<table>
<thead>
<tr>
<th>Factor</th>
<th>KC only vs ChIP-Seq</th>
<th>KC only total</th>
<th>TC and KC conserved vs ChIP-Seq</th>
<th>TC and KC conserved total</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Putative lncRNA</td>
<td>168</td>
<td>474</td>
<td>113</td>
<td>389</td>
<td>0.1664</td>
</tr>
<tr>
<td>CTCF</td>
<td>128</td>
<td>474</td>
<td>109</td>
<td>389</td>
<td>0.0297</td>
</tr>
<tr>
<td>SATB1</td>
<td>185</td>
<td>474</td>
<td>112</td>
<td>389</td>
<td>0.0297</td>
</tr>
<tr>
<td>SATB2</td>
<td>85</td>
<td>474</td>
<td>47</td>
<td>389</td>
<td>0.0477</td>
</tr>
<tr>
<td>RAD21</td>
<td>235</td>
<td>474</td>
<td>161</td>
<td>389</td>
<td>0.1593</td>
</tr>
<tr>
<td>H3K27me3</td>
<td>128</td>
<td>474</td>
<td>61</td>
<td>389</td>
<td>0.0015</td>
</tr>
<tr>
<td>H3K4me1</td>
<td>200</td>
<td>474</td>
<td>181</td>
<td>389</td>
<td>0.4589</td>
</tr>
<tr>
<td>H3K27ac</td>
<td>136</td>
<td>474</td>
<td>100</td>
<td>389</td>
<td>0.506</td>
</tr>
<tr>
<td>H3K4me1+H3K27ac</td>
<td>49</td>
<td>474</td>
<td>51</td>
<td>389</td>
<td>0.2893</td>
</tr>
<tr>
<td>H3K27me3+H3K4me1</td>
<td>36</td>
<td>474</td>
<td>34</td>
<td>389</td>
<td>0.6183</td>
</tr>
<tr>
<td>H3K27me3+H3K27ac</td>
<td>42</td>
<td>474</td>
<td>7</td>
<td>389</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>RING1B</td>
<td>5</td>
<td>474</td>
<td>9</td>
<td>389</td>
<td>0.1812</td>
</tr>
<tr>
<td>BRG1</td>
<td>109</td>
<td>474</td>
<td>125</td>
<td>389</td>
<td>0.0266</td>
</tr>
<tr>
<td>H3K27ac+H3K4me1</td>
<td>49</td>
<td>474</td>
<td>50</td>
<td>389</td>
<td>0.338</td>
</tr>
<tr>
<td>C/EBPα</td>
<td>33</td>
<td>474</td>
<td>12</td>
<td>389</td>
<td>0.02</td>
</tr>
<tr>
<td>C/EBPβ</td>
<td>98</td>
<td>474</td>
<td>73</td>
<td>389</td>
<td>0.6137</td>
</tr>
<tr>
<td>c-Myc</td>
<td>32</td>
<td>474</td>
<td>22</td>
<td>389</td>
<td>0.5747</td>
</tr>
<tr>
<td>Klf4</td>
<td>47</td>
<td>474</td>
<td>23</td>
<td>389</td>
<td>0.0307</td>
</tr>
<tr>
<td>MXI1</td>
<td>121</td>
<td>474</td>
<td>65</td>
<td>389</td>
<td>0.0115</td>
</tr>
<tr>
<td>Ovo2</td>
<td>38</td>
<td>474</td>
<td>18</td>
<td>389</td>
<td>0.0115</td>
</tr>
<tr>
<td>SATB1+SATB2</td>
<td>64</td>
<td>474</td>
<td>18</td>
<td>389</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>SATB1+RAD21</td>
<td>114</td>
<td>474</td>
<td>80</td>
<td>389</td>
<td>0.3385</td>
</tr>
<tr>
<td>SATB2+RAD21</td>
<td>83</td>
<td>474</td>
<td>38</td>
<td>389</td>
<td>0.0045</td>
</tr>
<tr>
<td>RAD21+Ctcf</td>
<td>80</td>
<td>474</td>
<td>81</td>
<td>389</td>
<td>0.2288</td>
</tr>
<tr>
<td>SATB1+BRG1</td>
<td>28</td>
<td>474</td>
<td>33</td>
<td>389</td>
<td>0.185</td>
</tr>
<tr>
<td>SATB1+Ctcf</td>
<td>20</td>
<td>474</td>
<td>28</td>
<td>389</td>
<td>0.076</td>
</tr>
<tr>
<td>SATB1+RING1B</td>
<td>0</td>
<td>474</td>
<td>0</td>
<td>389</td>
<td>0</td>
</tr>
<tr>
<td>SATB2+BRG1</td>
<td>28</td>
<td>474</td>
<td>20</td>
<td>389</td>
<td>0.6585</td>
</tr>
<tr>
<td>SATB2+Ctcf</td>
<td>13</td>
<td>474</td>
<td>14</td>
<td>389</td>
<td>0.4418</td>
</tr>
<tr>
<td>SATB2+RING1B</td>
<td>0</td>
<td>474</td>
<td>0</td>
<td>389</td>
<td>0</td>
</tr>
<tr>
<td>RAD21+BRG1</td>
<td>46</td>
<td>474</td>
<td>52</td>
<td>389</td>
<td>0.1359</td>
</tr>
<tr>
<td>RAD21+RING1B</td>
<td>0</td>
<td>474</td>
<td>1</td>
<td>389</td>
<td>0.4514</td>
</tr>
<tr>
<td>RBP2</td>
<td>175</td>
<td>474</td>
<td>83</td>
<td>389</td>
<td>0.0002</td>
</tr>
<tr>
<td>SIN3A</td>
<td>147</td>
<td>474</td>
<td>82</td>
<td>389</td>
<td>0.0132</td>
</tr>
<tr>
<td>RBP2+SIN3A</td>
<td>91</td>
<td>474</td>
<td>34</td>
<td>389</td>
<td>0.0001</td>
</tr>
<tr>
<td>SATB1+RBP2</td>
<td>121</td>
<td>474</td>
<td>48</td>
<td>389</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>SATB2+RBP2</td>
<td>84</td>
<td>474</td>
<td>44</td>
<td>389</td>
<td>0.0278</td>
</tr>
<tr>
<td>SATB2+SIN3A</td>
<td>56</td>
<td>474</td>
<td>18</td>
<td>389</td>
<td>0.0005</td>
</tr>
<tr>
<td>RAD21+RBP2</td>
<td>147</td>
<td>474</td>
<td>68</td>
<td>389</td>
<td>0.0004</td>
</tr>
<tr>
<td>RAD21+SIN3A</td>
<td>129</td>
<td>474</td>
<td>66</td>
<td>389</td>
<td>0.005</td>
</tr>
<tr>
<td>SATB1+MXI1</td>
<td>52</td>
<td>474</td>
<td>26</td>
<td>389</td>
<td>0.0562</td>
</tr>
<tr>
<td>SATB1+C/EBPβ</td>
<td>49</td>
<td>474</td>
<td>21</td>
<td>389</td>
<td>0.0169</td>
</tr>
<tr>
<td>SATB1+Klf4</td>
<td>29</td>
<td>474</td>
<td>8</td>
<td>389</td>
