**a** p.G20A and p.A42_P43insPP

```
Mus musculus               12  SNPELPVSGGSSTSGSRRSRRRSGDGEPSGAPPLPPPPPAVSYPDWIGQSYSEVMSLNEH 71
Rattus norvegicus          12  SNPELPLSGGSSTSGSRRSRRRSGDGEPTGAPPLPPPP-AVSYPDWIGQSYSEVMSLNEH 70
Canis lupus familiaris     121 NSPELPLGGGSTTSGSRRSRRRSGDGEPPGSPPPP---AAVTYPDWIGQTYSEVMSLNEH 177
Felis catus                12  NSPELPFSGGSTTSGSRRSRRRSGDGETPGSSPPP---AAVTYPDWIGQTYSEVMSLNEH 68
Bos taurus                 12  NSPELPLSGGNSTSGSRRSRRRSGDGEPPGSPPPPPP-PAVTYPDWIGQSYSEVMSLNEH 70
Sus scrofa                 12  NSPELPLSGGSTTSGSRRSRRHSGDGEPPGSPPPPPPPPAVTYPDWIGQSYSEVMSLNEH 71
Homo sapiens               12  SSPELPPSGGSTTSGSRRSRRRSGDGEPPGAPPPPP--SAVTYPDWIGQSYSEVMSLNEH 69
Gallus gallus                  ------------------------------------------------------MSLNEH 6
Xenopus laevis             7   -----------VETKSRPCSKQLQE--------------EVSYPEWISRSYVELMSLNEH 41
```

**b** p.S218G

```
Mus musculus               192 EVVLLCWVKFLPLKRQAGQPSPT-KPPAE-SVIVANESDSSGITPGEAAAIASTAIMVPC 249
Rattus norvegicus          191 EVVLLCWVKFLPLKRQAGQPSPT-KPPTEPAVVVANSSNNGGITPGEAAAIASTAIMVPC 249
Canis lupus familiaris     298 EVVLLCWVKFLPLKKQPGQPRPTSKPPAGSAVASVNGSSTGGITPGQAAAIASTTIMVPF 357
Felis catus                189 EVVLLCWVKFLPLKKQPGQLRPTSKPPATDAVANVS--STGGITPGQAAAIASTTIMVPF 246
Bos taurus                 191 EVVLLCWVKFLPLKKQPGQLRPTSKPPAGGAAANVS--STGGITPGQAAAIASTTIMVPF 248
Sus scrofa                 192 EVVLLCWVKFLPLKKQPGQPRPTSKPPPSSEATNVSSSSPGGITPGQAAAIASTTIMVPF 251
Homo sapiens               190 EVVLLCWVKFLPLKKQPGQPRPTSKPPASGAAANVS---TSGITPGQAAAIASTTIMVPF 246
Gallus gallus              127 EVVLLCWVKFLPLKKNPLDPAEN---------------SNSSITSGQAAAIASTSIMVPF 171
Xenopus laevis             162 EVVLLCWVKFLPVNSPKISSNET-----------------SAVSSGQAAAITSTAIMVPF 204
```

**c**

| | SIFT | Polyphen |
|---|---|---|
| p.G20A | Deleterious (0.02) | Unknown (0) |
| p.A42_P43insPP | NA | NA |
| p.S218G | Tolerated (0.5) | Benign (0.001) |

**S3 Fig. Prediction of impact of the amino acid sequence alterations on ORAI1 function.**
(a, b) Multiple species sequence alignment of ORAI1 proteins. Positions of variants are highlighted in boldface type and yellow background color.
(c) Results of *in silico* prediction of the nature of amino acid sequence alterations. Prediction by SIFT and Polyphen-2 methods were conducted with the Variant Effect Predictor (http://ensembl.org/info/docs/tools/vep/index.html) web tool.