

# RegulatorTrail: a web service for the identification of key transcriptional regulators

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Supplementary Table 1 – Alternative approaches

Name	Input	Output	Availability
TFACTS (14)	List of differentially expressed genes and collection of RTIs	Regulators with significantly over-represented target genes in the input list (p-value).	Webserver: <a href="http://www.tfacts.org/">http://www.tfacts.org/</a>
DCGL v2.0 (15)	List of differentially expressed genes and collection of RTIs	Regulators with significantly over-represented target genes in the input list (p-value).	R-package: <a href="https://cran.r-project.org/web/packages/DCGL/DCGL.pdf">https://cran.r-project.org/web/packages/DCGL/DCGL.pdf</a>
Regulator Impact Factors RIF1 + RIF2 (16)	A gene expression matrix with samples that belong to two groups and a collection of RTIs.	Impact score for each regulator.	-
Correlation set analysis (17)	A gene expression matrix and a collection of RTIs.	Regulators with a significant coherence between all target genes. (p-value)	-
REGGAE (18)	A gene expression matrix and a collection of RTIs	A prioritized list of influential regulators. (p-value)	Webserver: <a href="https://regulatortail.bioinf.uni-sb.de">https://regulatortail.bioinf.uni-sb.de</a>
TFRank (19)	A list of target genes (e.g. differentially expressed genes) and a collection of weighted RTIs in form of an adjacency list (network)	A prioritized / ranked list of influential regulators	Java implementation: <a href="http://web.tecnico.ulisboa.pt/aplf/code/tfrank/">http://web.tecnico.ulisboa.pt/aplf/code/tfrank/</a> + Adapted version of the algorithm in the Regulatory Snapshots webserver (22)
wPGSA (20)	A score list (e.g. fold-changes) and RTIs weighted by the number of experiments that confirm each RTI	A prioritized list of influential regulators (p-value)	Python script: <a href="https://github.com/eiryo-kawakami/wPGSA">https://github.com/eiryo-kawakami/wPGSA</a>
MIPRIP (21)	A gene expression matrix and weighted RTIs in form of an adjacency matrix (network)	A list of significant regulators per target gene (p-value)	R-package: <a href="http://www.leibniz-hki.de/de/miprip.html">http://www.leibniz-hki.de/de/miprip.html</a>
Regulatory Snapshots (22)	Gene expression time series and RTIs in form of regulatory networks	Important regulatory modules	Webserver: <a href="http://kdbio.inesc-id.pt/software/regulatorsnapshots/">http://kdbio.inesc-id.pt/software/regulatorsnapshots/</a>

Table 1A: Overview of methods based on regulator-target interactions (RTIs).

Name	Input	Output	Availability
CENTIPEDE (23)	Matrix of read counts around candidate binding sites from DNasel cut sites and/or histone marks	Posterior probabilities for all provided candidate binding sites to be true TF binding sites	R-package: <a href="http://centipede.uchicago.edu/">http://centipede.uchicago.edu/</a>
PIQ (24)	Bam file with DNasel data, and a collection of PWMs	List of purely PWM based motif matches and a list of motif matches incorporating the DNasel information as well as the corresponding scores	R-package: <a href="https://bitbucket.org/thashim/piq-single">https://bitbucket.org/thashim/piq-single</a>
MILLIPEDE (25)	Binned DNase data, TF binding information using PWM scores, optional: TF ChIP-seq labels	Probabilities for all candidate binding sites to be true TF binding sites	R-package: <a href="https://users.cs.duke.edu/~amink/software/millipede/">https://users.cs.duke.edu/~amink/software/millipede/</a>
BinDNase (26)	Training data contains PWM scores for bound and unbound regions and DNasel data, ideally in perBase resolution. Test data is composed of PWM scores and Dnasel data for all candidate regions	Probabilities for all candidate binding sites to be true TF binding sites	R-package: <a href="http://research.ics.aalto.fi/csb/software/bindnase/">http://research.ics.aalto.fi/csb/software/bindnase/</a>
HINT-BC (27)	BED file with regions of interest, e.g. DHS sites, a Bam file with DNasel data, and optionally Bam files with histone mark data	A Bed file with all predicted TF-footprints and the related scores	Part of the Regulatory Genomics Toolbox <a href="http://www.regulatory-genomics.org/rgt/basic-introduction/">http://www.regulatory-genomics.org/rgt/basic-introduction/</a>
TEPIC (28)	Candidate regions for TF binding, e.g. DHS sites, a collection of PCMs, and a reference genome. Optionally, a wig file with DNasel signal information	A file containing TF affinities calculated per peak and a file containing TF affinities calculated per gene	Bash and Python scripts as well as C++ code <a href="https://github.com/SchulzLab/TFAnalysis">https://github.com/SchulzLab/TFAnalysis</a>
PASTAA (29)	Ensembl IDs, Gene Symbols, or RefSeq IDs for Mouse or Human	List of TFs ranked according to the association with the input	Webserver: <a href="http://trap.molgen.mpg.de/cgi-bin/pastaa.cgi">http://trap.molgen.mpg.de/cgi-bin/pastaa.cgi</a> C++ Code: <a href="http://trap.molgen.mpg.de/PASTAA/">http://trap.molgen.mpg.de/PASTAA/</a>

Table 1B: Overview of methods based on genome-wide transcription factor (TF) binding predictions.

## Supplementary Table 2 – Expected runtimes

	Run 1 [ms]	Run 2 [ms]	Run 3 [ms]	Run 4 [ms]	Run 5 [ms]	Average runtime in s
<b>Hypergeometric test</b>	23724	23793	23644	23644	23577	<b>23.68</b>
<b>Fisher's exact test</b>	25281	25409	25485	25485	25140	<b>25.36</b>
<b>Binomial test</b>	247275	247336	247771	246396	246948	<b>247.15</b>
<b>REGGAE</b>	172959	172856	172620	172620	172665	<b>172.74</b>
<b>REGGAE (without bootstrapping)</b>	8645	8415	8402	8270	8058	<b>8.35</b>
<b>RIF1</b>	8338	8108	8272	8148	8174	<b>8.20</b>
<b>RIF2</b>	8194	8115	8346	8092	8229	<b>8.20</b>

Table 2A: Average runtime of all algorithms in Scenario 1 + 2. To perform the analyses, we used GSE10072 and calculated the expression differences for tumor and normal samples. We then selected the top 250 upregulated genes for each analysis. The analyses were performed using the entire RTI collection of Database V1 2016.

	Run 1 [ms]	Run 2 [ms]	Run 3 [ms]	Run 4 [ms]	Run 5 [ms]	Average runtime in s
<b>Hypergeometric test</b>	28619	28554	28643	28709	28651	<b>28.64</b>
<b>Fisher's exact test</b>	32003	31741	31793	32069	31710	<b>31.86</b>
<b>Binomial test</b>	250926	245165	243075	243993	244695	<b>245.57</b>
<b>REGGAE</b>	331289	331978	345028	344942	335938	<b>337.84</b>
<b>REGGAE (without bootstrapping)</b>	8470	8915	8731	8744	8337	<b>8.64</b>
<b>RIF1</b>	8425	8425	8280	8111	8320	<b>8.31</b>
<b>RIF2</b>	8474	8306	8305	8341	8473	<b>8.38</b>

Table 2B: Average runtime of all algorithms in Scenario 1 + 2. To perform the analyses, we used GSE10072 and calculated the expression differences for tumor and normal samples. We then selected the top 500 upregulated genes for each analysis. The analyses were performed using the entire RTI collection of Database V1 2016.

