

## Annotation sparse PCovR and sparse PLS weights and loadings with Panther and GSEA, 22/02/2018

1. Overrepresentation on official gene symbols of the probesets receiving non-zero component **weights**; GO biological process complete

SPCOVR1

	Homo sapiens (REF)		Client Text Box Input (▼ Hierarchy NEW! ?)				
	#	#	expected	Fold Enrichment	+/-	raw P value	FDR
<a href="#">GO biological process complete</a>							
<a href="#">histone acetylation</a>	<a href="#">103</a>	<a href="#">8</a>	.98	8.17	+	1.03E-05	5.73E-03
↳ <a href="#">internal peptidyl-lysine acetylation</a>	<a href="#">108</a>	<a href="#">8</a>	1.03	7.79	+	1.43E-05	7.16E-03
↳ <a href="#">internal protein amino acid acetylation</a>	<a href="#">113</a>	<a href="#">8</a>	1.07	7.45	+	1.95E-05	8.88E-03
↳ <a href="#">protein acetylation</a>	<a href="#">130</a>	<a href="#">10</a>	1.24	8.09	+	8.68E-07	1.03E-03
↳ <a href="#">protein acylation</a>	<a href="#">164</a>	<a href="#">10</a>	1.56	6.42	+	6.18E-06	3.99E-03
↳ <a href="#">macromolecule metabolic process</a>	<a href="#">7781</a>	<a href="#">111</a>	73.96	1.50	+	1.33E-07	2.95E-04
↳ <a href="#">organic substance metabolic process</a>	<a href="#">9520</a>	<a href="#">129</a>	90.49	1.43	+	6.25E-08	2.42E-04
↳ <a href="#">metabolic process</a>	<a href="#">9969</a>	<a href="#">133</a>	94.75	1.40	+	6.97E-08	2.16E-04
↳ <a href="#">nitrogen compound metabolic process</a>	<a href="#">8640</a>	<a href="#">120</a>	82.12	1.46	+	9.95E-08	2.57E-04
↳ <a href="#">primary metabolic process</a>	<a href="#">9162</a>	<a href="#">126</a>	87.08	1.45	+	5.43E-08	2.81E-04
↳ <a href="#">cellular macromolecule metabolic process</a>	<a href="#">6609</a>	<a href="#">96</a>	62.82	1.53	+	1.18E-06	1.22E-03
↳ <a href="#">cellular metabolic process</a>	<a href="#">9069</a>	<a href="#">125</a>	86.20	1.45	+	5.28E-08	4.09E-04
↳ <a href="#">cellular process</a>	<a href="#">15084</a>	<a href="#">170</a>	143.37	1.19	+	1.23E-05	6.38E-03
↳ <a href="#">peptidyl-lysine acetylation</a>	<a href="#">111</a>	<a href="#">8</a>	1.06	7.58	+	1.72E-05	8.10E-03
↳ <a href="#">peptidyl-lysine modification</a>	<a href="#">300</a>	<a href="#">14</a>	2.85	4.91	+	1.79E-06	1.63E-03
↳ <a href="#">covalent chromatin modification</a>	<a href="#">476</a>	<a href="#">17</a>	4.52	3.76	+	4.61E-06	3.58E-03
↳ <a href="#">chromatin organization</a>	<a href="#">667</a>	<a href="#">21</a>	6.34	3.31	+	2.33E-06	2.01E-03

