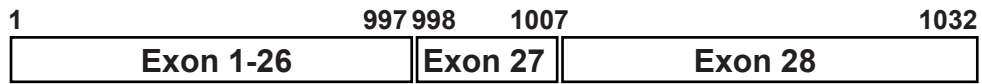


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**Wild-type KIF5A**

ATG.....KANMDN**GNATDINDN**RS**DLPCGYE**ADQAKLFPLHQETAAS\*

Frameshifting

**c.2987delA**

ATG.....KANM**AM**EMPQISMTIGVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

**c.2989delA**

ATG.....KANMD**M**EMPQISMTIGVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

**c.2993-1G>A**

ATG.....KANMDN**M**EMPQISMTIGVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

**c.2996delA**

ATG.....KANMDN**M**QPISMTIGVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

**c.2999delC**

ATG.....KANMDN**GN**AMPQISMTIGVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

Exon27 skipping

**c.2993-3C>A**

ATG.....KANMDN-----GVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

**c.2993-14G>T**

ATG.....KANMDN-----GVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

**c.3019A>G**

ATG.....KANMDN-----GVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

**c.3020+1G>A**

ATG.....KANMDN-----GVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

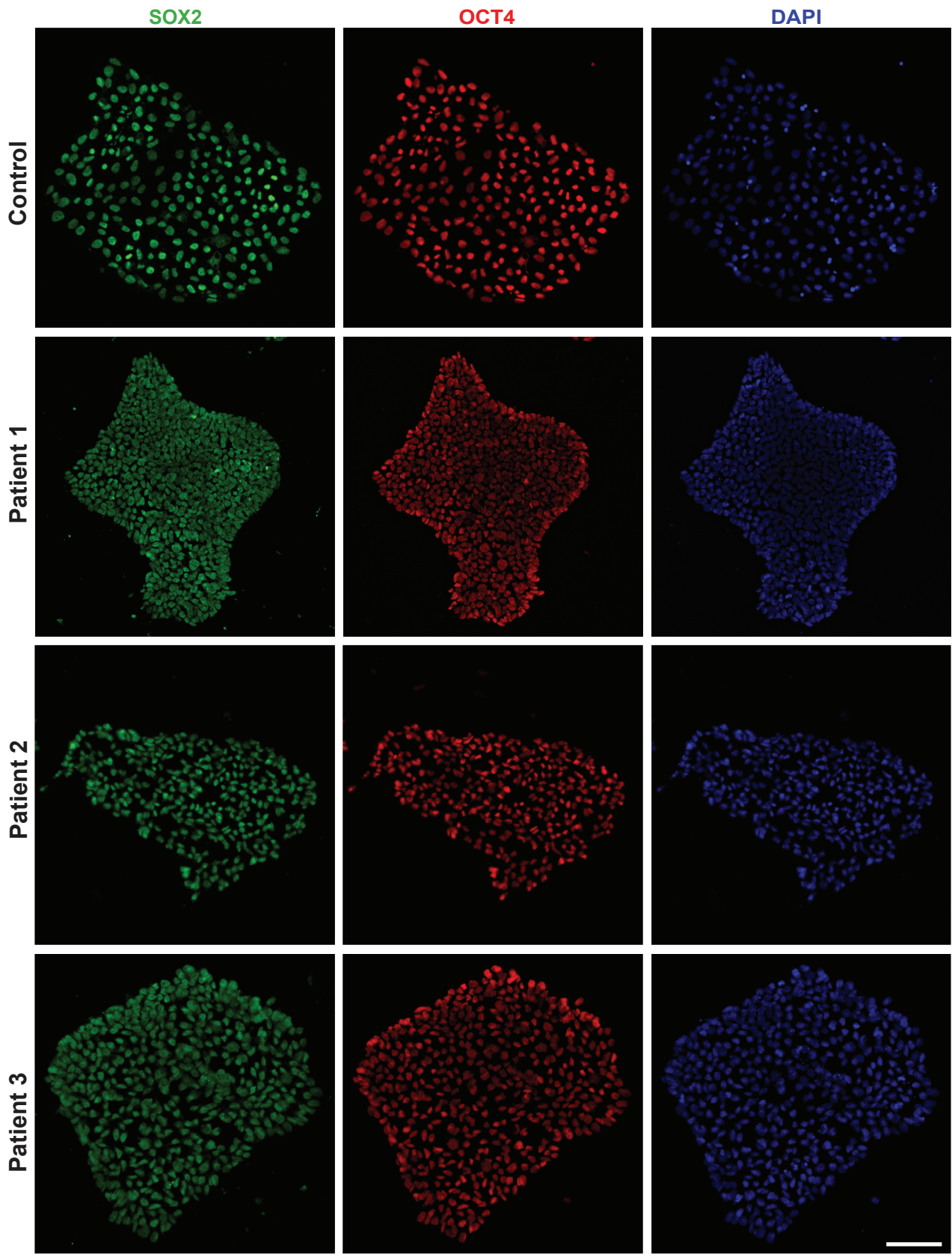
**c.3020+2T>A**

ATG.....KANMDN-----GVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

**c.3020+3A>T**

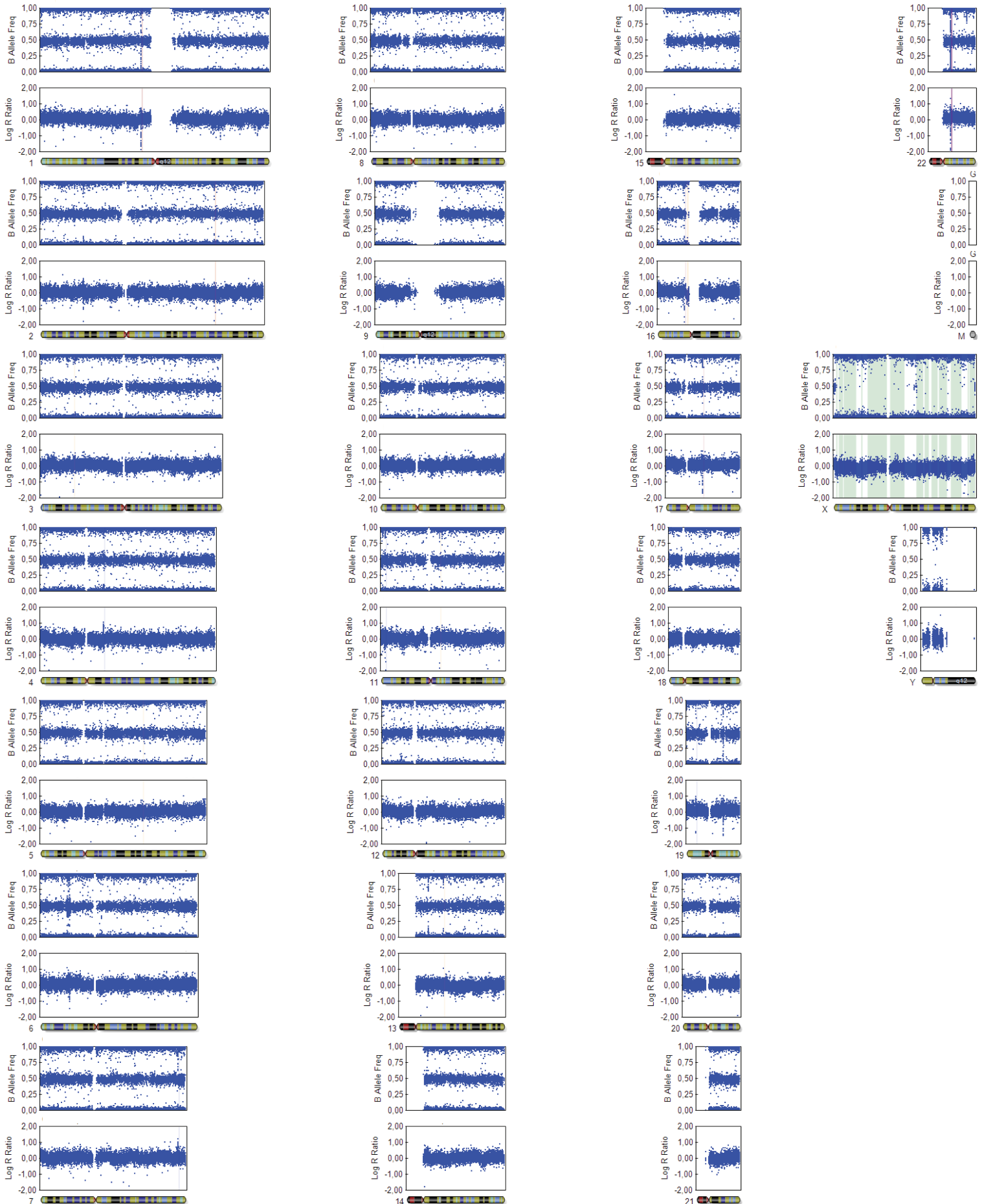
ATG.....KANMDN-----GVTCRVAMRLRTRPSFSLSTKRQQPANLPH**PHRLHTCTFSF**\*

**Appendix Figure S1. Comparison of amino acid sequences in the C-terminal tail domains of ALS-associated KIF5A.** The sequences in red are the “neopeptide” of aberrant 39 amino acids resulting from either exon27-skipping ( $\Delta$ Exon27) or non-exon27-skipping (frameshifting) ALS mutations.