	Run1 [s]	Run2 [s]	Run3 [s]	Run4 [s]	Run5 [s]	Average runtime in s
<b>TEPIC – all PSEM</b> s	469	471	471	476	470	<b>471.4</b>
<b>TEPIC – public PSEM</b> s	263	263	262	264	262	<b>262.8</b>
<b>INVOKE lasso penalty with performance measurement</b>	422	410	441	404	431	<b>421.6</b>
<b>INVOKE lasso penalty without performance measurement</b>	205	230	245	217	221	<b>224</b>
<b>INVOKE ridge penalty with performance measurement</b>	106	104	105	105	104	<b>105</b>
<b>INVOKE ridge penalty without performance measurement</b>	43	43	42	43	42	<b>43</b>
<b>INVOKE elastic net penalty with performance measurement</b>	3441	3606	3467	3470	3533	<b>3503</b>
<b>INVOKE elastic net penalty without performance measurement</b>	1683	1702	1738	1679	1772	<b>1715</b>

Table 2C: Average runtime of all algorithms in Scenario 3 + 4. To perform the analyses, we used BLUEPRINT Sample S001S7. We calculated binding affinities using TEPIC and trained predictive models of gene expression using INVOKE.

## Supplementary Table 3 – Methods for p-value adjustment

<b>Method</b>	<b>Reference</b>
<b>Bonferroni</b>	[S1.01]
<b>Šidák</b>	[S1.02]
<b>Holm</b>	[S1.03]
<b>Holm- Šidák</b>	[S1.02, S1.03]
<b>Finner</b>	[S1.04]
<b>Hochberg</b>	[S1.05]
<b>Benjamini-Hochberg</b>	[S1.06]
<b>Benjamini-Yekutieli</b>	[S1.07]

[S1.01] Bonferroni, Carlo E. Il calcolo delle assicurazioni su gruppi di teste. Tipografia del Senato, 1935.

[S1.02] Šidák, Zbyněk. "Rectangular confidence regions for the means of multivariate normal distributions." *Journal of the American Statistical Association* 62.318 (1967): 626-633.

[S1.03] Holm, Sture. "A simple sequentially rejective multiple test procedure." *Scandinavian journal of statistics* (1979): 65-70.

[S1.04] Finner, Helmut. "Some new inequalities for the range distribution, with application to the determination of optimum significance levels of multiple range tests." *Journal of the American Statistical Association* 85.409 (1990): 191-194.

[S1.05] Hochberg, Yosef. "A sharper Bonferroni procedure for multiple tests of significance." *Biometrika* 75.4 (1988): 800-802.

[S1.06] Benjamini, Yoav, and Yosef Hochberg. "Controlling the false discovery rate: a practical and powerful approach to multiple testing." *Journal of the royal statistical society. Series B (Methodological)* (1995): 289-300.

[S1.07] Benjamini, Yoav, and Daniel Yekutieli. "The control of the false discovery rate in multiple testing under dependency." *Annals of statistics* (2001): 1165-1188.

## Supplementary Table 4 – REGGAE Parameters

Parameter	Value
<b>Identifier level statistic</b>	Shrinkage t-test
<b>Upper-quantile filter</b>	0.05
<b>Enrichment method</b>	Wilcoxon rank-sum test
<b>Order of test set</b>	decreasingly
<b>Method to compute the influence of regulators</b>	Pearson correlation
<b>Scoring mode for influence scores</b>	Absolute correlation
<b>Method to adjust p-values</b>	Benjamini-Yekutieli
<b>Number of bootstrap replications</b>	1000
<b>Random seed</b>	8938479563690567223
<b>RTI collection</b>	Entire collection V1 2016

## Supplementary Table 5 – REGGAE Results

<b>Rank</b>	<b>Regulator</b>	<b>#Targets</b>	<b>Score</b>	<b>Adjusted p-value</b>	<b>Mean correlation</b>
<b>1</b>	FOSL2	968	27.07	4.88e-158	-0.319
<b>2</b>	CEBPA	861	26.16	7.70e-148	-0.328
<b>3</b>	ZBTB7A	917	25.58	1.76e-141	-0.318
<b>4</b>	SMAD1	780	25.49	1.35e-140	-0.317
<b>5</b>	GATA3	976	25.09	3.13e-136	-0.293
<b>6</b>	E2F6	983	24.14	3.92e-126	0.314
<b>7</b>	MITF	645	22.06	2.23e-105	0.355
<b>8</b>	FOXP1	813	21.92	4.92e-104	-0.294
<b>9</b>	TFAP2C	951	21.11	1.60e-96	-0.28
<b>10</b>	RXRA	802	20.81	7.42e-94	-0.277
<b>11</b>	CBX3	955	20.31	1.94e-89	0.301
<b>12</b>	BRCA1	741	19.6	3.03e-83	0.331
<b>13</b>	ATF2	925	18.98	4.00e-78	0.298
<b>14</b>	HEY1	941	18.92	1.37e-77	0.279
<b>15</b>	TP63	446	18.63	2.62e-75	-0.303
<b>16</b>	BCL11A	682	17.96	5.36e-70	-0.271
<b>17</b>	SP1	1018	17.62	2.49e-67	-0.231
<b>18</b>	RAD21	1017	16.91	5.14e-62	0.242
<b>19</b>	PBX1	624	16.8	2.85e-61	-0.268
<b>20</b>	KLF5	658	16.5	4.24e-59	-0.272
<b>21</b>	KDM5B	993	16.42	1.45e-58	-0.22
<b>22</b>	GRHL2	396	14.93	2.20e-48	-0.282
<b>23</b>	PRDM1	258	14.67	9.23e-47	-0.325
<b>24</b>	NANOG	922	14.49	1.31e-45	-0.232
<b>25</b>	ETV1	535	14.18	1.12e-43	0.318
<b>26</b>	NCOA1	419	13.64	1.97e-40	-0.3
<b>27</b>	RBL1	609	13.24	4.07e-38	0.280
<b>28</b>	NFIC	964	12.98	1.30e-36	-0.226
<b>29</b>	SMC1A	928	12.9	3.61e-36	0.246
<b>30</b>	CDK8	878	12.78	1.49e-35	0.244
<b>31</b>	ZMIZ1	860	12.67	5.94e-35	-0.214
<b>32</b>	RUNX1	964	12.59	1.64e-34	-0.219
<b>33</b>	ZNF750	415	12.51	4.32e-34	-0.258
<b>34</b>	ELL2	440	12.49	5.36e-34	-0.273
<b>35</b>	ATF1	750	12.39	1.98e-33	0.259
<b>36</b>	NIPBL	840	12.16	3.30e-32	-0.207
<b>37</b>	KLF4	384	12.1	6.60e-32	-0.271
<b>38</b>	STAT3	988	11.78	3.03e-30	-0.213
<b>39</b>	RB1	707	11.77	3.17e-30	0.254
<b>40</b>	SAP30	740	11.2	2.34e-27	0.255

