

**Supplementary information Table 1. OTS sequence information for the MCPH1-mutant monkey**

| Intronic loci |            |              |   |             |
|---------------|------------|--------------|---|-------------|
| No.           | Chromosome | GENE         | Sequence  | SCORE       |
| 1             | 1          | SRGAP2       | TTATCTTCTAAGCCAACCcageggtacactaaagggAGTGATGTTTGAAGATAA  | -1.36157295 |
| 2             | 6          | NC_022277.1  | TTATTTTAACAAATAACTtcattgtcaaattgatgAGCCATCTCTGAAGTTAA   | -1.43034945 |
| 3             | 1          | LOC101865519 | TCTCTTTCTCTCTCTGTctctctctatgtatgataGAGAGAGAGTGAAAGAGA   | -1.4875329  |
| 4             | 6          | SMAD5        | TCTCTTTTCAGGACTTGACcceaataagaagcataTGGCATTGTGAAGATAA    | -1.5332808  |
| 5             | X          | LOC102125728 | TTATCTTAAAAAATATCTtgaagtgcctaattcttCTCCATTTTTGAAGAATA   | -1.53434642 |
| 6             | 12         | NC_022283.1  | TTATCTCCAAAGATACCTtttctaaacttaggaacagAGGAAGTGATGAAGATGA | -1.55685565 |
| 7             | 1          | LOC101866504 | TCTCCTTCCATCCTTCCCtttgggcaaagacaatgGACAAATGTGGAAAGATA   | -1.56079065 |
| 8             | 14         | NC_022285.1  | TTTATTTCAAGCTTTAAGtagttgttggttaacAGCTGTTTTTGAAGATAA     | -1.56699624 |
| 9             | 5          | STIM2        | TTATATTCAAAGATAGCAcagttctgaatgatggtggGACAAGGCATGAGAGTGT | -1.5782592  |
| 10            | 6          | NC_022277.1  | TTAGCTACAAAGAAGGCTtggaaatgtagaggagcatAGGGATCTTTGATGATTT | -1.57925267 |
| 11            | 14         | LIN7C        | ATTTCTTCAAAGATAACGagtggtcagtaaactTGATGTCTTTGAAGATAA     | -1.58254374 |
| 12            | 15         | NC_022286.1  | TTATCCTCAAAGAGGGCTattggtgttctcatGGTGATGTTTGAAGAGAGA     | -1.59966103 |
| 13            | 8          | LOC102129130 | TCTCTTTCAAACCTTTTTcttgctagaatttattgATTTATTTTTTCATAGAA   | -1.60646616 |
| Exonic loci   |            |              |   |             |
| No.           | Chromosome | GENE         | Sequence  | SCORE       |
| 1             | 5          | LOC102115629 | TCTCTGTAGAGCTTGGTCctggcattatgggAGCCATTTTTGATGGTAT       | -1.42908846 |
| 2             | 7          | SYNE2        | TCATTTTCAAAGATGGCGaactacctatgccctaaccGTGAAAGCTGGAGAGAAG | -1.66901162 |
| 3             | 12         | FSIP2        | TCATCATTAACATATCTgtcaaaaacatctcAGCCATTTGTGAATGGAA       | -1.76553996 |
| 4             | 4          | HTR1B        | CTATCTGCAAAGATGCCTgctggtccacctAGCCATCTTTGACTTCTT        | -1.77345428 |
| 5             | 4          | PLEKHG1      | TCAGCATCAGAAATCCATgcacaagacctggcTGCCATCTTGAAGAGAA       | -1.84955674 |
| 6             | 6          | TRIM7        | TCTCTCAAGACCTTTGTcttaaaggatgctGAAGAAGTTCAAAGAGGA        | -1.86580685 |

|    |    |              |   |             |
|----|----|--------------|---|-------------|
| 7  | 11 | LOC101866275 | TTATCTTCAAACAACCTgatagaaaccattcctgaaaAGCCATTTGAGAATGCCA   | -1.87026626 |
| 8  | 7  | PARP2        | TCCCCTGCCAAGAAAACCTcgcagatgccagaGACAGGGGTCGAAAAAGA        | -1.88496406 |
| 9  | 9  | LIPN         | TCATCATCTACAATGGCTatcccagtgaagagtatgaAGTCACCACTGAAGATGG   | -1.91096956 |
| 10 | 3  | LHFPL3       | TGATCTTCCCTGATGGCTgggactcagatgaagtaaaACGGATGTGTGGAGAAAA   | -1.91152612 |
| 11 | 9  | DOCK1        | TATATTTCTGCTTCATAtattcatcttaaagaAGCGATAGTTGAAGGAAA        | -1.91540903 |
| 12 | 10 | SF3A1        | GCATCTTCAAAGGAGGATtctgcacctctaAGCCAGTTGTGGGGATTA          | -1.92415531 |
| 13 | 5  | FAM114A1     | AACTCTTAAAAAATGACCTaatttcattaaAGACATCTTTGCAGCCAA          | -1.92768991 |
| 14 | 2  | COL6A5       | TTACCTTCAAAGCCAAATgtttgagccacaaaataatGATCAATTATGAAAAAGA   | -1.93328637 |
| 15 | 20 | LOC102133268 | TCTCTTCCACCTATCCCtctgggtgggaccagaaatgaaGATGAAGATGGGGGGAGT | -1.93894436 |
| 16 | 7  | LOC101925900 | TTATCCTCAACAATGACAtgagtgagatggagctGGTCTTTGCAGAAGAGAA      | -1.93980089 |
| 17 | 3  | LOC101926614 | TCATTTCCAAGAGTTTTTctttggagctgggttattgaTGACATGTTTGAAGATAT  | -1.94673682 |
| 18 | 4  | VWA7         | TGATCTTCAACAAAGACCagcacattggagacgtggcAGCCATTGTTGGGGACAG   | -1.97128174 |