↳cellular component organization or biogenesis	<a href="#">5498</a>	<a href="#">77</a>	52.26	1.47	+	1.36E-04	4.23E-02
↳chromosome organization	<a href="#">1040</a>	<a href="#">28</a>	9.88	2.83	+	9.14E-07	1.01E-03
↳organelle organization	<a href="#">3182</a>	<a href="#">55</a>	30.24	1.82	+	6.92E-06	4.29E-03
signal transduction involved in DNA damage checkpoint	<a href="#">78</a>	<a href="#">6</a>	.74	8.09	+	1.43E-04	4.34E-02
↳cellular response to DNA damage stimulus	<a href="#">742</a>	<a href="#">20</a>	7.05	2.84	+	3.65E-05	1.62E-02
↳cellular response to stress	<a href="#">1599</a>	<a href="#">34</a>	15.20	2.24	+	1.15E-05	6.16E-03
↳signal transduction in response to DNA damage	<a href="#">109</a>	<a href="#">7</a>	1.04	6.76	+	1.16E-04	3.99E-02
↳signal transduction involved in DNA integrity checkpoint	<a href="#">78</a>	<a href="#">6</a>	.74	8.09	+	1.43E-04	4.26E-02
↳signal transduction involved in cell cycle checkpoint	<a href="#">79</a>	<a href="#">6</a>	.75	7.99	+	1.52E-04	4.46E-02
regulation of translation	<a href="#">403</a>	<a href="#">13</a>	3.83	3.39	+	1.68E-04	4.73E-02
↳regulation of primary metabolic process	<a href="#">6124</a>	<a href="#">92</a>	58.21	1.58	+	6.43E-07	9.07E-04
↳regulation of metabolic process	<a href="#">6672</a>	<a href="#">98</a>	63.42	1.55	+	5.38E-07	8.34E-04
↳regulation of nitrogen compound metabolic process	<a href="#">5958</a>	<a href="#">89</a>	56.63	1.57	+	1.25E-06	1.21E-03
↳regulation of macromolecule metabolic process	<a href="#">6151</a>	<a href="#">89</a>	58.46	1.52	+	5.22E-06	3.85E-03
↳regulation of cellular metabolic process	<a href="#">6187</a>	<a href="#">94</a>	58.81	1.60	+	2.00E-07	3.87E-04
↳posttranscriptional regulation of gene expression	<a href="#">538</a>	<a href="#">18</a>	5.11	3.52	+	5.74E-06	4.05E-03
↳regulation of gene expression	<a href="#">4625</a>	<a href="#">68</a>	43.96	1.55	+	1.04E-04	4.03E-02
↳regulation of cellular amide metabolic process	<a href="#">444</a>	<a href="#">14</a>	4.22	3.32	+	1.19E-04	3.91E-02
↳regulation of cellular macromolecule biosynthetic process	<a href="#">4119</a>	<a href="#">62</a>	39.15	1.58	+	1.53E-04	4.39E-02
↳regulation of cellular biosynthetic process	<a href="#">4400</a>	<a href="#">66</a>	41.82	1.58	+	7.64E-05	3.12E-02
↳regulation of biosynthetic process	<a href="#">4468</a>	<a href="#">66</a>	42.47	1.55	+	1.22E-04	3.93E-02
↳regulation of macromolecule biosynthetic process	<a href="#">4221</a>	<a href="#">63</a>	40.12	1.57	+	1.30E-04	4.11E-02
protein localization to organelle	<a href="#">618</a>	<a href="#">17</a>	5.87	2.89	+	1.13E-04	4.07E-02
↳cellular protein localization	<a href="#">1338</a>	<a href="#">28</a>	12.72	2.20	+	1.09E-04	4.12E-02
↳cellular macromolecule localization	<a href="#">1348</a>	<a href="#">28</a>	12.81	2.19	+	1.18E-04	3.98E-02

<a href="#">intracellular protein transport</a>	<a href="#">744</a>	<a href="#">20</a>	7.07	2.83	+	3.79E-05	1.63E-02
<a href="#">negative regulation of cellular macromolecule biosynthetic process</a>	<a href="#">1343</a>	<a href="#">28</a>	12.76	2.19	+	1.13E-04	3.99E-02
<a href="#">gene expression</a>	<a href="#">3782</a>	<a href="#">69</a>	35.95	1.92	+	2.88E-08	4.47E-04
<a href="#">RNA metabolic process</a>	<a href="#">3476</a>	<a href="#">56</a>	33.04	1.69	+	5.11E-05	2.14E-02
↳ <a href="#">nucleic acid metabolic process</a>	<a href="#">4003</a>	<a href="#">68</a>	38.05	1.79	+	7.39E-07	9.55E-04
↳ <a href="#">nucleobase-containing compound metabolic process</a>	<a href="#">4564</a>	<a href="#">71</a>	43.38	1.64	+	9.25E-06	5.31E-03
↳ <a href="#">organic cyclic compound metabolic process</a>	<a href="#">4997</a>	<a href="#">77</a>	47.50	1.62	+	3.72E-06	3.04E-03
↳ <a href="#">cellular nitrogen compound metabolic process</a>	<a href="#">5191</a>	<a href="#">77</a>	49.34	1.56	+	1.63E-05	7.92E-03
↳ <a href="#">heterocycle metabolic process</a>	<a href="#">4740</a>	<a href="#">73</a>	45.05	1.62	+	8.42E-06	5.02E-03
↳ <a href="#">cellular aromatic compound metabolic process</a>	<a href="#">4776</a>	<a href="#">74</a>	45.39	1.63	+	5.81E-06	3.92E-03
<a href="#">regulation of RNA metabolic process</a>	<a href="#">3909</a>	<a href="#">60</a>	37.15	1.61	+	1.11E-04	4.11E-02
↳ <a href="#">regulation of nucleobase-containing compound metabolic process</a>	<a href="#">4268</a>	<a href="#">72</a>	40.57	1.77	+	3.38E-07	5.82E-04
Unclassified	<a href="#">3542</a>	<a href="#">15</a>	33.67	.45	-	1.82E-04	4.96E-02
<a href="#">G-protein coupled receptor signaling pathway</a>	<a href="#">1306</a>	<a href="#">1</a>	12.41	.08	-	8.05E-05	3.20E-02