<b>41</b>	AR	1010	10.84	1.23e-25	-0.214
<b>42</b>	PRAME	426	10.81	1.72e-25	0.279
<b>43</b>	ASUN	498	10.76	2.66e-25	0.283
<b>44</b>	YAP1	774	10.72	4.00e-25	-0.206
<b>45</b>	TBL1X	435	10.54	2.70e-24	-0.259
<b>46</b>	FOXM1	922	10.5	4.26e-24	0.227
<b>47</b>	CBFB	871	9.807	5.05e-21	0.241
<b>48</b>	NME1	232	9.66	2.10e-20	0.259
<b>49</b>	RCOR1	967	9.596	3.83e-20	-0.129
<b>50</b>	LIN9	247	9.546	6.09e-20	0.313
<b>51</b>	BCL6	892	9.502	9.13e-20	-0.219
<b>52</b>	LDB1	231	9.184	1.80e-18	-0.258
<b>53</b>	CTBP2	412	9.162	2.16e-18	0.261
<b>54</b>	HOXA4	741	9.142	2.55e-18	0.251
<b>55</b>	GATAD1	536	9.102	3.63e-18	0.263
<b>56</b>	CHD8	937	8.904	2.17e-17	-0.184
<b>57</b>	EREG	243	8.848	3.51e-17	-0.235
<b>58</b>	BCLAF1	806	8.815	4.66e-17	-0.157
<b>59</b>	NOTCH1	858	8.762	7.33e-17	-0.193
<b>60</b>	THAP1	392	8.714	1.10e-16	0.278
<b>61</b>	HDAC3	120	8.471	9.02e-16	-0.292
<b>62</b>	WRNIP1	588	8.146	1.37e-14	0.234
<b>63</b>	NCAPG	126	7.988	4.91e-14	0.343
<b>64</b>	RFX5	915	7.951	6.53e-14	0.201
<b>65</b>	E2F1	942	7.69	5.10e-13	0.207
<b>66</b>	EZH2	913	7.614	9.09e-13	0.184
<b>67</b>	APOBEC3B	164	7.549	1.48e-12	0.281
<b>68</b>	CEPB	1024	7.324	7.97e-12	-0.177
<b>69</b>	TP73	241	7.114	3.68e-11	-0.223
<b>70</b>	TET3	95	7.026	6.85e-11	-0.305
<b>71</b>	RARG	189	6.918	1.45e-10	-0.255
<b>72</b>	GREB1	83	6.884	1.82e-10	0.323
<b>73</b>	RUNX3	969	6.819	2.83e-10	0.160
<b>74</b>	TCF4	361	6.783	3.59e-10	-0.199
<b>75</b>	SUMO2	944	6.592	1.30e-9	0.161
<b>76</b>	KDM6B	780	6.489	2.56e-9	-0.197
<b>77</b>	ING2	842	6.44	3.49e-9	-0.177
<b>78</b>	MAF	64	6.437	3.51e-9	-0.307
<b>79</b>	TET2	78	6.214	1.47e-8	-0.277
<b>80</b>	HOXB7	125	6.129	2.48e-8	0.272
<b>81</b>	VDR	632	5.947	7.60e-8	-0.188
<b>82</b>	SOX10	41	5.939	7.89e-8	0.343
<b>83</b>	SCLY	89	5.417	1.65e-6	0.221
<b>84</b>	ZNF143	971	5.329	2.64e-6	0.189

<b>85</b>	FOXO3	30	5.319	2.76e-6	-0.317
<b>86</b>	BRD3	755	5.283	3.32e-6	-0.158
<b>87</b>	LMNA	428	5.268	3.57e-6	-0.2
<b>88</b>	HDAC8	63	5.134	7.25e-6	0.302
<b>89</b>	GRHL1	36	5.053	1.10e-5	-0.339
<b>90</b>	JMJD6	84	5.045	1.14e-5	0.287
<b>91</b>	CHD2	966	4.946	1.88e-5	-0.132
<b>92</b>	E2F7	223	4.906	2.28e-5	0.240
<b>93</b>	SRF	975	4.863	2.79e-5	-0.175
<b>94</b>	GRHL3	37	4.599	1.02e-4	-0.314
<b>95</b>	KDM4C	791	4.583	1.09e-4	-0.205
<b>96</b>	ETV5	448	4.315	3.74e-4	0.224
<b>97</b>	REST	1006	4.277	4.40e-4	-0.101
<b>98</b>	BMI1	498	4.272	4.45e-4	0.204
<b>99</b>	MECP2	509	4.247	4.93e-4	0.186
<b>100</b>	TLE3	44	4.091	9.68e-4	-0.277
<b>101</b>	TFAP2A	953	4.007	0.001	0.125
<b>102</b>	SOX9	586	4.002	0.001	-0.171
<b>103</b>	FOXO1	385	3.982	0.001	-0.193
<b>104</b>	MAFF	894	3.96	0.002	0.165
<b>105</b>	ORC1	42	3.898	0.002	0.315
<b>106</b>	MBD2	72	3.809	0.003	-0.246
<b>107</b>	NCAPG2	48	3.783	0.003	0.298
<b>108</b>	TAF2	126	3.717	0.004	0.263
<b>109</b>	CREBBP	964	3.703	0.004	-0.034
<b>110</b>	RREB1	40	3.702	0.004	-0.28
<b>111</b>	MAFB	87	3.643	0.005	-0.242
<b>112</b>	PRKDC	108	3.608	0.006	0.249
<b>113</b>	CREB1	988	3.581	0.007	-0.099
<b>114</b>	AUTS2	59	3.568	0.007	-0.239
<b>115</b>	CDK9	868	3.565	0.007	-0.172
<b>116</b>	GABPA	970	3.542	0.008	0.116
<b>117</b>	NELFE	779	3.448	0.011	0.184
<b>118</b>	SP2	343	3.366	0.015	0.201
<b>119</b>	ZNF384	922	3.262	0.021	0.169
<b>120</b>	UBTF	756	3.062	0.041	-0.145
<b>121</b>	ELF1	995	2.978	0.054	-0.13
<b>122</b>	SUMO1	452	2.972	0.055	0.149
<b>123</b>	NR4A1	148	2.968	0.055	0.225
<b>124</b>	TERF1	226	2.919	0.064	0.231
<b>125</b>	DEK	147	2.855	0.078	0.230
<b>126</b>	GMEB2	238	2.846	0.079	-0.207
<b>127</b>	ELF5	71	2.833	0.082	-0.224
<b>128</b>	CDK7	799	2.805	0.089	-0.143

129	EHF	15	2.795	0.091	-0.286
130	BACH2	190	2.763	0.099	-0.203
131	OVOL2	21	2.759	0.099	-0.288
132	ASH2L	283	2.758	0.099	0.221
133	HLF	17	2.72	0.111	-0.21
134	PHF8	959	2.604	0.155	0.136
135	ZNF711	131	2.597	0.157	-0.136
136	YBX1	41	2.586	0.161	0.259
137	ZNF83	320	2.467	0.224	-0.221
138	MYB	867	2.463	0.225	-0.186
139	MBD1	4	2.447	0.234	-0.257
140	GTF2B	817	2.442	0.235	0.182
141	CBX8	14	2.403	0.259	0.313
142	BRIP1	7	2.402	0.259	0.333
143	YY1	1012	2.384	0.269	0.072
144	ETS1	955	2.333	0.307	0.154
145	NR3C1	980	2.279	0.352	-0.156
146	NCOA3	44	2.196	0.433	-0.259
147	ETV4	17	2.104	0.540	0.212
148	E2F4	991	2.102	0.540	-0.133
149	JUNB	658	2.1	0.540	-0.166
150	ZNF92	156	2.052	0.603	0.175
151	ARNT2	54	2.037	0.621	0.264
152	USF2	800	1.972	0.720	0.063
153	E2F8	228	1.965	0.728	0.224
154	CHD7	34	1.935	0.775	0.267
155	SPDEF	257	1.927	0.784	-0.177
156	SMAD3	730	1.924	0.786	-0.148
157	AREG	37	1.877	0.868	-0.175
158	ING4	2	1.867	0.883	-0.363
159	DNMT1	11	1.836	0.941	0.312
160	DDIT3	2	1.757	1	0.624
161	HECTD1	2	1.753	1	-0.379
162	PBX2	7	1.75	1	0.340
163	NFATC1	832	1.749	1	-0.184
164	WDHD1	1	1.721	1	0.763
165	DOT1L	1	1.708	1	0.593
166	RPA3	1	1.706	1	0.815
167	ZBTB33	718	1.703	1	0.118
168	DNAJC2	38	1.664	1	0.164
169	TTF2	109	1.656	1	0.229
170	MAX	1023	1.648	1	0.135
171	SFPQ	878	1.628	1	-0.109
172	PHF6	5	1.607	1	0.354