<td>0.0061</td>
</tr>
<tr>
<td>SATB1+Ovo2</td>
<td>36</td>
<td>474</td>
<td>7</td>
<td>389</td>
<td>0.0001</td>
</tr>
<tr>
<td>Protein Interaction</td>
<td>Chi-Sq</td>
<td>df</td>
<td>P</td>
<td>5C Score</td>
<td>FDR</td>
</tr>
<tr>
<td>---------------------</td>
<td>--------</td>
<td>----</td>
<td>---</td>
<td>----------</td>
<td>-----</td>
</tr>
<tr>
<td>SATB1+c-Myc</td>
<td>2</td>
<td>6</td>
<td>0.1507</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB1+C/EBPα</td>
<td>31</td>
<td>5</td>
<td>0.0001</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB1+AP-2γ</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB1+Ovo1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2+MXI1</td>
<td>23</td>
<td>5</td>
<td>0.0058</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2+C/EBPβ</td>
<td>50</td>
<td>32</td>
<td>0.2986</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2+Klf4</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2+Ovo2</td>
<td>15</td>
<td>3</td>
<td>0.0166</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2+c-Myc</td>
<td>0</td>
<td>2</td>
<td>0.204</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2+C/EBPα</td>
<td>13</td>
<td>2</td>
<td>0.0165</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2+AP-2γ</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2+Ovo1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21+MXI1</td>
<td>66</td>
<td>33</td>
<td>0.0321</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21+C/EBPβ</td>
<td>75</td>
<td>46</td>
<td>0.171</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21+Klf4</td>
<td>27</td>
<td>1</td>
<td>&lt;0.0001</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21+Ovo2</td>
<td>31</td>
<td>5</td>
<td>0.0001</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21+c-Myc</td>
<td>3</td>
<td>8</td>
<td>0.0759</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21+C/EBPα</td>
<td>26</td>
<td>3</td>
<td>0.0002</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21+AP-2γ</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21+Ovo1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB1-H3K27me3</td>
<td>96</td>
<td>36</td>
<td>0.0001</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB1-H3K4me1</td>
<td>58</td>
<td>53</td>
<td>0.6136</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB1+H3K27ac</td>
<td>50</td>
<td>17</td>
<td>0.002</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2-H3K27me3</td>
<td>60</td>
<td>20</td>
<td>0.0006</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2-H3K4me1</td>
<td>28</td>
<td>11</td>
<td>0.0471</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SATB2+H3K27ac</td>
<td>3</td>
<td>11</td>
<td>0.0147</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21-H3K27me3</td>
<td>96</td>
<td>39</td>
<td>0.0004</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21-H3K4me1</td>
<td>104</td>
<td>111</td>
<td>0.0927</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RAD21+H3K27ac</td>
<td>44</td>
<td>44</td>
<td>0.4317</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RBP2-H3K27me3</td>
<td>110</td>
<td>46</td>
<td>0.0003</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RBP2-H3K4me1</td>
<td>72</td>
<td>45</td>
<td>0.1975</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>RBP2+H3K27ac</td>
<td>52</td>
<td>16</td>
<td>0.0005</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SIN3A-H3K27me3</td>
<td>88</td>
<td>21</td>
<td>&lt;0.0001</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SIN3A-H3K4me1</td>
<td>52</td>
<td>46</td>
<td>0.7488</td>
<td>474</td>
<td>389</td>
</tr>
<tr>
<td>SIN3A+H3K27ac</td>
<td>67</td>
<td>39</td>
<td>0.12</td>
<td>474</td>
<td>389</td>
</tr>
</tbody>
</table>

Table A10 Comparison (Fisher’s exact test) between levels of enrichment for epigenomic marks and/or chromatin remodeler, architectural protein, transcription co-factor and/or transcription factor occupancy observed at sites of interaction identified as significant (5C score below an FDR of 1% in replicate KC IF matrices) only in KC and at sites identified as significant (5C score below an FDR of 1% in replicate TC and KC IF matrices) in both TC and KC. ChIP-chip tiling arrays for RBP2, SIN3A and transcription factors were generated by Nascimento et al.
(Nascimento et al., 2011). Otherwise, factor occupancy was mapped using ChIP-Seq as described here.