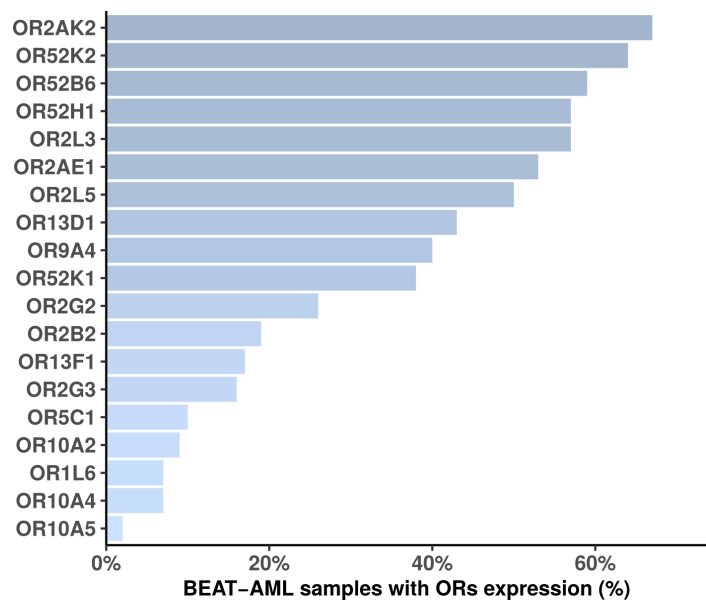


Supplementary Information

Supplementary Figures S1-S6

A)



B)

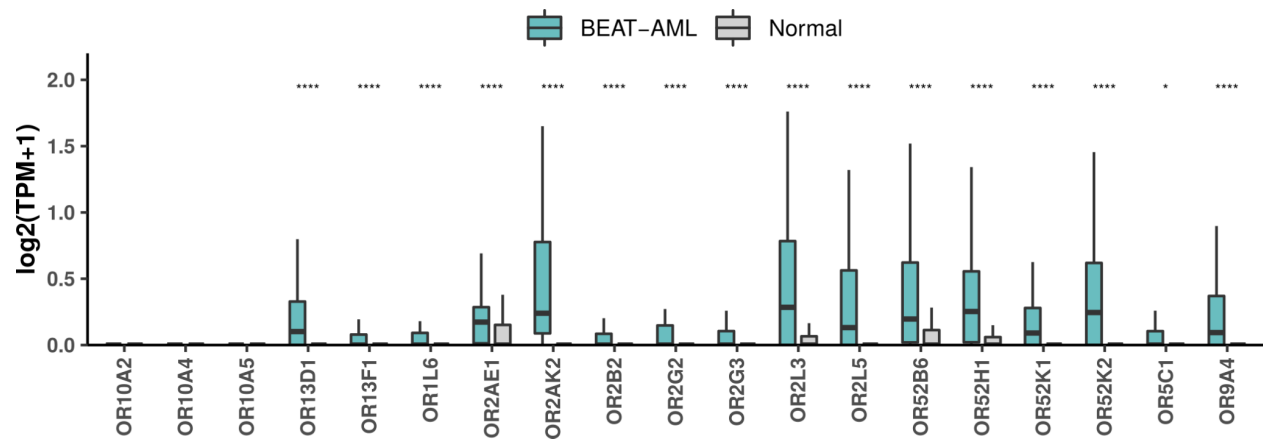


Figure S1. Expression of 19 ORs in samples from the BEAT - AML consortium. A) Percentage of AML samples showing expression of ORs. B) Boxplot showing expression of 19 ORs in AML or Normal samples. "****": p-value < 0.01; "*****": p-value < 0.00001;