173	TCF7L2	987	1.564	1	-0.116
174	NFKB2	1	1.521	1	0.408
175	ZMYND11	5	1.507	1	-0.264
176	TAF7	805	1.476	1	0.172
177	TRRAP	190	1.453	1	0.218
178	POU3F2	110	1.438	1	0.192
179	FOSB	1	1.429	1	0.333
180	FANCD2	1	1.421	1	0.423
181	BDP1	392	1.42	1	0.085
182	NR2F6	1	1.364	1	-0.324
183	ZC3H8	57	1.357	1	0.232
184	TRIM24	1	1.335	1	0.325
185	DEAF1	1	1.334	1	-0.339
186	NFE2	850	1.33	1	-0.183
187	PURA	1	1.303	1	0.288
188	KDM6A	48	1.298	1	-0.198
189	MBD3	4	1.291	1	-0.255
190	PLSCR1	1	1.281	1	0.344
191	NOLC1	1	1.277	1	0.415
192	ELOF1	10	1.25	1	0.145
193	KAT5	180	1.229	1	-0.141
194	PARP1	2	1.227	1	0.315
195	SOX4	171	1.224	1	-0.109
196	BATF	804	1.208	1	0.112
197	HES1	1	1.2	1	-0.232
198	ELF3	1	1.152	1	-0.164
199	NR1H3	58	1.119	1	0.174
200	DVL1	1	1.082	1	0.281
201	ZNF486	19	1.077	1	-0.198
202	DYRK1A	21	1.074	1	0.166
203	HTT	10	1.064	1	-0.195
204	HNRNPK	1	1.048	1	-0.098
205	MYCN	42	1.038	1	-0.114
206	HMGA2	1	1.036	1	0.363
207	DLX3	1	1.027	1	-0.242
208	PLAU	1	1.008	1	0.189
209	RAD51	1	0.983	1	0.425
210	CDK2	4	0.956	1	0.352
211	ERG	1004	0.954	1	-0.146
212	MIA3	3	0.908	1	0.262
213	IRF2	101	0.894	1	0.203
214	WHSC1	2	0.850	1	0.300
215	ATF7	1	0.845	1	-0.244
216	RELA	985	0.842	1	-0.086

217	NKX2-2	1	0.837	1	0.220
218	RPA1	1	0.827	1	0.334
219	CBX4	15	0.821	1	0.245
220	NR2F1	792	0.808	1	0.172
221	SP3	20	0.808	1	-0.186
222	XRCC5	1	0.803	1	-0.256
223	UBP1	1	0.784	1	-0.327
224	KLF8	1	0.776	1	-0.219
225	ATF7IP	6	0.772	1	-0.166
226	GABPB1	1	0.738	1	0.312
227	FLII	29	0.706	1	-0.037
228	STAT5A	800	0.690	1	0.120
229	PIAS1	400	0.686	1	-0.151
230	LHX2	49	0.677	1	-0.142
231	CBX2	7	0.636	1	0.217
232	HDAC2	956	0.630	1	-0.078
233	BCL11B	1	0.619	1	-0.228
234	TEAD4	990	0.611	1	0.122
235	NFATC4	1	0.610	1	0.234
236	TEAD1	436	0.592	1	0.162
237	THR8	1	0.567	1	-0.202
238	ETS2	3	0.549	1	-0.248
239	ESRRG	1	0.523	1	0.211
240	BRD7	27	0.493	1	-0.117
241	ARRB1	12	0.492	1	-0.25
242	ZZZ3	257	0.473	1	0.157
243	ZNF395	3	0.473	1	-0.272
244	SRCAP	8	0.468	1	-0.223
245	HAND2	4	0.453	1	0.169
246	GLI2	596	0.433	1	-0.15
247	FOXO4	1	0.431	1	-0.171
248	ARNT	325	0.426	1	-0.17
249	REL	3	0.413	1	-0.236
250	GDNF	3	0.410	1	-0.085
251	NFE2L2	88	0.401	1	-0.126
252	ZNF350	1	0.381	1	-0.166
253	BRF2	232	0.377	1	0.158
254	EGFR	4	0.370	1	-0.169
255	KCNIP3	1	0.369	1	0.156
256	HIF1A	941	0.360	1	0.115
257	CBX7	4	0.346	1	-0.174
258	LTF	1	0.319	1	-0.232
259	DROSHA	11	0.299	1	0.161
260	ELF2	11	0.294	1	-0.228

261	NFKB1	222	0.280	1	-0.142
262	OLIG2	1	0.277	1	0.155
263	NR3C2	2	0.271	1	-0.273
264	AGO1	232	0.256	1	-0.187
265	MZF1	2	0.251	1	-0.202
266	TCFL5	1	0.232	1	0.201
267	EBF1	946	0.217	1	-0.163
268	NFYB	775	0.202	1	-0.052
269	DAND5	3	0.161	1	-0.064
270	ISL2	2	0.160	1	0.089
271	IRF5	40	0.157	1	-0.058
272	HIC1	1	0.140	1	0.012
273	HOXC10	1	0.138	1	0.184
274	CREM	1	0.122	1	0.173
275	NR5A2	28	0.106	1	0.159
276	NFIB	1	0.098	1	-0.237
277	FOXE1	3	0.083	1	-0.103
278	TP53BP1	17	0.081	1	0.076
279	TDRD3	6	0.062	1	0.252
280	PPARD	200	0.030	1	-0.004
281	NFATC2	3	0.019	1	0.106
282	TFE3	1	-0.004	1	0.129
283	ZIC1	1	-0.012	1	-0.147
284	PALB2	9	-0.014	1	0.226
285	SETD2	2	-0.02	1	-0.15
286	MAPK1	4	-0.028	1	0.104
287	HOXC13	1	-0.034	1	0.149
288	RFX2	20	-0.036	1	-0.194
289	WDR5	914	-0.06	1	-0.113
290	ETV7	1	-0.061	1	-0.117
291	DR1	30	-0.072	1	0.194
292	SNAPC1	7	-0.078	1	0.186
293	HOXC11	1	-0.092	1	0.125
294	PSIP1	14	-0.106	1	0.207
295	FOXD1	1	-0.132	1	0.129
296	AGO2	29	-0.132	1	0.024
297	SNAPC2	1	-0.174	1	-0.06
298	KDM5C	53	-0.185	1	-0.148
299	C17ORF96	9	-0.2	1	-0.055
300	RYBP	2	-0.23	1	0.096
301	ZIC2	1	-0.279	1	-0.107
302	CHD1	839	-0.298	1	0.148
303	SFMBT1	12	-0.318	1	0.141
304	EGR2	24	-0.319	1	-0.063

