 1.29 |
| 222531_s_at | chromosome 14 open reading frame 108 | AW137526 | 55745 | 84.67 | 81.74 | 82.59 | 126.37 | 116.09 | 121.19 | 1.47 | 1.29 |
| 201946_s_at | chaperonin containing TCP1, subunit 2 (beta) | AL545982 | 10576 | 214.39 | 191.38 | 202.94 | 287.54 | 331.15 | 308.64 | 1.52 | 1.29 |
| 217362_x_at | major histocompatibility complex, class II, DR beta 6 (pseudogene) | AF005487 | 3128 | 41.85 | 36.93 | 39.47 | 64.04 | 60.52 | 61.95 | 1.57 | 1.29 |
| 212379_at | phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase | BE966876 | 2618 | 51.79 | 46.84 | 49.36 | 73.71 | 85.15 | 79.28 | 1.61 | 1.29 |
| 223318_s_at | alkB, alkylation repair homolog 7 (E. coli) | BC004393 | 84266 | 40.04 | 33.76 | 36.88 | 61.01 | 62.21 | 61.56 | 1.67 | 1.29 |
| 208306_x_at | Major histocompatibility complex, class II, DR beta 1 | NM_021983 | 3123 | 728.97 | 773.36 | 752.51 | 1033.17 | 1088.32 | 1057.13 | 1.4 | 1.3 |
| 208675_s_at | dolichyl-diphosphooligosaccharide-protein glycosyltransferase | D29643 | 1650 | 338.95 | 355.49 | 348.18 | 503.49 | 489.64 | 495.81 | 1.42 | 1.3 |
| 200722_s_at | GPI-anchored membrane protein 1 | BG258784 | 4076 | 88.95 | 95.19 | 91.88 | 132.48 | 135.68 | 134.28 | 1.46 | 1.3 |
| 221069_s_at | coiled-coil domain containing 44 | NM_016360 | 51204 | 41.15 | 43.58 | 42.63 | 65.55 | 64.24 | 64.87 | 1.52 | 1.3 |
| 221550_at | COX15 homolog, cytochrome c oxidase assembly protein (yeast) | BC002382 | 1355 | 37.34 | 42.53 | 40.2 | 61.76 | 67.08 | 64.33 | 1.6 | 1.3 |
| 202118_s_at | copine III | AA541758 | 8895 | 68.98 | 61.68 | 65.17 | 95.47 | 113.71 | 104.78 | 1.61 | 1.3 |
| 213104_at | hypothetical protein MGC24381 | AI799802 | 115939 | 32.37 | 23.87 | 28.25 | 45.81 | 50.06 | 48.06 | 1.7 | 1.3 |
| 202862_at | fumarylacetoacetate hydrolase (fumarylacetoacetase) | NM_000137 | 2184 | 85.66 | 80.71 | 83.19 | 120.01 | 122.41 | 120.93 | 1.45 | 1.31 |
| 203013_at | ecdysoneless homolog (Drosophila) | NM_007265 | 11319 | 78.42 | 79.59 | 78.91 | 110.88 | 121.01 | 116.11 | 1.47 | 1.31 |
| 228582_x_at | Metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA) | AI475544 | 378938 | 130.19 | 123.2 | 126.91 | 181.1 | 203.22 | 191.33 | 1.51 | 1.31 |
| 214836_x_at | immunoglobulin kappa constant /// immunoglobulin kappa variable 1-5 | BG536224 | 28299 /// 3514 | 65.05 | 71.88 | 68.93 | 100.72 | 113.31 | 106.6 | 1.55 | 1.31 |
| 1555730_a_at | cofilin 1 (non-muscle) | D00682 | 1072 | 233.42 | 203.68 | 219.04 | 373.43 | 332.44 | 354.76 | 1.62 | 1.31 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 205965_at | basic leucine zipper transcription factor, ATF-like | NM_006399 | 10538 | 513.82 | 461.76 | 485.77 | 774 | 697.77 | 735.88 | 1.51 | 1.32 |
| 225823_at | hypothetical protein P117 | AA699669 | 125988 | 83.75 | 75.65 | 79.49 | 117.06 | 131.82 | 123.84 | 1.56 | 1.32 |
| 204683_at | intercellular adhesion molecule 2 | NM_000873 | 3384 | 44.66 | 44.12 | 44.37 | 74.3 | 64.79 | 69.57 | 1.57 | 1.32 |
| 211600_at | gb:U20489.1 /DB_XREF=gi:885925 /GEN=GLEPP1 /FEA=FLmRNA /CNT=1 /TID=HsAffx.900321.277 /TIER=FL /STK=0 /DEF=Human glomerular epithelial protein 1 (GLEPP1) mRNA, complete cds. /PROD=glomerular epithelial protein 1 /FL=gb:U20489.1 | U20489 | | 661.4 | 556.65 | 610.28 | 907.29 | 1073.59 | 991.58 | 1.62 | 1.32 |
| 211716_x_at | Rho GDP dissociation inhibitor (GDI) alpha /// Rho GDP dissociation inhibitor (GDI) alpha | BC005851 | 396 | 297.22 | 292.48 | 294.83 | 406 | 421.58 | 413.44 | 1.4 | 1.33 |
| 217388_s_at | kynureninase (L-kynurenine hydrolase) | D55639 | 8942 | 373.53 | 372.97 | 373.17 | 540.06 | 519.84 | 529.28 | 1.42 | 1.33 |
| 202799_at | ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli) | NM_006012 | 8192 | 155.55 | 153.66 | 154.6 | 231.24 | 222.9 | 227.58 | 1.47 | 1.33 |
| 222703_s_at | yrdC domain containing (E. coli) | BE464161 | 79693 | 72.52 | 75.31 | 74.02 | 104.3 | 115.77 | 110.4 | 1.49 | 1.33 |
| 208965_s_at | interferon, gamma-inducible protein 16 | BG256677 | 3428 | 149.52 | 122.92 | 136.14 | 210.88 | 241.81 | 224.92 | 1.65 | 1.33 |
| 231821_x_at | hypothetical protein LOC284701 /// hypothetical gene supported by AK024248; AL137733 /// hypothetical gene supported by AK093729; BX647918 /// hypothetical protein LOC641693 /// hypothetical protein LOC642788 /// similar to hypothetical gene supported by AK024248; AL137733 | AK024248 | 284701 /// 401149 /// 441124 /// 641693 /// 642788 /// 653056 | 26.15 | 46.46 | 36.33 | 74.01 | 69.86 | 72.06 | 1.98 | 1.33 |
| 225647_s_at | cathepsin C | AI246687 | 1075 | 131.75 | 130.29 | 130.83 | 190.12 | 187.09 | 188.69 | 1.44 | 1.34 |
| 201391_at | TNF receptor-associated protein 1 | NM_016292 | 10131 | 245.4 | 229.29 | 237.58 | 343.18 | 346.75 | 344.96 | 1.45 | 1.34 |
| 202475_at | transmembrane protein 147 | NM_006326 | 10430 | 177.1 | 199.23 | 188.53 | 283.41 | 286.88 | 284.74 | 1.51 | 1.34 |
| 203105_s_at | dynamin 1-like | NM_012062 | 10059 | 100.78 | 92.59 | 96.91 | 150.34 | 145.99 | 148.38 | 1.53 | 1.34 |
| 216483_s_at | chromosome 19 open reading frame 10 | AC005339 | 56005 | 88.06 | 75.31 | 82.11 | 130.19 | 125.3 | 127.57 | 1.55 | 1.34 |
| 210154_at | malic enzyme 2, NAD(+)-dependent, mitochondrial | M55905 | 4200 | 37.74 | 41.63 | 39.6 | 65.43 | 61.25 | 63.12 | 1.59 | 1.34 |
| 203109_at | ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) | NM_003969 | 9040 | 75.02 | 59.52 | 67.23 | 109.31 | 112.37 | 111.06 | 1.65 | 1.34 |
| 215241_at | transmembrane protein 16C | AJ300461 | 63982 | 44.76 | 36.54 | 40.13 | 66.84 | 71.29 | 69.4 | 1.73 | 1.34 |
| 1553551_s_at | similar to NADH-ubiquinone oxidoreductase chain 2 (NADH dehydrogenase subunit 2) | NM_173709 | 643788 | 1375.43 | 1375.45 | 1375.44 | 1952.21 | 2152.52 | 2051.44 | 1.49 | 1.35 |
| 201476_s_at | ribonucleotide reductase M1 polypeptide | AI692974 | 6240 | 280.42 | 249.13 | 264.46 | 388.88 | 425.85 | 407.18 | 1.54 | 1.35 |
| 223578_x_at | PRO1073 protein | AF113016 | 29005 | 111.63 | 104.96 | 107.87 | 163.72 | 179.15 | 170.87 | 1.58 | 1.36 |
| 212338_at | myosin ID | AA621962 | 4642 | 46 | 46.48 | 46.24 | 86.43 | 70.96 | 78.63 | 1.7 | 1.36 |
| 200883_at | ubiquinol-cytochrome c reductase core protein II | NM_003366 | 7385 | 145.81 | 133.47 | 140.13 | 212.49 | 209.37 | 211.02 | 1.51 | 1.37 |
| 223037_at | PDZ domain containing 11 | AF151061 | 51248 | 116.64 | 121.8 | 119.55 | 179.47 | 183.76 | 181.59 | 1.52 | 1.37 |
| 214359_s_at | heat shock protein 90kDa alpha (cytosolic), class B member 1 | AI218219 | 3326 | 279.39 | 257.19 | 268.73 | 431.56 | 398.55 | 415.36 | 1.55 | 1.37 |
| 202151_s_at | ubiquitin associated domain containing 1 | NM_016172 | 10422 | 91.89 | 94.72 | 93.12 | 149.28 | 147.34 | 148.55 | 1.6 | 1.37 |
| 201118_at | phosphogluconate dehydrogenase /// phosphogluconate dehydrogenase /// UDP-glucose dehydrogenase /// UDP-glucose dehydrogenase | NM_002631 | 5226 /// 7358 | 75.01 | 79.57 | 76.82 | 119.32 | 129.96 | 124.75 | 1.62 | 1.37 |
| 212401_s_at | cell division cycle 2-like 1 (PITSLRE proteins) /// cell division cycle 2-like 2 (PITSLRE proteins) | AI767436 | 984 /// 985 | 63.67 | 58.52 | 61.38 | 114.99 | 98.19 | 106.74 | 1.74 | 1.37 |
| 212411_at | IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast) | BE747342 | 92856 | 81.82 | 74.89 | 77.84 | 119.26 | 122.21 | 121.06 | 1.56 | 1.38 |
| 202697_at | nudix (nucleoside diphosphate linked moiety X)-type motif 21 | NM_007006 | 11051 | 65.55 | 72.83 | 69.53 | 110.23 | 117.5 | 113.97 | 1.64 | 1.4 |
| 202833_s_at | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 | NM_000295 | 5265 | 70.26 | 81.76 | 75.66 | 131.04 | 121.5 | 126.65 | 1.67 | 1.4 |
| 224601_at | CDNA clone IMAGE:3831740 | BE891646 | | 167.41 | 154.1 | 161.25 | 246.56 | 256.86 | 251.04 | 1.56 | 1.41 |
| 212016_s_at | polypyrimidine tract binding protein 1 | AA679988 | 5725 | 65.92 | 58.58 | 62.48 | 100.42 | 99.12 | 99.67 | 1.6 | 1.41 |
| 223221_at | SCO cytochrome oxidase deficient homolog 1 (yeast) | AF183424 | 6341 | 69.34 | 69.49 | 69.41 | 108.3 | 114.49 | 111.2 | 1.6 | 1.41 |
| 233029_at | KIAA1639 protein | AB046859 | 57729 | 53.87 | 61.25 | 57.48 | 108.51 | 92.1 | 100.02 | 1.74 | 1.41 |
| 217791_s_at | aldehyde dehydrogenase 18 family, member A1 | NM_002860 | 5832 | 158.7 | 156.2 | 157.52 | 238.02 | 238.94 | 238.63 | 1.51 | 1.42 |
| 217741_s_at | zinc finger, AN1-type domain 5 | AW471220 | 7763 | 65.31 | 75.11 | 71.11 | 117.58 | 114.12 | 115.86 | 1.63 | 1.42 |
| 238623_at | CDNA FLJ37310 fis, clone BRAMY2016706 | AI633559 | | 87.44 | 98.22 | 93.12 | 150.96 | 153.33 | 152.23 | 1.63 | 1.42 |
| 1564494_s_at | procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide | AK075503 | 5034 | 44.4 | 42.98 | 43.64 | 78.41 | 72.44 | 75.6 | 1.73 | 1.42 |
| 206343_s_at | neuregulin 1 | NM_013959 | 3084 | 62.09 | 57.65 | 60.42 | 95.52 | 100.67 | 97.97 | 1.62 | 1.43 |
| 210663_s_at | kynureninase (L-kynurenine hydrolase) | BC000879 | 8942 | 134.81 | 128.46 | 131.34 | 210.89 | 210.36 | 210.68 | 1.6 | 1.47 |
| 1554464_a_at | cartilage associated protein | BC008745 | 10491 | 39.53 | 38.37 | 39.01 | 62.28 | 67.81 | 64.85 | 1.66 | 1.47 |
| 221782_at | DnaJ (Hsp40) homolog, subfamily C, member 10 | BG168666 | 54431 | 42.29 | 39.85 | 40.73 | 74.09 | 69.28 | 71.57 | 1.76 | 1.48 |
| 210338_s_at | heat shock 70kDa protein 8 | AB034951 | 3312 | 402.55 | 349.05 | 375.86 | 632.41 | 634.13 | 633.28 | 1.68 | 1.49 |
| 223360_at | chromosome 21 open reading frame 56 | AL136871 | 84221 | 30.06 | 27.64 | 28.65 | 54.27 | 52.42 | 53.44 | 1.87 | 1.49 |
| 203828_s_at | interleukin 32 /// interleukin 32 | NM_004221 | 9235 | 139.08 | 141.85 | 140.23 | 234.31 | 227.9 | 231.89 | 1.65 | 1.51 |
| 1555226_s_at | chromosome 1 open reading frame 43 | BC008306 | 25912 | 95.17 | 88.7 | 91.58 | 155.87 | 165.19 | 161.08 | 1.76 | 1.53 |
| 208677_s_at | basigin (Ok blood group) | AL550657 | 682 | 99.86 | 94.35 | 97.23 | 168.7 | 162.65 | 166.05 | 1.71 | 1.54 |
| 225070_at | chromosome 6 open reading frame 68 | BF112132 | 116150 | 84.58 | 81.01 | 82.65 | 142.34 | 150.14 | 145.93 | 1.77 | 1.55 |
| 37079_at | YDD19 protein | U82319 | 11049 | 39.95 | 37.46 | 38.73 | 67.04 | 85.66 | 76.43 | 1.97 | 1.55 |
| 225071_at | chromosome 6 open reading frame 68 | BG168247 | 116150 | 188.56 | 197.11 | 192.48 | 318.61 | 340.32 | 329.09 | 1.71 | 1.57 |
| 209692_at | eyes absent homolog 2 (Drosophila) | U71207 | 2139 | 37.49 | 42.96 | 40.43 | 73.01 | 78.56 | 75.81 | 1.88 | 1.57 |
| 49306_at | Ras association (RalGDS/AF-6) domain family 4 | AI890191 | 83937 | 36.48 | 31.75 | 33.9 | 65.7 | 62.78 | 64.2 | 1.89 | 1.57 |
| 219049_at | chondroitin beta1,4 N-acetylgalactosaminyltransferase | NM_018371 | 55790 | 53.38 | 46.55 | 50.41 | 95.77 | 92.42 | 94.63 | 1.88 | 1.58 |
| 212009_s_at | stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) | AL553320 | 10963 | 35.47 | 41.09 | 37.93 | 69.25 | 74.48 | 72.01 | 1.9 | 1.59 |
| 221972_s_at | stromal cell derived factor 4 | AL571362 | 51150 | 151.62 | 164.02 | 158 | 317.21 | 278.26 | 297.3 | 1.88 | 1.62 |
| 229640_x_at | Hypothetical protein LOC646201 | AW439242 | 646201 | 159.44 | 164.1 | 161.29 | 290.37 | 331.6 | 310.81 | 1.93 | 1.66 |
| 215207_x_at | YDD19 protein /// similar to CG4775-PA /// similar to CG4775-PA | BF695847 | 11049 /// 389850 /// 654174 | 50.75 | 48.35 | 49.27 | 93.74 | 111.13 | 102.38 | 2.08 | 1.73 |
| 206325_at | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6 | NM_001756 | 866 | 51.63 | 39.92 | 46.1 | 105.36 | 102.59 | 104.24 | 2.26 | 1.79 |
| 210342_s_at | thyroid peroxidase | M17755 | 7173 | 66.34 | 69.54 | 67.75 | 134.47 | 141.22 | 137.66 | 2.03 | 1.82 |
| 203559_s_at | amiloride binding protein 1 (amine oxidase (copper-containing)) | NM_001091 | 26 | 21.51 | 16.89 | 19.07 | 46.57 | 48.04 | 47.13 | 2.47 | 1.85 |