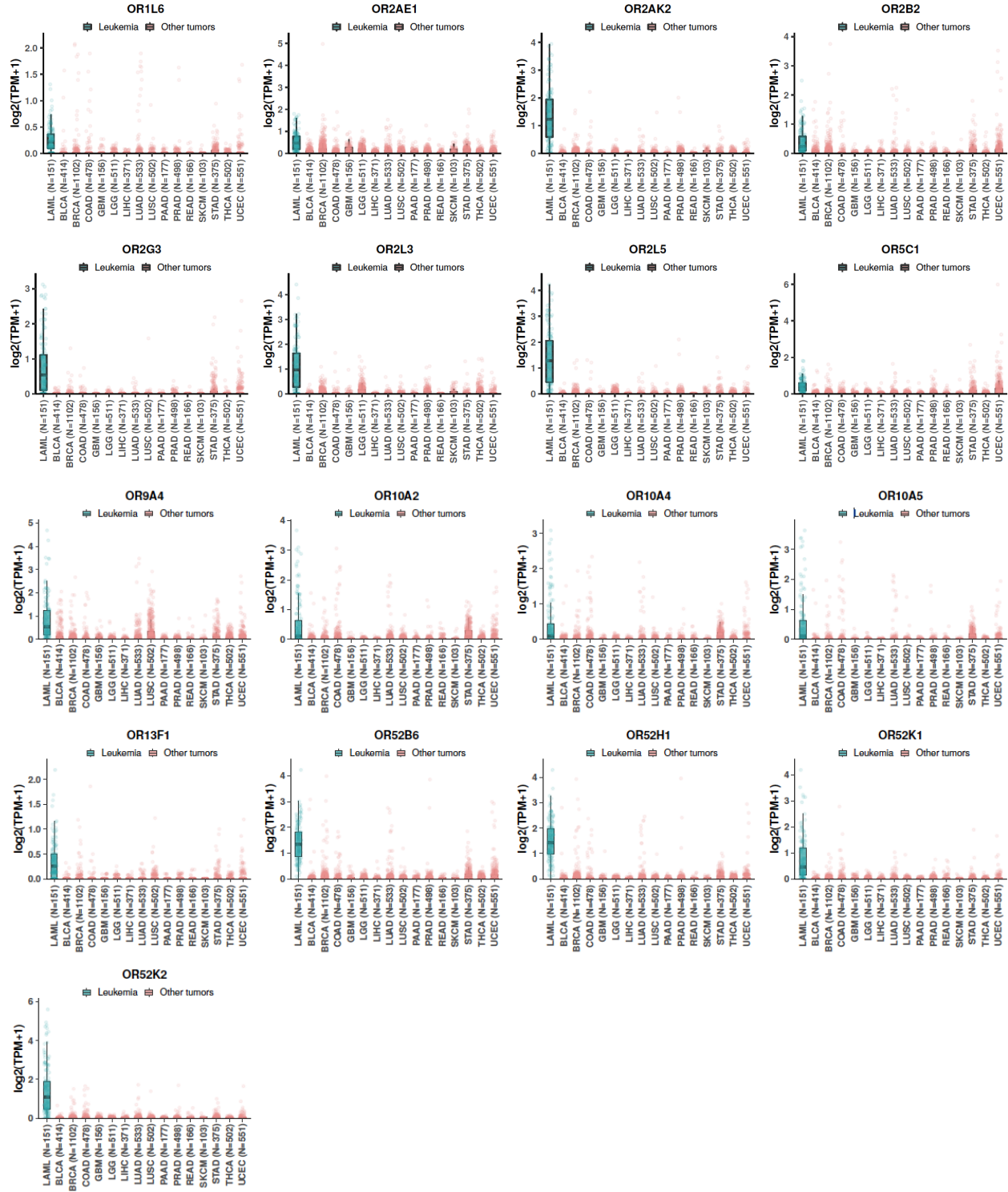
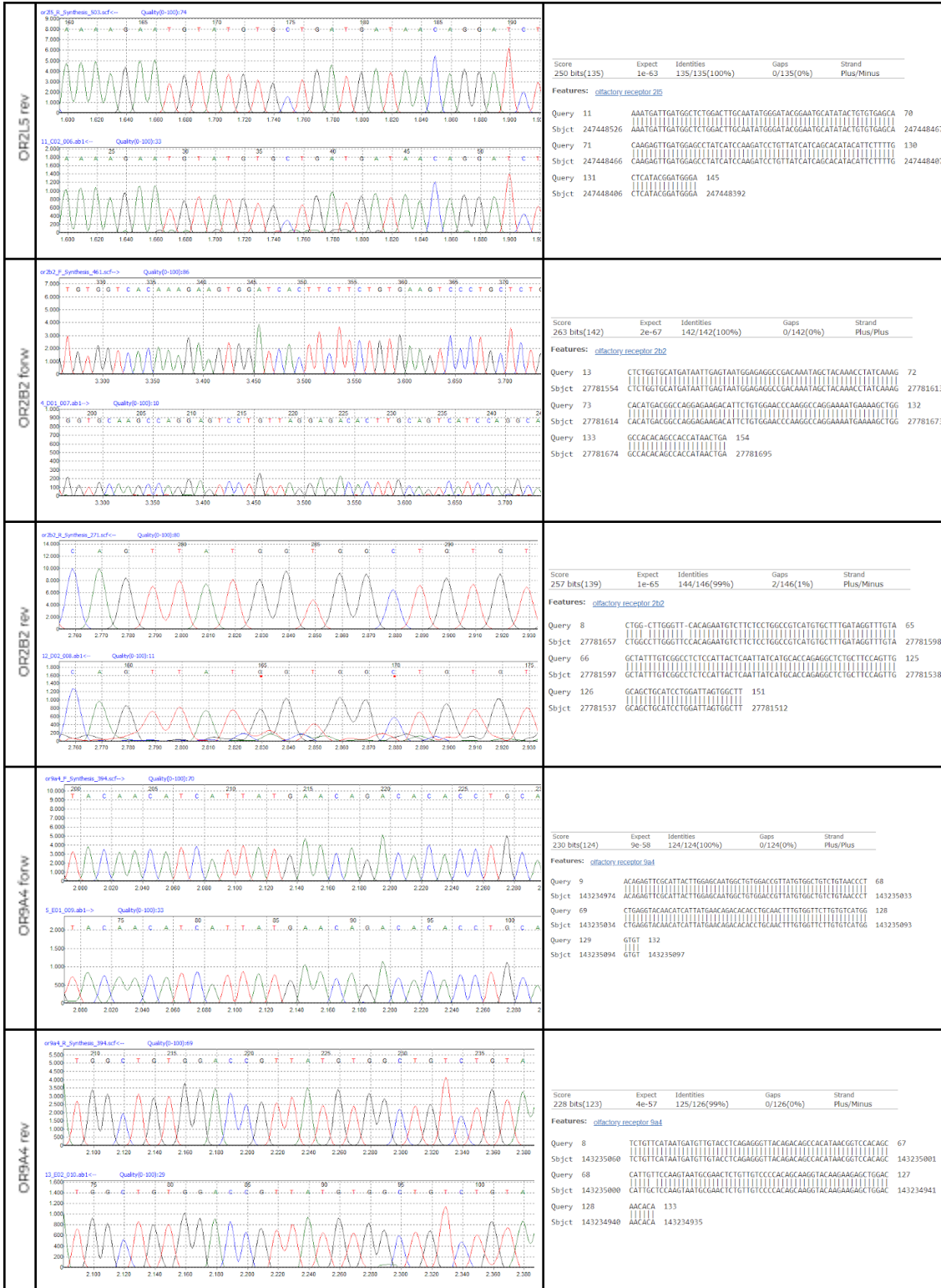