## SPCOVR2

	<a href="#">Homo sapiens</a> (REF)		<a href="#">Client Text Box Input</a> ( <a href="#">V</a> <a href="#">Hierarchy</a> <a href="#">NEW!</a> <a href="#">?</a> )				
<a href="#">GO biological process complete</a>	#	#	<a href="#">expected</a>	<a href="#">Fold Enrichment</a>	<a href="#">+/-</a>	<a href="#">raw P value</a>	<a href="#">FDR</a>
<a href="#">cytoplasmic translation</a>	<a href="#">45</a>	<a href="#">6</a>	.18	32.62	+	5.93E-08	9.19E-04
↳ <a href="#">translation</a>	<a href="#">383</a>	<a href="#">10</a>	1.57	6.39	+	4.45E-06	4.93E-03
↳ <a href="#">cellular process</a>	<a href="#">15084</a>	<a href="#">77</a>	61.65	1.25	+	9.72E-05	3.35E-02
↳ <a href="#">peptide biosynthetic process</a>	<a href="#">410</a>	<a href="#">10</a>	1.68	5.97	+	7.98E-06	7.73E-03
↳ <a href="#">peptide metabolic process</a>	<a href="#">537</a>	<a href="#">11</a>	2.19	5.01	+	1.36E-05	1.06E-02
↳ <a href="#">cellular amide metabolic process</a>	<a href="#">695</a>	<a href="#">11</a>	2.84	3.87	+	1.34E-04	4.01E-02
↳ <a href="#">amide biosynthetic process</a>	<a href="#">480</a>	<a href="#">10</a>	1.96	5.10	+	3.01E-05	1.79E-02
<a href="#">SRP-dependent cotranslational protein targeting to membrane</a>	<a href="#">93</a>	<a href="#">7</a>	.38	18.42	+	1.70E-07	1.32E-03

↳cotranslational protein targeting to membrane	<a href="#">99</a>	<a href="#">7</a>	.40	17.30	+	2.54E-07	9.85E-04
↳protein targeting to membrane	<a href="#">133</a>	<a href="#">7</a>	.54	12.88	+	1.68E-06	2.36E-03
↳protein targeting	<a href="#">278</a>	<a href="#">7</a>	1.14	6.16	+	1.63E-04	4.78E-02
↳localization	<a href="#">5436</a>	<a href="#">40</a>	22.22	1.80	+	3.64E-05	1.82E-02
↳transport	<a href="#">4324</a>	<a href="#">36</a>	17.67	2.04	+	1.10E-05	8.97E-03
↳establishment of localization	<a href="#">4440</a>	<a href="#">36</a>	18.15	1.98	+	1.46E-05	1.07E-02
↳protein transport	<a href="#">1362</a>	<a href="#">17</a>	5.57	3.05	+	3.45E-05	1.91E-02
↳establishment of protein localization	<a href="#">1439</a>	<a href="#">17</a>	5.88	2.89	+	6.82E-05	2.58E-02
↳peptide transport	<a href="#">1386</a>	<a href="#">17</a>	5.66	3.00	+	4.29E-05	2.02E-02
↳amide transport	<a href="#">1408</a>	<a href="#">17</a>	5.75	2.95	+	5.22E-05	2.19E-02
↳nitrogen compound transport	<a href="#">1672</a>	<a href="#">19</a>	6.83	2.78	+	3.96E-05	1.92E-02
↳organic substance transport	<a href="#">2043</a>	<a href="#">21</a>	8.35	2.52	+	6.15E-05	2.45E-02
↳establishment of protein localization to membrane	<a href="#">217</a>	<a href="#">7</a>	.89	7.89	+	3.62E-05	1.87E-02
↳protein targeting to ER	<a href="#">102</a>	<a href="#">7</a>	.42	16.79	+	3.08E-07	9.54E-04
↳establishment of protein localization to endoplasmic reticulum	<a href="#">106</a>	<a href="#">7</a>	.43	16.16	+	3.94E-07	1.02E-03
↳protein localization to endoplasmic reticulum	<a href="#">126</a>	<a href="#">7</a>	.51	13.59	+	1.19E-06	2.05E-03
viral transcription	<a href="#">114</a>	<a href="#">7</a>	.47	15.02	+	6.27E-07	1.39E-03
↳viral gene expression	<a href="#">128</a>	<a href="#">7</a>	.52	13.38	+	1.31E-06	2.04E-03
↳viral process	<a href="#">662</a>	<a href="#">12</a>	2.71	4.44	+	1.78E-05	1.15E-02
↳symbiont process	<a href="#">734</a>	<a href="#">12</a>	3.00	4.00	+	4.79E-05	2.19E-02
↳interspecies interaction between organisms	<a href="#">771</a>	<a href="#">12</a>	3.15	3.81	+	7.62E-05	2.68E-02
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	<a href="#">119</a>	<a href="#">7</a>	.49	14.39	+	8.25E-07	1.60E-03
↳nuclear-transcribed mRNA catabolic process	<a href="#">199</a>	<a href="#">7</a>	.81	8.61	+	2.12E-05	1.31E-02
↳mRNA catabolic process	<a href="#">214</a>	<a href="#">7</a>	.87	8.00	+	3.32E-05	1.91E-02
↳negative regulation of macromolecule metabolic process	<a href="#">2546</a>	<a href="#">26</a>	10.41	2.50	+	6.76E-06	6.99E-03