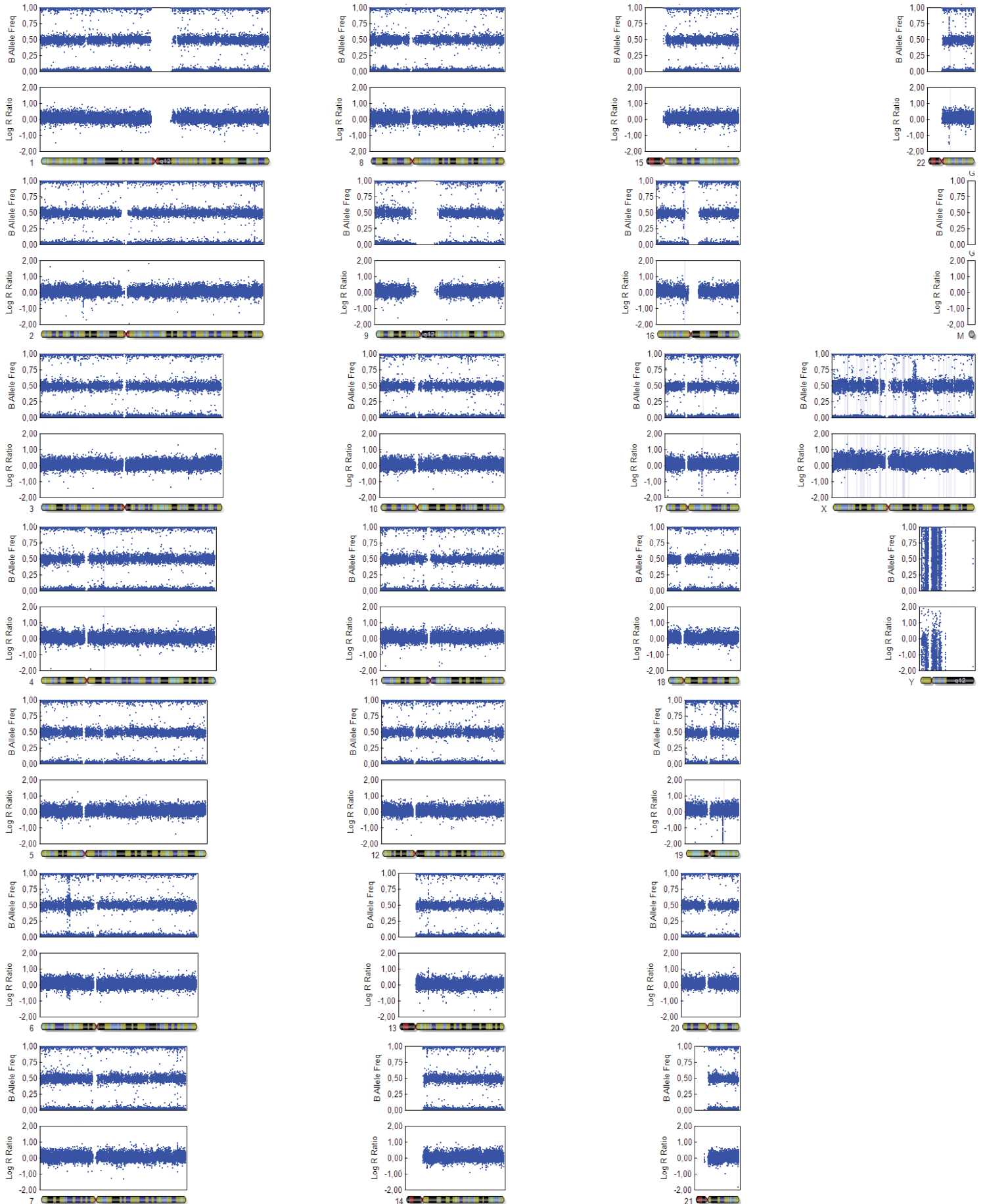
Appendix Figure S2. iPSC lines stained for the pluripotent markers Oct4 and Sox2. Scale bar, 50  $\mu$ m