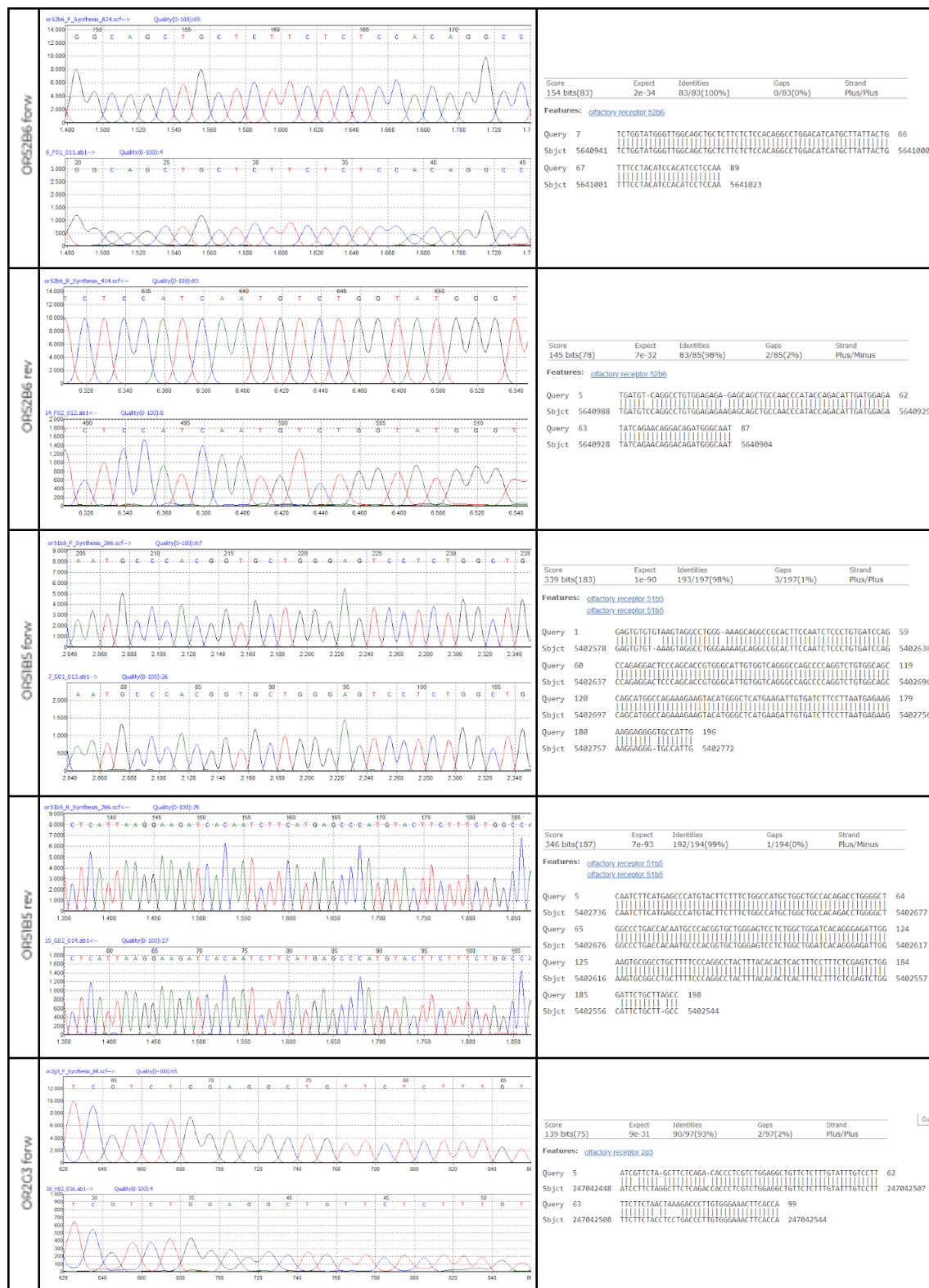
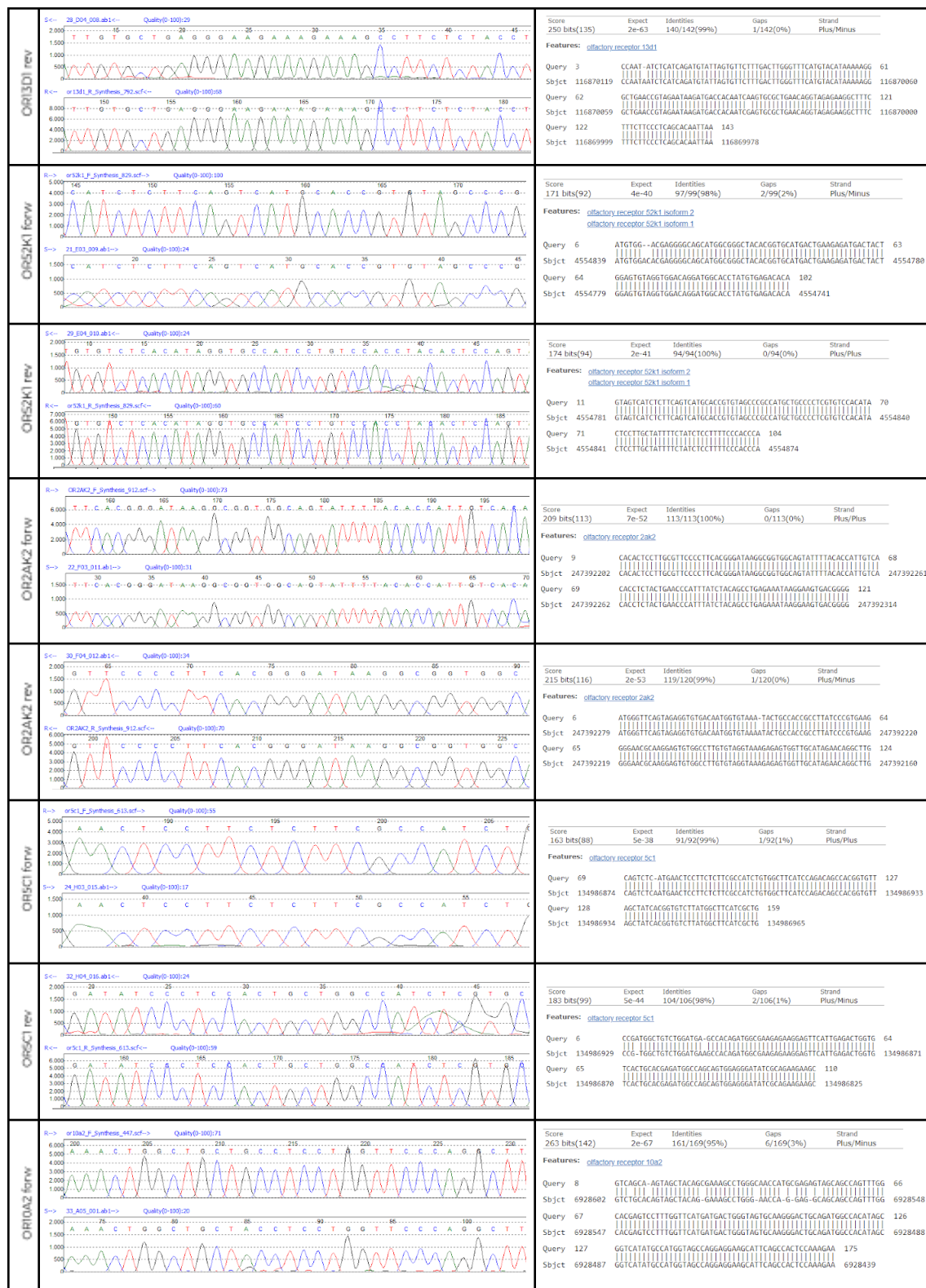