↳ <a href="#">negative regulation of metabolic process</a>	<a href="#">2795</a>	<a href="#">28</a>	11.42	2.45	+	3.74E-06	4.83E-03
↳ <a href="#">regulation of metabolic process</a>	<a href="#">6672</a>	<a href="#">46</a>	27.27	1.69	+	3.61E-05	1.93E-02
↳ <a href="#">regulation of gene expression</a>	<a href="#">4625</a>	<a href="#">35</a>	18.90	1.85	+	1.15E-04	3.55E-02
↳ <a href="#">RNA catabolic process</a>	<a href="#">243</a>	<a href="#">7</a>	.99	7.05	+	7.24E-05	2.67E-02
↳ <a href="#">nucleobase-containing compound catabolic process</a>	<a href="#">362</a>	<a href="#">8</a>	1.48	5.41	+	1.33E-04	4.03E-02
↳ <a href="#">aromatic compound catabolic process</a>	<a href="#">422</a>	<a href="#">9</a>	1.72	5.22	+	6.46E-05	2.50E-02
↳ <a href="#">cellular nitrogen compound catabolic process</a>	<a href="#">409</a>	<a href="#">9</a>	1.67	5.38	+	5.10E-05	2.20E-02
↳ <a href="#">organic cyclic compound catabolic process</a>	<a href="#">454</a>	<a href="#">9</a>	1.86	4.85	+	1.11E-04	3.68E-02
↳ <a href="#">heterocycle catabolic process</a>	<a href="#">407</a>	<a href="#">9</a>	1.66	5.41	+	4.92E-05	2.18E-02
↳ <a href="#">mRNA metabolic process</a>	<a href="#">680</a>	<a href="#">11</a>	2.78	3.96	+	1.11E-04	3.76E-02
<a href="#">translational initiation</a>	<a href="#">143</a>	<a href="#">8</a>	.58	13.69	+	1.87E-07	9.67E-04
<a href="#">rRNA processing</a>	<a href="#">261</a>	<a href="#">7</a>	1.07	6.56	+	1.12E-04	3.61E-02
↳ <a href="#">ribosome biogenesis</a>	<a href="#">334</a>	<a href="#">9</a>	1.37	6.59	+	1.08E-05	9.32E-03
↳ <a href="#">ribonucleoprotein complex biogenesis</a>	<a href="#">468</a>	<a href="#">11</a>	1.91	5.75	+	3.84E-06	4.58E-03
<a href="#">myeloid leukocyte activation</a>	<a href="#">564</a>	<a href="#">10</a>	2.31	4.34	+	1.12E-04	3.56E-02
↳ <a href="#">leukocyte activation</a>	<a href="#">873</a>	<a href="#">13</a>	3.57	3.64	+	5.80E-05	2.37E-02
↳ <a href="#">cell activation</a>	<a href="#">1019</a>	<a href="#">15</a>	4.16	3.60	+	1.67E-05	1.17E-02
↳ <a href="#">immune system process</a>	<a href="#">2575</a>	<a href="#">26</a>	10.52	2.47	+	8.29E-06	7.57E-03
<a href="#">immune effector process</a>	<a href="#">1026</a>	<a href="#">14</a>	4.19	3.34	+	7.42E-05	2.67E-02
<a href="#">immune response</a>	<a href="#">1720</a>	<a href="#">20</a>	7.03	2.85	+	1.70E-05	1.15E-02

## SGCCA1

No statistically significant results. [Click to see all results.](#)

## SGCCA2

No statistically significant results. [Click to see all results.](#)

2. Enrichment, based on the **loadings** (full list of probe sets): Only GO-Slim could be obtained with PANTHER; GSEA was used as an alternative to include more GO terms

