

Supplementary Data

A Gene Expression Pattern in Blood for the Early Detection of Alzheimer's Disease

Birgitte Boonstra Booi^{a,1}, Torbjørn Lindahl^a, Peter Wetterberg^a, Nina Voss Skaane^b, Solve Sæbø^c, Guri Feten^c, Phil D. Rye^{a,2}, Lena Iren Kristiansen^a, Nina Hagen^a, Marianne Jensen^a, Ken Bårdsen^a, Bengt Winblad^d, Praveen Sharma^a and Anders Lönneborg^{a,*}

^a*DiaGenic ASA, Grenseveien, Oslo, Norway*

^b*Memory Clinic, Department of Geriatrics, Medical Division, Ullevål University Hospital, Oslo, Norway*

^c*Department of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, Ås, Norway*

^d*Department of Neurobiology, Care Sciences and Society, Karolinska Institutet Alzheimer Disease Research Center, Huddinge, Sweden*

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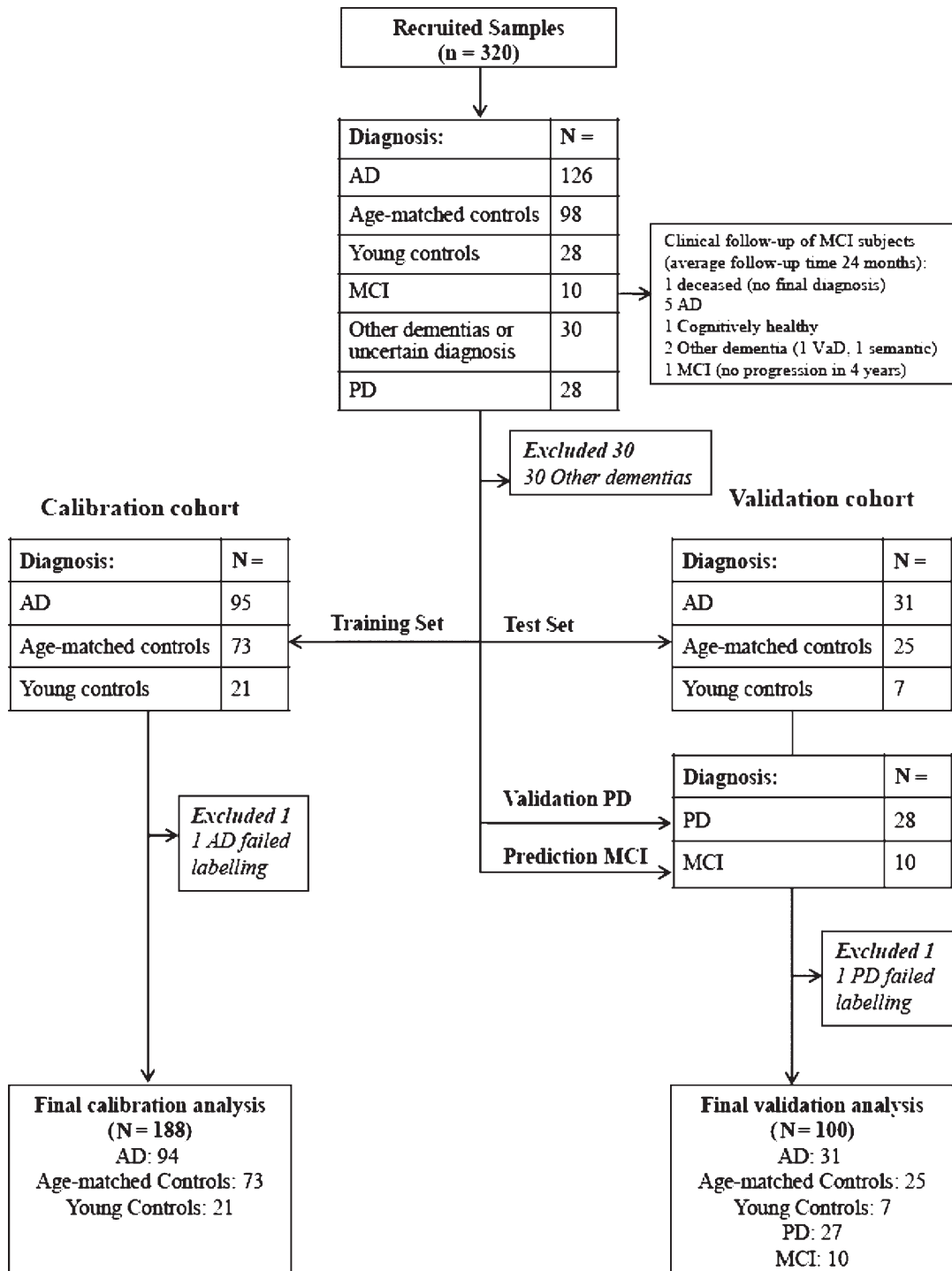
The study flow diagram is given in Figure SI-1. Figures SI-2A-G shows quality checks performed on the microarray data and Figure SI-3 shows the

classification error as a function of number of PLS components for different models.