Figure S2. Expression of 19 individual ORs in AML and 15 other cancers from the TCGA. Expression unit is shown in $\log_2(\text{TPM}+1)$. Only tumors with RNAseq data were used.





OR2G3 rev	<p>R-> or2g3_F_synthes_88.acf-- Quality(0-100):62</p> <p>S17_A03_015.ab1-- Quality(0-100):24</p>	<table><tr><th>Score</th><th>Expect</th><th>Identities</th><th>Gaps</th><th>Strand</th></tr><tr><td>89.8 bits(48)</td><td>1e-15</td><td>67/75(89%)</td><td>5/75(6%)</td><td>Plus/Minus</td></tr></table> <p>Features: olfactory receptor 293</p> <p>Query 10 ATAC-AAGAG-ACAGCCT-CAGACGAGGCTGCTGAGAAGCTAGAGGATGAA-TCGA 65 Sbjct 247042499 ATACAGAGAGACAGCCTCCAGACGAGGCTGCTGAGAAGCTAGAGGATGAAATCA 247042440</p> <p>Query 66 CTACTGAGACTCTCA 80 Sbjct 247042439 TTAGGGA-ACCTCA 247042426</p>	Score	Expect	Identities	Gaps	Strand	89.8 bits(48)	1e-15	67/75(89%)	5/75(6%)	Plus/Minus
Score	Expect	Identities	Gaps	Strand								
89.8 bits(48)	1e-15	67/75(89%)	5/75(6%)	Plus/Minus								
OR52H1 forw	<p>R-> or52h1_F_synthes_065.acf-- Quality(0-100):57</p> <p>S17_A03_001.ab1-- Quality(0-100):25</p>	<table><tr><th>Score</th><th>Expect</th><th>Identities</th><th>Gaps</th><th>Strand</th></tr><tr><td>152 bits(82)</td><td>1e-34</td><td>84/85(99%)</td><td>0/85(0%)</td><td>Plus/Plus</td></tr></table> <p>Features: olfactory receptor 52h1</p> <p>Query 1 ACCTTATCTGATCTGCTGGTCTTCACTCCGTAACCATGGGTTGAGTCAGGTGGG 60 Sbjct 5603967 ACCTTATCTGATCTGCTGGTCTTCACTCCGTAACCATGGGTTGAGTCAGGTGGG 5604026</p> <p>Query 61 ATACAATGTAGAGATTGGCAACA 85 Sbjct 5604027 ATACAATGTAGAGATTGGCAACA 5604051</p>	Score	Expect	Identities	Gaps	Strand	152 bits(82)	1e-34	84/85(99%)	0/85(0%)	Plus/Plus
Score	Expect	Identities	Gaps	Strand								
152 bits(82)	1e-34	84/85(99%)	0/85(0%)	Plus/Plus								
OR52H1 rev	<p>S17_A04_002.ab1-- Quality(0-100):24</p> <p>R-> or52h1_R_synthes_065.acf-- Quality(0-100):57</p>	<table><tr><th>Score</th><th>Expect</th><th>Identities</th><th>Gaps</th><th>Strand</th></tr><tr><td>65.8 bits(35)</td><td>2e-08</td><td>45/49(92%)</td><td>3/49(6%)</td><td>Plus/Minus</td></tr></table> <p>Features: olfactory receptor 52h1</p> <p>Query 5 CCATGG-ATACGGAGTGAAGACCAAGCAGATCAGAGATAAG-T-ATACT 50 Sbjct 5604009 CCATGGTTTACGGAGTGAAGACCAAGCAGATCAGAGATAAGTTATACT 5603961</p>	Score	Expect	Identities	Gaps	Strand	65.8 bits(35)	2e-08	45/49(92%)	3/49(6%)	Plus/Minus
Score	Expect	Identities	Gaps	Strand								
65.8 bits(35)	2e-08	45/49(92%)	3/49(6%)	Plus/Minus								
OR52K2 forw	<p>R-> or52k2_F_synthes_87.acf-- Quality(0-100):94</p> <p>S17_A03_003.ab1-- Quality(0-100):27</p>	<table><tr><th>Score</th><th>Expect</th><th>Identities</th><th>Gaps</th><th>Strand</th></tr><tr><td>154 bits(83)</td><td>4e-35</td><td>83/83(100%)</td><td>0/83(0%)</td><td>Plus/Plus</td></tr></table> <p>Features: olfactory receptor 52k2</p> <p>Query 2 TGCTTTCTTGGTGGGATTCAGGCTTGGACACCTGCACATCTGGATCTCCATCCC 61 Sbjct 4449375 TGCTTTCTTGGTGGGATTCAGGCTTGGACACCTGCACATCTGGATCTCCATCCC 4449434</p> <p>Query 62 TTTCTGCTTAGCATATACATCG 84 Sbjct 4449435 TTTCTGCTTAGCATATACATCG 4449457</p>	Score	Expect	Identities	Gaps	Strand	154 bits(83)	4e-35	83/83(100%)	0/83(0%)	Plus/Plus
Score	Expect	Identities	Gaps	Strand								
154 bits(83)	4e-35	83/83(100%)	0/83(0%)	Plus/Plus								
OR52K2 rev	<p>S17_A04_004.ab1-- Quality(0-100):22</p> <p>R-> or52k2_R_synthes_87.acf-- Quality(0-100):36</p>	<table><tr><th>Score</th><th>Expect</th><th>Identities</th><th>Gaps</th><th>Strand</th></tr><tr><td>111 bits(60)</td><td>2e-22</td><td>63/64(98%)</td><td>1/64(1%)</td><td>Plus/Minus</td></tr></table> <p>Features: olfactory receptor 52k2</p> <p>Query 7 GATGTGAGGTGTTTCAGGCTTGA-TCCTCCACCAAGAGGAGTGTGATGTGTTAA 65 Sbjct 4514541 GATGTGAGGTGTTTCAGGCTTGAATCCCTCCACCAAGAGGAGTGTGATGTGTTAA 4514482</p> <p>Query 66 GGTG 69 Sbjct 4514481 GGTG 4514478</p>	Score	Expect	Identities	Gaps	Strand	111 bits(60)	2e-22	63/64(98%)	1/64(1%)	Plus/Minus
Score	Expect	Identities	Gaps	Strand								
111 bits(60)	2e-22	63/64(98%)	1/64(1%)	Plus/Minus								
OR2G2 forw	<p>R-> or2g2_F_synthes_108.acf-- Quality(0-100):94</p> <p>S17_A03_005.ab1-- Quality(0-100):20</p>	<table><tr><th>Score</th><th>Expect</th><th>Identities</th><th>Gaps</th><th>Strand</th></tr><tr><td>169 bits(91)</td><td>1e-39</td><td>90/101(97%)</td><td>1/101(0%)</td><td>Plus/Plus</td></tr></table> <p>Features: olfactory receptor 292</p> <p>Query 9 GGATGACTCAGTGG-ATAGCCACACCTTGTACAGTCCACCTACCCCGAGCTGCC 67 Sbjct 247025652 GGATGACTCAGTGGATAGCCACACCTTGTACAGTCCACCTACCCCGAGCTGCC 247025711</p> <p>Query 68 CTCTGTGGGATGCCAGATGATCATCTCTGGAGG 108 Sbjct 247025712 CTCTGTGGGATGCCAGATGATCATCTCTGGAGG 247025752</p>	Score	Expect	Identities	Gaps	Strand	169 bits(91)	1e-39	90/101(97%)	1/101(0%)	Plus/Plus
Score	Expect	Identities	Gaps	Strand								
169 bits(91)	1e-39	90/101(97%)	1/101(0%)	Plus/Plus								
OR2G2 rev	<p>S17_A04_006.ab1-- Quality(0-100):39</p> <p>R-> or2g2_R_synthes_108.acf-- Quality(0-100):97</p>	<table><tr><th>Score</th><th>Expect</th><th>Identities</th><th>Gaps</th><th>Strand</th></tr><tr><td>167 bits(90)</td><td>3e-38</td><td>92/93(99%)</td><td>0/93(0%)</td><td>Plus/Minus</td></tr></table> <p>Features: olfactory receptor 292</p> <p>Query 12 GCAGCTGCGGGTGAGGGTGAGTGTACAGGCTGGCTATTCCACTGAGCATGCCA 71 Sbjct 247588867 GCAGCTGCGGGTGAGGGTGAGTGTACAGGCTGGCTATTCCACTGAGCATGCCA 247588808</p> <p>Query 72 TAGATCCAGGCGATGACAGATGATGCA 104 Sbjct 247588807 TAGATCCAGGCGATGACAGATGATGCA 247588775</p>	Score	Expect	Identities	Gaps	Strand	167 bits(90)	3e-38	92/93(99%)	0/93(0%)	Plus/Minus
Score	Expect	Identities	Gaps	Strand								
167 bits(90)	3e-38	92/93(99%)	0/93(0%)	Plus/Minus								
OR1301 forw	<p>R-> or1301_F_synthes_92.acf-- Quality(0-100):95</p> <p>S17_A03_007.ab1-- Quality(0-100):26</p>	<table><tr><th>Score</th><th>Expect</th><th>Identities</th><th>Gaps</th><th>Strand</th></tr><tr><td>241 bits(130)</td><td>8e-61</td><td>136/139(98%)</td><td>0/139(0%)</td><td>Plus/Plus</td></tr></table> <p>Features: olfactory receptor 1301</p> <p>Query 7 CTGATAGCGCACTGATTCGCTACCTTATTTCTAGCGTCCAGCCCTTTTATGACAT 66 Sbjct 116870015 CTGATAGCGCACTGATTCGCTACCTTATTTCTAGCGTCCAGCCCTTTTATGACAT 116870074</p> <p>Query 67 GAAACCAAGTCAAGAAACATATACATCTGATGATTTATGGGCTGCTTATGGAGT 126 Sbjct 116870075 GAAACCAAGTCAAGAAACATATACATCTGATGATTTATGGGCTGCTTATGGAGT 116870134</p> <p>Query 127 GGTAAAGCCAAATGTTAAAT 145 Sbjct 116870135 GGTAAAGCCAAATGTTAAAT 116870153</p>	Score	Expect	Identities	Gaps	Strand	241 bits(130)	8e-61	136/139(98%)	0/139(0%)	Plus/Plus
Score	Expect	Identities	Gaps	Strand								
241 bits(130)	8e-61	136/139(98%)	0/139(0%)	Plus/Plus								