#### SPCOVR1

<a href="#">PANTHER GO-Slim Biological Process</a>		#	+/-	P value
<input type="checkbox"/>	↳ <a href="#">metabolic process (GO:0008152)</a>	<a href="#">5244</a>	-	2.30E-09
<input type="checkbox"/>	↳ <a href="#">RNA metabolic process (GO:0016070)</a>	<a href="#">1419</a>	-	0.00E00
<input type="checkbox"/>	↳ <a href="#">nucleobase-containing compound metabolic process (GO:0006139)</a>	<a href="#">2514</a>	-	6.75E-13
<input type="checkbox"/>	↳ <a href="#">primary metabolic process (GO:0044238)</a>	<a href="#">4215</a>	-	6.72E-11
<input type="checkbox"/>	↳ <a href="#">mRNA processing (GO:0006397)</a>	<a href="#">227</a>	-	1.23E-11
<input type="checkbox"/>	↳ <a href="#">biological regulation (GO:0065007)</a>	<a href="#">2403</a>	+	6.77E-09
<input type="checkbox"/>	↳ <a href="#">developmental process (GO:0032502)</a>	<a href="#">1372</a>	+	1.52E-06
<input type="checkbox"/>	↳ <a href="#">protein metabolic process (GO:0019538)</a>	<a href="#">1361</a>	-	8.00E-03
<input type="checkbox"/>	↳ <a href="#">cellular component organization or biogenesis (GO:0071840)</a>	<a href="#">1811</a>	-	1.18E-03
<input type="checkbox"/>	↳ <a href="#">signal transduction (GO:0007165)</a>	<a href="#">1926</a>	+	7.22E-05
<input type="checkbox"/>	↳ <a href="#">cell communication (GO:0007154)</a>	<a href="#">2258</a>	+	1.64E-09
<input type="checkbox"/>	↳ <a href="#">synaptic transmission (GO:0007268)</a>	<a href="#">344</a>	+	3.67E-07
<input type="checkbox"/>	↳ <a href="#">cell-cell signaling (GO:0007267)</a>	<a href="#">510</a>	+	1.53E-12
<input type="checkbox"/>	↳ <a href="#">biological adhesion (GO:0022610)</a>	<a href="#">317</a>	+	3.64E-03
<input type="checkbox"/>	↳ <a href="#">sensory perception of chemical stimulus (GO:0007606)</a>	<a href="#">87</a>	+	1.32E-05
<input type="checkbox"/>	↳ <a href="#">sensory perception (GO:0007600)</a>	<a href="#">222</a>	+	1.06E-02

<input type="checkbox"/>	↳ <a href="#">neurological system process (GO:0050877)</a>	<a href="#">684</a>	+	1.96E-08
<input type="checkbox"/>	↳ <a href="#">system process (GO:0003008)</a>	<a href="#">777</a>	+	5.00E-10
<input type="checkbox"/>	↳ <a href="#">single-multicellular organism process (GO:0044707)</a>	<a href="#">1291</a>	+	0.00E00
<input type="checkbox"/>	↳ <a href="#">multicellular organismal process (GO:0032501)</a>	<a href="#">1307</a>	+	0.00E00
<input type="checkbox"/>	↳ <a href="#">organelle organization (GO:0006996)</a>	<a href="#">1064</a>	-	7.54E-05
<input type="checkbox"/>	↳ <a href="#">intracellular protein transport (GO:0006886)</a>	<a href="#">612</a>	-	3.67E-05
<input type="checkbox"/>	↳ <a href="#">protein transport (GO:0015031)</a>	<a href="#">647</a>	-	2.83E-05
<input type="checkbox"/>	↳ <a href="#">system development (GO:0048731)</a>	<a href="#">406</a>	+	8.76E-04
<input type="checkbox"/>	↳ <a href="#">response to stimulus (GO:0050896)</a>	<a href="#">2076</a>	+	1.21E-04

## SPCOVR2

<a href="#">PANTHER GO-Slim Biological Process</a>	#	+/-	P value
<input type="checkbox"/> ↳ <a href="#">transport (GO:0006810)</a>	<a href="#">1464</a>	+	1.82E-04
<input type="checkbox"/> ↳ <a href="#">localization (GO:0051179)</a>	<a href="#">1733</a>	+	8.81E-03
<input type="checkbox"/> ↳ <a href="#">RNA metabolic process (GO:0016070)</a>	<a href="#">1419</a>	-	6.96E-08
<input type="checkbox"/> ↳ <a href="#">protein transport (GO:0015031)</a>	<a href="#">647</a>	+	2.40E-02
<input type="checkbox"/> ↳ <a href="#">transcription, DNA-dependent (GO:0006351)</a>	<a href="#">921</a>	-	6.51E-04

## SGCCA1

<a href="#">PANTHER GO-Slim Biological Process</a>	#	+/-	P value
<input type="checkbox"/> ↳ <a href="#">RNA metabolic process (GO:0016070)</a>	<a href="#">1419</a>	-	4.03E-08
<input type="checkbox"/> ↳ <a href="#">nucleobase-containing compound metabolic process (GO:0006139)</a>	<a href="#">2514</a>	-	9.13E-03

<input type="checkbox"/>	<a href="#">↳biological adhesion (GO:0022610)</a>	<a href="#">317</a>	+	3.23E-02
<input type="checkbox"/>	<a href="#">↳mRNA processing (GO:0006397)</a>	<a href="#">227</a>	-	1.71E-02
<input type="checkbox"/>	<a href="#">↳localization (GO:0051179)</a>	<a href="#">1733</a>	+	2.91E-03

## SGCCA2

<a href="#">PANTHER GO-Slim Biological Process</a>		<a href="#">#</a>	<a href="#">+/-</a>	<a href="#">P value</a>
<input type="checkbox"/>	<a href="#">↳RNA metabolic process (GO:0016070)</a>	<a href="#">3220</a>	-	8.82E-11
<input type="checkbox"/>	<a href="#">↳nucleobase-containing compound metabolic process (GO:0006139)</a>	<a href="#">4233</a>	-	6.45E-03
<input type="checkbox"/>	<a href="#">↳endocytosis (GO:0006897)</a>	<a href="#">503</a>	+	1.25E-04
<input type="checkbox"/>	<a href="#">↳vesicle-mediated transport (GO:0016192)</a>	<a href="#">1612</a>	+	0.00E00
<input type="checkbox"/>	<a href="#">↳transport (GO:0006810)</a>	<a href="#">3972</a>	+	5.35E-09
<input type="checkbox"/>	<a href="#">↳localization (GO:0051179)</a>	<a href="#">5019</a>	+	4.60E-04