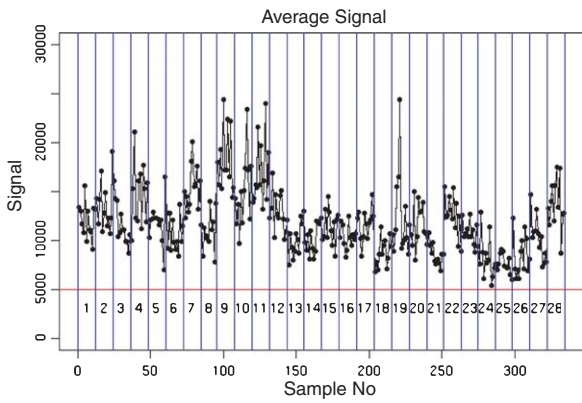
¹ Present address: Birgitte Boonstra Booi, Clavis Pharma ASA, Oslo, Norway.

² Present address: Phil D. Rye, GE Healthcare Europe GmbH, Oslo, Norway.

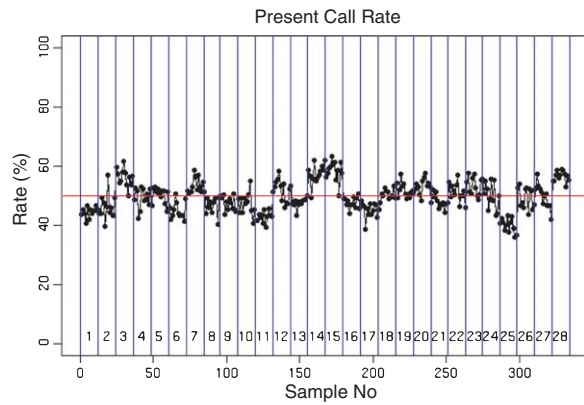
*Correspondence to: Dr. A. Lönneborg, DiaGenic ASA, Grenseveien 92, 0663 Oslo, Norway. E-mail: anders.lonneborg@diagenic.com.



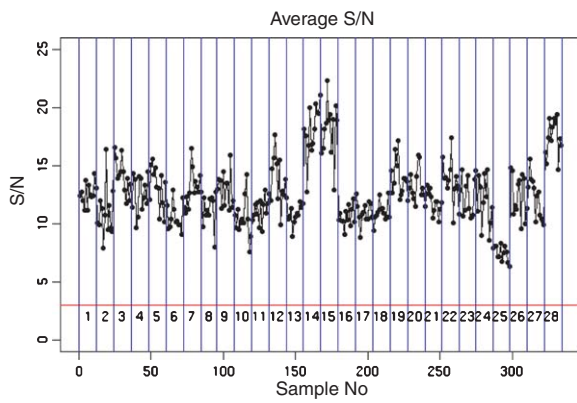
Supplementary Figure S1. Study flow diagram.



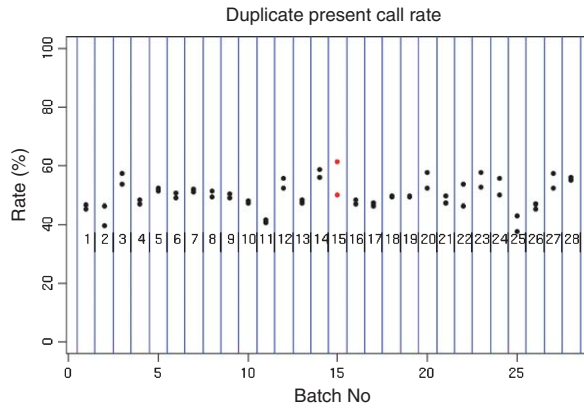
Supplementary Figure S2A. Microarray data quality control. Average signal for all samples. Red line marks minimum criteria and numbers below show batch number.