**Supplementary Table S3:** Frequency of *CIITA* rearrangements detected by FISH in 263 B cell lymphomas

| **Histology** | **# samples** | **CIITA break-apart (%)** | **Unbalanced rearrangements (%)** |
|---|---|---|---|
| Diffuse large B cell lymphoma (DLBCL) | 131 | 4 (3%) | 3 (75%) |
| Primary mediastinal B cell lymphoma (PMBCL) | 77 | *29 (38%)** | 13 (45%) |
| Classical Hodgkin lymphoma (cHL) | 55 | 8 (15%) | 4 (50%) |
| All cases | 263 | 41 (16%) | 20 (49%) |

*significant overrepresentation compared to all cases: p<0.0001

**Supplementary Table S4:** Clinical characteristics in a selected cohort of 57 patients with PMBCL, homogeneously treated with CHOP or CHOP-like chemotherapy

| | ***CIITA+*** (n=22) [‡] | ***CIITA-*** (n=35) | **p-value** |
|---|---|---|---|
| **Age in years:**<br>mean (SD) | 37.5 (15.3) | 40.0 (16.9) | p=0.604 |
| **Gender** (%) | | | |
| Male | 68 | 46 | p=0.097 |
| Female | 32 | 54 | |
| **Mass size in cm:**<br>mean (SD) | 12.1 (2.2) | 10.9 (4.4) | p=0.158 |
| **LDH** (%) | | | |
| Normal | 18 | 26 | p=0.509 |
| Elevated | 82 | 74 | |
| **Extranodal sites** (%) | | | |
| 0-1 | 52 | 72 | p=0.068 |
| >1 | 48 | 28 | |
| **Clinical stage** (%) | | | |
| limited* | 5 | 14 | p=0.243 |
| advanced | 95 | 86 | |
| **Performance Status 2-4 (WHO) (%)** | 36.4 | 34.3 | p=0.226 |
| **IPI Score (%)** | | | |
| 0-2 | 59 | 77 | p=0.147 |
| 3-5 | 41 | 23 | |
| **CHOP or CHOP-like polychemotherapy (%)** | 100 | 100 | p=1.000 |
| **Radiation therapy (%)** | 36.4 | 37.1 | p=0.953 |

[‡] *CIITA+* = *CIITA* break-apart present; *CIITA-* = *CIITA* break-apart absent
*limited=stage I/II and maximal tumor diameter <10 cm and the absence of B symptoms
SD = standard deviation

**Supplementary Table S5:** Cox regression model for disease-specific survival in 57 patients with PMBCL

| **Variable** | **Class** | **N (%)** | **Univariate analysis p-value** | **Multivariate analysis p-value** |
|---|---|---|---|---|
| **Fluorescence in situ hybridization** | | | | |
| *CIITA* rearrangement | present | 22 (38.6%) | *0.043* | *0.013* |
| **Clinical parameters** | | | | |
| Age (years) | >60 | 6 (10.5%) | 0.622 | |
| Ann Arbor Stage | III,IV | 16 (28.1%) | 0.347 | |
| Serum LDH | elevated | 44 (77.2%) | 0.0001 | *0.0008* |
| WHO performance status | >1 | 20 (35.1%) | 0.301 | |
| Number of extranodal sites | >1 | 21 (36.8%) | 0.144 | |
| IPI score | >2 | 17 (29.8%) | *0.042* | |

[1)] Univariate Cox proportional hazards regression model

[2)] Multivariate Cox proportional hazards regression model (forward stepwise, likelihood ratio)

IPI = International Prognostic Index

**Supplementary Table S6:** Translocation partners of *CIITA* resulting in expressed gene fusions (identified by RNA-seq and *CIITA* 3` RACE)

| **Sample** | **Translocation partners** | | **Chromosomal location** | **Retained *CIITA* exons** | **Reading frame of fusion partner** | **Putative translation*** |
|---|---|---|---|---|---|---|
| | Gene symbol (HGNC database) | Description | | | | |
| KM-H2 | ***BX648577*** | hypothetical LOC145788 | 15q21.3 | 1-4 | conserved | CIITA N-terminus (119aa), BX648577 C-terminus (136aa) |
| #5 | ***CD274*** | programmed cell death 1 ligand 1, *CD274* antigen, B7-H1 | 9p24.1 | 1 | conserved | Wild type CD274 (+22aa N-terminus CIITA) |
| *#6,#7* | ***CD273***[†] | programmed cell death 1 ligand 2, CD273 antigen, PDCD1LG2 | 9p24.1 | 1 | conserved | Wild type CD273[††] |
| *#1* | ***RUNDC2A*** | RUN domain containing 2A | 16p13.13 | 1 | conserved | Wild type RUNDC2A (+22aa N-terminus CIITA) |
| *#6* | ***RALGDS*** | ral guanine nucleotide dissociation stimulator | 9q34.3 | 1 | disrupted | Truncated CIITA (24aa) with large C-terminal deletion |
| *#3* | ***C16ORF75*** | chromosome 16 open reading frame 75, RMI2 | 16p13.13 | 1 | disrupted | Truncated CIITA with additional intron-derived sequence (56aa) |

*For cDNA sequence and amino acid sequence see supplemental text; aa = amino acids.