305	TFCP2	1	-0.32	1	0.205
306	TFDP1	2	-0.322	1	0.192
307	TERF2	2	-0.328	1	0.100
308	POLR2A	1002	-0.33	1	-0.143
309	PPARA	5	-0.333	1	-0.059
310	APEX1	1	-0.334	1	0.176
311	DNTTIP1	1	-0.336	1	0.133
312	DSCAM	2	-0.347	1	-0.139
313	EPAS1	50	-0.349	1	-0.104
314	BRD4	959	-0.352	1	-0.124
315	RUNX2	194	-0.354	1	0.147
316	POLR3G	4	-0.368	1	0.168
317	ARNTL	897	-0.369	1	-0.159
318	POU2F1	125	-0.378	1	-0.066
319	SPANXC	1	-0.384	1	-0.106
320	CIITA	45	-0.42	1	-0.056
321	TFAP2D	2	-0.424	1	-0.104
322	TOP2B	96	-0.431	1	0.027
323	HOXA5	7	-0.437	1	0.171
324	INO80	20	-0.441	1	-0.073
325	CKAP4	545	-0.459	1	-0.124
326	PPARGC1A	134	-0.462	1	0.170
327	CBFA2T3	3	-0.476	1	-0.093
328	KDM2B	1	-0.487	1	-0.15
329	BLVRA	1	-0.516	1	0.143
330	XRCC4	9	-0.519	1	0.081
331	HLTF	1	-0.531	1	0.084
332	MRE11A	57	-0.552	1	0.124
333	HOXA2	1	-0.556	1	-0.064
334	ZBTB24	2	-0.57	1	0.229
335	SLC6A4	2	-0.636	1	-0.122
336	ARHGEF7	9	-0.643	1	0.072
337	CDX1	1	-0.661	1	-0.175
338	DEC1	1	-0.688	1	-0.108
339	IRF9	2	-0.698	1	-0.115
340	HNF1B	11	-0.699	1	0.049
341	AFF4	704	-0.707	1	-0.003
342	SIRT3	1	-0.719	1	0.073
343	EWSR1	46	-0.72	1	0.130
344	SORBS2	1	-0.727	1	-0.061
345	TCF7L1	1	-0.751	1	-0.074
346	FABP4	1	-0.76	1	-0.121
347	HNRNPL	1	-0.805	1	-0.144
348	ARNTL2	1	-0.807	1	-0.028

349	CARM1	5	-0.841	1	0.128
350	SNAPC5	3	-0.845	1	0.157
351	PLAG1	29	-0.851	1	-0.119
352	HOXA13	2	-0.851	1	-0.03
353	CTNNB1	261	-0.875	1	0.167
354	FOXK1	4	-0.89	1	0.109
355	GLI1	7	-0.9	1	-0.08
356	TFF2	1	-0.901	1	0.100
357	RXRB	1	-0.904	1	-0.016
358	E2F2	7	-0.911	1	0.059
359	HOXA10	1	-0.93	1	0.084
360	ZNF148	1	-0.933	1	-0.087
361	MTA1	1	-0.947	1	-0.059
362	SALL2	1	-0.952	1	0.109
363	PES1	1	-0.962	1	-0.006
364	AFF1	227	-0.963	1	-0.165
365	ELL	11	-0.965	1	-0.183
366	ZC3H11A	28	-0.965	1	0.007
367	XRN2	139	-0.97	1	0.156
368	LIN54	139	-0.999	1	0.047
369	RXRG	1	-1.004	1	0.069
370	RPA2	1	-1.01	1	0.099
371	CEBPZ	16	-1.012	1	0.130
372	PCGF2	79	-1.043	1	0.014
373	PIAS4	11	-1.106	1	-0.052
374	HSF1	887	-1.109	1	0.123
375	GFI1	1	-1.114	1	-0.013
376	PRDM2	1	-1.132	1	0.020
377	MTF1	1	-1.132	1	0.043
378	CBX6	4	-1.154	1	0.089
379	ZFHX4	10	-1.176	1	0.129
380	GTF2I	567	-1.179	1	0.153
381	IRF8	14	-1.185	1	0.076
382	E2F5	2	-1.186	1	0.105
383	ZNF652	5	-1.199	1	0.034
384	FUBP1	1	-1.2	1	0.064
385	HMGAI	3	-1.202	1	0.078
386	FOXF2	51	-1.211	1	0.144
387	ELF4	1	-1.216	1	-0.025
388	CBX5	5	-1.226	1	-0.091
389	SCML2	180	-1.228	1	0.149
390	MEF2C	447	-1.231	1	0.166
391	BCL10	1	-1.244	1	0.007
392	DPPA3	2	-1.246	1	-0.038

393	ZNF281	3	-1.247	1	0.110
394	NR1H4	28	-1.264	1	0.036
395	CTBP1	263	-1.271	1	-0.159
396	ICE2	10	-1.279	1	0.068
397	HMBOX1	24	-1.302	1	-0.105
398	TFAM	1	-1.304	1	0.143
399	RLF	2	-1.307	1	0.031
400	T	147	-1.311	1	0.147
401	SOX11	50	-1.333	1	0.038
402	ZNF12	23	-1.351	1	0.218
403	NFYC	364	-1.358	1	-0.122
404	INSM1	51	-1.375	1	0.083
405	GLI3	6	-1.386	1	-9.85e-4
406	ASF1A	170	-1.395	1	-0.104
407	L3MBTL2	12	-1.396	1	0.073
408	NR5A1	8	-1.4	1	0.095
409	ZNF280D	255	-1.402	1	0.144
410	HSF4	1	-1.456	1	-0.023
411	ZNF84	21	-1.484	1	-0.021
412	KCNH8	23	-1.499	1	-0.04
413	KDM3A	165	-1.507	1	0.099
414	GPS2	19	-1.522	1	-0.076
415	ATRX	3	-1.532	1	0.068
416	ELK1	646	-1.537	1	0.100
417	BCOR	869	-1.547	1	0.142
418	ZFP42	95	-1.648	1	-0.172
419	SALL1	5	-1.671	1	0.041
420	SLC22A1	1	-1.692	1	-0.052
421	KMT2A	651	-1.708	1	-0.144
422	CLOCK	28	-1.727	1	-0.075
423	NRF1	919	-1.742	1	-0.092
424	ZKSCAN1	315	-1.747	1	0.154
425	ERCC3	184	-1.753	1	0.146
426	NR2C2	501	-1.764	1	-0.078
427	LMTK3	31	-1.782	1	-0.13
428	STAT6	36	-1.79	1	-0.07
429	HOXC8	4	-1.798	1	0.072
430	GBX2	11	-1.803	1	-0.055
431	CDX2	970	-1.81	1	0.064
432	SVIL	2	-1.847	1	-0.056
433	DACH1	138	-1.873	1	-0.149
434	SSRP1	73	-1.928	1	0.057
435	ZBTB10	106	-1.93	1	0.174
436	HSF2	4	-1.933	1	0.002

437	DCP1A	487	-2.001	1	0.146
438	ZFX	229	-2.044	1	0.139
439	EZH1	57	-2.09	1	-0.125
440	LEF1	74	-2.102	1	0.137
441	RBL2	328	-2.126	1	-0.101
442	HINFP	3	-2.17	1	0.080
443	SETDB1	709	-2.218	1	-0.026
444	SMAD2	355	-2.235	1	0.024
445	KAT2B	22	-2.249	1	-0.024
446	PRKCQ	29	-2.255	1	-0.129
447	NHLH1	39	-2.308	1	0.060
448	CCNT2	824	-2.342	1	0.015
449	MYC	1026	-2.353	1	0.134
450	STAT4	93	-2.371	1	0.031
451	HMGN3	793	-2.424	1	-0.083
452	TFAP4	442	-2.467	1	0.135
453	NR2F2	951	-2.476	1	0.092
454	TFEB	71	-2.484	1	-0.088
455	ONECUT1	30	-2.494	1	0.077
456	HDAC6	128	-2.503	1	-0.049
457	FOXH1	539	-2.505	1	0.102
458	WWTR1	145	-2.524	1	0.135
459	KAT8	111	-2.566	1	-0.13
460	MEIS1	58	-2.685	1	-0.092
461	HEYL	19	-2.692	1	0.007
462	LMO3	164	-2.744	1	-0.118
463	MYBL2	819	-2.812	1	0.148
464	ZNF274	101	-2.854	1	-0.074
465	TBP	993	-2.869	1	-0.127
466	GFI1B	30	-2.932	1	-0.07
467	TOP1	306	-2.954	1	0.048
468	ALKBH3	26	-2.988	1	-0.001
469	SMC3	959	-3.007	1	0.009
470	NFYA	821	-3.016	1	0.142
471	NOS2	12	-3.02	1	-0.005
472	FOXI1	46	-3.063	1	-0.094
473	SMARCB1	933	-3.074	1	0.101
474	HNF1A	23	-3.109	1	-0.067
475	TCF3	906	-3.141	1	0.068
476	NCOR2	337	-3.175	1	-0.122
477	ESRRA	225	-3.197	1	-0.051
478	ELK4	484	-3.245	1	-0.114
479	BACH1	653	-3.257	1	0.053
480	TP53	851	-3.282	1	-0.086

