

LG01	Gac	Tetr	Ola	Tru	Dre
<i>Sma-E191</i>	-	6	-	10	2
SmaUSC-E42	sc120	15-un	17	22un	-
Sma-USC268	2	5	-	-	25
<b>Sma-USC1</b>	18	14	24	16	-
<i>Sma-E231</i>	3	un	17	-	-
<b>Sma-USC15</b>	3	15	17	22un	-
<b>SmaUSC-E15</b>	3	-	17	-	-
<b>SMAC09</b>	3	un	17	22	-
<b>1/4AC18</b>	3	15	17	22	22
<b>Sma-USC271</b>	3	-	-	-	-
<b>SmaSNP204</b>	3	15	17	22un	2
<b>Sma-E277</b>	3	-	-	22	-
<b>SMAC07</b>	3	un	17	22	-
Sma-USC218	sc111	un	-	12un	-
Sma-USC222	10	21	11	12	-
<i>SmaSNP19</i>	10	un	11	12	19
<i>SmaSNP153</i>	10	un	11	12	19

LG02	Gac	Tetr	Ola	Tru	Dre
<i>SmaSNP143</i>	20	8	16	7	-
<i>SmaSNP145</i>	20	8	16	7	16
<i>SmaSNP40</i>	6	17	-	4	-
<i>Sma-USC51</i>	-	2	19	1	-
<i>SmaUSC-E17</i>	6	-	-	-	-
<b>Sma-USC46</b>	20	8	16	7	-
<i>SmaSNP103</i>	1	3	-	8	7
<b>Sma-USC242</b>	20	-	-	-	-
<i>SMAC01</i>	sc47	-	-	-	7
<i>SmaSNP149</i>	1	3	-	-	-
<b>Sma-USC168</b>	20	8	-	-	-
<i>SmaSNP71</i>	20	8	-	-	-
<i>SmaSNP30</i>	20	8	16	-	16
<b>Sma-USC84</b>	20	-	16	-	-
<b>Sma-USC249</b>	-	-	16	-	-
<b>Sma-USC185</b>	-	-	16	-	-
<i>Sma-USC36</i>	20	-	-	-	-
<b>Sma-USC187</b>	1	-	2	8	-
<i>Sma-USC64</i>	20	8	16	-	-
<b>Sma-USC43</b>	sc74	-	2	-	-

LG03	Gac	Tetr	Ola	Tru	Dre
<i>Sma-USC93</i>	15	un	sc604	2	-
<b>Sma-USC17</b>	-	10	-	2	-
<b>SmaUSC-E34</b>	15	10	22	2	-
<b>Sma-USC157</b>	15	10	22	2	-
<b>Sma-USC179</b>	15	10	-	-	-
<b>Sma-E118</b>	15	10	22	2	-
<b>Sma-E72</b>	15	10	22	2	-
<b>Sma-E272</b>	-	10	-	-	-

LG04	Gac	Tetr	Ola	Tru	Dre
<i>SmaSNP190</i>	2	5	3	13	18
<b>SmaSNP181</b>	2	5	3	13	7
<b>Sma-USC100</b>	2	5	3	13	-
<b>Sma-USC167</b>	-	-	-	17	-
<b>Sma-USC102</b>	2	5	3	13	sc_3485

LG05	Gac	Tetr	Ola	Tru	Dre
<b>SmaUSC-E30</b>	8	-	-	-	-
<b>SmaSNP31</b>	8	1	-	20	-
<b>Sma-USC12</b>	8	1	4	20	8
<b>Sma-USC202</b>	8	-	-	-	-
<b>Sma-USC265</b>	8	1	4	20	-
<b>Sma-USC88</b>	8	1	-	20	-
<b>Sma-E254</b>	-	-	4	-	-
<b>Sma-USC225</b>	8	un	-	20un	-

LG06	Gac	Tetr	Ola	Tru	Dre
<i>SmaUSC-E7</i>	19	13	uc72	9	-
<b>SmaSNP29</b>	19	13	-	-	25
<b>Sma-USC188</b>	19	-	-	-	-
<b>Sma-USC107</b>	19	13	-	9	-
<b>Sma-USC110</b>	19	13	6	9	18
<b>SmaUSC-E29</b>	19	13	6	9	25
<b>Sma-E315</b>	19	13	6	9	25
<b>Sma-USC132</b>	-	-	-	-	6
<b>Sma-USC264</b>	19	-	-	-	-

