

Additional File 7:
**Ingenuity Pathway Analysis for the CpGs that are
used for calculating DNA methylation age.**

**Horvath S. DNA Methylation age of
human tissues and cell types.**

Top Bio Functions

Diseases and Disorders

Name	p-value	# Molecules
Cancer	9.20E-05 - 3.17E-02	109
Developmental Disorder	2.55E-04 - 3.17E-02	28
Endocrine System Disorders	2.55E-04 - 3.17E-02	22
Hereditary Disorder	2.55E-04 - 3.17E-02	50
Reproductive System Disease	2.55E-04 - 3.12E-02	37

Molecular and Cellular Functions

Name	p-value	# Molecules
Cell Death and Survival	1.07E-07 - 3.17E-02	74
Cellular Growth and Proliferation	3.65E-05 - 3.17E-02	71
Lipid Metabolism	2.13E-04 - 3.17E-02	35
Molecular Transport	2.13E-04 - 3.17E-02	35
Small Molecule Biochemistry	2.13E-04 - 3.17E-02	44

Physiological System Development and Function

Name	p-value	# Molecules
Immune Cell Trafficking	2.58E-04 - 2.64E-02	28
Hematological System Development and Function	2.90E-04 - 3.17E-02	57
Organismal Development	4.61E-04 - 3.17E-02	56
Embryonic Development	6.06E-04 - 3.17E-02	36
Tissue Development	6.06E-04 - 3.17E-02	27

Top Canonical Pathways

Name	p-value	Ratio
Sertoli Cell-Sertoli Cell Junction Signaling	7.71E-03	8/187 (0.043)
Death Receptor Signaling	1.38E-02	4/63 (0.063)
Dopamine-DARPP32 Feedback in cAMP Signaling	1.6E-02	7/167 (0.042)
D-mannose Degradation	1.6E-02	1/1 (1)
Circadian Rhythm Signaling	1.68E-02	3/36 (0.083)