<b>481</b>	SOX17	40	-3.309	1	0.012
<b>482</b>	ASCL1	236	-3.326	1	0.090
<b>483</b>	RUNX1T1	672	-3.472	1	-0.137
<b>484</b>	GLYR1	17	-3.484	1	0.108
<b>485</b>	HIRA	130	-3.594	1	0.009
<b>486</b>	TAL1	968	-3.599	1	-0.074
<b>487</b>	TCF12	997	-3.632	1	0.059
<b>488</b>	FOXA3	81	-3.719	1	0.090
<b>489</b>	RNF2	255	-3.77	1	0.118
<b>490</b>	SIN3A	996	-3.796	1	-0.093
<b>491</b>	INTS3	686	-3.811	1	0.063
<b>492</b>	EED	113	-3.818	1	0.059
<b>493</b>	MXD3	27	-3.855	1	-0.038
<b>494</b>	HDAC1	870	-3.941	1	0.118
<b>495</b>	CYP27B1	17	-3.962	1	-0.045
<b>496</b>	CTCF	1022	-3.974	1	-0.037
<b>497</b>	LMNB1	744	-3.974	1	0.124
<b>498</b>	HOXC9	170	-4.038	1	0.108
<b>499</b>	SUPT5H	867	-4.049	1	-0.045
<b>500</b>	SALL4	104	-4.102	1	0.105
<b>501</b>	LYL1	175	-4.314	1	0.043
<b>502</b>	GTF3C2	228	-4.387	1	0.081
<b>503</b>	ICE1	636	-4.417	1	0.124
<b>504</b>	STAT2	574	-4.504	1	0.047
<b>505</b>	PRDM14	89	-4.519	1	0.042
<b>506</b>	C17ORF49	188	-4.521	1	-0.093
<b>507</b>	BRD1	703	-4.569	1	-0.117
<b>508</b>	TBX21	166	-4.693	1	0.031
<b>509</b>	AHR	210	-4.724	1	0.020
<b>510</b>	ARID3A	745	-4.739	1	-0.003
<b>511</b>	SIRT6	301	-4.762	1	-0.08
<b>512</b>	IRF4	931	-4.831	1	0.072
<b>513</b>	CSNK2A1	148	-4.863	1	0.101
<b>514</b>	IRF3	167	-4.898	1	-0.005
<b>515</b>	KDM5A	188	-4.983	1	-0.085
<b>516</b>	CDK12	99	-5.013	1	0.059
<b>517</b>	BRF1	339	-5.03	1	-0.068
<b>518</b>	CTCFL	919	-5.032	1	0.003
<b>519</b>	GTF2F1	799	-5.065	1	0.013
<b>520</b>	ERCC2	112	-5.089	1	-0.11
<b>521</b>	HMGN1	112	-5.199	1	0.039
<b>522</b>	E2F3	712	-5.226	1	0.149
<b>523</b>	ZNF263	941	-5.264	1	-0.07
<b>524</b>	TRIM28	995	-5.321	1	0.016

<b>525</b>	FOXA2	989	-5.357	1	0.068
<b>526</b>	JUN	1010	-5.373	1	-0.082
<b>527</b>	ELK3	362	-5.417	1	0.077
<b>528</b>	MTA3	786	-5.473	1	-0.15
<b>529</b>	KAT2A	247	-5.496	1	0.063
<b>530</b>	PADI4	98	-5.542	1	-0.114
<b>531</b>	PAF1	131	-5.571	1	-0.01
<b>532</b>	PAX6	218	-5.581	1	-0.076
<b>533</b>	GATA2	969	-5.599	1	-0.112
<b>534</b>	CHD4	151	-5.656	1	-0.03
<b>535</b>	ZNF76	173	-5.752	1	0.106
<b>536</b>	ESR2	289	-5.768	1	-0.06
<b>537</b>	JUND	1018	-5.773	1	-0.075
<b>538</b>	WT1	199	-5.852	1	0.072
<b>539</b>	TBL1XR1	791	-5.859	1	-7.94e-4
<b>540</b>	FOSL1	885	-6.022	1	0.125
<b>541</b>	PDX1	277	-6.065	1	3.50e-4
<b>542</b>	SP4	631	-6.084	1	0.082
<b>543</b>	FUS	211	-6.093	1	-0.015
<b>544</b>	EOMES	609	-6.226	1	0.110
<b>545</b>	ZNF217	354	-6.261	1	0.030
<b>546</b>	THAP11	153	-6.345	1	-0.113
<b>547</b>	SUPT20H	191	-6.352	1	0.034
<b>548</b>	BCL3	855	-6.361	1	-0.071
<b>549</b>	POLR3A	507	-6.385	1	-0.029
<b>550</b>	IRF1	951	-6.4	1	-0.074
<b>551</b>	SREBF1	557	-6.406	1	-0.107
<b>552</b>	SREBF2	236	-6.481	1	-0.033
<b>553</b>	SMARCA4	909	-6.492	1	0.013
<b>554</b>	MED12	328	-6.56	1	0.034
<b>555</b>	SMARCC1	867	-6.701	1	0.006
<b>556</b>	CUX1	851	-6.726	1	-0.007
<b>557</b>	STAT5B	350	-6.75	1	0.025
<b>558</b>	NKX3-1	375	-6.775	1	0.047
<b>559</b>	HNF4G	645	-6.791	1	0.129
<b>560</b>	SNAI2	903	-6.905	1	-0.057
<b>561</b>	DAXX	564	-6.959	1	-0.042
<b>562</b>	SMAD4	455	-6.985	1	-0.011
<b>563</b>	EHMT2	301	-7.056	1	-0.005
<b>564</b>	STAG1	886	-7.069	1	-0.054
<b>565</b>	EGR1	984	-7.205	1	-0.104
<b>566</b>	LMO2	320	-7.297	1	0.009
<b>567</b>	MED1	952	-7.385	1	-0.017
<b>568</b>	ZEB1	776	-7.407	1	-0.006

569	CPSF3L	507	-7.414	1	-0.022
570	MYH11	818	-7.418	1	-0.138
571	RBBP5	967	-7.422	1	0.052
572	DDX5	914	-7.429	1	0.026
573	TAF3	821	-7.482	1	-0.084
574	STAT1	992	-7.487	1	0.067
575	PROX1	192	-7.675	1	-0.056
576	SUZ12	420	-7.69	1	0.079
577	CDK6	351	-7.73	1	0.008
578	RBPJ	706	-7.755	1	-0.034
579	FOXP3	163	-7.764	1	-0.016
580	ZBTB17	503	-7.768	1	0.030
581	KAT7	760	-7.797	1	0.035
582	TCP1	453	-7.826	1	-0.042
583	BRD2	599	-7.916	1	-0.051
584	HCFC1	915	-8.076	1	0.061
585	KLF1	899	-8.233	1	0.004
586	ATF3	927	-20.45	1	-0.016
587	PAX5	914	-20.54	1	0.026
588	RAG2	867	-20.22	1	-0.018
589	OTX2	623	-16.67	1	-0.036
590	FOS	995	-16.96	1	-0.036
591	GATA1	980	-16.18	1	-0.026
592	NKX2-1	762	-14.74	1	0.056
593	MAFK	1010	-14.37	1	0.012
594	PBX3	952	-14.12	1	0.050
595	KDM4A	842	-14.64	1	0.030
596	CEBDP	803	-13.43	1	-0.03
597	XBP1	597	-13.87	1	0.045
598	RARA	834	-13.29	1	0.060
599	MEF2B	352	-13.74	1	-0.014
600	MYOD1	510	-12.56	1	-0.035
601	HOXA6	667	-12.7	1	0.004
602	GATA4	871	-12.05	1	0.075
603	NPAT	530	-12.23	1	0.061
604	MXI1	986	-12.01	1	-0.026
605	EP300	1022	-12.65	1	0.055
606	TCF21	290	-11.81	1	0.049
607	MAZ	970	-11.54	1	0.034
608	TAF1	1005	-11.71	1	0.006
609	MBD4	480	-11.57	1	-0.003
610	FOXP2	861	-11.31	1	-0.093
611	SOX2	605	-11.69	1	0.059
612	PPARG	839	-10.2	1	-0.101

