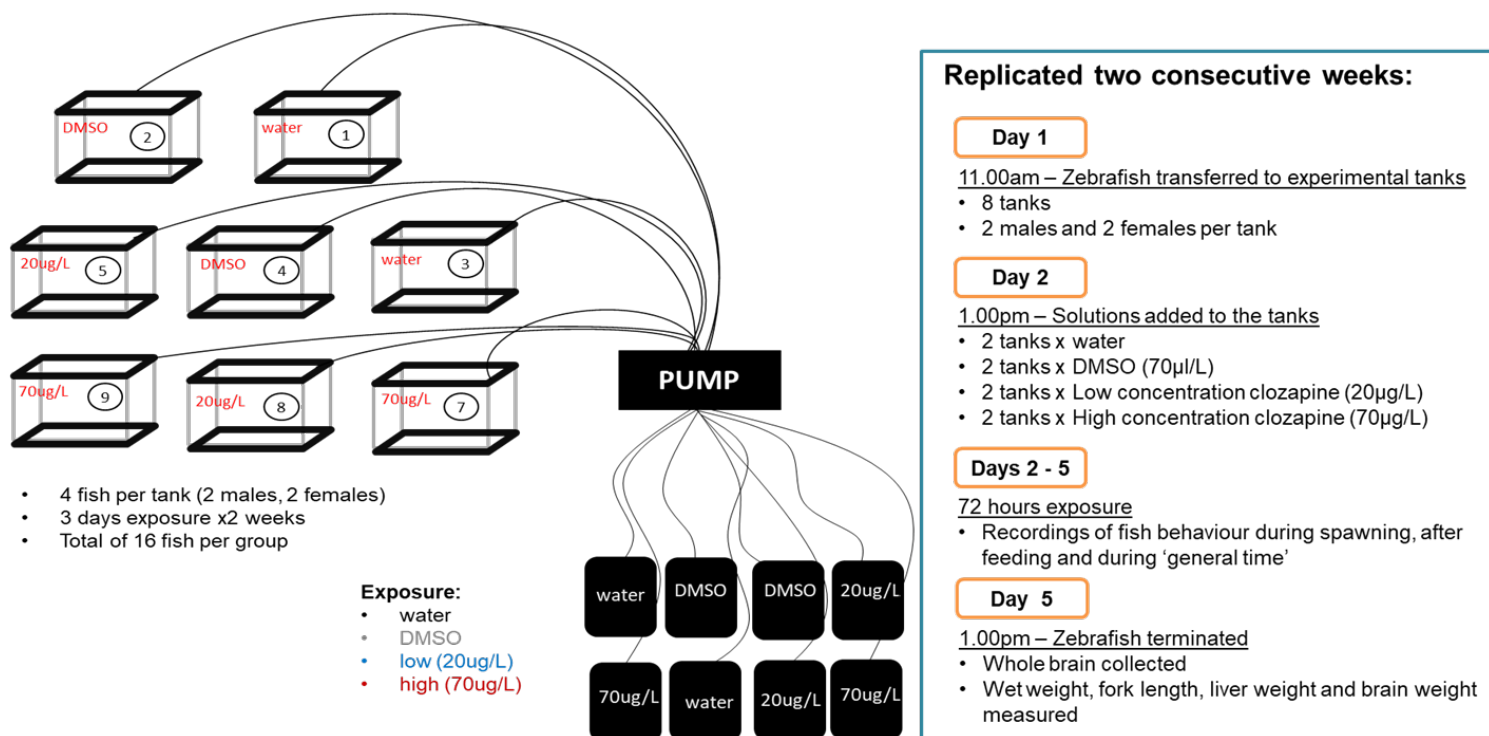
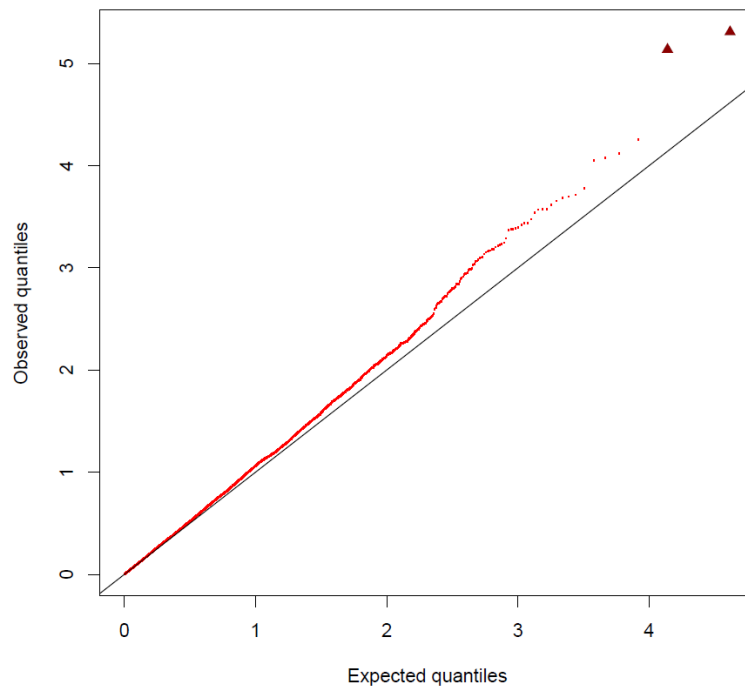
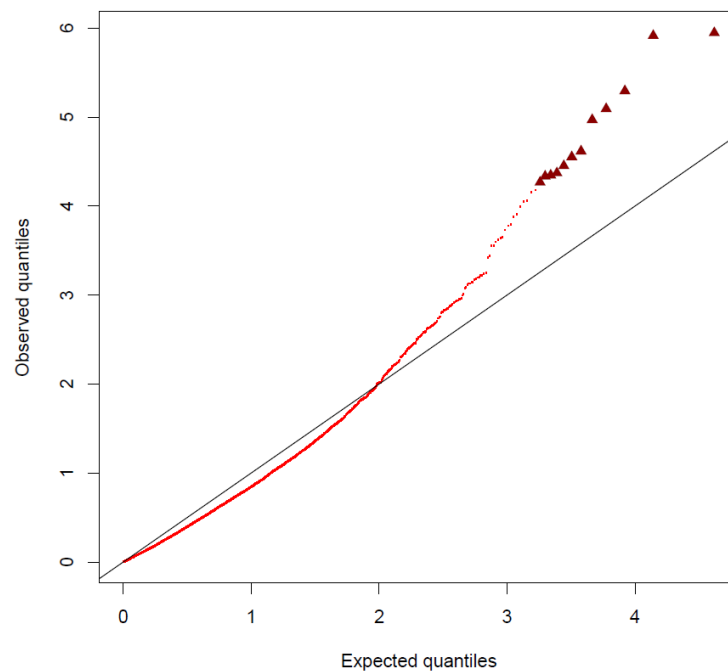