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## GENE SET ENRICHMENT USING GSEA

See Github for detailed GSEA results; here only terms with FWER < 0.01 are shown

### SPCOVR, PC1: upregulated

NAME	SIZE	ES	NES	FDR q-val	FWER p-val
GO_OLFACTORY_RECEPTOR_ACTIVITY	85	0.5523735	2.9037292	0.0	0.0
GO_CATECHOLAMINE_BINDING	16	0.7713403	2.6421924	0.0	0.0
GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	498	0.39954886	2.5883408	0.0	0.0
GO_G_PROTEIN_COUPLED_AMINE_RECEPTOR_ACTIVITY	43	0.5666132	2.5787802	0.0	0.0

### SPCOVR, PC1: downregulated

NAME	SIZE	ES	NES	FDR q-val	FWER p-val
GO_SPLICEOSOMAL_COMPLEX	166	-0.59278405	-2.3329313	0.0	0.0
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	257	-0.5724424	-2.3189914	0.0	0.0
GO_REGULATION_OF_MRNA_SPLICING_VIA_SPLICEOSOME	60	-0.6388619	-2.2792573	0.0	0.0
GO_RNA_SPLICING	347	-0.55220693	-2.2555594	8.758427E-5	0.001
GO_CATALYTIC_STEP_2_SPLICEOSOME	89	-0.59892035	-2.2503347	8.028558E-5	0.001
GO_NUCLEOCYTOPLASMIC_TRANSPORTER_ACTIVITY	24	-0.73497456	-2.2494276	7.410976E-5	0.001
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	187	-0.56319565	-2.2379725	6.881621E-5	0.001
GO_RNA_LOCALIZATION	173	-0.55625093	-2.2228682	6.4228465E-5	0.001
GO_MRNA_PROCESSING	408	-0.54179156	-2.2172828	6.0214184E-5	0.001
GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	82	-0.58647484	-2.186687	5.6672176E-5	0.001
GO_REGULATION_OF_MRNA_METABOLIC_PROCESS	115	-0.562678	-2.168169	1.0686039E-4	0.002
GO_TRANSLATION_INITIATION_FACTOR_ACTIVITY	47	-0.6384447	-2.1573462	2.0230771E-4	0.004
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	74	-0.58296704	-2.1446252	3.351314E-4	0.007
GO_SOMATIC_CELL_DNA_RECOMBINATION	33	-0.65276366	-2.1402295	3.649013E-4	0.008

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**SPCOVR, PC2: upregulated**

NAME	SIZE	ES	NES	FDR q-val	FWER p-val
GO_RESPONSE_TO_TYPE_I_INTERFERON	59	0.6511073	2.9652436	0.0	0.0
GO_PHAGOCYTIC_VESICLE	77	0.5391335	2.5681438	0.0	0.0
GO_GLUCOSE_6_PHOSPHATE_METABOLIC_PROCESS	21	0.72087175	2.5457456	5.4443E-4	0.001
GO_INTERFERON_GAMMA_MEDIATED_SIGNALING_PATHWAY	51	0.561533	2.4764407	0.0016018079	0.004
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	40	0.6057513	2.4546037	0.0015833693	0.005
GO_PHAGOCYTIC_VESICLE_MEMBRANE	50	0.57382715	2.4543846	0.0013194744	0.005
GO_CELL_KILLING	48	0.5661053	2.4530938	0.0011309781	0.005
GO_SIGNALING_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	17	0.7266218	2.4522817	9.896059E-4	0.005
GO_LYSOSOMAL_LUMEN	85	0.5055462	2.4496143	8.7964965E-4	0.005
GO_VACUOLAR_LUMEN	107	0.48013738	2.4330363	9.4927574E-4	0.006
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	57	0.5476536	2.4312923	8.6297793E-4	0.006
GO_ACTIVATION_OF_INNATE_IMMUNE_RESPONSE	198	0.43532375	2.423329	9.284209E-4	0.007
GO_MEMBRANE_LIPID_CATABOLIC_PROCESS	22	0.68985933	2.4196868	8.570039E-4	0.007
GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY	30	0.62470967	2.4049668	7.9578935E-4	0.007
GO_REGULATION_OF_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	30	0.6192405	2.3994396	7.4273674E-4	0.007