<b>613</b>	FOXA1	1017	-10.43	1	0.042
<b>614</b>	FLI1	923	-10.98	1	-0.022
<b>615</b>	PGR	661	-10.97	1	0.003
<b>616</b>	BHLHE40	951	-10.39	1	0.081
<b>617</b>	USF1	1002	-10.68	1	0.086
<b>618</b>	KDM1A	618	-10.8	1	0.062
<b>619</b>	RING1	731	-10.96	1	-0.039
<b>620</b>	ING5	782	-10.48	1	0.082
<b>621</b>	GATA6	976	-10.56	1	0.098
<b>622</b>	JARID2	457	-9.195	1	0.038
<b>623</b>	BARX1	212	-9.714	1	0.061
<b>624</b>	NCOR1	561	-9.266	1	-0.046
<b>625</b>	HNF4A	1009	-9.104	1	0.050
<b>626</b>	ESR1	978	-9.884	1	-0.019
<b>627</b>	SMARCC2	751	-9.853	1	0.036
<b>628</b>	IKZF1	442	-9.8	1	-0.015
<b>629</b>	PRDM11	297	-9.212	1	-0.083
<b>630</b>	MEF2A	716	-9.703	1	-0.038
<b>631</b>	NELFA	612	-9.118	1	-0.057
<b>632</b>	ATF4	305	-9.377	1	0.009
<b>633</b>	KLF11	836	-8.336	1	-0.134
<b>634</b>	POU2F2	926	-8.296	1	-0.02
<b>635</b>	DMC1	386	-8.833	1	-0.034
<b>636</b>	PML	939	-8.536	1	-0.07
<b>637</b>	SIX5	589	-8.395	1	-0.027
<b>638</b>	SPI1	1003	-8.825	1	0.038
<b>639</b>	KMT2D	832	-8.434	1	0.083
<b>640</b>	TLX1	208	-8.992	1	0.074

Supplementary Table 6 – Top 15 Regulators – Associations to melanoma

Regulators	Adjusted p-value	Melanoma	Metastasis or tumor progression	Tumor suppressor gene	Oncogene
<i>FOSL2</i>	4.88e-158		[S4.01]		
<i>CEBPA</i>	7.70e-148		[S4.02]	[S4.03]	
<i>ZBTB7A</i>	1.76e-141	[S4.04]	[S4.02, S4.04]	[S4.05]	
<i>SMAD1</i>	1.35e-140	[S4.06, S4.07]	[S4.08]		
<i>GATA3</i>	3.13e-136	[S4.09]	[S4.10]		
<i>E2F6</i>	3.92e-126	[S4.11, S4.12]			
<i>MITF</i>	2.23e-105	[S4.13, S4.14]	[S4.13, S4.14]		[S4.13, S4.14]
<i>FOXP1</i>	4.92e-104	[S4.15]	[S4.16]	[S4.17]	
<i>TFAP2C</i>	1.60e-96	[S4.18]			
<i>RXRA</i>	7.42e-94	[S4.19, S4.20]	[S4.19, S4.20]		
<i>CBX3</i>	1.94e-89	[S4.21]	[S4.22]		
<i>BRCA1</i>	3.03e-83	[S4.23]	[S4.24, S4.25]	[S4.26]	
<i>ATF2</i>	4.00e-78	[S4.27]	[S4.27]	[S4.28]	[S4.28]
<i>HEY1</i>	1.37e-77	[S4.29, S4.30]			
<i>TP63</i>	2.62e-75	[S4.31]	[S4.32]	[S4.32]	

[S4.01] Kim, Seung Woo, et al. "Association study of FOS-like antigen-2 promoter polymorphisms with papillary thyroid cancer in Korean population." Clinical and experimental otorhinolaryngology 7.1 (2014): 42. APA

[S4.02] Shi, Duan-Bo, et al. "C/EBP $\alpha$ -induced miR-100 expression suppresses tumor metastasis and growth by targeting ZBTB7A in gastric cancer." Cancer letters 369.2 (2015): 376-385.

[S4.03] Sato, Atsuyasu, et al. "CCAAT/enhancer-binding protein- $\alpha$  suppresses lung tumor development in mice through the p38 $\alpha$  MAP kinase pathway." PLoS One 8.2 (2013): e57013.

[S4.04] Liu, Xue-Song, et al. "ZBTB7A suppresses melanoma metastasis by transcriptionally repressing MCAM." Molecular Cancer Research 13.8 (2015): 1206-1217.

[S4.05] Liu, Xue-Song, et al. "ZBTB7A acts as a tumor suppressor through the transcriptional repression of glycolysis." Genes & development 28.17 (2014): 1917-1928.

[S4.06] Rungsimanond, N., et al. "Stable isoform of the Smad1 protein inhibits melanoma cell proliferation and migration." JOURNAL OF INVESTIGATIVE DERMATOLOGY. Vol. 130. 75 VARICK ST, 9TH FLR, NEW YORK, NY 10013-1917 USA: NATURE PUBLISHING GROUP, 2010.

[S4.07] Tang, Ming-Rui, et al. "CSMD1 exhibits antitumor activity in A375 melanoma cells through activation of the Smad pathway." Apoptosis 17.9 (2012): 927-937.

- [S4.08] Pangas, Stephanie A., et al. "Conditional deletion of Smad1 and Smad5 in somatic cells of male and female gonads leads to metastatic tumor development in mice." *Molecular and cellular biology* 28.1 (2008): 248-257.
- [S4.09] Riker, Adam I., et al. "The gene expression profiles of primary and metastatic melanoma yields a transition point of tumor progression and metastasis." *BMC medical genomics* 1.1 (2008): 13.
- [S4.10] Chou, Jonathan, et al. "GATA3 suppresses metastasis and modulates the tumour microenvironment by regulating microRNA-29b expression." *Nature cell biology* 15.2 (2013): 201-213.
- [S4.11] Deng, Tao, et al. "An essential role for DNA methyltransferase 3a in melanoma tumorigenesis." *Biochemical and biophysical research communications* 387.3 (2009): 611-616.
- [S4.12] Halaban, Ruth, et al. "Deregulated E2F transcriptional activity in autonomously growing melanoma cells." *The Journal of experimental medicine* 191.6 (2000): 1005-1016. APA
- [S4.13] Levy, Carmit, Mehdi Khaled, and David E. Fisher. "MITF: master regulator of melanocyte development and melanoma oncogene." *Trends in molecular medicine* 12.9 (2006): 406-414.
- [S4.14] Garraway, Levi A., et al. "Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma." *Nature* 436.7047 (2005): 117-122.
- [S4.15] Spritz, Richard A. "The genetics of generalized vitiligo: autoimmune pathways and an inverse relationship with malignant melanoma." *Genome medicine* 2.10 (2010): 78.
- [S4.16] Feng, Jian, et al. "High expression of FoxP1 is associated with improved survival in patients with non-small cell lung cancer." *American journal of clinical pathology* 138.2 (2012): 230-235.
- [S4.17] Banham, Alison H., et al. "The FOXP1 winged helix transcription factor is a novel candidate tumor suppressor gene on chromosome 3p." *Cancer research* 61.24 (2001): 8820-8829.
- [S4.18] Penna, Elisa, et al. "microRNA-214 contributes to melanoma tumour progression through suppression of TFAP2C." *The EMBO journal* 30.10 (2011): 1990-2007.
- [S4.19] Chakravarti, Nitin, et al. "Decreased expression of retinoid receptors in melanoma: entailment in tumorigenesis and prognosis." *Clinical Cancer Research* 13.16 (2007): 4817-4824.
- [S4.20] Klopper, Joshua P., et al. "Combination PPAR and RXR Agonist Treatment in Melanoma Cells: Functional Importance of S100A2." *PPAR research* 2010 (2009).
- [S4.21] Schmid, Rainer, et al. "Melanoma inhibitory activity promotes melanoma development through activation of YBX1." *Pigment cell & melanoma research* 26.5 (2013): 685-696.
- [S4.22] Hammoudi, Abeer T. Proteomic dissection of the early genetic changes in a colorectal cancer model. Diss. University of Liverpool, 2012.
- [S4.23] Liede, Alexander, Beth Y. Karlan, and Steven A. Narod. "Cancer risks for male carriers of germline mutations in BRCA1 or BRCA2: a review of the literature." *Journal of Clinical Oncology* 22.4 (2004): 735-742.