Supplementary Information File

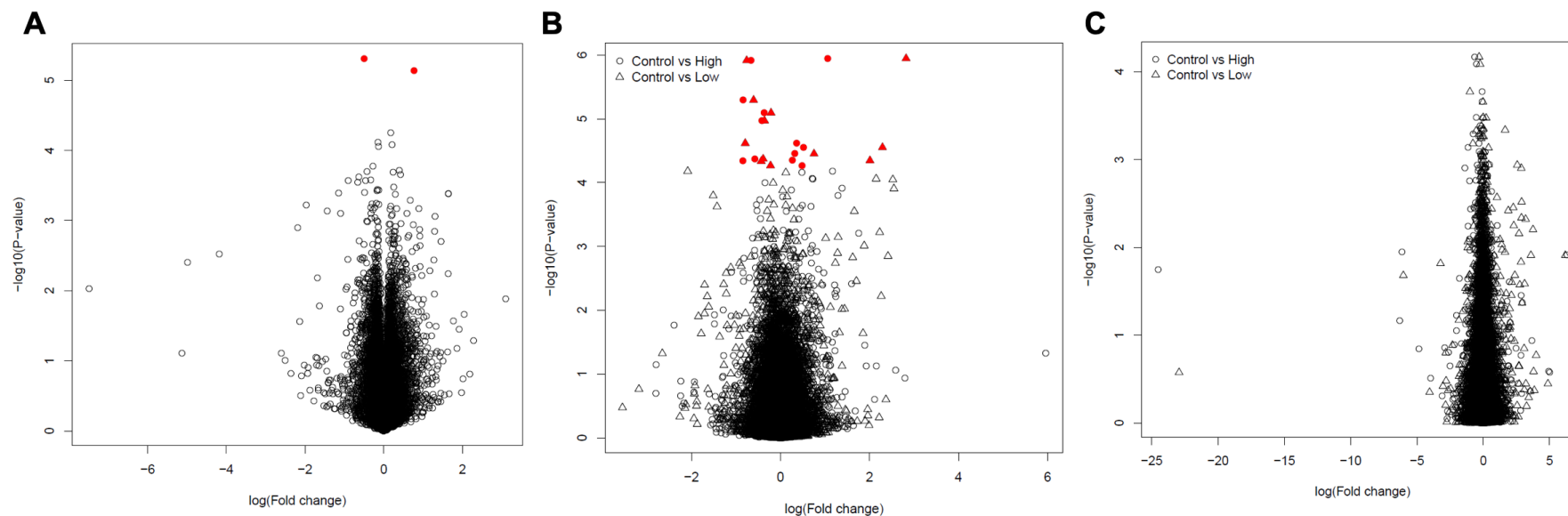
Supplementary Data Set 1 - Results of differential gene expression analysis following clozapine exposure for all detectable transcripts in zebrafish brain. FDR – False Discovery Rate.



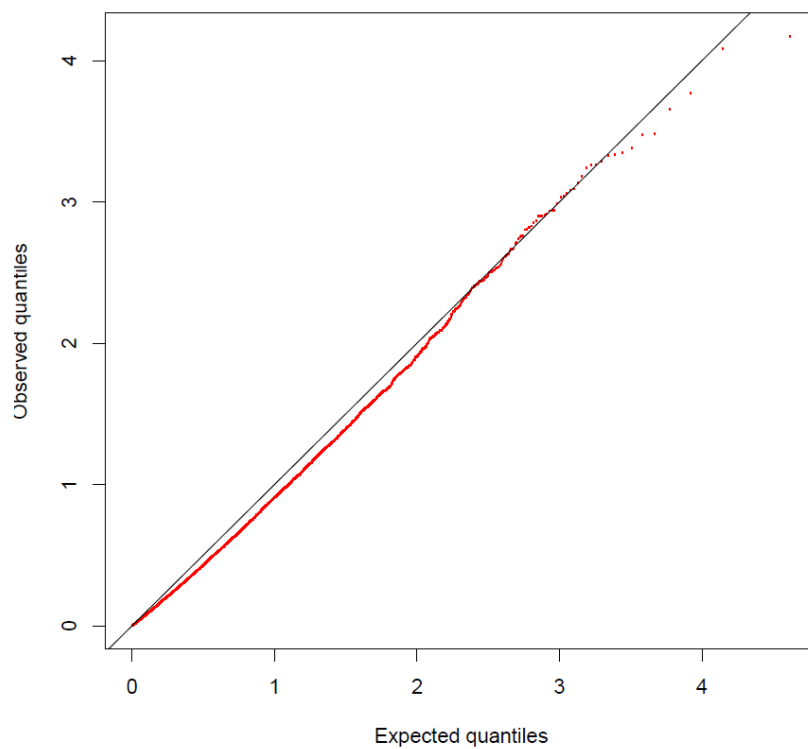
Supplementary Figure 1 – An overview of the experimental design used in this study.

A**B**

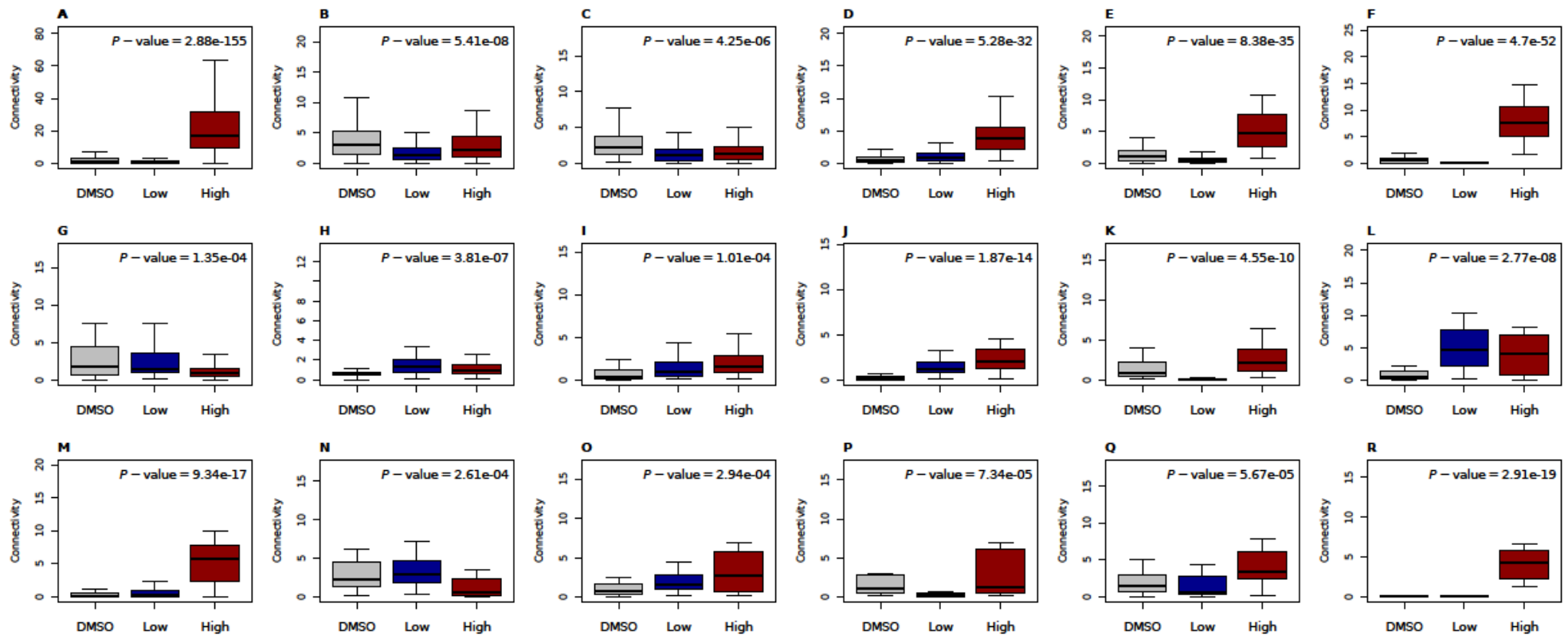
Supplementary Figure 2 – Quantile-quantile (QQ) plot of association statistics from a model designed to identify gene expression differences between zebrafish exposed to A) water and DMSO and B) DMSO and clozapine. Twelve transcripts were characterized by significant differences ($FDR < 0.10$) in gene expression associated with clozapine exposure. Results for all expressed genes are given in **Supplementary Table 4**. Triangles highlight transcripts with $FDR < 0.10$.