**SPCOVR, PC2: downregulated**

NAME	SIZE	ES	NES	FDR q-val	FWER p-val
		-			
GO_CYTOSOLIC_RIBOSOME	105	0.85517776	-3.3593915	0.0	0.0
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	103	-0.8358008	-3.2791746	0.0	0.0
		-			
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	114	0.81367624	-3.2390933	0.0	0.0
GO_TRANSLATIONAL_INITIATION	141	-0.7838875	-3.1838377	0.0	0.0
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	58	-0.8933256	-3.1608417	0.0	0.0
		-			
GO_MULTI_ORGANISM_METABOLIC_PROCESS	136	0.76602846	-3.0791237	0.0	0.0
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	122	-0.7684152	-3.074301	0.0	0.0
GO_PROTEIN_TARGETING_TO_MEMBRANE	152	-0.7295566	-2.9729335	0.0	0.0
		-			
GO_RIBOSOMAL_SUBUNIT	154	0.72525024	-2.965513	0.0	0.0
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	39	-0.8606321	-2.8496747	0.0	0.0

GO_LARGE_RIBOSOMAL_SUBUNIT	92	-0.7404751	-2.8079078	0.0	0.0
GO_RNA_CATABOLIC_PROCESS	222	-0.6552078	-2.752109	0.0	0.0
GO_SMALL_RIBOSOMAL_SUBUNIT	62	-0.7364	-2.7163181	0.0	0.0
GO_RIBOSOME	213	-0.6461315	-2.701998	0.0	0.0
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	203	-0.6407391	-2.690537	0.0	0.0
GO_RIBOSOME_BIOGENESIS	292	-0.6073094	-2.642923	0.0	0.0
	-				
GO_RRNA_METABOLIC_PROCESS	243	0.61870116	-2.6330783	0.0	0.0
GO_CYTOPLASMIC_TRANSLATION	39	-0.7513726	-2.5263064	0.0	0.0
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	416	-0.5670321	-2.4776976	0.0	0.0
GO_CYTOSOLIC_PART	211	-0.5932626	-2.4762723	0.0	0.0
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	257	-0.5819919	-2.4702015	0.0	0.0
	-				
GO_RRNA_BINDING	53	0.69001496	-2.4559703	0.0	0.0
	-				
GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	23	0.82642543	-2.450063	0.0	0.0
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	349	-0.5547134	-2.4000766	0.0	0.0
	-				
GO_VIRAL_LIFE_CYCLE	279	0.55658644	-2.377337	0.0	0.0
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	49	-0.6748234	-2.3508432	0.0	0.0
GO_RIBOSOME_ASSEMBLY	50	-0.6812716	-2.3468845	0.0	0.0
GO_NCRNA_PROCESSING	366	-0.5252052	-2.279406	0.0	0.0
	-				
GO_PROTEIN_TARGETING	390	0.51842475	-2.2659748	2.92959E-5	0.001
	-				
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	187	0.53329897	-2.2212324	8.438709E-5	0.003
				1.6387452E-	
GO_FORMATION_OF_TRANSLATION_PREINITIATION_COMPLEX	19	-0.7609968	-2.1570296	4	0.006

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**SGCCA, PC1: up-regulated**

NAME	SIZE	ES	NES	FDR q-val	FWER p-val
GO_SIGNALING_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	17	0.7801607	2.7426445	0.0	0.0
GO_PHAGOCYTIC_VESICLE_MEMBRANE	50	0.5389346	2.520449	0.002016922	0.003
GO_RESPONSE_TO_TYPE_I_INTERFERON	59	0.532611	2.4800665	0.0013446147	0.003

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**SGCCA, PC1: down-regulated**

NAME	SIZE	ES	NES	FDR q-val	FWER p-val
GO_CYTOSOLIC_RIBOSOME	105	-0.7935739	-3.2303927	0.0	0.0
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	114	-0.77939844	-3.180997	0.0	0.0
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	103	-0.7831753	-3.1313484	0.0	0.0
GO_TRANSLATIONAL_INITIATION	141	-0.7553972	-3.1208994	0.0	0.0
GO_MULTI_ORGANISM_METABOLIC_PROCESS	136	-0.7219156	-2.9993246	0.0	0.0
GO_PROTEIN_TARGETING_TO_MEMBRANE	152	-0.7060951	-2.9671252	0.0	0.0
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	58	-0.7918059	-2.9500847	0.0	0.0
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	122	-0.72174466	-2.9381292	0.0	0.0
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	39	-0.8278393	-2.8409433	0.0	0.0
GO_RIBOSOMAL_SUBUNIT	154	-0.6735611	-2.8263013	0.0	0.0
GO_RNA_CATABOLIC_PROCESS	222	-0.62582684	-2.6839817	0.0	0.0
GO_LARGE_RIBOSOMAL_SUBUNIT	92	-0.6667735	-2.6380684	0.0	0.0
GO_RRNA_METABOLIC_PROCESS	243	-0.6083013	-2.635567	0.0	0.0
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	203	-0.60534596	-2.6310205	0.0	0.0
GO_RIBOSOME_BIOGENESIS	292	-0.5916168	-2.6146305	0.0	0.0
GO_RIBOSOME	213	-0.60719	-2.602018	0.0	0.0
GO_SMALL_RIBOSOMAL_SUBUNIT	62	-0.68423474	-2.547275	0.0	0.0
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	416	-0.5584154	-2.4875066	0.0	0.0
GO_RIBOSOME_ASSEMBLY	50	-0.68844694	-2.478708	0.0	0.0
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	257	-0.57129306	-2.472497	0.0	0.0
GO_CYTOPLASMIC_TRANSLATION	39	-0.6949343	-2.4177115	0.0	0.0
GO_RIBOSOMAL_LARGE_SUBUNIT_ASSEMBLY	23	-0.7724781	-2.3959248	0.0	0.0
GO_CYTOSOLIC_PART	211	-0.5546334	-2.3951297	0.0	0.0
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	49	-0.65599936	-2.3552089	0.0	0.0