[†] Identical fusion transcript was found in two cases

[††]Missense mutations in CIITA translational start codon

## Supplementary Table S7: Primer sequences used for validation

| Name | Sequence | Purpose |
|---|---|---|
| *CIITA F1* | GTTCAGCAGGCTGTTGTGTG | *CIITA-BX648577* RT-PCR |
| *BX648577 R1* | TTCACACAAGGAGGCAGTTG | *CIITA-BX648577* RT-PCR |
| *CIITA F4* | CTGCTGGGTCCTACCTGTCAGAG | CIITA 3'RACE and genomic *CIITA-BX648577* PCR |
| *CIITA F5* | TGTAAAACGACGGCCAGT<br>CTGCTCCACCGGCTCAGG | CIITA 3'RACE (nested) |
| *BX648577 R2* | GCAGTCGCAGCTCATTGTAA | genomic *CIITA-BX648577* PCR |
| *CIITA F3* | TGTAAAACGACGGCCAGT<br>AAGGCATCCTTGGGGAAG | *CIITA-Fusion* RT-PCR |
| *CIITA exon 3 F (q)* | GTGACATGGAAGGTGATGAAGA | *CIITA- BX648577* qRT-PCR |
| *BX648577 intron 1 R (q)* | AAAGCCTGTTTGGTGGTCTCT | *CIITA- BX648577* qRT-PCR |
| *ELMO1 F2* | TGTAAAACGACGGCCAGT<br>CGTCAAGGTGGCCATAGAAT | *ELMO1-SLCO3A1* RT-PCR |
| *SLCO3A1 R1* | CAGGAAACAGCTATGAC<br>TGTGGAAACCCAAACATCAA | *ELMO1-SLCO3A1* RT-PCR |
| *BAT2L1 F1* | TGTAAAACGACGGCCAGT<br>GCGGAACCAGACCAGGTAC | *BAT2L1-MGMT* RT-PCR |
| *MGMT R4* | CAGGAAACAGCTATGAC<br>CTCGGGCTGGTGGAAATAG | *BAT2L1-MGMT* RT-PCR |
| *CD274 R3* | CAGGAAACAGCTATGAC<br>TCACTGCTTGTCCAGATGACTT | *CIITA-CD274* RT-PCR |

| | | |
|---|---|---|
| *CD274 F (q)* | TGACCTACTGGCATTTGCTG | *CIITA-CD274* qRT-PCR |
| *CD274 R (q)* | TGAACCTTCAGGTCTTCCTCTC | *CIITA-CD274* qRT-PCR |
| *PDCD1LG2 R3* | CAGGAAACAGCTATGAC<br>CAGAACACTGGTGACCTGGTAG | *CIITA- PDCD1LG2* RT-PCR |
| *PDCD1LG2 F (q)* | CCTGGGACTACAAGTACCTGAC | *CIITA- PDCD1LG2* qRT-PCR |
| *PDCD1LG2 R (q)* | CAGAACACTGGTGACCTGGTAG | *CIITA- PDCD1LG2* qRT-PCR |
| *RALGDS R3* | CAGGAAACAGCTATGAC<br>GATGCAGCCGTATCTAGAGGAG | *CIITA-RALGDS* RT-PCR |
| *RUNDC2A R2* | CAGGAAACAGCTATGAC<br>CGTTCAAATCCTTGTTGTCG | *CIITA- RUNDC2A* RT-PCR |
| *C16ORF75 R1* | *CAGGAAACAGCTATGAC*<br>TGTGGTGTTGCACACCTGTA | *CIITA- C16ORF75* RT-PCR |

Underlined: M13 sequence tags

## Sequences:

**1) Full length *CIITA-BX648577* (BX648577.1) cDNA in KM-H2 (longest transcript) and putative translation (used for forced expression in SUDHL4).** Expressed "intronic" *BX648577* sequence underlined. Translational start and stop codons in bold.

GGTTAGTGATGAGGCTAGTGATGAGGCTGTGTGCTTCTGAGCTGGGCATCCGAAG
GCATCCTTGGGGAAGCTGAGGGCACGAGGAGGGGCTGCCAGACTCCGGGAGCT
GCTGCCTGGCTGGGATTCCTACACA**ATG**CGTTGCCTGGCTCCACGCCCTGCTGGG
TCCTACCTGTCAGAGCCCCAAGGCAGCTCACAGTGTGCCACCATGGAGTTGGGGC
CCCTAGAAGGTGGCTACCTGGAGCTTCTTAACAGCGATGCTGACCCCCTGTGCCT
CTACCACTTCTATGACCAGATGGACCTGGCTGGAGAAGAAGAGATTGAGCTCTACT
CAGAACCCGACACAGACACCATCAACTGCGACCAGTTCAGCAGGCTGTTGTGTGA
CATGGAAGGTGATGAAGAGACCAGGGAGGCTTATGCCAATATCGCGGAACTGGAC
CAGTATGTCTTCCAGGACTCCCAGCTGGAGGGCCTGAGCAAGGACATTTTCAGTG
TATGTGATTTTAAGGGTAGTCTTCAACGTCAAGAGAAGAGACCACCAAACAGGCTT
TGTGATAAGAAAAGTACTTCACCTTCAAATTCAGACACAGAAATGAAATCTGAACAA
CTGCCTCCTTGTGTGAACCCTGGCAATCCTGTGTTTTCATGTATGTTGGATCCAAA
GACACTCCAGACAGCCACCTCACTATCAAAACCTCAAATGATTATGTATAAAACCAA
TTCAAGTCATTATGGTGAATTTCTACCTATTCCACAGTTTTTCCCCTGCAATTATACT
CCAAAGGAGCAAGTATTTTCAAGCCATATCAGAGCAACTGGATTTTATCAAAATAAC
ACTCTAAATACTGCACCTGACAGAACCAGAACTCTTGATTTTCCTAATATTCAACAC
ACTCTA**TGA**AAATATATTCCTTTGTATATTGAAGAGAAAATATACTCGGGAAAAATG
AGTGTTAAATCTAAGGGTAGAATACCTAATAAAGAAGATAAAAAGTTTTGAATCAAT
TTTTAAAATAAGTTAAATAAAGTATTTCAACTGATAAAAAAAAAAAAAAAAA

**Putative translation (255 residues):**

M R C L A P R P A G S Y L S E P Q G S S Q C A T M E L G P L E G G Y L E L L N S
D A D P L C L Y H F Y D Q M D L A G E E E I E L Y S E P D T D T I N C D Q F S R L L
C D M E G D E E T R E A Y A N I A E L D Q Y V F Q D S Q L E G L S K D I F S V C D
F K G S L Q R Q E K R P P N R L C D K K S T S P S N S D T E M K S E Q L P P C V
N P G N P V F S C M L D P K T L Q T A T S L S K P Q M I M Y K T N S S H Y G E F L
P I P Q F F P C N Y T P K E Q V F S S H I R A T G F Y Q N N T L N T A P D R T R T L
D F P N I Q H T L Stop

**2) Full length *CIITA-CD274* cDNA in a PMBCL case and putative translation (used for forced expression in U2940).** Translational start and stop codons in bold.

GGTTAGTGATGAGGCTAGTGATGAGGCTGTGTGCTTCTGAGCTGGGCATCCGAAG
GCATCCTTGGGGAAGCTGAGGGCACGAGGAGGGGCTGCCAGACTCCGGGAGCT
GCTGCCTGGCTGGGATTCCTACACA**ATG**CGTTGCCTGGCTCCACGCCCTGCTGGG
TCCTACCTGTCAGAGCCCCAAGGGCATTCCAGAAAGATGAGGATATTTGCTGTCTT
TATATTCATGACCTACTGGCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGA
CCTATATGTGGTAGAGTATGGTAGCAATATGACAATTGAATGCAAATTCCCAGTAG
AAAAACAATTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAAC
ATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCTACAG
ACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCTGCACTTCAG
ATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTGCATGATCAGCTATG
GTGGTGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCCATACAACAAAATC
AACCAAAGAATTTTGGTTGTGGATCCAGTCACCTCTGAACATGAACTGACATGTCA
GGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAAGTC
CTGAGTGGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGT
GACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCACTTTTAG
GAGATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTACCTC
TGGCACATCCTCCAAATGAAAGGACTCACTTGGTAATTCTGGGAGCCATCTTATTA
TGCCTTGGTGTAGCACTGACATTCATCTTCCGTTTAAGAAAAGGGAGAATGATGGA
TGTGAAAAAATGTGGCATCCAAGATACAAACTCAAAGAAGCAAAGTGATACACATTT
GGAGGAGACG**TAA**TCCAGCATTGGAACTTCTGATCTTCAAGCAGGGATTCTCAAC
CTGTGGTTTAGGGGTTCATCGGGGCTGAGCGTGACAAGAGGAAGGAATGGGCCC
GTGGGATGCAGGCAATGTGGGACTTAAAAGGCCCAAGCACTGAAAATGGAACCTG
GCGAAAGCAGAGGAGGAGAATGAAGAAAGATGGAGTCAAACAGGGAGCCTGGAG
GGAGACCTTGATACTTTCAAATGCCTGAGGGGCTCATCGACGCCTGTGACAGGGA
GAAAGGATACTTCTGAACAAGGAGCCTCCAAGCAAATCATCCATTGCTCATCCTAG
GAAGACGGGTTGAGAATCCCTAATTTGAGGGTCAGTTCCTGCAGAAGTGCCCTTT
GCCTCCACTCAATGCCTCAATTTGTTTTCTGCATGACTGAGAGTCTCAGTGTTGGA
ACGGGACAGTATTTATGTATGAGTTTTTCCTATTTATTTTGAGTCTGTGAGGTCTTCT
TGTCATGTGAGTGTGGTTGTGAATGATTTCTTTTGAAGATATATTGTAGTAGATGTT
ACAATTTTGTCGCCAAACTAAACTTGCTGCTTAATGATTTGCTCACATCTAGTAAAA
CATGGAGTATTTGTAAAAAAAAAAAAAAA

**Putative translation (312 residues):**

M R C L A P R P A G S Y L S E P Q G H S R K M R I F A V F I F M T Y W H L L N A F
T V T V P K D L Y V V E Y G S N M T I E C K F P V E K Q L D L A A L I V Y W E M E
D K N I I Q F V H G E E D L K V Q H S S Y R Q R A R L L K D Q L S L G N A A L Q I T
D V K L Q D A G V Y R C M I S Y G G A D Y K R I T V K V N A P Y N K I N Q R I L V V
D P V T S E H E L T C Q A E G Y P K A E V I W T S S D H Q V L S G K T T T T N S K
R E E K L F N V T S T L R I N T T T N E I F Y C T F R R L D P E E N H T A E L V I P E

L P L A H P P N E R T H L V I L G A I L L C L G V A L T F I F R L R K G R M M D V K
K C G I Q D T N S K K Q S D T H L E E T Stop

### 3) Full length *CIITA-PDCD1LG2* cDNA in a PMBCL case and putative translation (used for forced expression in U2940). CIITA start codon mutation underlined. The putative translation starts at the PDCD1LG2 start codon (bold).

GGTTAGTGATGAGGCTAGTGATGAGGCTGTGTGCTTCTGAGCTGGGCATCCGAAG
GCATCCTTGGGGAAGCTGAGGGCACGAGGAGGGGCTGCCAGACTCCGGGAGCT
GCTGCCTGGCTGGGATTCCTACACA**CTG**CGTTGCCTGGCTCCACGCCCTGCTGGG
TCCTACTTGTCAGAACCCCAAGATCAAATACAGAAC***ATG***ATCTTCCTCCTGCTAATG
TTGAGCCTGGAATTGCAGCTTCACCAGATAGCAGCTTTATTCACAGTGACAGTCCC
TAAGGAACTGTACATAATAGAGCATGGCAGCAATGTGACCCTGGAATGCAACTTTG
ACACTGGAAGTCATGTGAACCTTGGAGCAATAACAGCCAGTTTGCAAAAGGTGGAA
AATGATACATCCCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCC
TAGGGAAGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGGCAGTA
CCAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAG
TCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGGTTCCAGAAACAGAT
GAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGCAGAAGTATCCTGGC
CAAACGTCAGCGTTCCTGCCAACACCAGCCACTCCAGGACCCCTGAAGGCCTCTA
CCAGGTCACCAGTGTTCTGCGCCTAAAGCCACCCCCTGGCAGAAACTTCAGCTGT
GTGTTCTGGAATACTCACGTGAGGGAACTTACTTTGGCCAGCATTGACCTTCAAAG
TCAGATGGAACCCAGGACCCATCCAACTTGGCTGCTTCACATTTTCATCCCCTCCT
GCATCATTGCTTTCATTTTCATAGCCACAGTGATAGCCCTAAGAAAACAACTCTGTC
AAAAGCTGTATTCTTCAAAAGACACAACAAAAAGACCTGTCACCACAACAAAGAGG
GAAGTGAACAGTGCTATC***TGA***ACCTGTGGTCTTGGGAGCCAGGGTGACCTGATAT
GACATCTAAAGAAGCTTCTGGACTCTGAACAAGAATTCGGTGGCCTGCAGAGCTTG
CCATTTGCACTTTTCAAATGCCTTTGGATGACCCAGCACTTTAATCTGAAACCTGCA
ACAAGACTAGCCAACACCTGGCCATGAAACTTGCCCCTTCACTGATCTGGACTCAC
CTCTGGAGCCTATGGCTTTAAGCAAGCACTACTGCACTTTACAGAATTACCCCACT
GGATCCTGGACCCACAGAATTCCTTCAGGATCCTTCTTGCTGCCAGACTGAAAGCA
AAAGGAATTATTTCCCCTCAAGTTTTCTAAGTGATTTCCAAAAGCAGAGGTGTGTGG
AAATTTCCAGTAACAGAAACAGATGGGTTGCCAATAGAGTTATTTTTTATCTATAGC
TTCCTCTGGGTACTAGAAGAGGCTATTGAGACTATGAGCTCACAGACAGGGCTTC
GCACAAACTCAAATCATAATTGACATGTTTTATGGATTACTGGAATCTTGATAGCAT
AATGAAGTTGTTCTAATTAACAGAGAGCATTTAAATATACACTAAGTGCACAAATTG
TGGAGTAAAGTCATCAAGCTCTGTTTTTGAGGTCTAAGTCACAAAGCATTTGTTTTA
ACCTGTAATGGCACCATGTTTAATGGTGGTTTTTTTTTTGAACTACATCTTTCCTTTA
AAAATTATTGGTTTCTTTTTATTTGTTTTTACCTTAGAAATCAATTATATACAGTCAAA
AATATTTGATATGCTCATACGTTGTATCTGCAGCAATTTCAGATAAGTAGCTAAAAT
GGCCAAAGCCCCAAACTAAGCCTCCTTTTCTGGCCCTCAATATGACTTTAAATTTGA
CTTTTCAGTGCCTCAGTTTGCACATCTGTAATACAGCAATGCTAAGTAGTCAAGGC
CTTTGATAATTGGCACTATGGAAATCCTGCAAGATCCCACTACATATGTGTGGAGC