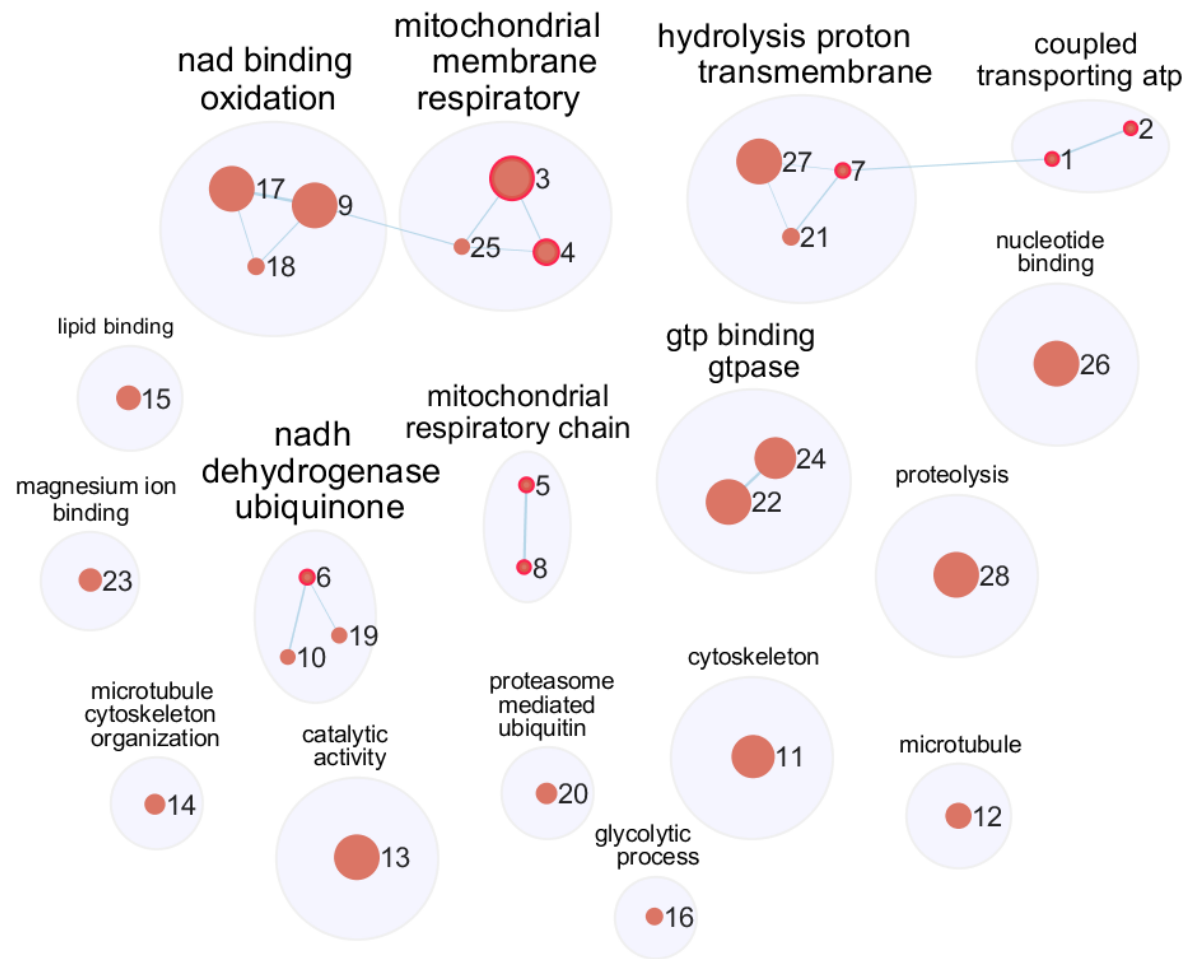
Supplementary Figure 3 – Volcano plots highlighting association statistics for gene expression analyses of A) water vs DMSO, B) clozapine vs DMSO, and C) a test of interaction between sex and clozapine exposure. Results for all expressed genes are given in Supplementary Table 4.



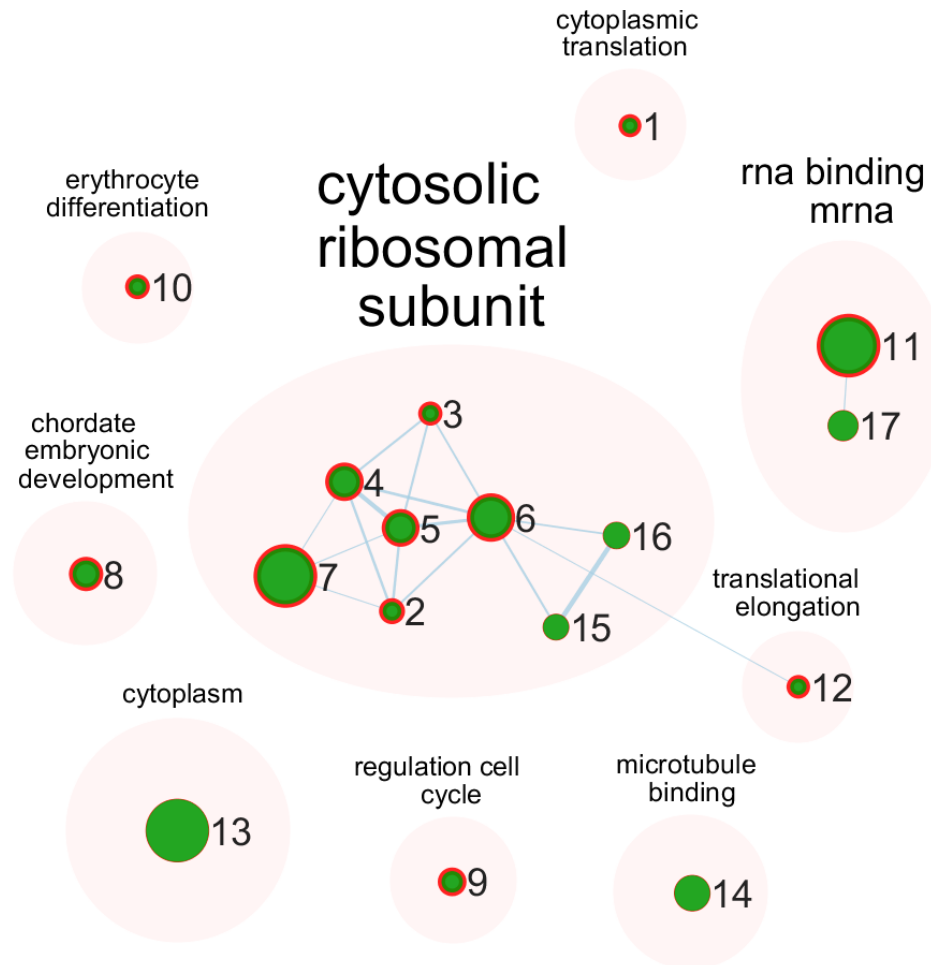
Supplementary Figure 4 – Quantile-quantile (Q-Q) plot of association statistics from a model testing gene expression differences reflecting an interaction between clozapine exposure and sex. No significant differences were identified, indicating that exposure to clozapine does not have differential effects on gene expression in males and females. Results for all expressed genes are given in **Supplementary Table 4**.