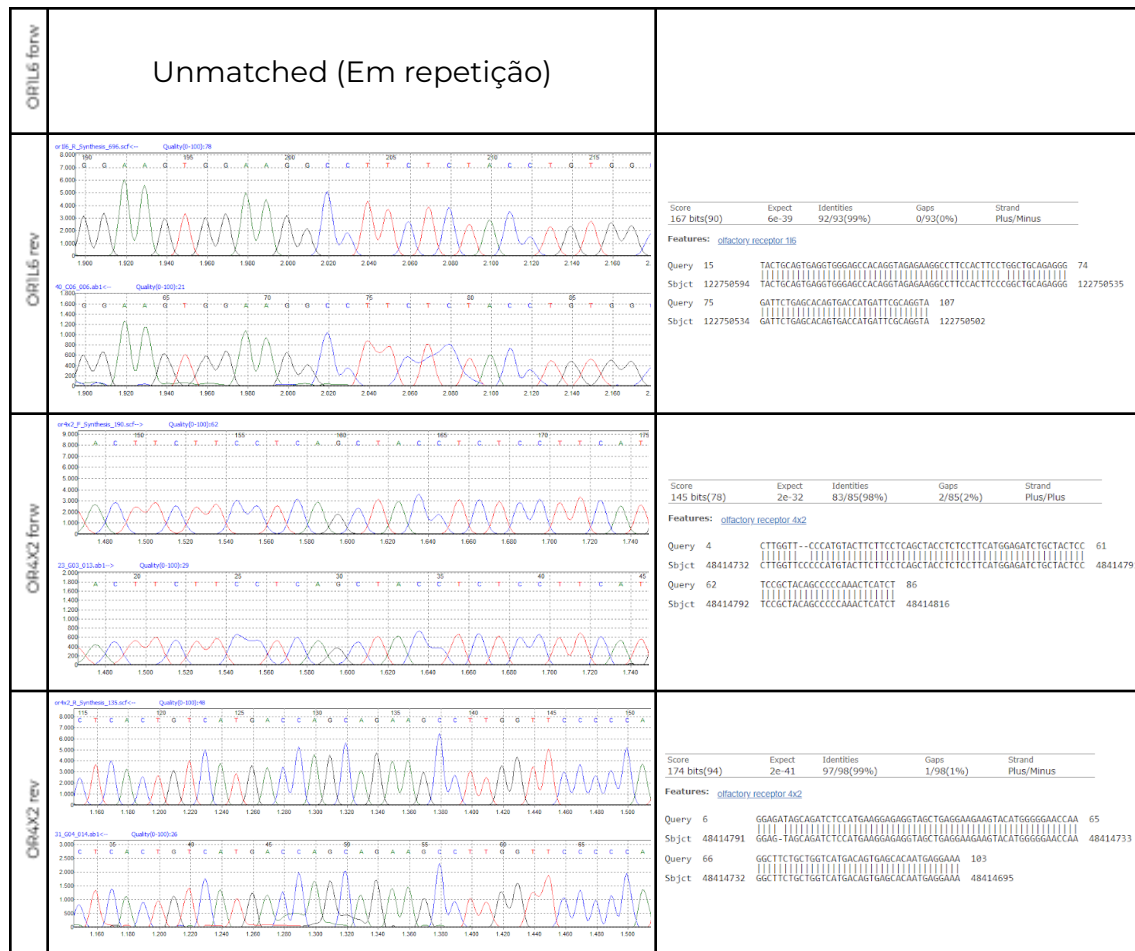
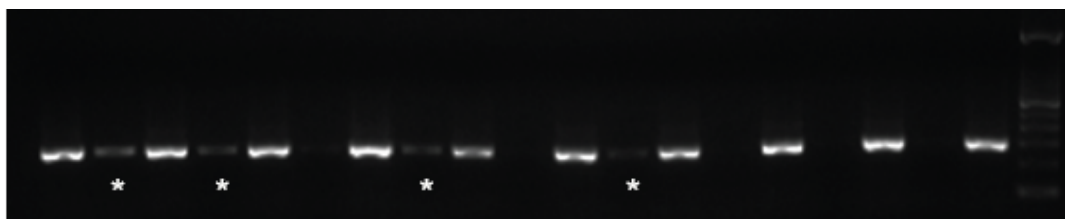