### SNP Karyotyping



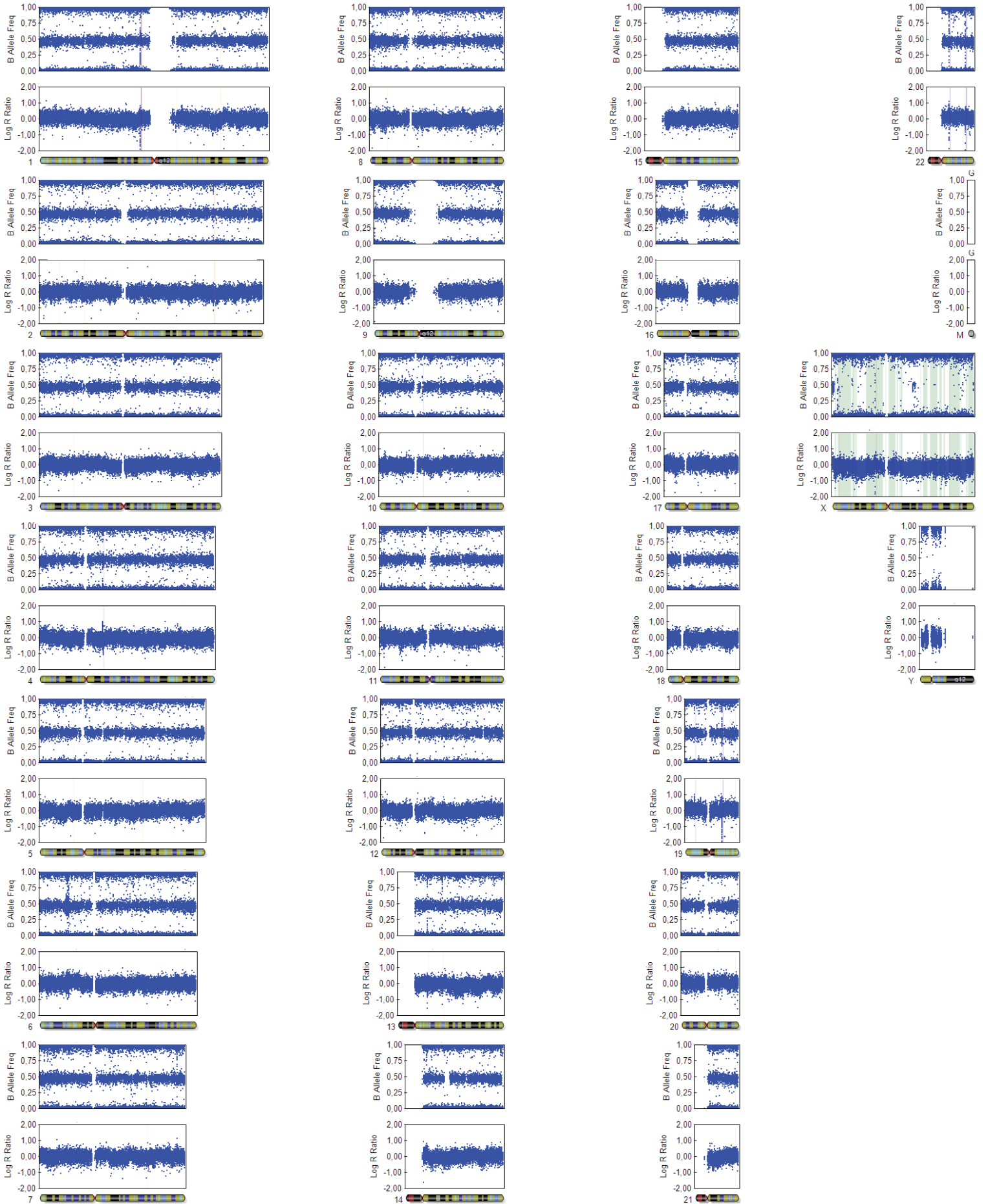
Appendix Figure S3. SNP Karyotyping analysis of iPSCs generated from Patient 1.

### SNP Karyotyping



Appendix Figure S4. SNP Karyotyping analysis of iPSCs generated from Patient 2.

### SNP Karyotyping



Appendix Figure S5. SNP Karyotyping analysis of iPSCs generated from Patient 3.