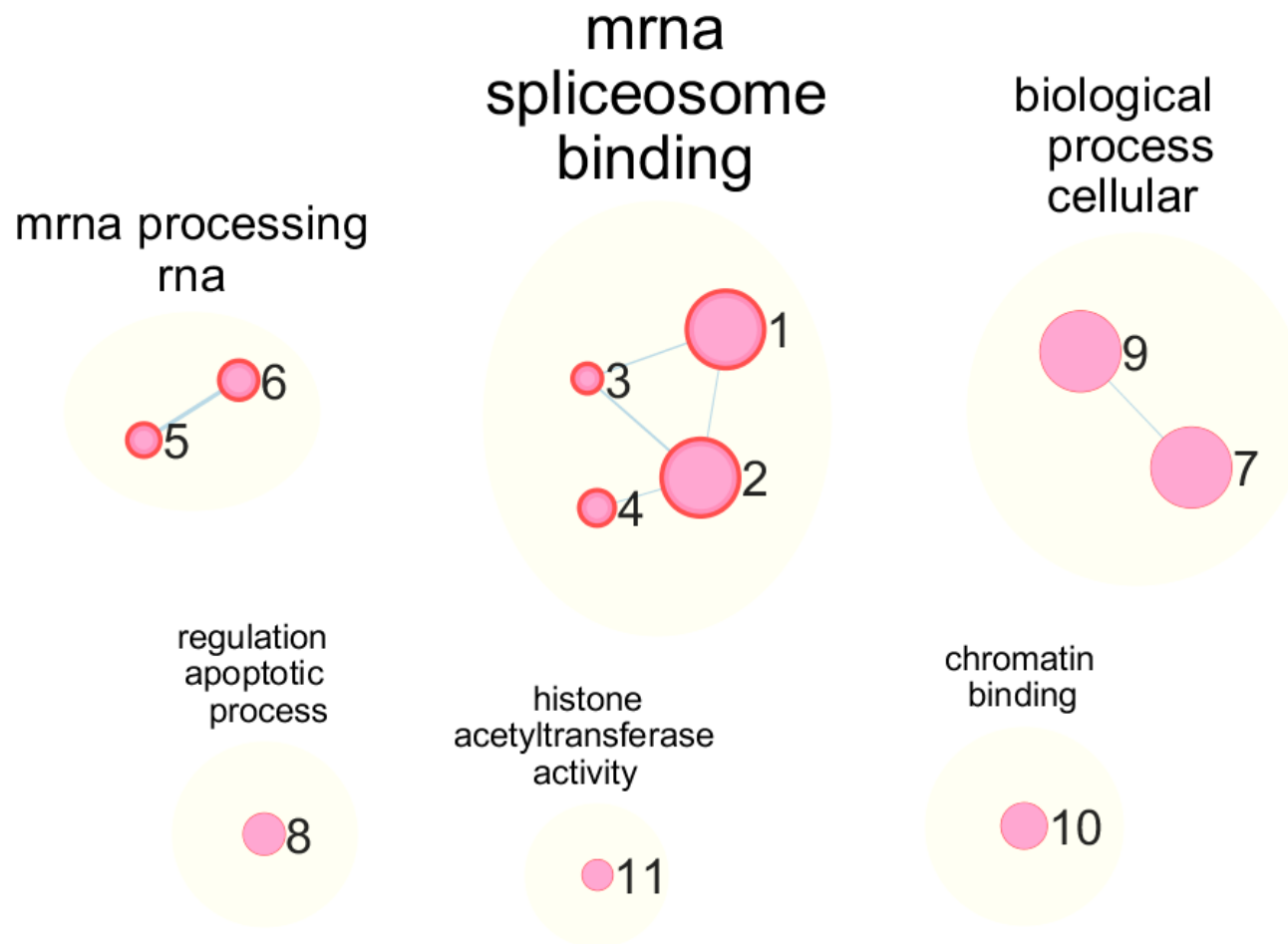
Supplementary Figure 5 – Clozapine exposure is associated with altered transcript connectivity in multiple brain co-expression modules. Shown is the relationship between mean connectivity and clozapine exposure for transcripts in eighteen additional modules. The results for two other modules ('Module 1' and 'Module 5') are shown in **Figure 3** and **Figure 4**, respectively.



Supplementary Figure 6 – Clusters of gene ontology (GO) categories enriched in ‘Module 4’. The applications ‘EnrichmentMap” (v3.2.0) and AutoAnnotate’ (v1.3) in Cytoscape (v3.7.1) were used to generate this figure. GO terms are ordered by enrichment *P*-value with smaller numbers representing smaller *P*-values. GO terms were clustered by ‘gene set description’ (‘EnrichmentMap’). Overrepresented GO terms are circled with a red border (Bonferroni $P < 3.34\text{E-}05$, see **Supplementary Table 6**). The width of the edges is proportional to the number of genes in common between GO terms.

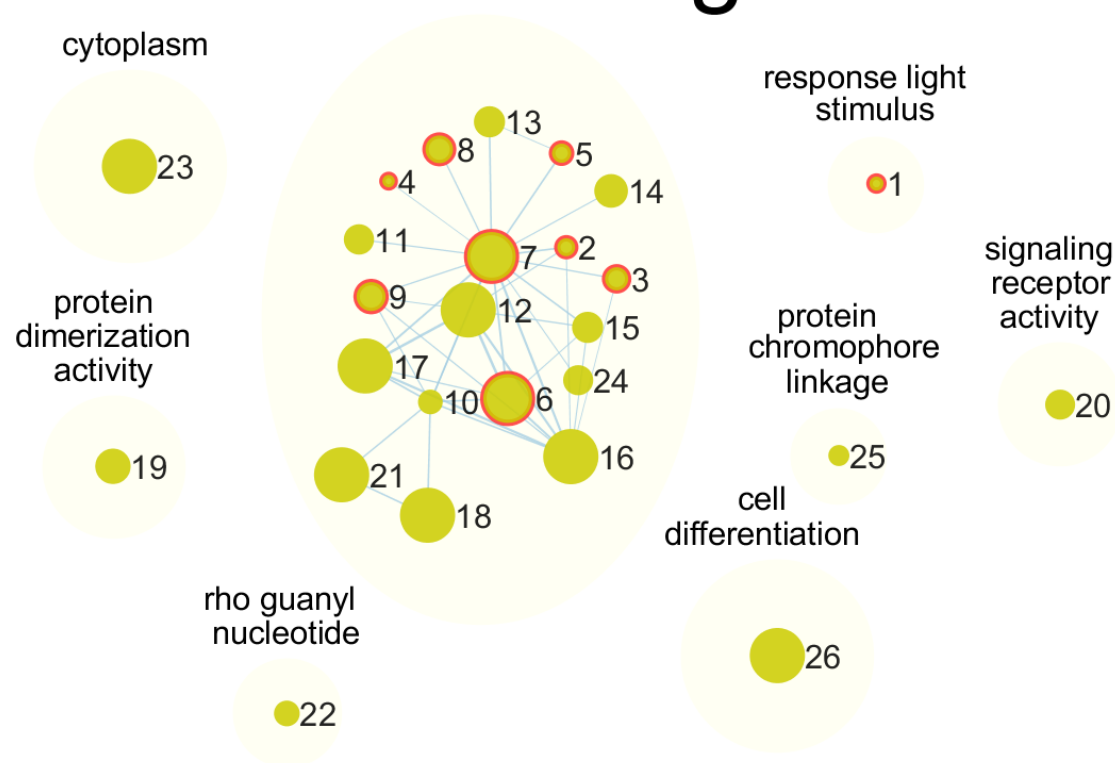


Supplementary Figure 7 – Clusters of gene ontology (GO) categories enriched in ‘Module 5’. The applications ‘EnrichmentMap” (v3.2.0) and AutoAnnotate’ (v1.3) in Cytoscape (v3.7.1) were used to generate this figure. GO terms are ordered by enrichment *P*-value with smaller numbers representing smaller *P*-values. GO terms were clustered by ‘gene set description’ (‘EnrichmentMap’). Overrepresented GO terms are circled with a red border (Bonferroni $P < 3.34\text{E-}05$, see **Supplementary Table 6**). The width of the edges is proportional to the number of genes in common between GO terms.