[S4.24] Seery, Liam T., et al. "BRCA1 expression levels predict distant metastasis of sporadic breast cancers." *International journal of cancer* 84.3 (1999): 258-262.

[S4.25] Szabova, Ludmila, et al. "Perturbation of Rb, p53, and Brca1 or Brca2 cooperate in inducing metastatic serous epithelial ovarian cancer." *Cancer research* 72.16 (2012): 4141-4153.

[S4.26] Chang, Suhwan, et al. "Tumor suppressor BRCA1 epigenetically controls oncogenic microRNA-155." *Nature medicine* 17.10 (2011): 1275-1282.

[S4.27] Bhoumik, Anindita, et al. "An ATF2-derived peptide sensitizes melanomas to apoptosis and inhibits their growth and metastasis." *The Journal of clinical investigation* 110.5 (2002): 643-650.

[S4.28] Bhoumik, Anindita, and Ze'ev Ronai. "ATF2: a transcription factor that elicits oncogenic or tumor suppressor activities." *Cell cycle* 7.15 (2008): 2341-2345.

[S4.29] Bedogni, Barbara, et al. "Notch1 is an effector of Akt and hypoxia in melanoma development." *The Journal of clinical investigation* 118.11 (2008): 3660-3670.

[S4.30] Hoek, Keith, et al. "Expression profiling reveals novel pathways in the transformation of melanocytes to melanomas." *Cancer research* 64.15 (2004): 5270-5282.

[S4.31] Matin, Rubeta N., et al. "p63 is an alternative p53 repressor in melanoma that confers chemoresistance and a poor prognosis." *Journal of Experimental Medicine* (2013): jem-20121439.

[S4.32] Su, Xiaohua, Deepavali Chakravarti, and Elsa R. Flores. "p63 steps into the limelight: crucial roles in the suppression of tumorigenesis and metastasis." *Nature Reviews Cancer* 13.2 (2013): 136-143.

## Supplementary Table 7 – Macrophages

<b>TF</b>	<b>Regression Coefficient</b>	
<b>HOXA3</b>	0.148367202	[S6.01]
<b>HLTF</b>	0.089891363	[S6.02]
<b>ETV5</b>	0.078639561	[S6.03]
<b>GMEB1</b>	0.045548794	[S6.04]
<b>HOXA5</b>	0.04494131	[S6.05]
<b>NRF1</b>	0.039230003	[S6.06, S6.07, S6.08]
<b>PAX2 (paralog of PAX5)</b>	0.038496525	[S6.09]
<b>ETS2</b>	0.034375522	[S6.10]
<b>ELF5</b>	0.033069267	[S6.11]
<b>NFATC1</b>	0.032528012	[S6.12]
<b>KLF4</b>	0.025539592	[S6.13]
<b>NKX2.5</b>	0.025418796	[S6.14]
<b>RAD21</b>	-0.052709626	[S6.15]

[S6.01] Al Sadoun, Hadeel, et al. "Enforced Expression of Hoxa3 Inhibits Classical and Promotes Alternative Activation of Macrophages In Vitro and In Vivo." *The Journal of Immunology* 197.3 (2016): 872-884.

[S6.02] Lahouassa, Hichem, et al. "HIV-1 Vpr degrades the HLTF DNA translocase in T cells and macrophages." *Proceedings of the National Academy of Sciences* 113.19 (2016): 5311-5316.

[S6.03] Roy, Sugata, et al. "Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics." *Nucleic acids research* 43.14 (2015): 6969-6982.

[S6.04] Kawabe, Kiyokazu, et al. "IL-12 inhibits glucocorticoid-induced T cell apoptosis by inducing GMEB1 and activating PI3K/Akt pathway." *Immunobiology* 217.1 (2012): 118-123.

[S6.05] Gordon, Siamon, ed. *The macrophage as therapeutic target*. Vol. 158. Page 14, Springer Science & Business Media, ISBN 978-3-642-55742-2, 2012.

[S6.06] Beyer, T. A., et al. "Roles and mechanisms of action of the Nrf2 transcription factor in skin morphogenesis, wound repair and skin cancer." *Cell death and differentiation* 14.7 (2007): 1250.

[S6.07] Liou, Geou-Yarh, and Peter Storz. "Reactive oxygen species in cancer."

[S6.08] Zhang, Shu-Tao, et al. "Nrf1 is time-dependently expressed and distributed in the distinct cell types after trauma to skeletal muscles in rats." *Histol Histopathol* 28 (2013): 725-735. *Free radical research* 44.5 (2010): 479-496.

[S6.09] Hodawadekar, Suchita, et al. "B-lymphoma cells with epigenetic silencing of Pax5 trans-differentiate into macrophages, but not other hematopoietic lineages." *Experimental cell research* 313.2 (2007): 331-340.

[S6.10] Zabuawala, Tahera, et al. "An ets2-driven transcriptional program in tumor-associated macrophages promotes tumor metastasis." *Cancer research* 70.4 (2010): 1323-1333.

[S6.11] Tuomisto, Tiina T., et al. "Analysis of gene and protein expression during monocyte-macrophage differentiation and cholesterol loading—cDNA and protein array study." *Atherosclerosis* 180.2 (2005): 283-291.

[S6.12] Zanoni, Ivan, and Francesca Granucci. "Regulation and dysregulation of innate immunity by NFAT signaling downstream of pattern recognition receptors (PRRs)." *European journal of immunology* 42.8 (2012): 1924-1931.

[S6.13] Liao, Xudong, et al. "Krüppel-like factor 4 regulates macrophage polarization." *The Journal of clinical investigation* 121.7 (2011): 2736-2749. Schuetz, Anja, et al. "The structure of the Klf4 DNA-binding domain links to self-renewal and macrophage differentiation." *Cellular and Molecular Life Sciences* 68.18 (2011): 3121-3131.

[S6.14] Ravasi, Timothy, et al. "Generation of diversity in the innate immune system: macrophage heterogeneity arises from gene-autonomous transcriptional probability of individual inducible genes." *The Journal of Immunology* 168.1 (2002): 44-50.

[S6.15] Bowers, Sarion R., et al. "A conserved insulator that recruits CTCF and cohesin exists between the closely related but divergently regulated interleukin-3 and granulocyte-macrophage colony-stimulating factor genes." *Molecular and cellular biology* 29.7 (2009): 1682-1693.