

**Supplemental Figure 2. Alignments between scaffolds containing more than one disagreement with the BEAT consensus sequence, the BEAT consensus, and the human reference.** Scaffolds that meet these criteria were found to belong to two categories: likely paralogs, and possible assembly errors. Paralogs are indicated when the entire sequence can be reconstructed from shotgun sequence reads, while assembly errors are marked by regions of scaffold-read disagreement. All alignments to scaffolds shown were conducted with BWA-MEM (Li 2013), and used only the original reads from Perry, Reeves et al. (2012). Titles with a light blue border indicate likely paralogs, while titles with a red border indicate possible assembly error.



# CDH23 Scaffold with disagreement 2

<b>Human</b>	ATGCTGGTGGGGATCCGGGTGCTGGACATCAACGACAACGACCCCTGTGCTGAACCTGCCCATGAACATCACCATCAGCGAGAAGACGCCCTGTCTCCAGCTTTGTCGCCATGTCTGGCCAGTGACCTGACAGTGGCTGCAATGACGCCTCACCTTCAACATCACTGCGGCAACCGCGAGCGGGCCTTCTT
<b>BEAT</b>	ATGTTGGTGGGGATCCGGGTGCTGGATATCAACGACAACGACCCCGTGTGCTGAACCTGCCCATGAACATCACCATCAGTGAGAAGACGCCCTGTCTCCAGCTTTGTCGCCACATCTGGCCAGCGATGACAGAGTGGCTGCAACGCGCTCACCTTCAACATCACTGCAGGCAACCGCGAGCGGGCCTTCTC
<b>Scaffold</b>	<div style="display: flex; justify-content: space-between; font-size: small;"> <span>1</span> <span>11</span> <span>21</span> <span>31</span> <span>41</span> <span>51</span> <span>61</span> <span>71</span> <span>81</span> <span>91</span> <span>101</span> <span>111</span> <span>121</span> <span>131</span> <span>141</span> <span>151</span> <span>161</span> <span>171</span> <span>181</span> <span>191</span> </div> <p>ATGTTGGTGGGGATCCGGGTGCTGGATATCAACGACAACGACCCCGTGTGCTGAACCTGCCCATGAACATCACCATCAGTGAGAAGACGCCCTGTCTCCAGCTTTGTCGCCACATCTGGCCAGCGATGACAGAGTGGCTGCAATGACGCCTCACCTTCAACATCACTGCAGGCAACCGCGAGCGGGCCTTCTT</p>
<b>BWA alignment to scaffold</b>	<pre> .....,c,t,,,a,,,,,tg,a,,,,,c,g,t,,,,, .....T.....G.....T..... .....C.....C,T.....A.....TG,A.....A,G..... .....C,g,C,,,,,t,,,,,C,,,,,C,t,,,a,,,,, .....t,C,,,,,gt,,,,,C,g,C,t,,,a,,,,,tg,a,,,,, .....C.....C,T.....A.....TG,C.....C..... .....C.....C,T.....A.....C.....C,T..... .....g,t,,,g,,,,,C,,,,,C,t,,,a,,,,,tg,a,,,,, .....C.....C,T.....C,g,t,,,,, .....C,,,,,g,,,,,a,,,,,tg,a,,,,,c,g,t,,,,, .....C,,,,,C,t,,,a,,,,,g,,,,,C,,,,,C,t,,,a,,,,, .....C.....C,T.....A.....g,,,,,C,,,,,C,t,,,a,,,,, .....C.....C,T.....A.....A.....TG,A.....C,g,T.....C..... .....a,t,,,,,C,,,,,C,t,,,a,,,,, .....g,,,,,C,,,,,C,t,,,a,,,,, .....C.....C,T.....A..... .....C.....C,T.....A..... .....C..... .....C,,,,,C,t,,,a,,,,,tg,a,,,,, .....C,,,,,C,t,,,a,,,,,tg,a,,,,, .....C.....C,T.....A..... </pre>