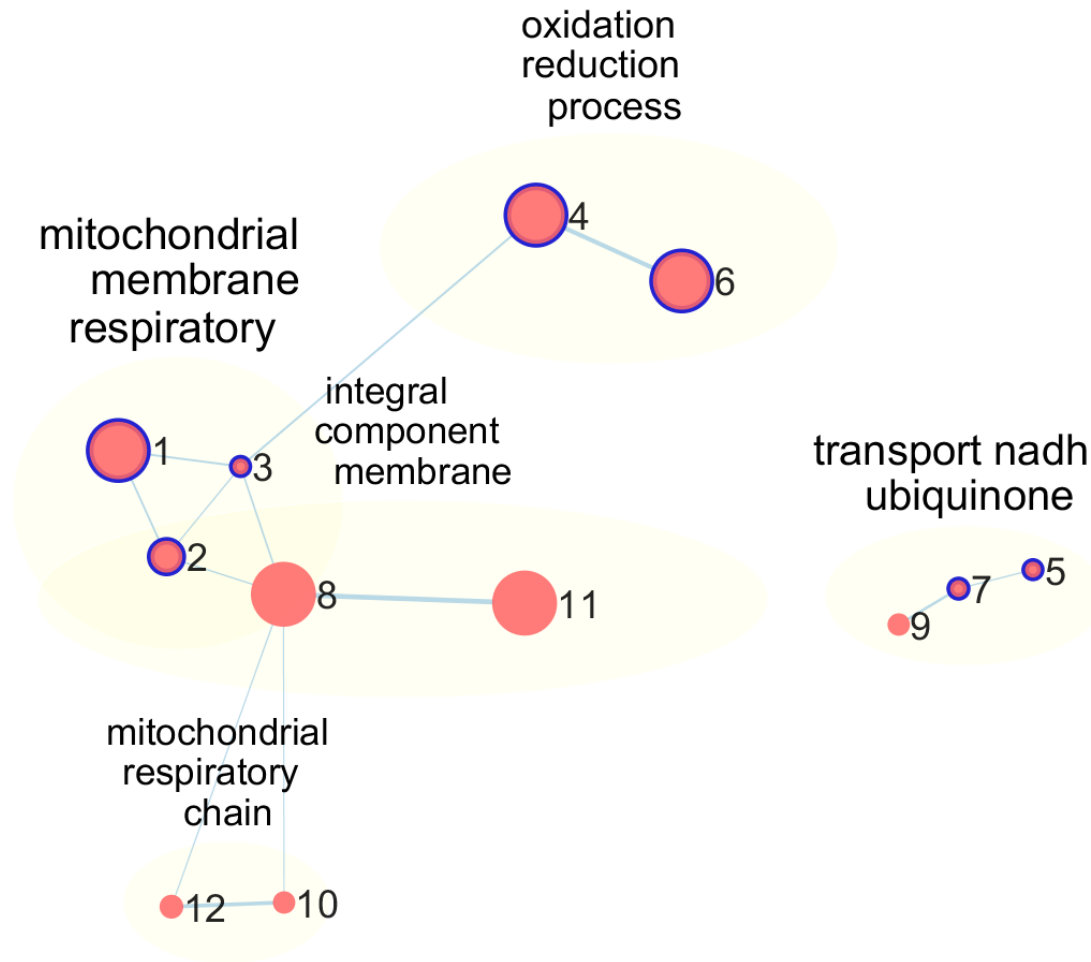


Supplementary Figure 8 – Clusters of gene ontology (GO) categories enriched in ‘Module 8’. The applications ‘EnrichmentMap” (v3.2.0) and AutoAnnotate’ (v1.3) in Cytoscape (v3.7.1) were used to generate this figure. GO terms are ordered by enrichment *P*-value with smaller numbers representing smaller *P*-values. GO terms were clustered by ‘gene set description’ (‘EnrichmentMap’). Overrepresented GO terms are circled with a red border (Bonferroni $P < 3.34\text{E-}05$, see **Supplementary Table 6**). The width of the edges is proportional to the number of genes in common between GO terms.