AGAAGGGTAACTCGGCTACAGTAACAGCTTAATTTTGTTAAATTTGTTCTTTATACT
GGAGCCATGAAGCTCAGAGCATTAGCTGACCCTTGAACTATTCAAATGGGCACATT
AGCTAGTATAACAGACTTACATAGGTGGGCCTAAAGCAAGCTCCTTAACTGAGCAA
AATTTGGGGCTTATGAGAATGAAAGGGTGTGAAATTGACTAACAGACAAATCATAC
ATCTCAGTTTCTCAATTCTCATGTAAATCAGAGAATGCCTTTAAAGAATAAAACTCAA
TTGTTATTCTTCAACGTTCTTTATATATTCTACTTTTGGGTAAAAAAAAAAAAAAA

**Putative translation (295 residues):**
M I F L L L M L S L E L Q L H Q I A A L F T V T V P K E L Y I I E H G S N V T L E C N
F D T G S H V N L G A I T A S L Q K V E N D T S P H R E R A T L L E E Q L P L G K
A S F H I P Q V Q V R D E G Q Y Q C I I I Y G V A W D Y K Y L T L K V K A S Y R K I
N T H I L K V P E T D E V E L T C Q A T G Y P L A E V S W P N V S V P A N T S H S
R T P E G L Y Q V T S V L R L K P P P G R N F S C V F W N T H V R E L T L A S I D
L Q S Q M E P R T H P T W L L H I F I P S C I I A F I F I A T V I A L R K Q L C Q K L Y
S S K D T T K R P V T T T K R E V N S A I Stop

## 4) Full length *CIITA-RALGDS* cDNA in a PMBCL case and putative translation.

GGTTAGTGATGAGGCTAGTGATGAGGCTGTGTGCTTCTGAGCTGGGCATCCGAAG
GCATCCTTGGGGAAGCTGAGGGCACGAGGAGGGGCTGCCAGACTCCGGGAGCT
GCTGCCTGGCTGGGATTCCTACACA***ATG***CGTTGCCTGGCTCCACGCCCTGCTGGG
TCCTACCTGTCAGAGCCCCAAGAGCTCCACGCAGGAGATCGG**TGA**GGAGCTGATC
AACGGAGTCATCTACTCCATCTCCCTGCGCAAGGTGCAGCTGCACCACGGAGGCA
ACAAGGGGCAGCGCTGGCTCGGGTATGAGAATGAGTCGGCCCTGAACCTTTATGA
GACTTGCAAGGTGCGGACCGTGAAGGCTGGCACGCTGGAGAAGCTGGTGGAGCA
CCTGGTGCCAGCCTTCCAGGGCAGCGACCTCTCCTACGTCACCATCTTCCTGTGT
ACCTATAGAGCCTTCACCACCACCCAACAGGTCCTGGACCTGCTGTTCAAAAGGTA
CGGTAGATGTGACGCCCTCACGGCCTCCTCTAGATACGGCTGCATCCTCCCCTAT
TCCGACGAGGATGGTGGACCCCAGGACCAACTTAAAAATGCCATCTCCTCCATCC
TGGGCACCTGGCTGGACCAGTACTCGGAGGATTTCTGTCAACCTCCGGACTTTCC
CTGCCTCAAGCAGCTGGTGGCCTACGTGCAGCTCAACATGCCAGGCTCAGACCTG
GAGCGCCGTGCCCACCTTCTCCTGGCCCAGCTGGAGCACTCGGAACCCATTGAG
GCAGAGCCTGAGGCTCTGTCACCAGTGCCAGCTCTAAAACCAACTCCAGAGCTCG
AGCTAGCTCTAACACCAGCTCGAGCACCCAGCCCAGTGCCGGCTCCAGCCCCGG
AGCCAGAGCCAGCTCCAACACCAGCTCCAGGTTCAGAGCTAGAAGTAGCTCCAGC
ACCAGCTCCGGAGCTCCAGCAGGCTCCAGAGCCAGCTGTGGGACTAGAATCGGC
TCCAGCGCCAGCTCTGGAACTAGAGCCAGCTCCAGAACAGGATCCAGCTCCCTCA
CAAACTCTAGAGCTGGAGCCAGCTCCAGCACCAGTTCCATCATTACAGCCTTCCTG
GCCTTCACCTGTGGTTGCAGAGAACGGGCTGAGTGAGGAGAAGCCTCACCTCTTG
GTGTTCCCTCCAGATCTGGTGGCAGAGCAGTTTACACTGATGGATGCGGAACTGTT
CAAGAAGGTGGTGCCCTACCACTGCCTGGGCTCCATCTGGTCCCAGCGGGACAA
GAAGGGCAAGGAGCACCTGGCGCCCACCATCCGCGCCACTGTCACCCAGTTCAA
CAGTGTGGCCAACTGTGTCATCACCACCTGCCTCGGGAACCGAAGCACGAAAGCC
CCAGACAGGGCCAGGGTGGTGGAGCACTGGATCGAGGTGGCCAGGGAGTGCCG
GATCCTCAAGAACTTCTCGTCACTGTATGCCATCCTCTCTGCCCTGCAGAGCAACT
CCATCCACCGTCTGAAGAAGACGTGGGAAGACGTTTCCAGGGACAGTTTCCGGAT
CTTTCAGAAGCTGTCAGAGATCTTCTCAGATGAGAACAACTACTCATTGAGCCGGG
AGCTGCTCATCAAGGAGGGCACCTCCAAGTTTGCCACCCTGGAGATGAACCCCAA
GAGAGCCCAGAAACGGCCGAAGGAGACGGGCATCATCCAGGGCACCGTTCCCTA
CCTGGGCACGTTCCTCACCGACCTGGTGATGCTGGACACTGCCATGAAGGACTAT
CTGTATGGCAGACTCATCAACTTTGAGAAGAGGAGGAAGGAGTTCGAGGTGATCG
CCCAGATCAAGCTGCTGCAGTCGGCCTGCAACAACTACAGCATCGCGCCAGATGA
GCAATTTGGGGCCTGGTTCCGGGCCGTGGAGCGGCTCAGCGAGACTGAGAGCTA
CAACCTGTCGTGCGAGCTGGAGCCCCCATCCGAGTCAGCCAGCAACACCCTCAG
GACCAAGAAGAACACAGCCATTGTCAAGCGCTGGAGCGACCGCCAGGCCCCCAG
CACTGAGCTCAGTACCAGTGGCAGCTCCCACTCCAAGTCCTGTGACCAGCTCAGG
TGTGGCCCCTACCTCAGCAGCGGGGACATCGCTGACGCGCTCAGCGTGCACTCG
GCCGGCTCCTCTAGCTCCGACGTGGAGGAGATCAACATCAGCTTCGTCCCGGAGT
CTCCTGATGGCCAGGAAAAGAAGTTCTGGGAATCAGCCTCACAGTCATCCCCGGA
GACCTCCGGCATCAGCTCAGCCTCCAGCAGCACCTCGTCCTCCTCAGCCTCCACC
ACGCCCGTGGCTGCCACACGCACCCACAAGCGCTCTGTCTCAGGGCTCTGCAACT
CCAGCTCCGCGCTGCCGCTCTACAACCAGCAGGTGGGCGACTGCTGTATCATCCG

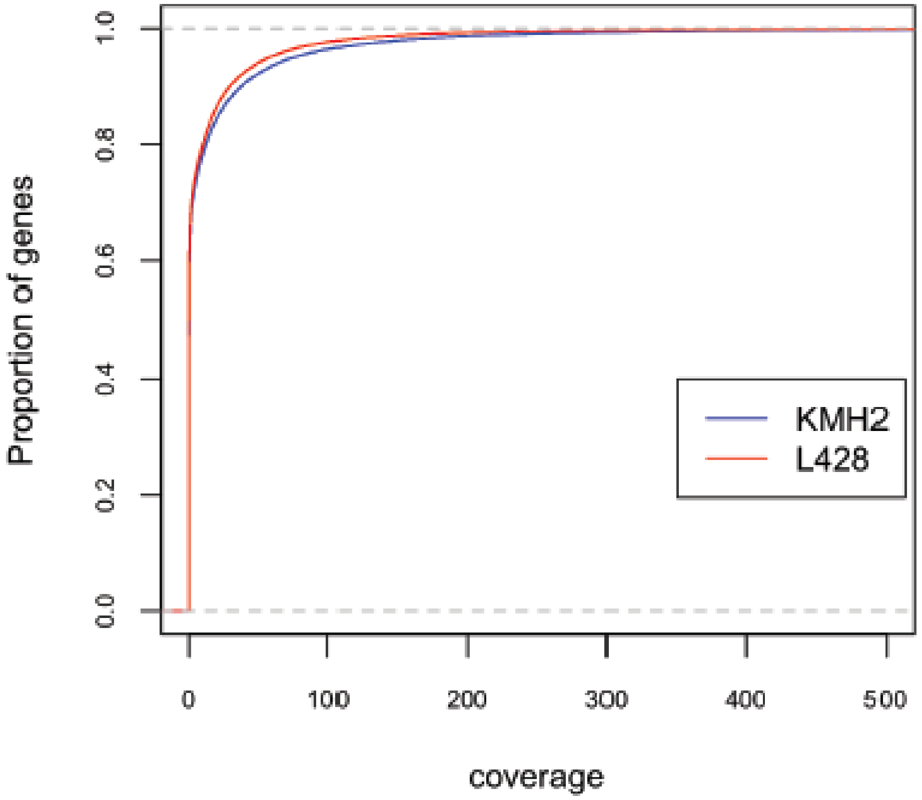
CGTCAGCCTGGACGTGGACAATGGCAACATGTACAAGAGCATCCTGGTGACCAGC
CAAGATAAGGCTCCGGCTGTAATCCGCAAGGCCATGGACAAACACAACCTGGAGG
AGGAGGAGCCGGAGGACTATGAGCTGCTGCAGATTCTCTCAGATGACCGGAAGCT
GAAGATCCCTGAAAACGCCAACGTCTTCTATGCCATGAACTCTACCGCCAACTATG
ACTTTGTCCTCAAGAAGCGGACCTTCACCAAGGGAGTGAAGGTCAAGCACGGAGC
CAGCTCCACCCTCCCTCGCATGAAGCAGAAAGGACTCAAGATTGCCAAGGGCATC
TTCTGAGGGCATCCTCCCAGGGTCTGGCTGGCTGGTAGCCAAGCACTTATGGACC
AGAGTGGCCCAGGCCAGCTGGGCGCCTTCCTCCCACCTGCCAGCCCAGGGTACC
CCAGACTCCAGTTTCATCCTGAACCTCTCCCGCTGCTGGGATTGACGCCTGCCATT
GGTCAGGCTGACCTGGCCTCCCGTGGACCACTCGCTGCCTTAGGTGCCTTCTGCT
CTCTGGAACCAGAGGACTAGCTGACTTTTGCCAAGGAGCAGTGCCAACGGGCATG
GCATGGTGCCCTGCCTGCCCCCGGGCGCCACCTCTGTACACTTCCCTGACACCTT
CCCAGGTGTGGGTCACTGCCACCTGTGCCCATGGGCACCCCAGAGCACCCACTG
TGACCACTGCAGTTCTCTCATGCCCACAGGCACTGGCCTGTGACCTTCGCAGGGG
TCCCGGCCCCTCCCACCACTCTAGCCTTTCTCAGGCTGCACCAAAGATTCCATCAT
CAGGGCCAACTGAGAGTGAGGGAGTCTCACCCACCGCTTACCCCAGCCCTCCCCT
GGGAGCAGAGAGAGAAACCCTCTTCATGGACCAGACTCTGCACCCGGTGAGTGA
GGACAGTCCCAGCTGAGTCCCATCGATGTTGAATCTCATGCCACTGCAAGTGCCA
TTCACCACTGCGTCCTGGGCTTTACGAGACCATGCAAGACGGGGGTTAGTGAGGA
AGGAGGATTTGGGGTGGGGGTGGGGTGATTGAATATTTGTATAAAAAGCAAAAAG
AAAAAAAAAATGTTTGTTTACTGATTGGGGAGGGGCAATATTTATTTGTTGTAAATA
GCAAATGCTAGACTTGAATATTATATTAAAATCCTGTTTCTACTATAAAAAAAAAAAA
AAAAAAAAAAA