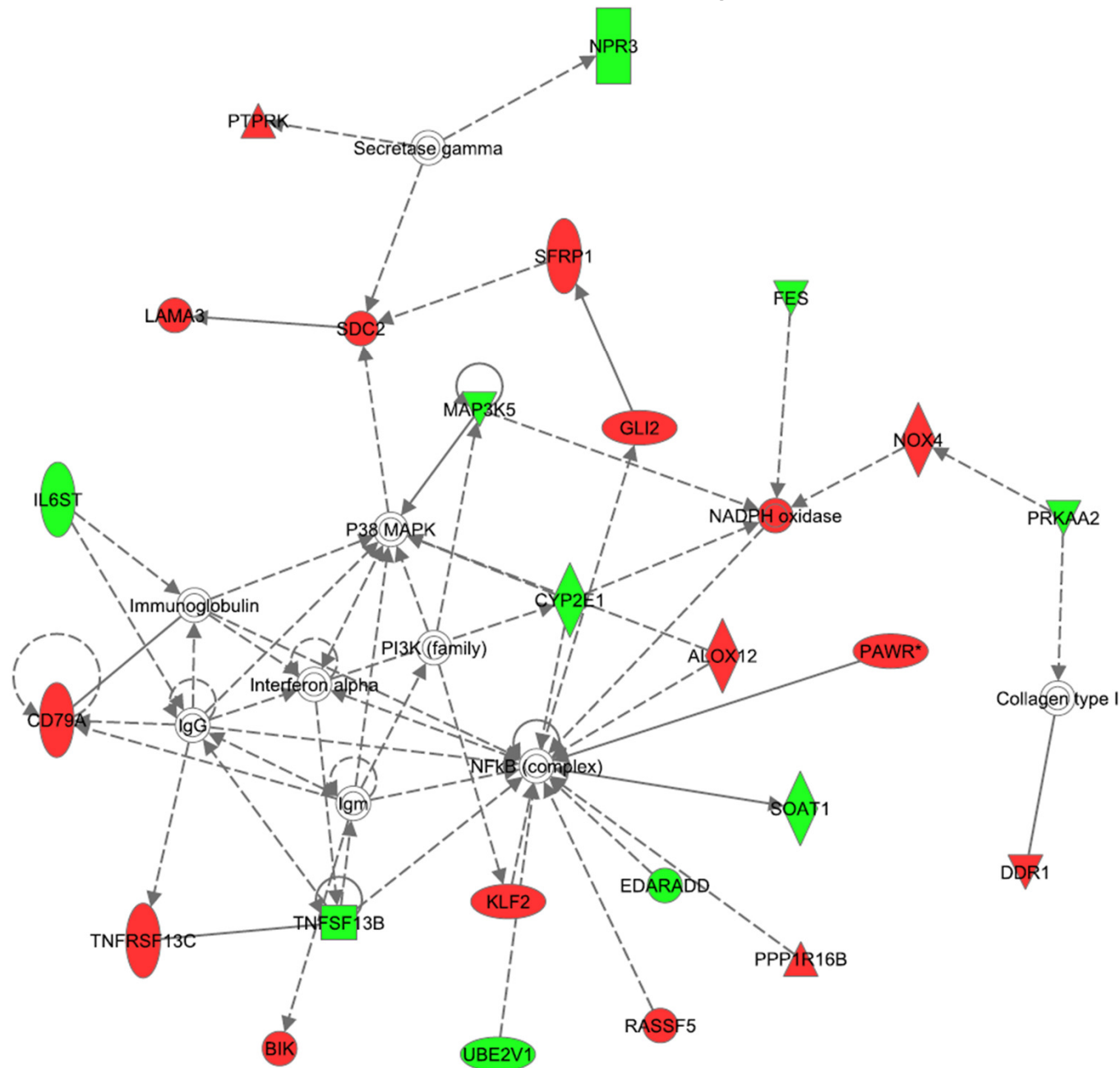
Top Upstream Regulators

Upstream Regulator	p-value of overlap	Predicted Activation State
RHOA	2.83E-04	
PHC1	7.00E-04	
TNF	9.73E-04	
ZFYVE9	1.39E-03	
PI3K (family)	2.43E-03	

Top Networks

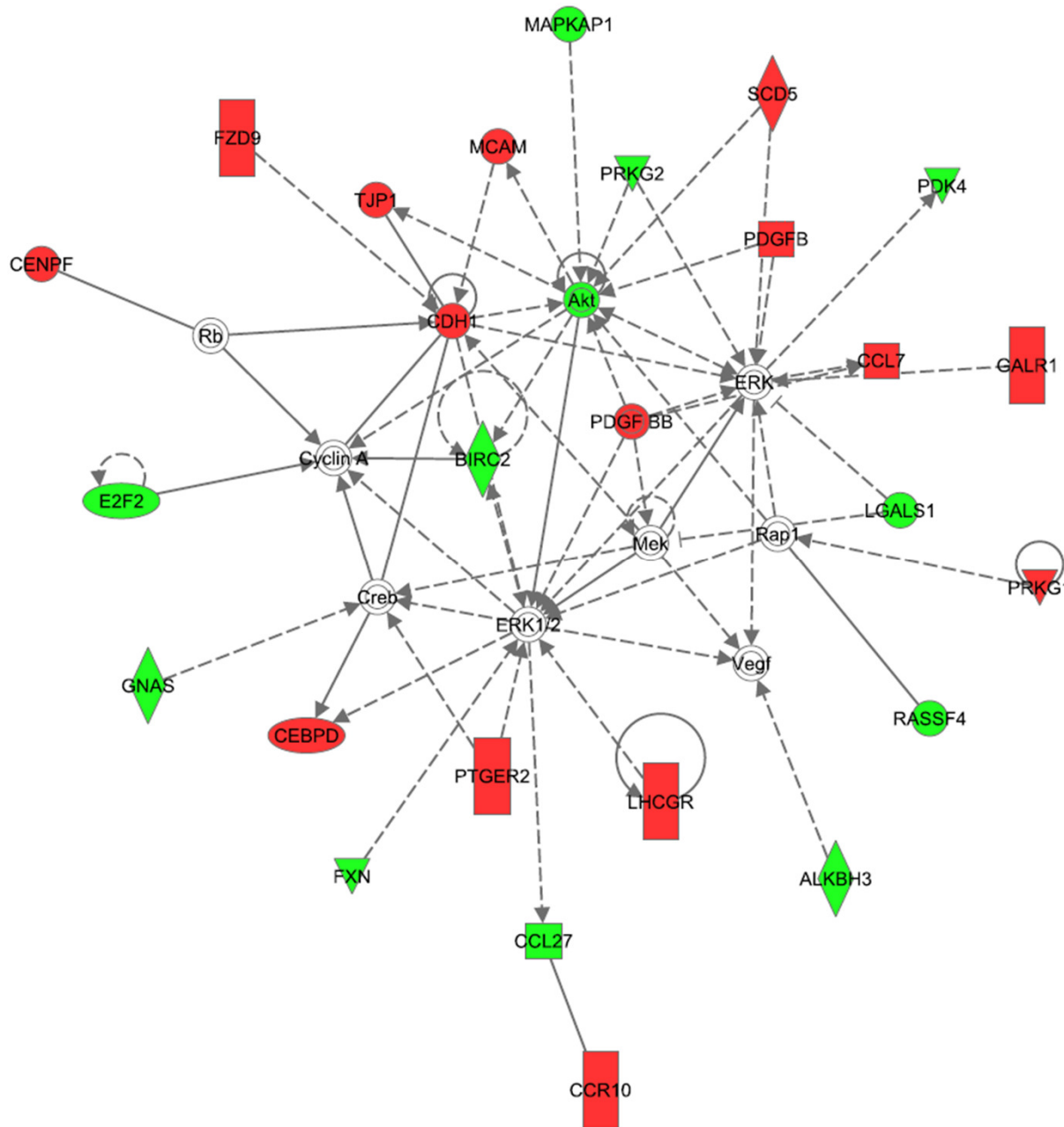
ID	Associated Network Functions	Score
1	Hematological System Development and Function, Tissue Morphology, Cell Death and Survival	37
2	Cellular Growth and Proliferation, Cell Signaling, Developmental Disorder	37
3	Hepatocellular Peroxisome Proliferation, Organismal Functions, Cellular Assembly and Organization	30
4	Cellular Development, Hematological System Development and Function, Hematopoiesis	19
5	Cardiovascular Disease, Hematological Disease, Cell-To-Cell Signaling and Interaction	19