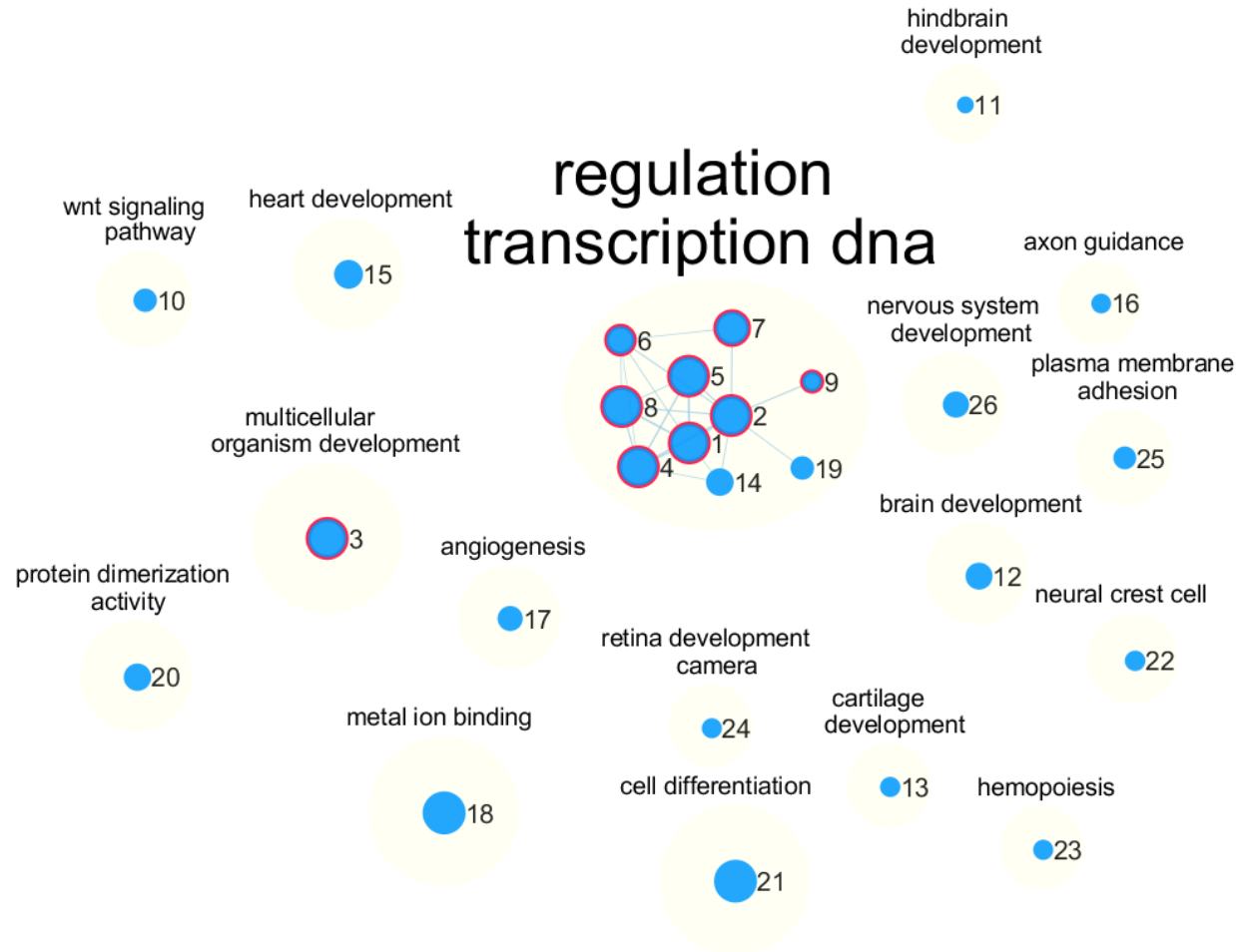
transcription dna binding



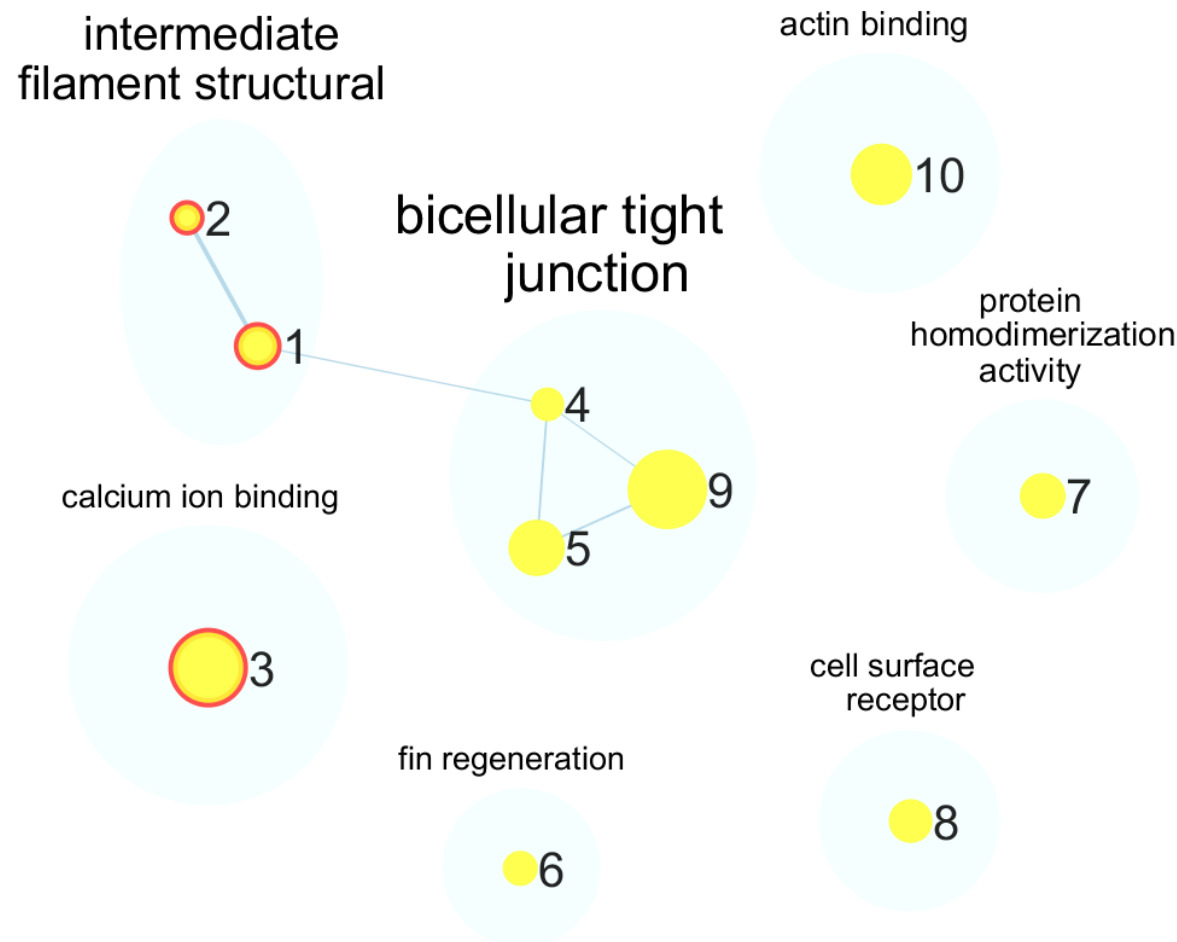
Supplementary Figure 9 – Clusters of gene ontology (GO) categories enriched in ‘Module 11’. The applications ‘EnrichmentMap’ (v3.2.0) and AutoAnnotate’ (v1.3) in Cytoscape (v3.7.1) were used to generate this figure. GO terms are ordered by enrichment *P*-value with smaller numbers representing smaller *P*-values. GO terms were clustered by ‘gene set description’ (‘EnrichmentMap’). Overrepresented GO terms are circled with a red border (Bonferroni $P < 3.34E-05$, see **Supplementary Table 6**). The width of the edges is proportional to the number of genes in common between GO terms.



Supplementary Figure 10 – Clusters of gene ontology (GO) categories enriched in ‘Module 13’. The applications ‘EnrichmentMap” (v3.2.0) and AutoAnnotate’ (v1.3) in Cytoscape (v3.7.1) were used to generate this figure. GO terms are ordered by enrichment *P*-value with smaller numbers representing smaller *P*-values. GO terms were clustered by ‘gene set description’ (‘EnrichmentMap’). Overrepresented GO terms are circled with a blue border (Bonferroni *P* < 3.34E-05, see **Supplementary Table 6**). The width of the edges is proportional to the number of genes in common between GO terms.