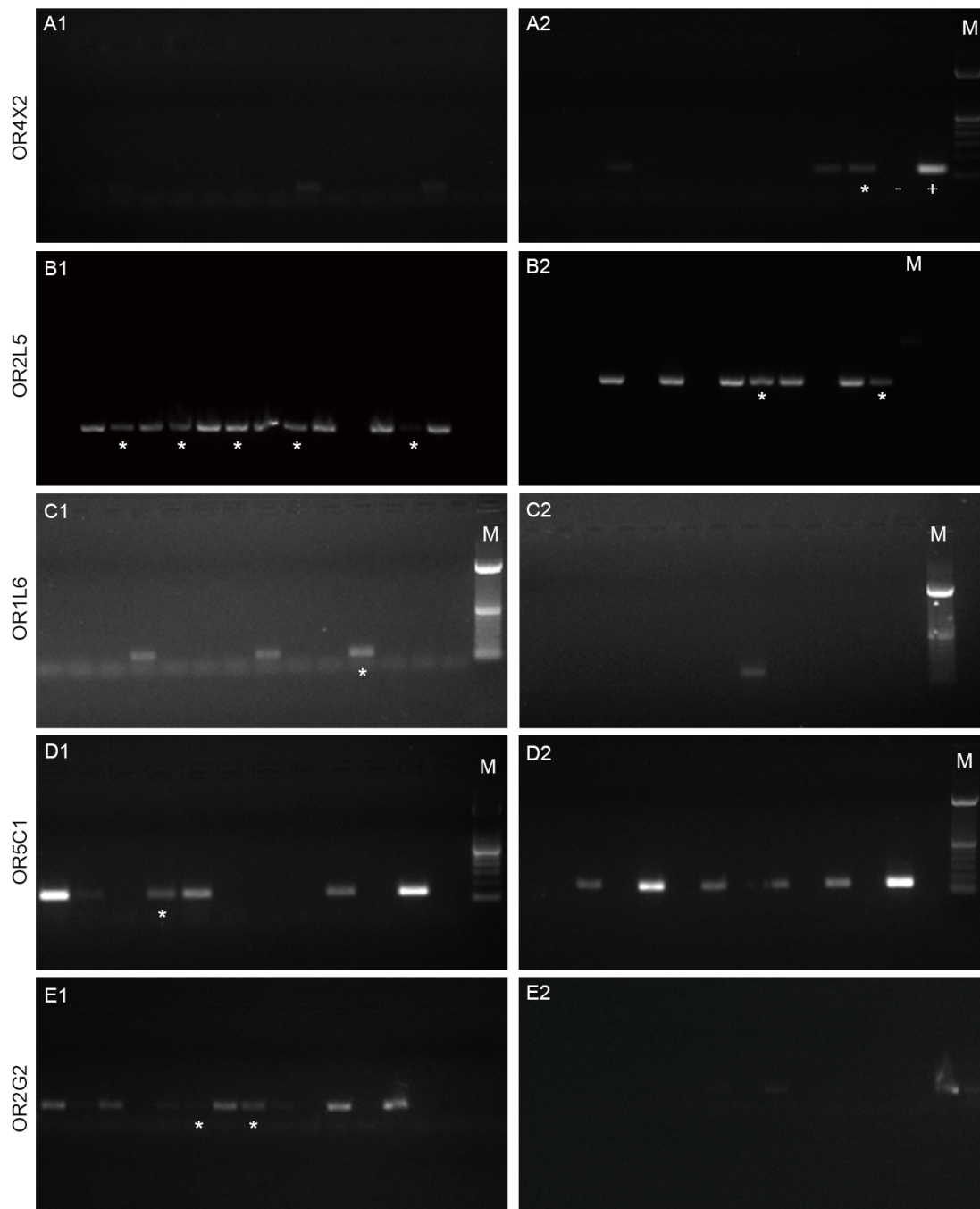
Figure S3. Confirmation of specificity of ORs PCRs. Since ORs have 40-90% homology with each other, all OR PCRs were double checked with forward and reverse sequencing. A healthy donor genomic DNA was used to amplify all OR PCRs. The first column shows the electropherogram aligned to the corresponding reference sequence in Mutation Surveyor Software (Soft Genetics), following, the sequence was aligned to the human genome with the BLAST tool (NCBI). The majority of sequences aligned over 95% with the corresponding targeted OR in at least forward or reverse sequencing, with exception of OR13F1, which showed 92% of alignment. As expected, in some BLAST analysis, the corresponding OR was not the only target listed, however, it was the target with highest score and longer and highest identity (bp, %).

