

Effects of RAGE Deletion on the Cardiac Transcriptome during Aging

Francesco Scavello ^{1,†}, Luca Piacentini ^{2,†}, Stefania Castiglione ¹, Filippo Zeni ¹, Federica Macrì ¹, Manuel Casaburo ³, Maria Cristina Vinci ⁴, Gualtiero I. Colombo ^{5,*} and Angela Raucchi ^{1,3,*}

¹ Unit of Experimental Cardio-Oncology and Cardiovascular Aging, Centro Cardiologico Monzino IRCCS, 20138 Milan, Italy

² Bioinformatics and Artificial Intelligence Facility, Centro Cardiologico Monzino IRCCS, 20138 Milan, Italy

³ Animal Facility, Centro Cardiologico Monzino IRCCS, 20138 Milan, Italy

⁴ Vascular Biology and Regenerative Medicine Unit, Centro Cardiologico Monzino IRCCS, 20138 Milan, Italy

⁵ Unit of Immunology and Functional Genomics, Centro Cardiologico Monzino IRCCS, 20138 Milan, Italy

* Correspondence: gualtiero.colombo@cardiologicomonzino.it (G.I.C.); araucchi@ccfm.it (A.R.);
Tel.: +39-025-800-2464 (G.I.C.); +39-025-800-2802 (A.R.); Fax: +39-025-800-2342 (G.I.C. & A.R.)

† These authors contributed equally to this work.

Table S3. Sequences of mouse forward and reverse primers used for RT-qPCR

Gene	Forward	Reverse
<i>Adgrf5</i>	5'-GGAAGAACAGGACATCCGCTCA-3'	5'-CCAGGAGTTCAAGGCAGACTTG-3'
<i>Igtp</i>	5'-AGCCCGTCTTTTCACGACTT-3'	5'-CTCCAGGTTGGCAGTGTTCAT-3'
<i>Irgm2</i>	5'-GGCAGTTGAGTCACCTGAGG-3'	5'-CCCCTTCTTTCACGGCAGT-3'
<i>Ifit3</i>	5'-CGAGCAAAAATGTGCTTTGA-3'	5'-GCTCCCCTTCAGCTTCTTCT-3'
<i>P2ry1</i>	5'-CCTGCTATGACACCACGTCCAA-3'	5'-AGCGGAGAGTTGTCCAGGTCAT-3'
<i>Rgs4</i>	5'-CTGAAGTCGGAATACAGCGAGG-3'	5'-CTGGTGCAAGAGTCCAGGTTCA-3'
<i>Hmgcs2</i>	5'-TGCTATGCAGCCTACCGCAAGA-3'	5'-GCCAGGGATTTCTGGACCATCT-3'
<i>Rps24</i>	5'-TGGTGGCAAGACCACTGGCTTT-3'	5'-CTGTTCTTGCGTTCCTTTCGCTG-3'
<i>C4a</i>	5'-GGAGAGTGGAACCTGTAGACAG-3'	5'-CACTCGAACACGAGTTGGCTTG-3'
<i>Fitm2</i>	5'-TGCATGAGGTGAAGACGGAc-3'	5'-AGTGCCTTGAGGCATTGGG-3'
<i>Hprt</i>	5'-GGAGCGGTAGCACCTCCT-3'	5'-CCAAATCCTCGGCATAATGA-3'
<i>Ldha</i>	5'-AGACAAACTCAAGGCGGAGA-3'	5'-CAGCTTGCAGTGTGGACTGT-3'

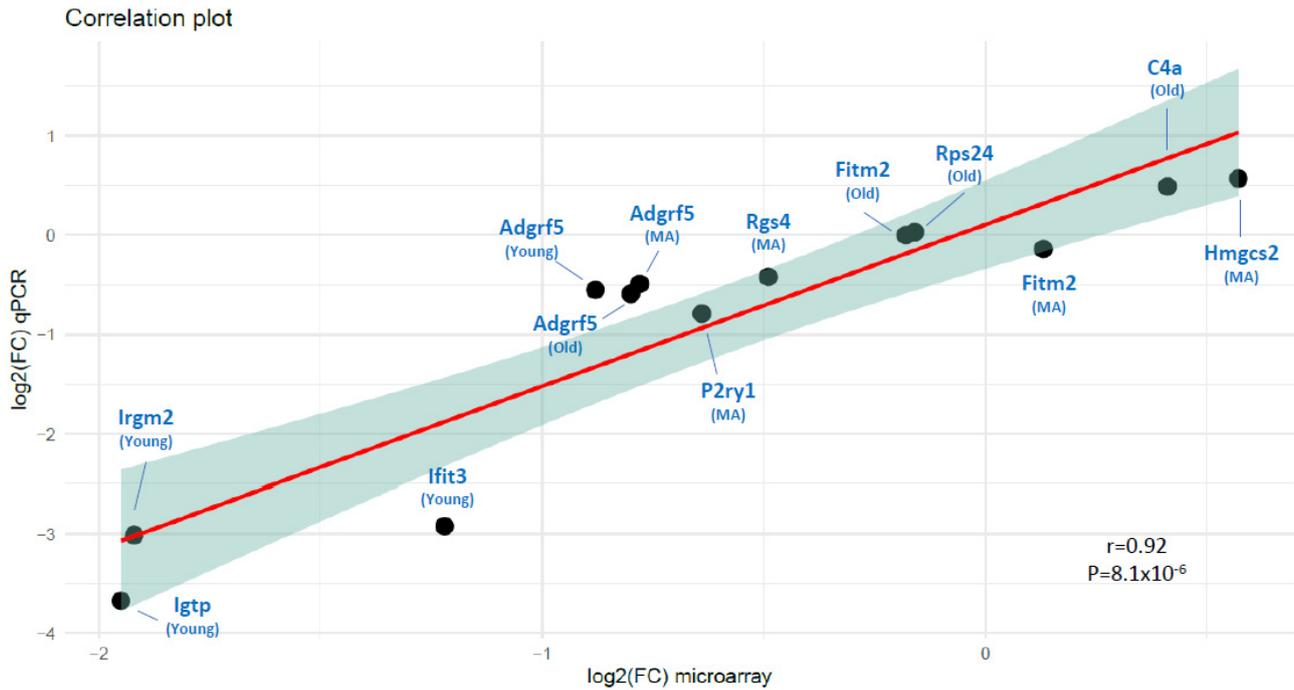


Figure S1. Correlation plot. Technical validation by RT-qPCR of 10 selected genes (*Igtp*, *Irgm2*, *Ifit3*, *Adgrf5*, *P2ry1*, *Rgs4*, *Fitm2*, *Rps24*, *C4a*, and *Hmgcs2*) differentially expressed in at least one of the comparisons between *Rage*^{-/-} vs. WT in Young, MA or Old mice (*cf.* in brackets). Pearson's correlation coefficient (*r*) was computed to assess the degree of association between the log₂ mean fold differences (log₂FC) of these genes tested by microarray (x-axis) and RT-qPCR (y-axis). The trendline is colored in red whereas the 95% confidence interval of the trendline is depicted in light green.