

Supplementary Table 3. Twenty-four pathogenic variants in *ARR3* that identified in our cohort (including three previously reported)

| No. | Position(at chrX)<br>(GRCh37/hg19) | NM_004312.2   |              | Family<br>Count | ACMG/AMP<br>Evidence | gnomAD |         | RE<br>VEL | CA<br>DD | SIFT | Poly-<br>phen2 | PRO<br>VEAN | BD<br>GP | NetG<br>ene2 | HSF  |
|-----|------------------------------------|---------------|--------------|-----------------|----------------------|--------|---------|-----------|----------|------|----------------|-------------|----------|--------------|------|
|     |                                    | Change        | Effect       |                 |                      | CA     | AF      |           |          |      |                |             |          |              |      |
| 1   | 69489238                           | c.3G>A        | p.M11?       | 1               | PVS1,PS4,PM2,PP1,PP4 | P      | none    | NA        | 0.01     | NA   | NA             | NA          | NSSC     | NSSC         | NSSC |
| 2   | 69489511                           | c.9-1G>A      | SA           | 1               | PVS1,PS4,PM2,PP1     | P      | none    | NA        | 22.7     | NA   | NA             | NA          | SSC      | SSC          | SSC  |
| 3   | 69489952                           | c.103G>A      | p.G35S       | 1               | PS2,PS4,PM2,PP3      | P      | none    | 0.54      | 28.6     | D    | D              | D           | NSSC     | NSSC         | SSC  |
| 4   | 69489988                           | c.139C>T      | p.R47*       | 2               | PVS1,PS2,PS4,PM2,PP4 | P      | none    | NA        | 35.0     | NA   | NA             | NA          | NSSC     | NSSC         | NSSC |
| 5   | 69495932                           | c.146T>G      | p.L49W       | 1               | PS4,PM2,PP1,PP3,PP4  | LP     | none    | 0.21      | 24.1     | D    | Pr             | D           | NSSC     | NSSC         | NSSC |
| 6   | 69495935                           | c.149T>C      | p.F50S       | 1               | PS4,PM2,PP1,PP3,PP4  | LP     | 5.5E-06 | 0.43      | 23.9     | D    | D              | D           | NSSC     | NSSC         | NSSC |
| 7   | 69496018                           | c.232C>T      | p.Q78*       | 1               | PVS1,PS4,PM2,PP1,PP4 | P      | none    | NA        | 32.0     | NA   | NA             | NA          | SSC      | NSSC         | NSSC |
| 8   | 69496025                           | c.239T>C      | p.L80P       | 1               | PS1,PS4,PM2,PP1,PP4  | P      | none    | 0.08      | 9.2      | T    | B              | D           | NSSC     | SSC          | NSSC |
| 9   | 69496084                           | c.298C>T      | p.R100*      | 3               | PVS1,PS1,PS4,PM2     | P      | none    | NA        | 34.0     | NA   | NA             | NA          | SSC      | NSSC         | SSC  |
| 10  | 69496131                           | c.345G>C      | p.Q115H      | 1               | PVS1,PS4,PM2         | P      | none    | 0.07      | 34.0     | T    | Pr             | N           | SSC      | SSC          | SSC  |
| 11  | 69496281                           | c.346-2A>T    | SA           | 1               | PVS1,PS4,PM2,PP4     | P      | none    | NA        | 33.0     | NA   | NA             | NA          | SSC      | SSC          | SSC  |
| 12  | 69496298                           | c.361C>A      | p.P121T      | 1               | PS4,PM2,PM6,PP3      | LP     | none    | 0.63      | 25.3     | D    | D              | D           | NSSC     | NSSC         | NSSC |
| 13  | 69496323                           | c.386_389del  | 4            | 1               | PVS1,PS4,PM2         | P      | none    | NA        | NA       | NA   | NA             | NA          | NSSC     | NSSC         | SSC  |
| 14  | 69497269                           | c.499A>T      | p.K167*      | 1               | PVS1,PS4,PM2,PP4     | P      | none    | NA        | 37.0     | NA   | NA             | NA          | SSC      | NSSC         | SSC  |
| 15  | 69497290                           | c.520G>T      | p.E174*      | 1               | PVS1,PS4,PM2         | P      | none    | NA        | 35.0     | NA   | NA             | NA          | NSSC     | NSSC         | SSC  |
| 16  | 69497290                           | c.520delG     | 0            | 1               | PVS1,PS4,PM2,PM4,PP4 | P      | none    | NA        | NA       | NA   | NA             | NA          | NSSC     | NSSC         | SSC  |
| 17  | 69497928                           | c.707C>G      | p.T236R      | 1               | PS4,PM2,PM6,PP3      | LP     | none    | 0.33      | 24.7     | D    | D              | D           | NSSC     | NSSC         | SSC  |
| 18  | 69497978                           | c.757delC     | p.Q253Rfs*7  | 1               | PVS1,PS4,PM2,PP4     | P      | none    | NA        | NA       | NA   | NA             | NA          | NSSC     | NSSC         | SSC  |
| 19  | 69498430                           | c.844_845insT | p.R282Lfs*10 | 1               | PVS1,PS4,PM2,PP1,PP4 | P      | none    | NA        | NA       | NA   | NA             | NA          | NSSC     | NSSC         | NSSC |
| 20  | 69498479                           | c.893C>A      | p.A298D      | 1               | P4                   | LP     | none    | 0.63      | 26.2     | D    | D              | D           | NSSC     | NSSC         | NSSC |
| 21  | 69500067                           | c.928G>T      | p.E310*      | 1               | PVS1,PS4,PM2,PP1,PP4 | P      | none    | NA        | 38.0     | NA   | NA             | NA          | NSSC     | NSSC         | NSSC |
| 22  | 69500068                           | c.929_930del  | 6            | 1               | PVS1,PS4,PM2         | P      | none    | NA        | NA       | NA   | NA             | NA          | NSSC     | NSSC         | SSC  |
| 23  | 69500102                           | c.963_964del  | 5            | 3               | PVS1,PS4,PM2,PP4     | P      | none    | NA        | NA       | NA   | NA             | NA          | NSSC     | Un           | SSC  |
| 24  | 69500614                           | c.1014-2A>G   | SA           | 1               | PVS1,PS4,PS2,PM2     | P      | none    | NA        | 32.0     | NA   | NA             | NA          | SSC      | SSC          | SSC  |

Abbreviations: AF = allele Frequency; B = benign; CA = classification; D = damage; N = neutral; NA = not applicable; NSSC = no splicing site change; P = pathogenic; Pr = probably damage; T = tolerant; Un = unknown splicing effect; SA = splicing acceptor; SSC = splicing site change. The p.L80P, p.R100\*, and p.A298D were reported before.