ACTB



AML Patients at diagnostic

Healthy individuals



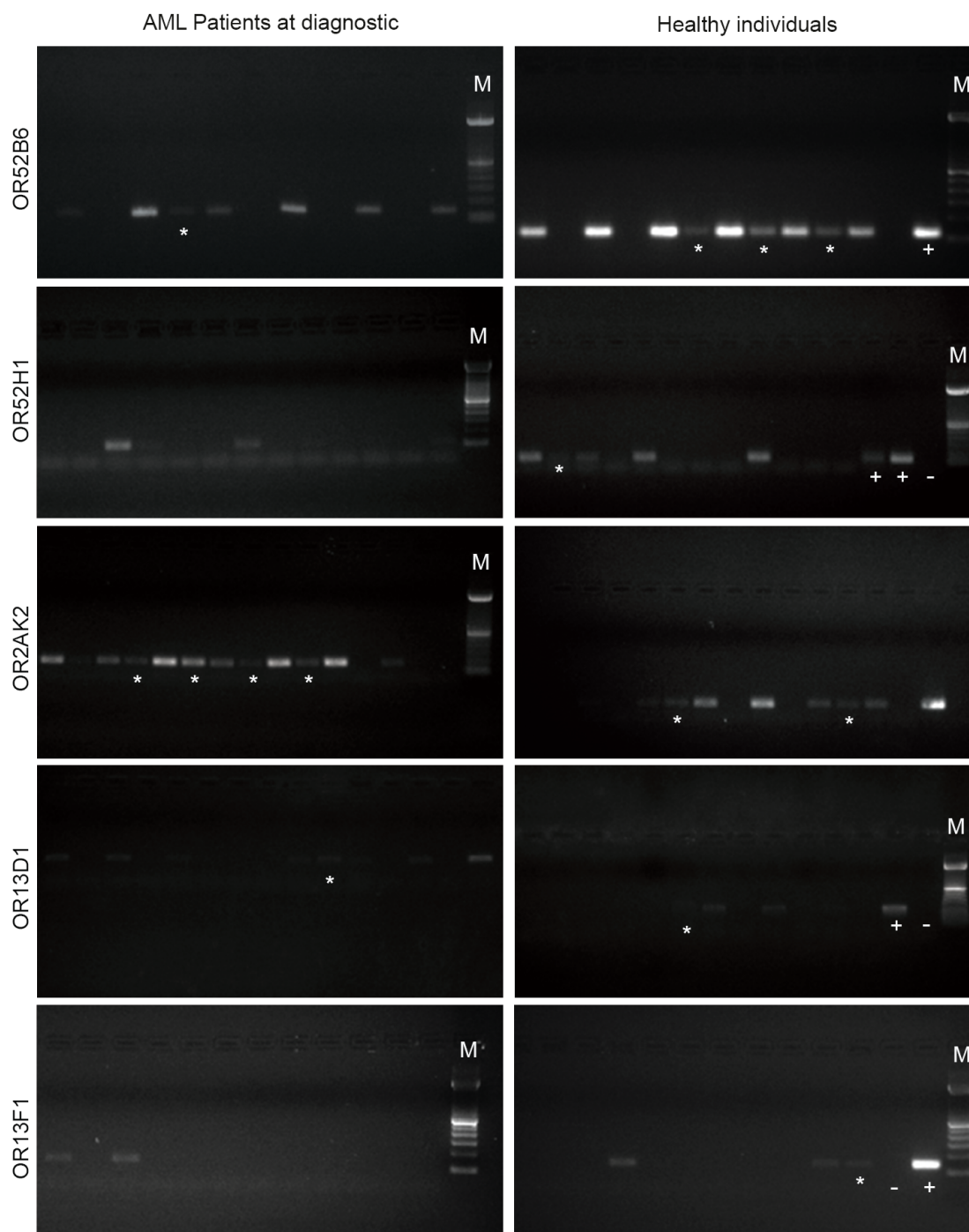


Figure S4. Expression of ORs in AML patients or healthy donors samples.

PCR products subjected to electrophoresis in agarose gel 1.5% stained with Ethidium Bromide. PCR were performed in patient or donor cDNA

synthesized with and without RT enzyme, disposed in this sequence in gel for ACTB and ORs PCR. All samples were pre-selected with PCR for ACTB (295 bp), each sample with amplification in cDNA synthesized without RT enzyme (marked by an asterisk), were removed from our cohort. However, despite this selection, some cDNA without RT were positive for one or more OR PCR and were also removed from our cohort (marked with asterisk). PCR products for OR4X2 (131 bp, A), found not expressed in AML or donor samples; OR2L5 (180 bp, B); OR1L6 (142 bp, C); OR5C1 (140 bp; D); OR2G2 (136bp; E); OR52B6 (120 bp; F); OR52H1 (114 bp; G); OR2AK2 (155 bp; H); OR13D1 (171 bp; I); OR13F1 (150 bp; J). All PCRs were confirmed in at least two independent experiments.