**Putative translation (24 residues):**
M R C L A P R P A G S Y L S E P Q E L H A G D R Stop

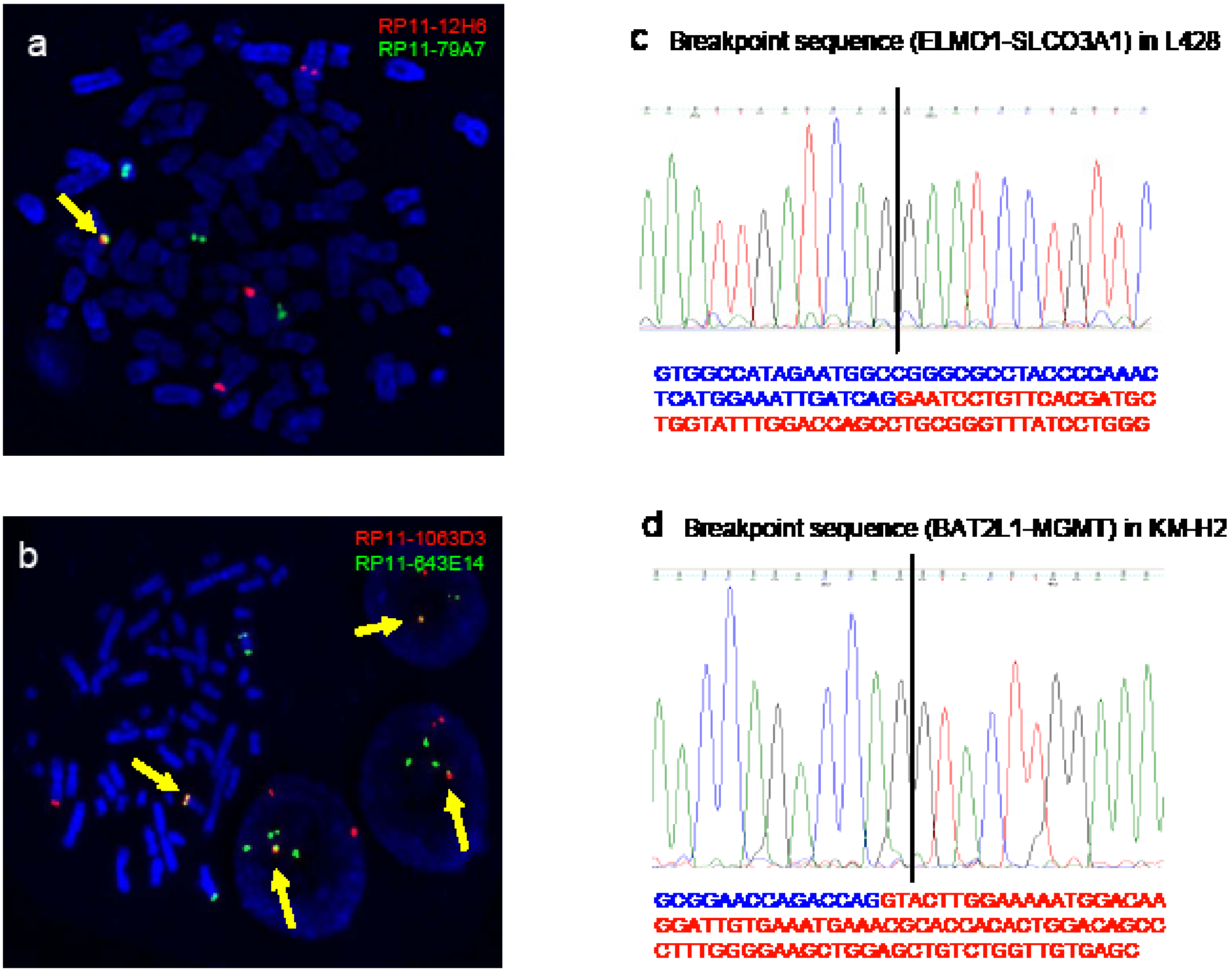
## 5) Full length *CIITA-C16ORF75* cDNA in a PMBCL case and putative translation.

GGTTAGTGATGAGGCTAGTGATGAGGCTGTGTGCTTCTGAGCTGGGCATCCGAAG
GCATCCTTGGGGAAGCTGAGGGCACGAGGAGGGGCTGCCAGACTCCGGGAGCT
GCTGCCTGGCTGGGATTCCTACACA***ATG***CGTTGCCTGGCTCCACGCCCTGCTGGG
TCCTACCTGTCAGAGCCCCAAGGGTCTCGCTCTGCTGCCCAGGCTGGAGTGCAGT
GGCGCCATCTCAGCTGCAACGTCTGCCTCCGAGTTCAAGCAGTCCTCCCGCTGGG
ACTACAGGTGTGCAACACCACACCCAGC**TAA**TTTTGTTTATTTTTTGTAGAGATAGG
GTTTCATCATGTTGCCCAGGCTGGTCTCGAACTGCTGGGCTCCAACGATCCACCC
ACCTCAGCCTCCCAAAGTGCTAGGATGACAAGTGTGAGTCACTGCACCCAGCCTG
AATCATTTTTTAAAGAGCATGTGTCCATTAAAAATTATTTTAATGAAAAAAAAAAAAA
AAAAAAAAAAAAA

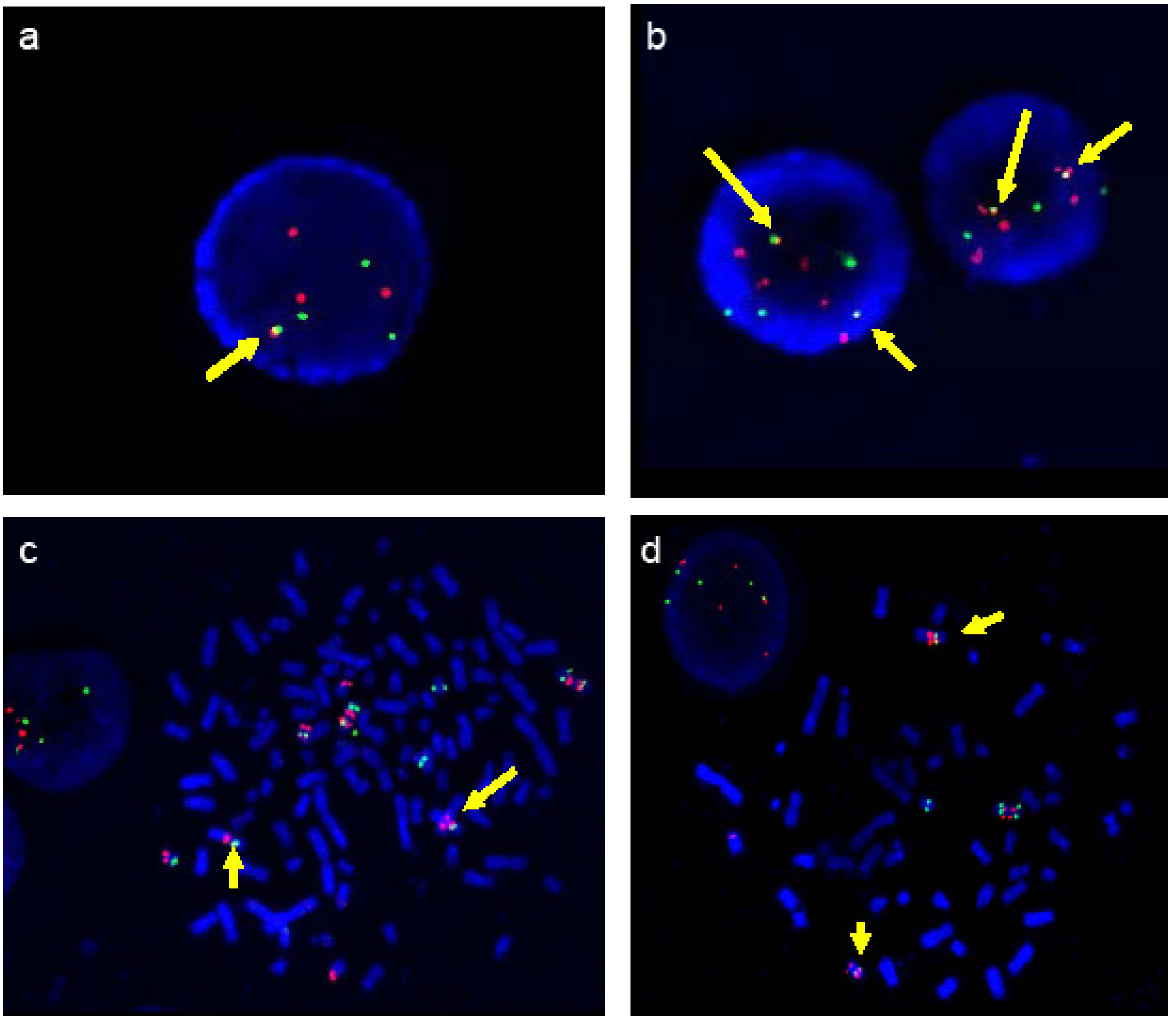
**Putative translation (56 residues):**
M R C L A P R P A G S Y L S E P Q G S R S A A Q A G V Q W R H L S C N V C L R V
Q A V L P L G L Q V C N T T P S Stop