GO_RRNA_BINDING	53	-0.6350739	-2.308317	0.0	0.0
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	349	-0.5165153	-2.3066065	0.0	0.0
GO_VIRAL_LIFE_CYCLE	279	-0.5226155	-2.3027966	0.0	0.0
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	187	-0.53257316	-2.273793	0.0	0.0
GO_PROTEIN_TARGETING	390	-0.50373465	-2.2540925	6.190569E-5	0.002
GO_NCRNA_PROCESSING	366	-0.50357664	-2.2397313	8.975735E-5	0.003
GO_PROTEIN_LOCALIZATION_TO_MEMBRANE	368	-0.4866734	-2.1729841	2.6119975E-4	0.009
GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX	15	-0.7703866	-2.1055505	5.061501E-4	0.018
GO_RNA_SPLICING	347	-0.46358165	-2.062049	0.001310709	0.048
GO_SPLICEOSOMAL_COMPLEX	166	-0.48273832	-2.0617046	0.0012732602	0.048
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	257	-0.47102594	-2.0574887	0.0013155583	0.051
GO_V_D_J_RECOMBINATION	16	-0.7308054	-2.046089	0.0015059627	0.058
GO_FORMATION_OF_TRANSLATION_PREINITIATION_COMPLEX	19	-0.70031685	-2.043863	0.0014908811	0.059
GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	56	-0.5533796	-2.0417216	0.001524672	0.062
GO_AMIDE_BIOSYNTHETIC_PROCESS	475	-0.45047367	-2.0297978	0.0018827651	0.079
GO_EXOSOME_RNASE_COMPLEX	21	-0.6664727	-2.0274847	0.0019510984	0.083
GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	415	-0.44874346	-2.01352	0.002323747	0.098
GO_TRANSLATION_INITIATION_FACTOR_ACTIVITY	47	-0.56817347	-2.012878	0.0022910081	0.099
GO_NUCLEAR_SPECK	188	-0.4709208	-2.0117073	0.0022389397	0.099

#### SGCCA, PC2: upregulated

NAME	SIZE	ES	NES	FDR q-val	FWER p-val
GO_SIGNALING_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	17	0.7134674	2.5039656	0.0055457987	0.004

#### SGCCA, PC2: downregulated

NAME	SIZE	ES	NES	FDR q-val	FWER p-val
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	103	-0.7013349	-2.8528984	0.0	0.0
GO_CYTOSOLIC_RIBOSOME	105	-0.7037573	-2.8403244	0.0	0.0
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	114	0.68200475	-2.7806325	0.0	0.0
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	122	-0.6591273	-2.6968784	0.0	0.0

GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	58	-0.7203712	-2.6769874	0.0	0.0
GO_TRANSLATIONAL_INITIATION	141	-0.6403597	-2.673831	0.0	0.0
GO_MULTI_ORGANISM_METABOLIC_PROCESS	136	-0.6374333	-2.6203103	0.0	0.0
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	39	0.74154854	-2.5256913	0.0	0.0
GO_RIBOSOMAL_SUBUNIT	154	-0.5854627	-2.4573472	0.0	0.0
GO_CYTOPLASMIC_TRANSLATION	39	-0.708512	-2.4500306	0.0	0.0
GO_PROTEIN_TARGETING_TO_MEMBRANE	152	0.58291674	-2.4325953	0.0	0.0
GO_SMALL_RIBOSOMAL_SUBUNIT	62	-0.6391664	-2.4221063	0.0	0.0
GO_RNA_CATABOLIC_PROCESS	222	0.55633384	-2.4143775	0.0	0.0
GO_RIBOSOME	213	-0.5285721	-2.2863271	0.0	0.0
GO_RRNA_METABOLIC_PROCESS	243	-0.5220171	-2.275546	0.0	0.0
GO_LARGE_RIBOSOMAL_SUBUNIT	92	0.56670266	-2.2701104	0.0	0.0
GO_RIBOSOME_BIOGENESIS	292	-0.5159737	-2.2628715	5.1323022E-5	0.001
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	416	-0.4997258	-2.2371614	9.742066E-5	0.002
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	203	-0.5121918	-2.2125604	1.392731E-4	0.003