LG08	Gac	Tetr	Ola	Tru	Dre
<b>Sma-USC194</b>	7	-	-	-	-
<b>Sma-E218</b>	7	7	-	15	18
<b>SMAC08</b>	7	7	14	15	5
<b>SmaUSC-E43</b>	7	7	14	15un	5
<b>SmaSNP147</b>	7	-	-	-	-
<i>Sma-USC269</i>	7	7	14	15	-
<b>Sma-USC170</b>	14	4	12	6	21
<b>Sma-USC18</b>	7	-	-	8	-

LG09	Gac	Tetr	Ola	Tru	Dre
<i>SmaSNP61</i>	-	18	-	-	-
<b>Sma-USC216</b>	9	-	1	17	-
<b>Sma-USC150</b>	9	-	-	-	-
<b>Sma-USC118</b>	21	-	-	-	-
<b>SmaUSC-E16</b>	9	-	1	17	-
<b>Sma-E99</b>	-	-	-	-	1
<i>SmaSNP100</i>	9	18	-	17	1
<i>SmaUSC-E36</i>	9	18	1	17	-
<b>Sma-USC126</b>	9	18	1	17	-
<b>SmaUSC-E23</b>	9	18	1	-	-
<b>Sma-E71</b>	9	18	1	17	1
<b>SmaSNP35</b>	9	un	-	-	-
<b>Sma-E197</b>	9	un	-	-	3
<b>Sma-E139</b>	18	14	24	16	20
<b>SmaUSC-E5</b>	-	-	1	-	-
<b>Sma-E302</b>	9	18	1	17	-
<b>F12-ITG16</b>	-	un	-	-	-
<b>SmaUSC-E41</b>	9	18	1	17un	3
<b>Sma-USC57</b>	1	-	-	-	-
<b>Sma-E248</b>	-	un	1	un	19
<b>SmaUSC-E2</b>	9	-	-	-	-
<b>Sma-USC21</b>	9	18	1	17	-
<b>Sma-E117</b>	9	un	-	17	-
<b>SMAC05</b>	9	un	1	17	1
<b>Sma-USC226</b>	9	-	-	-	-

LG10	Gac	Tetr	Ola	Tru	Dre
<i>SmaSNP64</i>	12	-	7	3	23
<i>Sma-USC175</i>	12	-	-	-	-
<b>Sma-USC217</b>	sc68	9	7	3	-
<b>SmaUSC-E20</b>	sc68	-	7	-	-
<b>SmaUSC-E27</b>	12	9	-	3	-
<b>SmaUSC-E32</b>	sc114	un	uc90	-	-
<b>Sma-USC162</b>	sc180	-	7	-	23
<b>SmaSNP157</b>	12	un	7	-	-
<b>Sma-USC244</b>	sc114	un	uc90	3	-
<b>Sma-USC113</b>	-	9	7	3	-
<b>Sma-USC96</b>	12	-	-	-	23
<b>Sma-E144</b>	-	5	-	-	-
<b>Sma-E290</b>	12	un	7	un	-
<b>Sma-E224</b>	12	un	7	un	-
<b>Sma-USC79</b>	-	un	7	un	8
<i>SmaSNP3</i>	12	-	7	3	8

LG07	Gac	Tetr	Ola	Tru	Dre
<b>Sma-USC206</b>	4	-	10	14	-
<b>SmaSNP62</b>	4	1	-	un	9
<b>Sma-E100</b>	4	1	10	14	-
<b>B11-112/6/3</b>	4	-	10	-	-
<b>Sma-USC135</b>	4	un	10	14un	-
<b>Sma-USC272</b>	4	1	10	14	-
<i>Sma-USC37</i>	-	-	-	14	-
<b>Sma-E78</b>	4	-	10	14un	14
<b>Sma-E194</b>	4	20	uc115	14	-