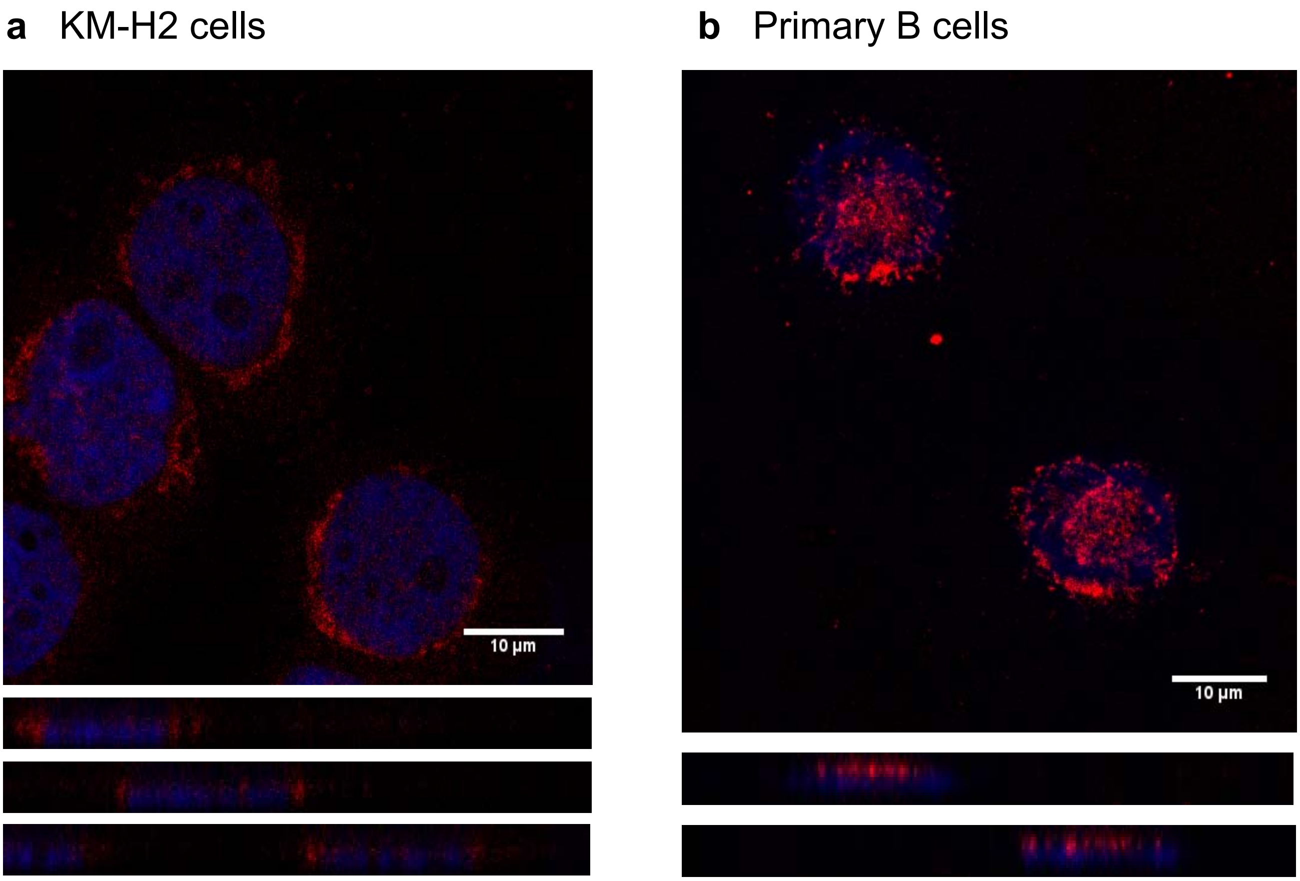
**Supplementary Figure S1:** Cumulative distribution plots of expression for both KM-H2 and L428 showing the proportion of genes expressed at increasing coverage levels.



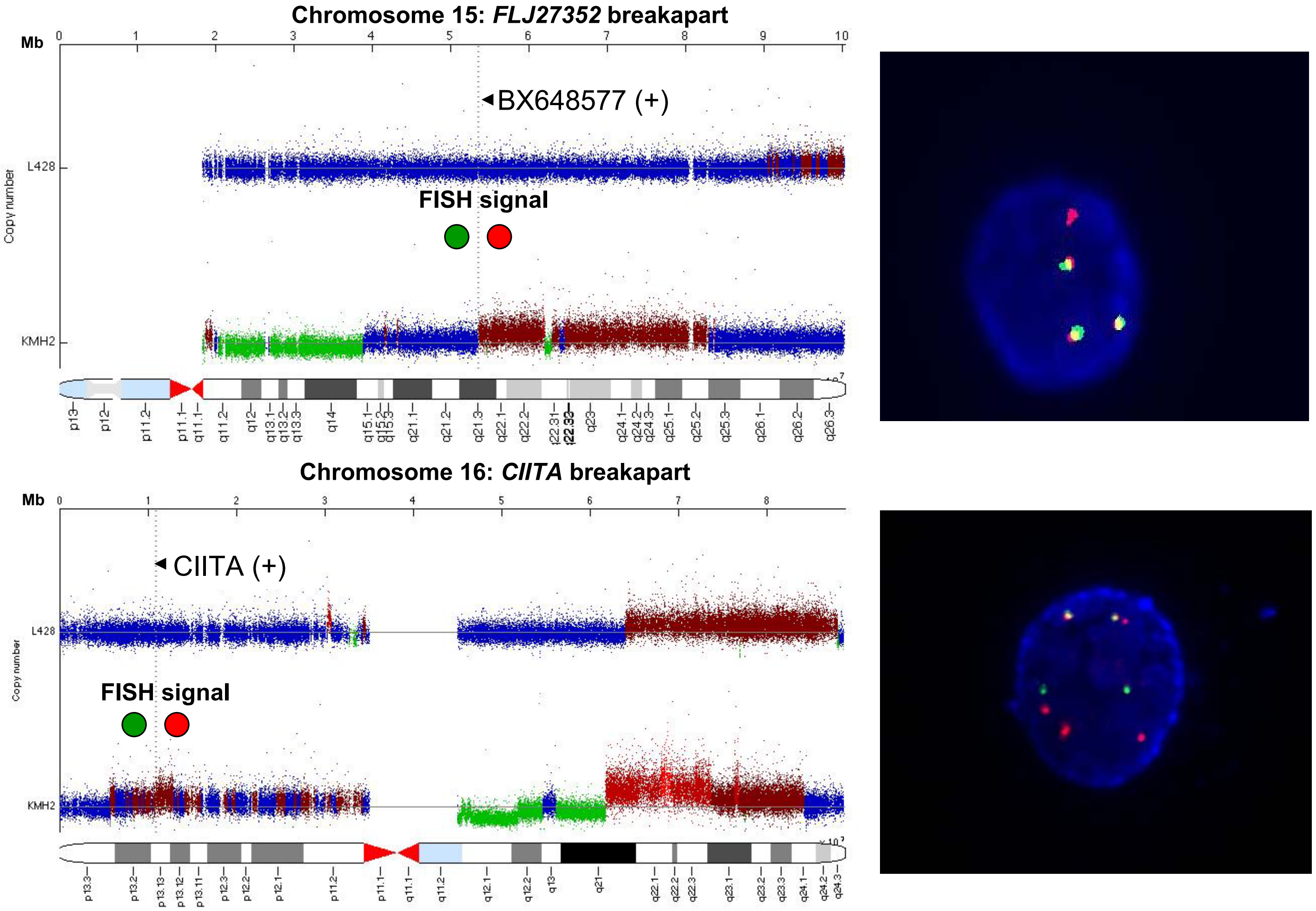
**Supplementary Figure S2:** Validation of fusion transcripts by FISH and direct sequencing. **a,** L428 metaphase cell with co-localization of the *SLCO3A1* (RP11-79A7) and *ELMO1* (RP11-12H6) gene loci (yellow arrow). **b,** Direct sequencing and breakpoint sequence of an ELMO1-SLCO3A1 fusion transcript as predicted by RNAseq. **c,** KM-H2 interphase and metaphase cell with co-localization of the *BAT2L1* (RP11-643E14) and *MGMT* (RP11-1063D3) gene loci (yellow arrows). **d,** Direct sequencing and breakpoint sequence of a BAT2L1-MGMT fusion transcript as predicted by RNA-seq.



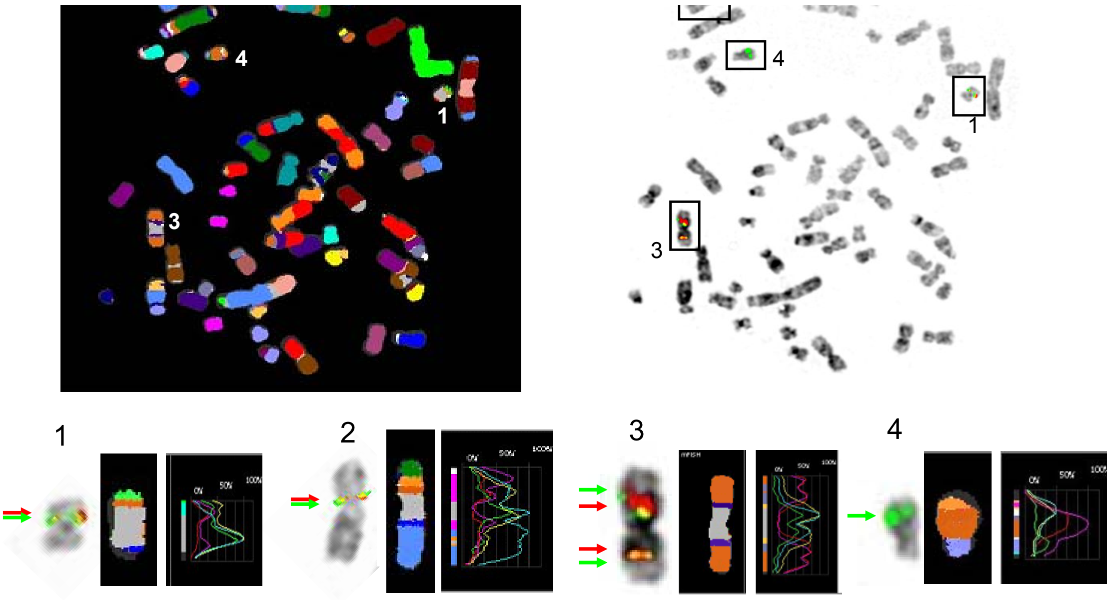
**Supplementary Figure S3:** Validation of complex chromosome 16 rearrangements in KM-H2 leading to expression of CIITA-BX648577 fusion transcripts. Yellow arrows indicate co-localization of the gene loci of *CIITA* and *BX648577* in interphase **(a+b)** and metaphase **(c+d)** cells. Green signals: *BX648577* locus (15q21.3, RP11-460A24); Red signals: *CIITA* locus (16p13.13, RP11-1057F14).



**Supplementary Figure S4:** Immuno-fluorescence staining with N-terminal CIITA antibody. **a,** Confocal microscopy shows a perinuclear staining pattern of the fusion protein in KM-H2 cells. **b,** The staining pattern in primary B cells is predominantly nuclear. The lower panels show slice views from the side which were derived from Z stack image series.