Network 1 p=E-37



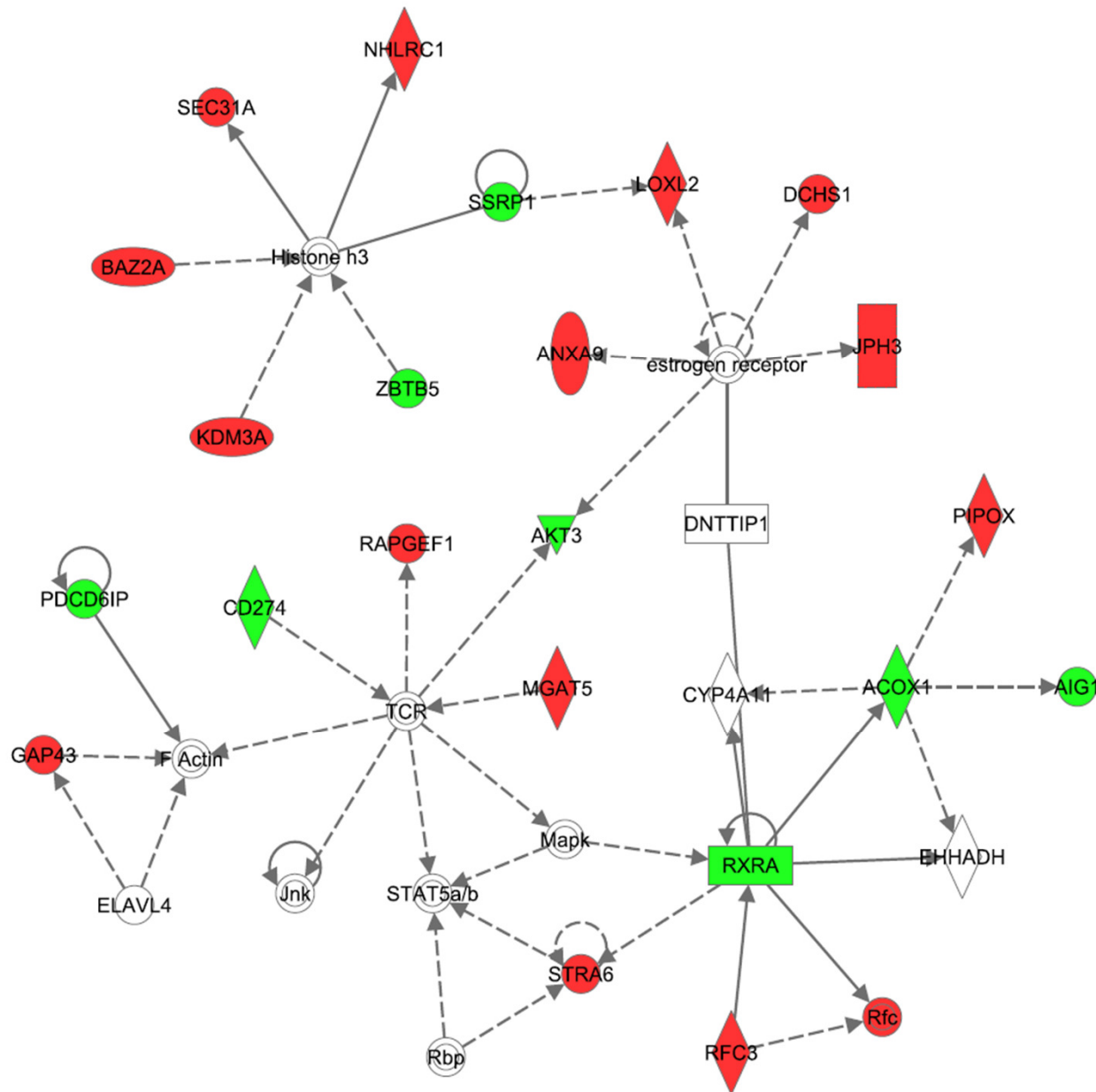
Genes colored in red (green) co-located with a CpG whose DNA methylation level positively (negatively) correlated with chronological age.