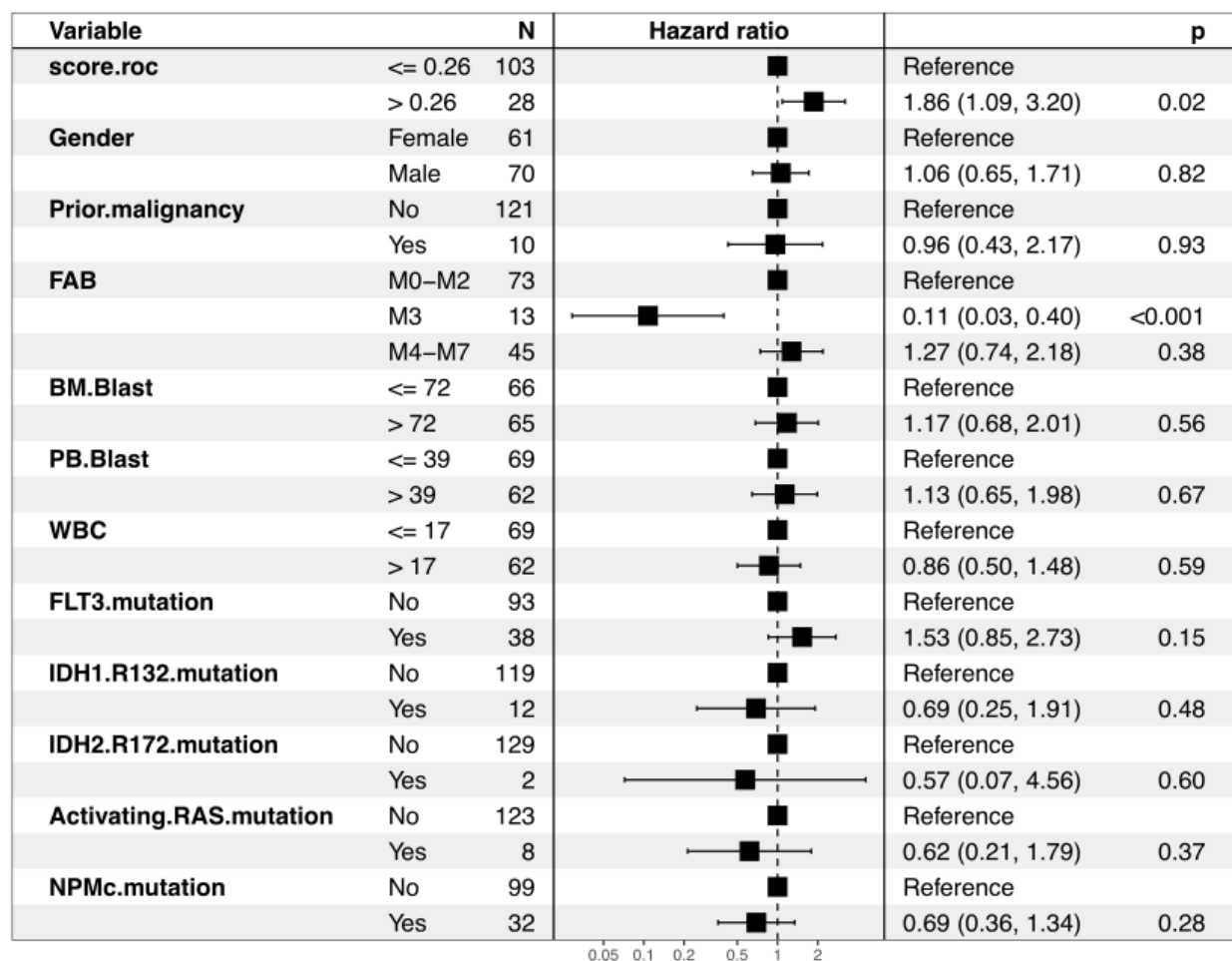


Figure S5. Multivariate Cox survival analysis of the OR expression signature in AML samples from TCGA.

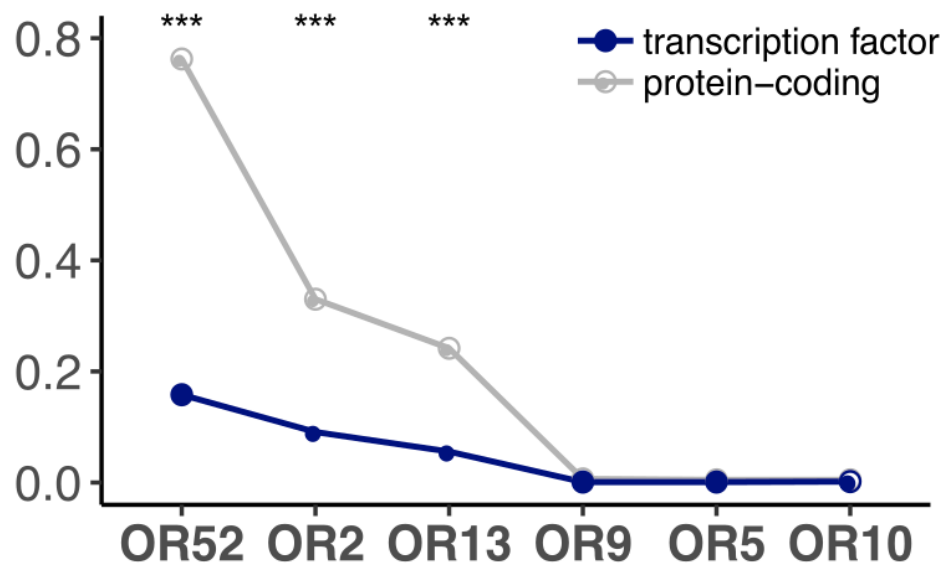


Figure S6. Enrichment of transcription factors coexpressed with ORs from subfamilies OR2, OR13 and OR52.