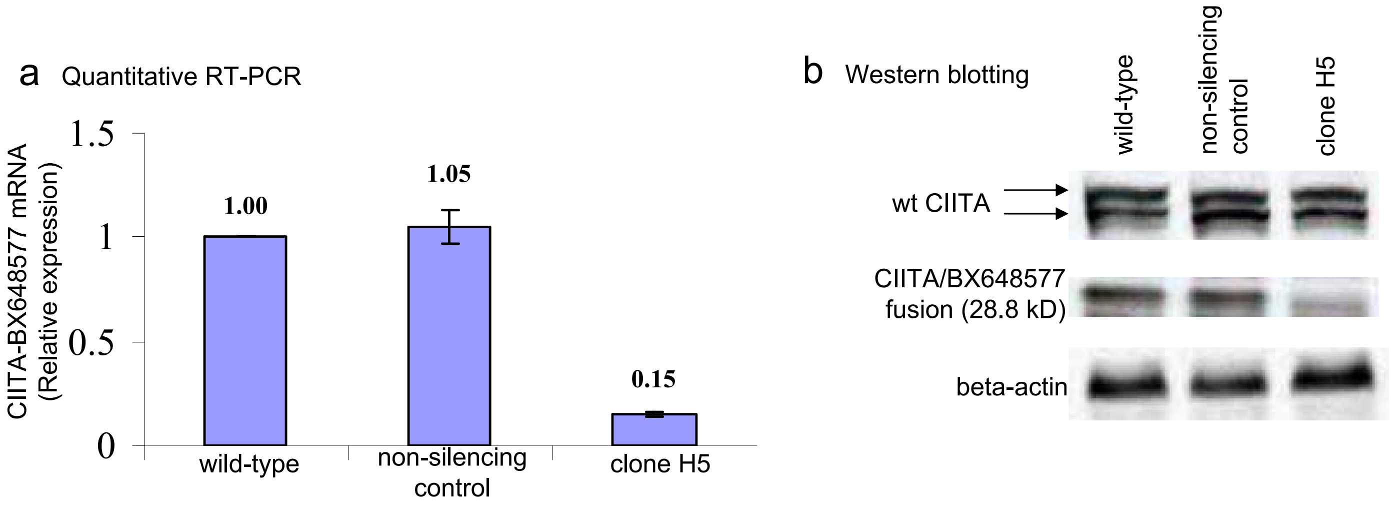


**Supplementary Figure S5:** High-resolution single nucleotide polymorphism analysis and FISH confirm chromosomal unbalances accompanying complex rearrangements involving chromosomes 15 and 16 in KM-H2. Results of high-resolution genotyping arrays and FISH using *CIITA* (RP11-109M19, RP11-66H6) and *BX648577* (RP11-139H15, RP11-161E4) break-apart probes are shown. Copy number changes are color-coded according to five discrete copy number states: green=loss; blue=neutral; dark red=gain; medium red=amplification; bright red=high level amplification. Predicted breakpoints in *CIITA* and *BX648577* by RNA-seq are indicated by the hatched lines. **Upper panel:** Relative amplification of chromosomal material telomeric of the *BX648577* breakpoint in KM-H2 is confirmed by FISH (4 fused + 1 red signal). **Lower panel:** Relative amplification of chromosomal material centromeric of the *CIITA* breakpoint in KM-H2 is confirmed by FISH (2 fused + 2 green + 3 red signals). L428 is shown as reference.

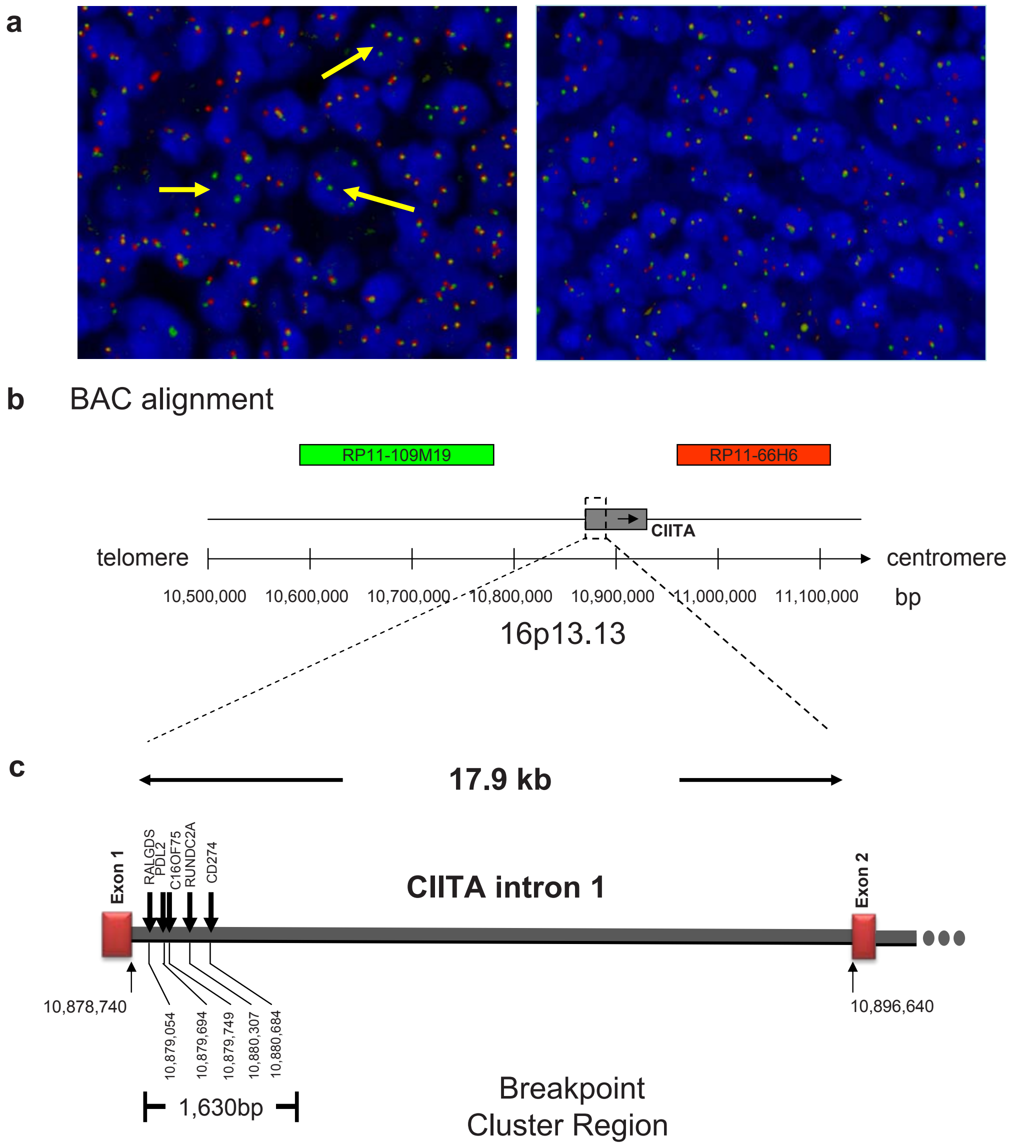


**der(16)t(6;15;16;8)** **der(16)t(3;7;15;16;8;2)** **der(?)(15;9;16;9;15)** **der(15)(7;15;11)**

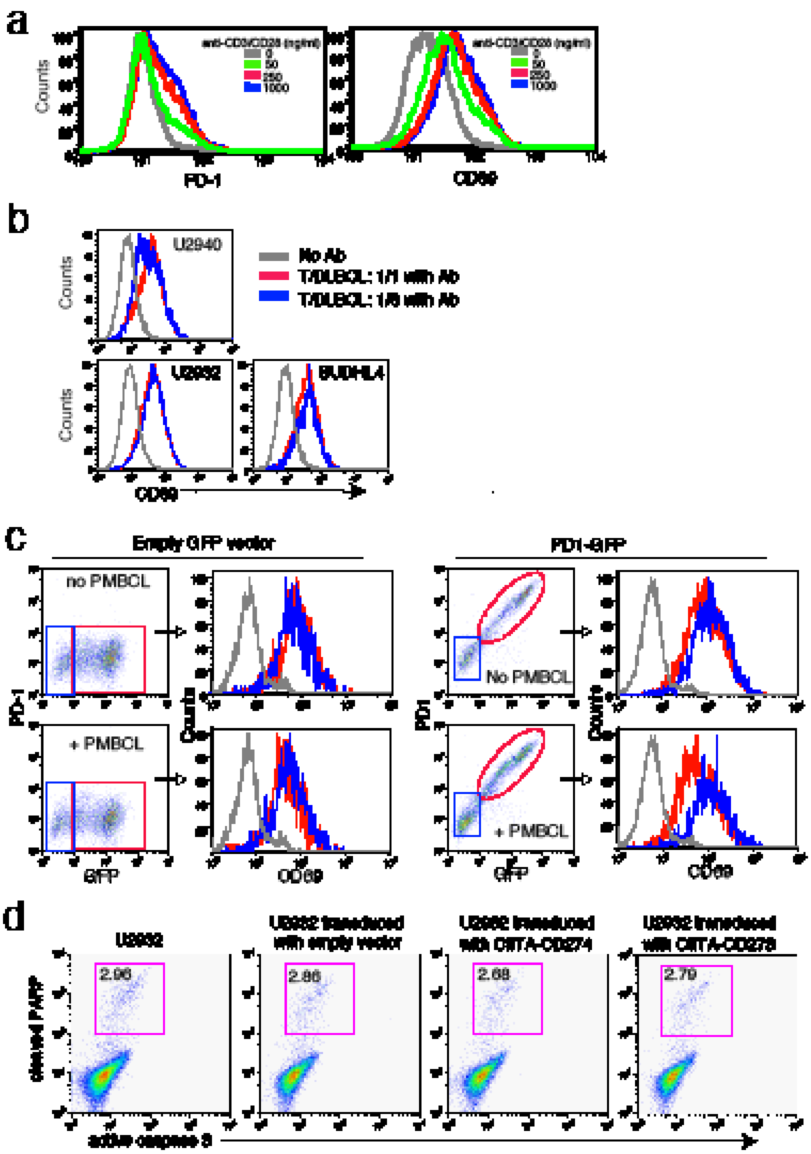
**Supplementary Figure S6:** Detailed molecular-cytogenetic characterization of KM-H2. **a,** 24-colour FISH of a representative KM-H2 metaphase matching the same metaphase in **b,** stained with locus-specific FISH probes for the *CIITA* (WI2-1388I10) and *BX648577* (WI2-2329H16) gene loci (Fosmid probes). The Banding pattern is shown in inverted DAPI. The four derivative chromosomes with involvement of the CIITA and BX648577 loci are shown in higher magnification (1-4). As part of complex rearrangements between chromosomes 15 and 16, chromosomal material telomeric of the CIITA breakpoint is fused with chromosomal material telomeric of the BX648577 breakpoint on two derivative chromosomes 16 (1+2). Note that the derivative chromosome der(?)(15;9;16;9;15) (3) does not harbour CIITA-BX648577 gene fusions as FISH showed no break-apart signals for the *CIITA* and *BX648577* gene loci on this derivative chromosome (data not shown).