# KCNQ4 Scaffold with disagreement

<b>Human</b>	GCCGCGGGTACCCAGGGCAACATCTTCGCCACGTCCGCGCTGCGCAGCATGCGCTTCTGCAGATCTGCGCATGGTGCATGGACCGCGCGGGCCACCTGGAAGCTGCTGGGCTCAGTGGTCTACGCGCATAGCAAGG
<b>BEAT</b>	GCTGCGGGCACACAGGGCAACATCTTCGCCACGTCTGCGCTGCGCAGCATGCGCTTCTGCAGATCTGCGCATGCTGCGGATGGACCGGAGGGGCGGCACCTGGAAGCTGCTGGGCTCGGTGGTCTACGCGCACAGCAAGG
<b>Scaffold</b>	<div style="display: flex; justify-content: space-between; font-size: small;"> <span>1</span> <span>11</span> <span>21</span> <span>31</span> <span>41</span> <span>51</span> <span>61</span> <span>71</span> <span>81</span> <span>91</span> <span>101</span> <span>111</span> <span>121</span> <span>131</span> <span>141</span> </div> <pre> GCCGCGGGTCCAGGGCAATGCTTTGCCACGTCTGCACTCCGGAGCCTGCGGTTCTGCAGATCTGCGGATGATCCGCATGGACCGGAGGGGAGGCACCTGGAAGCTCCTGGGCTCCGCCATCTGCGCCACAGCAAGGN ..... .....C.....C.....C..G..... .....G.....CA.....C.....C..G..... ..... .....C.....T..T..... .....TGG..A..... .....C.....C.....C..g.....tgg..a..... .....C.....C.....C..g.....TGG..A..... .....a.....G..C..... .....C..C.....C..... .....t.....C.....g..... .....g..tg..g..C..C..... .....a.....a.....a.....a..a..... .....g.....g.....C..... .....A..G..G.....C.....T..A..... .....C..g.....G..... .....C.....C..g..g.....C..... .....C.....C..g..g.....C..... .....g..C.....C..g..g.....C..... .....g..g.....g.....C.....C.....C..... .....C.....C..G..G.....C.....C..... .....g.....C.....C..g..g.....C..g.....TGG..A..... .....C.....C..G..G.....C..... .....C.....C..... .....C.....TGG..A..... ..... ..... </pre>
BWA alignment to scaffold	

# OTOF Scaffold with disagreement

Human	GCCGCTTCCTCCCTCGCTGACAAGGACCAGGGCCACTCATCCCGCACCAGGCTTGACCGGGAGCGCCTCAAGTCCTGCATGAGGGAGCTGG
BEAT	GCCGCTTCCTCCCTCGCTGACAAGGACCAGAGCCACTCGTCCCGCACCAGGCTTGACCGGGAGCGCCTCAAGTCCTGCATGAGGGAGCTGG
Scaffold	<div style="display: flex; justify-content: space-between; width: 100%;"> <span>1</span> <span>11</span> <span>21</span> <span>31</span> <span>41</span> <span>51</span> <span>61</span> <span>71</span> <span>81</span> <span>91</span> </div> <p>GCCGCTTCCTCCCTCGCGGACAAGGACCAGAGCCACTCGTCCCGCACCAGGCTGGACCGGGAGCGCCTCAAGTCCTGCATGAGGGAGCTGGNNN</p>
BWA alignment to scaffold	<p>The alignment visualization shows approximately 15 reads aligned to the scaffold. The scaffold sequence is: GCCGCTTCCTCCCTCGCGGACAAGGACCAGAGCCACTCGTCCCGCACCAGGCTGGACCGGGAGCGCCTCAAGTCCTGCATGAGGGAGCTGGNNN. The reads are mostly aligned to the first 91 positions of the scaffold. Mismatches are indicated by 't' (thymine) or 'g' (guanine) characters below the alignment lines. For example, one read has a 't' at position 51, and another has a 'g' at position 61. The alignment also shows some indels and gaps, particularly towards the end of the reads.</p>