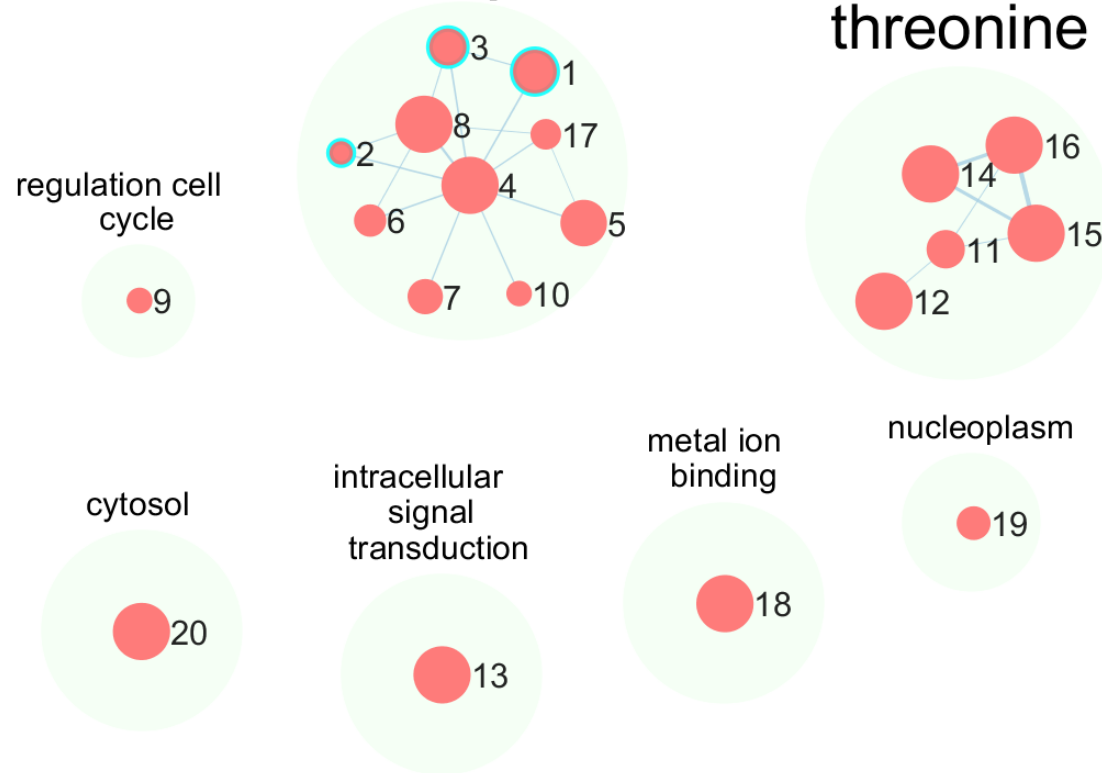
Supplementary Figure 11 – Clusters of gene ontology (GO) categories enriched in ‘Module 16’. The applications ‘EnrichmentMap’ (v3.2.0) and AutoAnnotate’ (v1.3) in Cytoscape (v3.7.1) were used to generate this figure. GO terms are ordered by enrichment P -value with smaller numbers representing smaller P -values. GO terms were clustered by ‘gene set description’ (‘EnrichmentMap’). Overrepresented GO terms are circled with a blue border (Bonferroni $P < 3.34\text{E-}05$, see **Supplementary Table 6**). The width of the edges is proportional to the number of genes in common between GO terms.



Supplementary Figure 12 – Clusters of gene ontology (GO) categories enriched in ‘Module 19’. The applications ‘EnrichmentMap” (v3.2.0) and AutoAnnotate’ (v1.3) in Cytoscape (v3.7.1) were used to generate this figure. GO terms are ordered by enrichment *P*-value with smaller numbers representing smaller *P*-values. GO terms were clustered by ‘gene set description’ (‘EnrichmentMap’). Overrepresented GO terms are circled with a red border (Bonferroni $P < 3.34E-05$, see **Supplementary Table 6**). The width of the edges is proportional to the number of genes in common between GO terms.

rna polymerase transcription

protein serine threonine



Supplementary Figure 13 – Clusters of gene ontology (GO) categories enriched in 'Module 13'. The applications 'EnrichmentMap' (v3.2.0) and AutoAnnotate' (v1.3) in Cytoscape (v3.7.1) were used to generate this figure. GO terms are ordered by enrichment P -value with smaller numbers representing smaller P -values. GO terms were clustered by 'gene set description' ('EnrichmentMap'). Overrepresented GO terms are circled with a blue border (Bonferroni $P < 3.34E-05$, see **Supplementary Table 6**). The width of the edges is proportional to the number of genes in common between GO terms.

Supplementary Table 1 – Phenotypic data for each of the samples used in this study. Shown is the body weight (g), fork length (cm), liver weight (mg) and brain weight (mg), Fulton's condition factor (*k*), hepatosomatic index (HSI), brain-body ratio (BBR) and RNA integrity number (RIN) for each individual fish (see **Methods**).

Fish ID	Exposure	Sex	Week	Tank	Body weight (g)	Length (cm)	Condition factor	Brain (mg)	Brain-body ratio	Liver (mg)	Hepatosomatic index	RIN
1	high	F	2	5	0.36	3.30	0.99	4.81	1.35	8.64	2.42	9.4
2	high	M	1	5	0.42	3.40	1.06	5.87	1.4	1.79	0.43	9.2
3	DMSO	M	1	4	0.45	3.40	1.13	6.33	1.42	5.01	1.12	9.5
4	low	F	2	3	0.32	3.00	1.19	4.68	1.46	7.01	2.19	9.5
5	high	F	1	5	0.31	3.00	1.13	3.22	1.05	5.81	1.9	9.1
6	DMSO	F	1	6	0.54	3.50	1.26	5.34	0.99	11.9	2.21	9.3
7	DMSO	F	1	4	0.37	3.20	1.14	4.6	1.23	13.16	3.52	9.3
8	water	M	1	8	0.35	3.30	0.97	5.51	1.57	1.51	0.43	9.2
9	low	F	1	1	0.34	3.10	1.15	4.33	1.26	4.25	1.24	9.2
10	DMSO	F	2	4	0.34	3.20	1.02	4.23	1.26	9.13	2.73	9.3
11	high	M	1	7	0.36	3.40	0.92	4.64	1.28	2.35	0.65	9.3
12	low	M	1	1	0.39	3.50	0.91	5.95	1.53	1.7	0.44	9.9
13	water	F	2	8	0.32	3.10	1.09	5.19	1.6	6.97	2.15	9
14	low	F	1	3	0.36	3.10	1.21	4.88	1.36	3.24	0.9	9.4
15	low	M	1	1	0.5	3.20	1.52	5.52	1.11	1.15	0.23	9.3
16	high	M	1	5	0.34	3.30	0.94	5.61	1.65	1.25	0.37	9.4
17	DMSO	M	1	6	0.34	3.10	1.15	5.83	1.7	2.21	0.64	9.7
18	water	M	2	8	0.41	3.50	0.96	5.3	1.29	1.98	0.48	9.3
19	water	F	1	8	0.34	3.10	1.14	4.62	1.36	3.86	1.14	9.4
20	high	M	2	5	0.34	3.20	1.04	3.88	1.14	2.43	0.71	9.6
21	DMSO	M	2	4	0.52	3.60	1.11	6.55	1.26	3.3	0.64	8.7
22	DMSO	F	1	4	0.36	3.20	1.10	5.5	1.53	10.18	2.83	10
23	high	M	2	5	0.32	3.20	0.98	5.59	1.74	1.22	0.38	9.9
24	low	M	2	1	0.42	3.50	0.98	5.97	1.42	1.16	0.28	9.4
25	DMSO	M	2	6	0.38	3.40	0.97	5.9	1.55	1.71	0.45	9.1