**pplementary Figure S7:** Inhibition of CIITA/BX648577 fusion gene expression by a tiviral shRNAmir vector. KM-H2 cells stably transduced by either an shRNAmir (clone ), or a non-silencing control were examined for mRNA and protein expression of the TA/BX648577 fusion by **a,** qRT-PCR and **b,** Western blotting



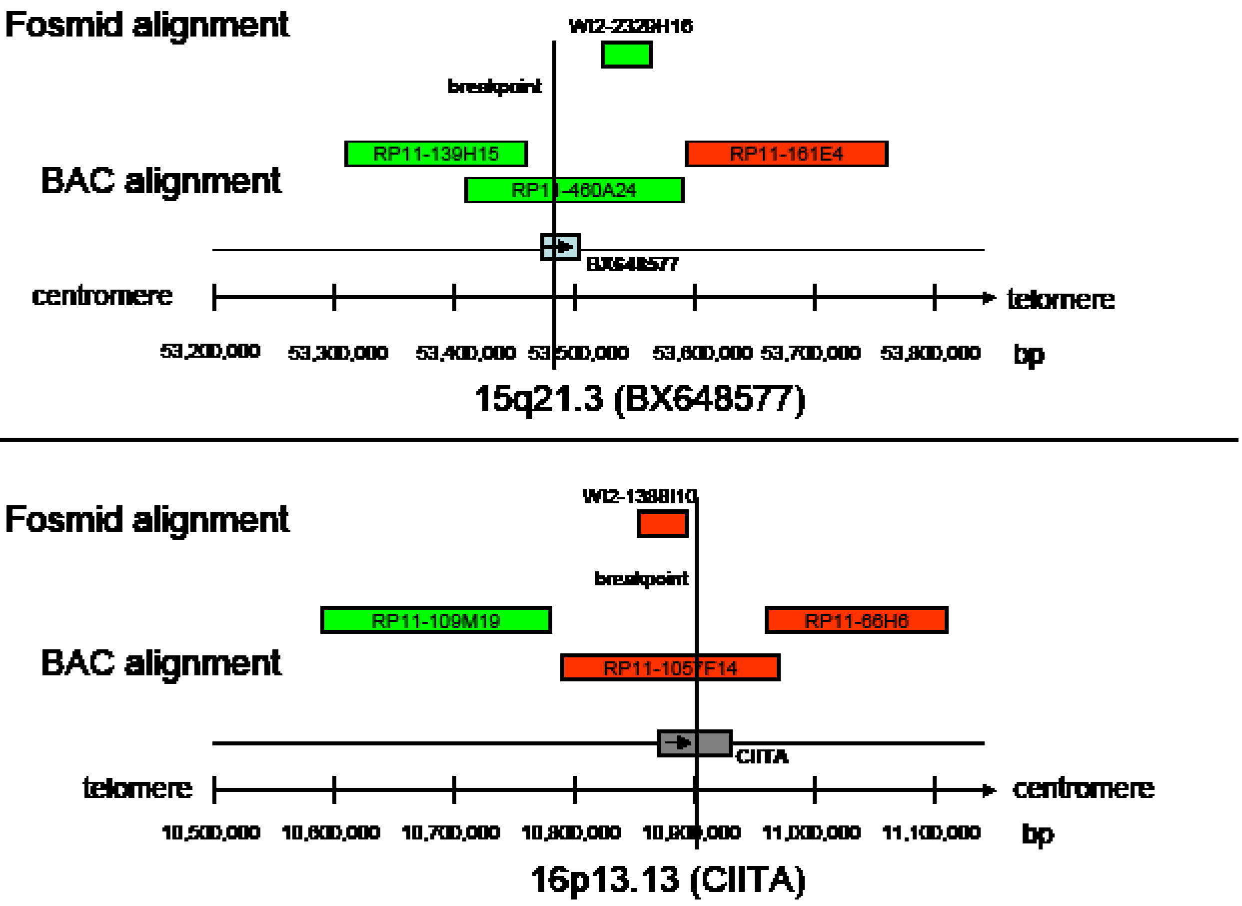
**Supplementary Figure S8:** Genomic breakpoints in the *CIITA* gene defining a 1,630bp breakpoint cluster region in intron1 based on 5 cases with CIITA rearrangements. **a,** Left panel: cHL case with unbalanced *CIITA* rearrangement in aberrant large HRS (yellow arrows) cells displaying 1 fusion signal and 3 green signals (telomere side of the breakpoint) Right panel: PMBCL case with rearrangement of one allele while the other *CIITA* allele seems intact (1 fused + 1 red + 1 green signal). **b,** BAC alignment for *CIITA* break-apart assay. Hatched box indicates location of *CIITA* intron 1 containing **c,** breakpoint cluster region defined by genomic breakpoints found in 5 PMBCL cases.



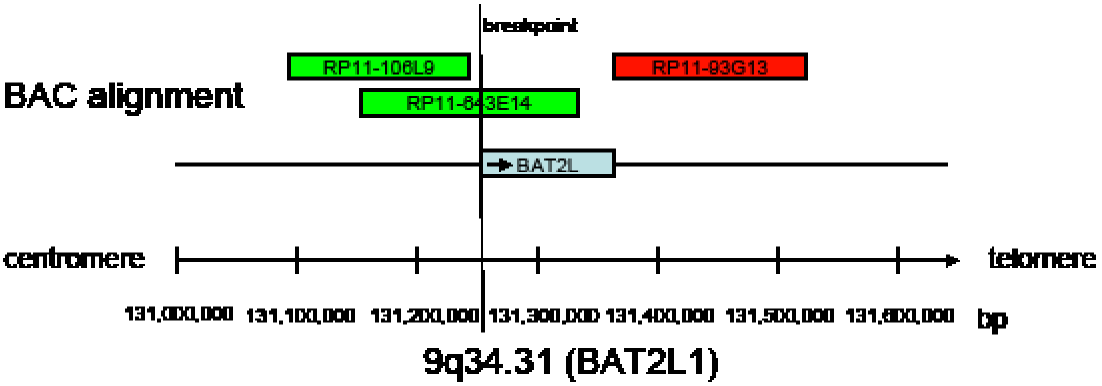
**Supplementary Figure S9: a,** Induction of PD-1 and CD69 by anti-CD3 and anti-CD28 antibodies in Jurkat T cells. **b,** Inhibition of T cell activation by PMBCL (U2940) cells but not by ABC (U2932) or GCB (SUDHL4) DLBCL cells. **c,** Forced PD1 expression on Jurkat T cells augments T cell inhibition by PMBCL cells. Jurkat T cells transduced with bicistronic PD1-GFP vector (right panel) or empty GFP vector (left panel) in mono-culture (upper panel) and in co-culture mixed with U2940 cells (ratio 1:4) (bottom panel) were stimulated with anti-CD3 and anti-CD28 for 4 h before harvesting. Shown are FACS plots of Jurkat T cells (CD-2 positive). Dot plots display the expression levels of PD1 *vs* GFP. Histograms show the expression levels of CD69 in GFP positive cells (red histograms) vs GFP negative cells (blue histograms, internal controls). Non-stimulated

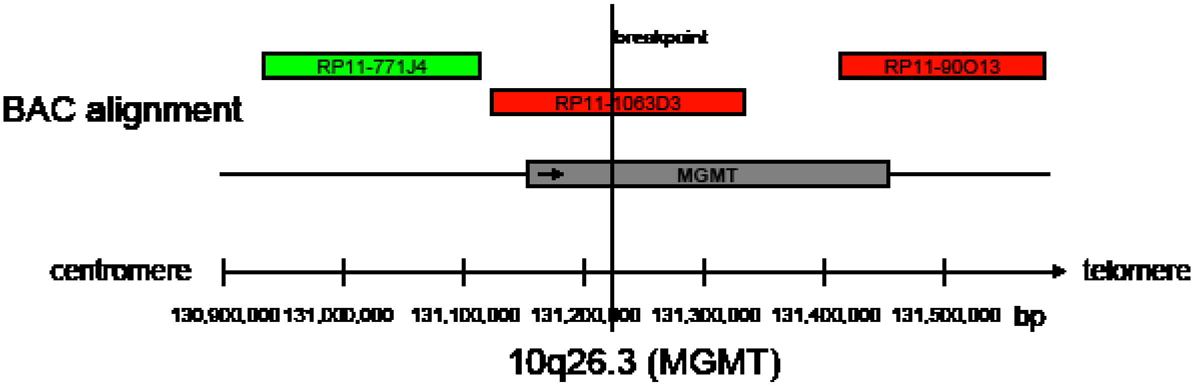
Jurkat cells served as negative controls (gray histograms). **d,** Flow cytometric analysis of intracellular cleaved PARP and active caspase 3 do not show differences between transduced and wildtype U2932 cells.

**Supplementary Figure S10a:** Probe design for FISH-validation of *CIITA-BX648577* fusion in KM-H2

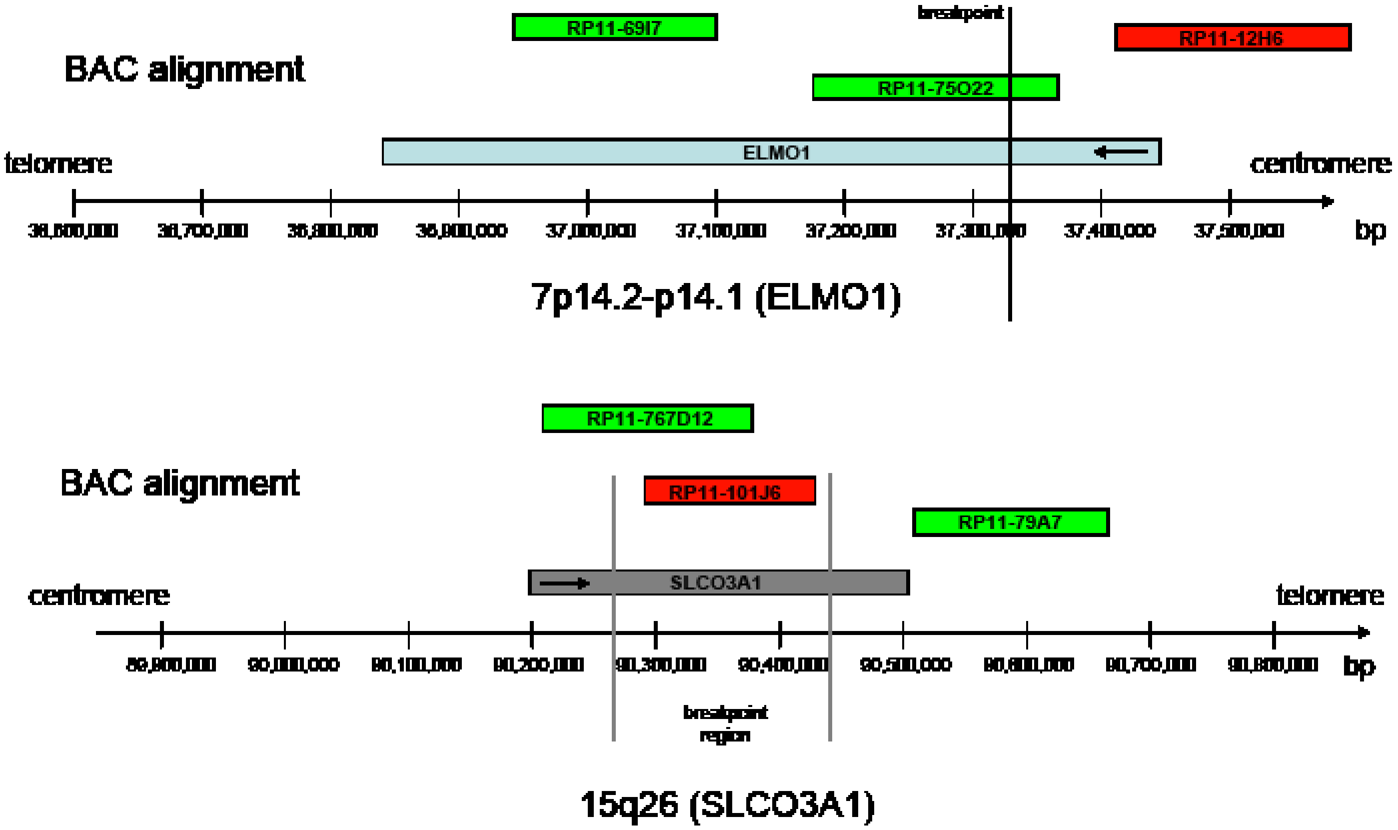


**Supplementary Figure S10b:** Probe design for FISH-validation of *BAT2L1-MGMT* fusion in KM-H2





**Supplementary figure S10c:** Probe design for FISH-validation, *ELMO1-SLCO3A1* fusion in L428



**Supplementary Figure S10:** Probe design for FISH-validation experiments. **a,** BAC and Fosmid alignments for *CIITA-BX648577* fusion and break-apart assays. Red: probes labeled in SpO Green: probes labeled in SpG. **b,** BAC alignments for *BAT2L1-MGMT* fusion and break-apart assays. **c,** BAC alignments for *ELMO1-SLCO3A1* fusion and break-apart assays.