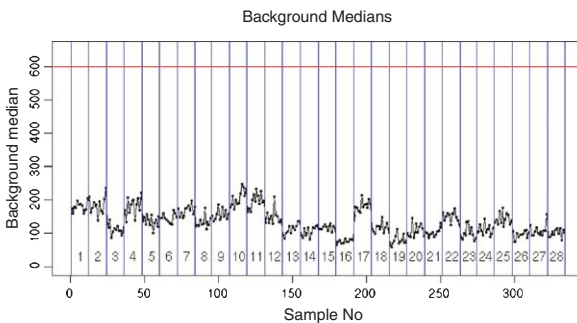
Supplementary Figure S2D. Present call rate per sample. Red line marks expected rate and numbers below show batch number.



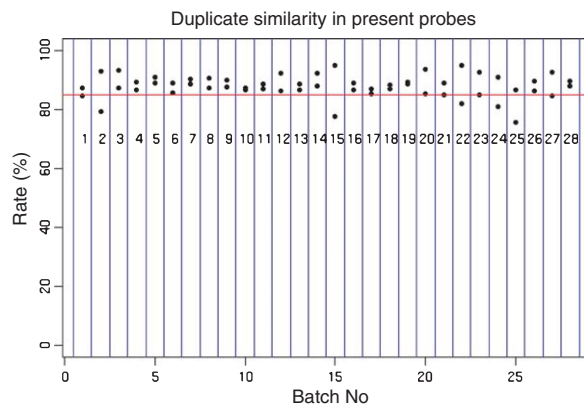
Supplementary Figure S2B. Average probe Signal-to-Noise (S/N) per sample. Red line marks minimum criteria and numbers below show batch number.



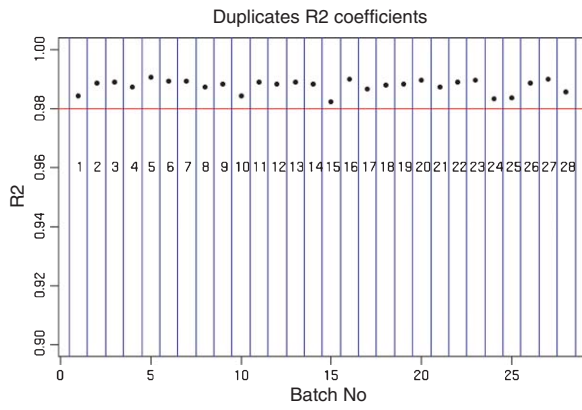
Supplementary Figure S2E. Present call rates of technical replicates in each batch. Batch 15 shows a too large spread. Maximum spread is a ratio of 1.21. Numbers below data points show batch number.



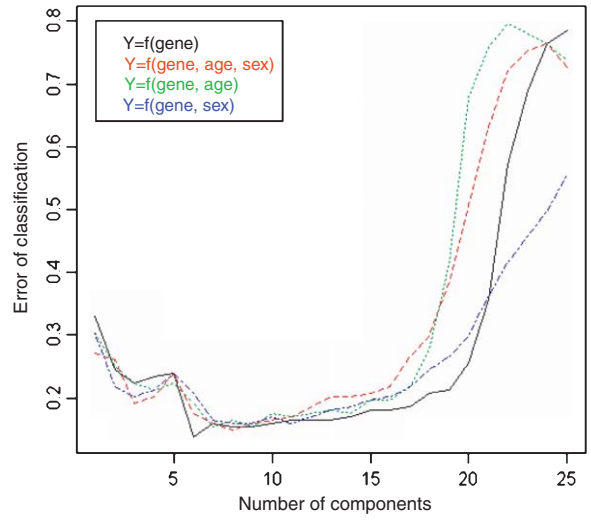
Supplementary Figure S2C. Median background values per sample. Red line marks maximum criteria and numbers below show batch number.



Supplementary Figure S2F. Present call repeatability. Rate shows how many probes present in one replicate were also found present in the other replicate. Red line marks the criteria. Numbers below give batch number.



Supplementary Figure S2G. Correlation coefficient on technical replicates. Calculated on log values for probes called present in both replicates. Red line marks the criteria. Numbers below give batch number.



Supplementary Figure S3. Classification error as a function of number of PLS components. Minimum error rate is observed for 6 components (in black, $Y = f(\text{gene})$). The figure also shows the additional effect on age and/or gender on the classification error (in green; $Y = f(\text{gene, age})$, in blue; $Y = f(\text{gene, sex})$ and in red; $Y = f(\text{gene, age, sex})$).