Network 2 p=E-37



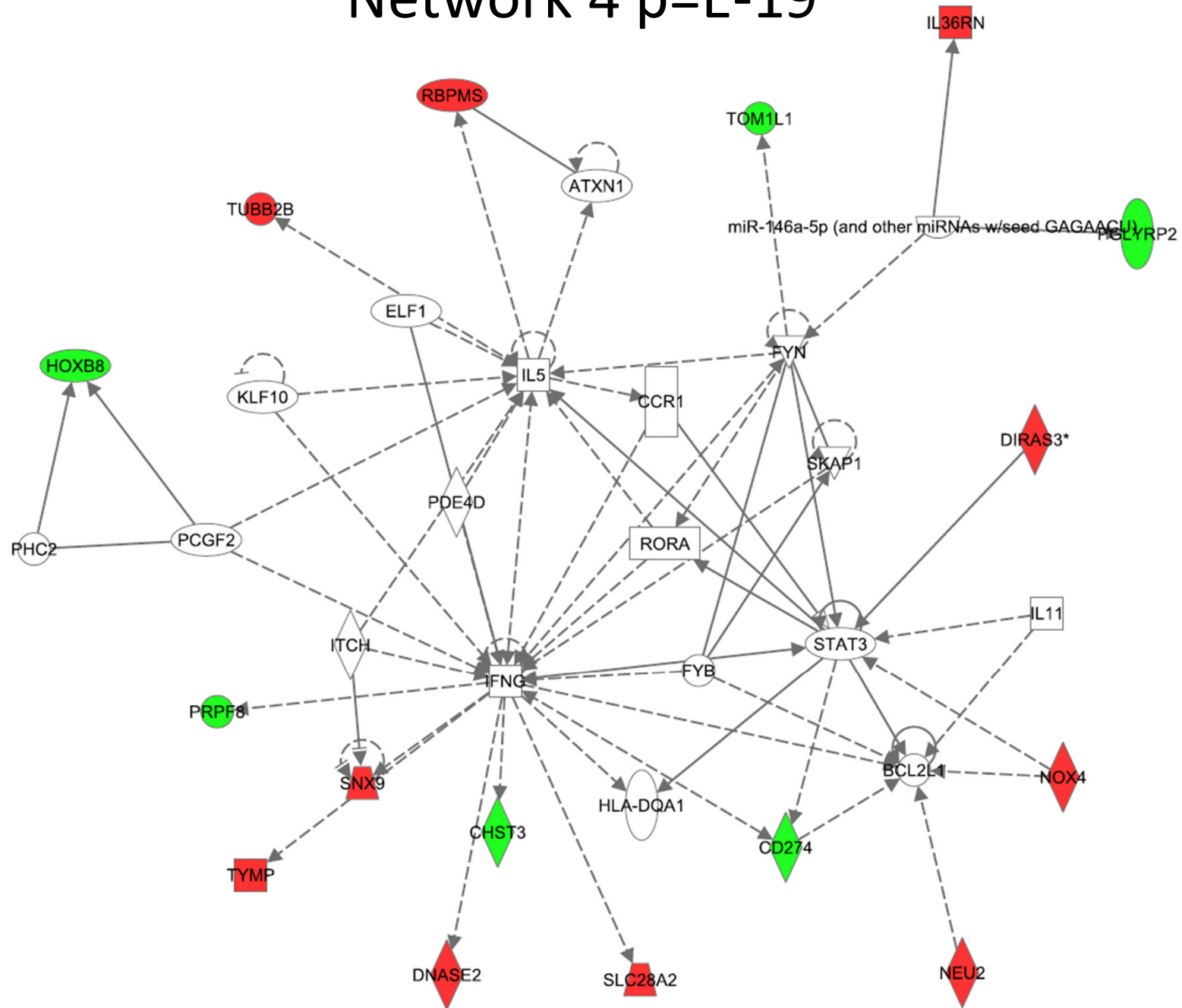
Genes colored in red (green) co-located with a CpG whose DNA methylation level positively (negatively) correlated with chronological age.

Network 3 p=E-30



Genes colored in red (green) co-located with a CpG whose DNA methylation level positively (negatively) correlated with chronological age.

Network 4 p=E-19



Network 5 p=E-19