LG11					LG12					LG13					LG14									
Gac	Tetr	Ola	Tru	Dre	Gac	Tetr	Ola	Tru	Dre	Gac	Tetr	Ola	Tru	Dre	Gac	Tetr	Ola	Tru	Dre					
<i>SmaSNP87</i>	sc27	-	sc1179	19	-	<i>Sma-USC169</i>	13	-	-	-	-	<b>Sma-USC280</b>	-	<i>un</i>	-	5	-	<i>Sma-E50</i>	14	-	-	6	-	
<b>Sma-USC201</b>	sc27	-	5	19	-	<i>SmaUSC-E25</i>	13	12	-	21	5	<b>Sma-E82</b>	11	<b>un</b>	8	5	-	<i>SmaSNP200</i>	14	4	12	6	<b>un</b>	
<b>Sma-USC152</b>	sc27	-	-	-	-	<b>Sma-USC60</b>	13	-	-	-	-	<b>Sma-USC76</b>	sc151	-	8	-	-	<i>SmaSNP32</i>	-	-	12	6	5	
<b>Sma-USC158</b>	17	-	-	19	-	<b>SmaSNP140</b>	13	<i>un</i>	9	<b>un</b>	-	<i>SmaSNP150</i>	11	3	8	-	-	<i>SmaSNP45</i>	14	4	12	-	-	
<b>SmaUSC-E24</b>	17	-	-	19	-	<b>3/9CA15</b>	13	-	-	21	-	<b>Sma-USC16</b>	-	-	8	-	-	<b>SmaUSC-E28</b>	14	-	-	-	10	
<b>Sma-USC62</b>	-	-	-	19	-	<b>4/4CA4/13</b>	-	-	9	-	-	<b>Sma-E120</b>	11	3	8	5	3	<b>Sma-USC85</b>	14	-	12	-	-	
<b>Sma-E96</b>	17	-	-	-	-	<b>Sma-USC89</b>	13	-	9	21	-	<b>Sma-E215</b>	11	-	-	1	12	<b>Sma-USC82</b>	-	-	-	6	-	
<b>Sma-USC22</b>	17	-	-	-	-	<b>Sma-USC20</b>	-	-	-	-	5	<b>SmaUSC-E10</b>	11	2	-	1	-	<b>Sma-E164</b>	20	<i>un</i>	16	7	-	
<i>Sma-E156</i>	17	-	-	-	-	<b>SmaUSC-E14</b>	13	<i>un</i>	-	21	-	<b>SmaUSC-E38</b>	11	3	8	5	-							
<b>Sma-USC235</b>	17	<i>un</i>	5	-	-	<b>Sma-USC19</b>	13	-	9	-	-	<b>Sma-USC155</b>	11	-	-	-	5	-						
						<b>Sma-USC133</b>	-	-	9	-	-	<i>SmaSNP44</i>	-	-	-	-	3	-						
						<b>Sma-USC56</b>	13	-	-	-	-	<b>SmaSNP192</b>	11	3	-	5	3	-						
						<b>SmaSNP73</b>	-	12	-	21	21													
						<b>SmaUSC-E21</b>	13	-	-	21	-													
						<b>SmaUSC-E22</b>	13	-	-	21	-													
						<i>Sma-E310</i>	13	-	-	21	-													
						<b>SmaSNP126</b>	13	-	-	21	-													
						<b>Sma-USC266</b>	13	12	9	21	5													

  

LG16					LG17					LG18					LG19								
Gac	Tetr	Ola	Tru	Dre	Gac	Tetr	Ola	Tru	Dre	Gac	Tetr	Ola	Tru	Dre	Gac	Tetr	Ola	Tru	Dre				
<i>Sma-E279</i>	-	<i>un</i>	-	8 <i>un</i>	-	<b>Sma-USC91</b>	21	-	-	10	-	<b>SmaUSC-E40</b>	7	7	<i>uc170</i>	-	-	<b>3/20CA17</b>	4	19	23	18	-
<b>Sma-E137</b>	7	<b>un</b>	18	8 <i>un</i>	-	<b>Sma-E112</b>	21	-	20	-	-	<b>SmaUSC-E13</b>	7	7	<b>uc170</b>	-	-	<i>SmaSNP101</i>	-	-	-	4	-
<b>Sma-USC128</b>	4	<b>un</b>	23	18	4	<b>Smax-02</b>	21	-	20	10	-	<b>Sma-E195</b>	7	7	<i>uc170</i>	-	-	<i>SmaSNP74</i>	6	17	-	4	-
<b>Sma-USC136</b>	4	19	23	-	-	<b>Sma-USC138</b>	21	<b>un</b>	-	10	-	<b>Sma-USC160</b>	-	7	-	15 <i>un</i>	7	<i>SmaSNP28</i>	6	17	15	4	-
<b>3/20CA17</b>	4	19	23	18	-	<b>Sma-USC55</b>	21	-	-	10 <i>un</i>	12	<b>SmaUSC-E19</b>	7	<b>un</b>	14	15	-	<i>Sma-E142</i>	6	<b>un</b>	15	4	-
<b>Sma-USC282</b>	4	-	23	18	-	<b>Sma-E159</b>	sc37	<b>un</b>	<i>uc236</i>	<b>un</b>	-							<i>Sma-USC108</i>	6	-	-	-	-
<b>Sma-USC285</b>	4	19	23	18	-	<b>Sma-USC134</b>	21	6	-	10	-							<b>Sma-E205</b>	6	-	sc521	<b>un</b>	13
<b>Sma-USC223</b>	4	19	23	18	-	<b>Sma-USC142</b>	sc67	-	-	10	-							<b>Sma-USC86</b>	6	17	-	-	-
<b>Sma-E183</b>	4	19	23	18	4	<b>Sma-E184</b>	sc126	-	20	10	-							<i>Sma-USC263</i>	6	-	-	-	-
						<b>SmaUSC-E1</b>	sc126	<b>un</b>	20	10	24							<b>Smax-04b</b>	6	17	-	4	-
																		<b>Sma-USC23</b>	-	-	<i>uc72</i>	4	-

  

LG20					LG21					LG22					LG23								
Gac	Tetr	Ola	Tru	Dre	Gac	Tetr	Ola	Tru	Dre	Gac	Tetr	Ola	Tru	Dre	Gac	Tetr	Ola	Tru	Dre				
<i>SmaSNP163</i>	1	-	13	<i>un</i>	-	<b>SmaSNP210</b>	20	8	16	7	-	<i>Sma-E91</i>	1	<b>un</b>	sc2179	<b>un</b>	18	<b>Sma-E168</b>	18	14	24	16	20
<b>SmaSNP194</b>	-	-	21	-	-	<b>Sma-USC231</b>	-	2	19	1	-	<i>SmaSNP141</i>	10	21 <i>un</i>	11	12	15	<b>Sma-USC273</b>	18	14	24	16	-
<b>Sma-USC29</b>	-	-	-	1	-	<b>Sma-USC234</b>	5	-	-	-	-	<b>Sma-E167</b>	10	<b>un</b>	11	-	16	<b>Sma-USC38</b>	18	14	-	16	-
<b>Sma-E189</b>	-	2	-	1	1	<b>Sma-E316</b>	5	-	19	1	12	<b>SmaUSC-E39</b>	10	21 <i>un</i>	-	12	-	<b>Sma-USC54</b>	-	-	24	-	-
<b>Sma-E244</b>	16	2	21	1	-							<b>Sma-USC58</b>	10	-	-	-	-	<b>SmaSNP68</b>	18	-	-	-	-
<b>Sma-E270</b>	-	2	21	1	-							<i>SmaSNP160</i>	10	-	-	-	-	<b>Sma-E127</b>	18	14	24	16	-
																		<b>Sma-E154</b>	-	-	24	-	-
																		<b>SmaUSC-E33</b>	-	14	-	16	-
																		<i>SmaUSC-E31</i>	18	-	-	16	20

**FIGURE S3. Comparative mapping between the turbot map and the five model teleost genomes.** Turbot linkage groups: LG1-LG24; stickleback (Gac), Tetraodon (Tni), Medaka (Ola), Fugu (Tru) and zebrafish (Dre). Markers yielding significant matches against at least one model fish genome are ordered on the left of each turbot linkage group (framework markers in boldface, markers at LOD<3.0 in normal type and accessory markers in italic type; see Figure 1 and Table S1). Details on similarity matches against each model genome are recorded as either the number of the specific chromosome or as the code of the unallocated genomic regions of the model species: (sc) stickleback or medaka scaffolds, (uc) medaka ultracontigs, (un) unrandom genomic or unassigned chromosomal sequences of *Tetraodon* and fugu. The significant unique hits under  $E \leq 10^{-5}$  threshold are presented in boldface type; the remaining at  $E < 10^{-10}$  in italic type.