26	water	M	2	2	0.42	3.40	1.08	NA	NA	5.14	1.21	9.7
27	water	M	2	8	0.37	3.40	0.94	5.87	1.59	1.56	0.42	9.8
28	low	M	1	3	0.36	3.20	1.08	5.57	1.57	1.72	0.48	9.6
29	water	F	2	8	0.41	3.30	1.14	5.62	1.38	12.6	3.09	9.6
30	water	M	1	8	0.39	3.30	1.09	5.46	1.39	2.88	0.73	9.6
31	DMSO	M	2	4	0.37	3.30	1.02	6.35	1.73	1.3	0.35	9.9
32	high	F	1	7	0.41	3.40	1.04	5.25	1.28	10.09	2.46	9.4
33	DMSO	F	2	6	0.42	3.50	0.99	5.75	1.36	8.89	2.1	-
34	water	M	2	2	0.33	3.20	1.01	6.1	1.84	2.02	0.61	9.8
35	high	F	2	7	0.35	3.00	1.28	4.87	1.41	11.54	3.34	9.2
36	high	M	2	7	0.34	3.40	0.85	3.61	1.08	2.26	0.67	9.3
37	water	F	2	2	0.44	3.40	1.12	4.16	0.95	12.91	2.93	9.4
38	high	F	2	5	0.36	3.20	1.10	4.66	1.29	9.03	2.51	9
39	water	F	1	2	0.37	3.10	1.24	4.64	1.25	10.68	2.89	9.1
40	water	M	1	2	0.37	3.30	1.03	6.54	1.76	3.45	0.93	9.2
41	water	F	1	8	0.47	3.40	1.19	4.54	0.97	11.56	2.48	9.1
42	low	F	2	3	-	3.00	-	2.64	-	10.8	-	9.4
43	water	F	1	2	0.35	3.10	1.16	5.46	1.58	7.84	2.27	9.3
44	DMSO	F	2	6	0.38	3.35	1.01	5.62	1.48	9.01	2.37	9.8
45	low	F	1	1	0.35	3.20	1.07	4.1	1.17	10.72	3.05	9.8
46	low	M	2	3	0.45	3.50	1.05	6.37	1.42	3.1	0.69	9.3
47	DMSO	F	2	4	0.46	3.40	1.16	5.48	1.2	10.71	2.34	9.2
48	DMSO	M	1	6	0.45	3.70	0.89	5.64	1.25	4.42	0.98	9.3
49	low	M	2	3	0.41	3.50	0.95	5.24	1.29	1.98	0.49	9.4
50	low	F	2	1	0.32	3.10	1.07	4.49	1.41	9.08	2.85	9.3
51	high	F	2	7	0.32	3.10	1.07	4.68	1.47	8.89	2.79	9.3
52	high	M	1	7	0.43	3.40	1.09	1.77	0.41	3.6	0.84	9.4
53	water	M	1	2	0.39	3.40	1.00	5.56	1.41	1.9	0.48	8.3
54	low	M	1	3	0.26	3.00	0.98	5.1	1.93	2.62	0.99	9.5
55	high	F	1	7	0.53	3.60	1.13	5.87	1.12	11.95	2.27	9.4
56	low	F	2	1	0.43	3.30	1.19	6.54	1.53	22.83	5.35	9.3
57	high	M	2	7	0.37	3.50	0.87	5.69	1.53	1.29	0.35	9.5

58	water	F	2	2	0.38	3.40	0.96	4.15	1.09	6.78	1.79	9.2
59	DMSO	M	2	6	0.4	3.50	0.94	6.4	1.58	1.95	0.48	9.4
60	high	F	1	5	0.43	3.40	1.08	4.64	1.09	10.5	2.46	9.4
61	low	M	2	1	0.32	3.30	0.89	5.58	1.74	0.54	0.17	8.7
62	low	F	1	3	0.42	3.30	1.15	4.42	1.07	8.85	2.13	9.3
63	DMSO	F	1	6	0.35	3.10	1.16	5.51	1.6	8.83	2.56	9.4
64	DMSO	M	1	4	0.33	3.30	0.93	5.78	1.73	2.51	0.75	9.6

Supplementary Table 2 – Exposure to clozapine is not associated with changes in any of the measured physiological characteristics. The first two columns show t-test *P*-values comparing the water and DMSO samples for body weight (g), fork length (cm), Fulton’s condition factor (*k*), hepatosomatic index (HSI) and brain-body ratio (BBR) (see **Methods**). The two last columns show the ANOVAs *P*-values comparing the DMSO, ‘low’ (20µg/L) and ‘high’ (70µg/L) exposure groups for body weight, fork length, *k*, HSI and BBR. These tests were done separately for males and females since the two sexes can present large differences in these measurements.

	t-test water vs DMSO <i>P</i> -value		ANOVA DMSO, low and high <i>P</i> -value	
	Females	Males	Females	Males
Body weight	0.58	0.34	0.48	0.44
Fork length	0.35	0.42	0.15	0.63
k	0.48	0.85	0.52	0.55
HSI	0.43	0.92	0.99	0.21
BBR	0.64	0.82	0.60	0.25

Supplementary Table 3 – Exposure to clozapine is associated with changes in tank position. Shown are the estimates, standard deviations (SD) and *P*-values of an analysis comparing the time spent in the top, middle or bottom of the tank during spawning, feeding and ‘general time’ (see **Methods**). **A)** shows the results of the linear regression comparing the water and DMSO samples (see **Methods**) and **B)** shows the ANOVA results comparing the DMSO, ‘low’ (20µg/L) and ‘high’ (70µg/L) exposure groups (see **Methods**). Highlighted are all *P*-values < 2.78E-03 (Bonferroni corrected *P*-value).

			Spawning	Feeding	'General time'
A) DMSO vs water	Top	Estimate	1.79	1.50	1.60
		SD	0.91	1.34	1.30
		<i>P</i> -value	0.05	0.27	0.22
	Middle	Estimate	0.69	1.31	0.65
		SD	1.05	0.86	1.38
		<i>P</i> -value	0.52	0.13	0.64
	Bottom	Estimate	-2.48	-2.81	-2.25
		SD	1.06	1.08	1.18
		<i>P</i> -value	0.02	0.01	0.02
B) DMSO vs clozapine	Top	Estimate DMSO vs low	4.25	0.78	3.00
		SD DMSO vs low	1.20	1.56	1.61
		Estimate DMSO vs high	6.67	5.19	13.44
		SD DMSO vs high	1.20	1.56	1.61
		<i>P</i> -value	6.144E-07	2.41E-03	4.34E-14
	Middle	Estimate DMSO vs low	2.88	2.88	0.15
		SD DMSO vs low	1.11	1.23	1.47
		Estimate DMSO vs high	-2.35	-0.25	-6.15
		SD DMSO vs high	1.11	1.23	1.47
		<i>P</i> -value	0.00003282	2.22E-02	1.55E-05
	Bottom	Estimate DMSO vs low	-7.13	-3.66	-3.15
		SD DMSO vs low	1.07	1.44	1.11

		Estimate DMSO vs high	-4.31	-4.94	-7.29
		SD DMSO vs high	1.07	1.44	1.11
		<i>P</i>-value	3.009E-09	2.69E-03	6.74E-09

Supplementary Table 4 – RNA-seq quality control metrics for each sample. Shown are the number of raw paired reads, number of paired reads after trimming (see **Methods**), percentage of trimmed paired reads in relation to the raw reads, number of mapped paired reads (see **Methods**), number of unique mapped reads (see **Methods**), percentage of unique mapped reads in relation to the raw reads and percentage of unique mapped reads in relation to the trimmed reads.

Fish ID	Exposure	Raw paired reads	Trimmed paired reads	% Trimmed paired reads	Mapped paired reads	Unique mapped reads	% unique mapped reads (in relation to raw)	% unique mapped reads (in relation to trimmed)
1	high	25,857,546	24,662,322	95.38	37,008,984	17,527,942	67.79	71.07
2	high	29,277,732	27,533,538	94.04	42,247,030	18,895,135	64.54	68.63
3	DMSO	34,694,030	32,859,138	94.71	49,884,656	23,037,310	66.40	70.11
4	low	21,518,362	20,173,874	93.75	30,558,882	14,366,569	66.76	71.21
5	high	23,459,864	22,511,080	95.96	32,875,582	16,301,997	69.49	72.42
6	DMSO	31,644,800	30,453,254	96.23	46,492,494	21,096,057	66.67	69.27
7	DMSO	43,804,656	41,519,558	94.78	61,731,348	29,616,887	67.61	71.33
8	water	43,474,072	41,061,480	94.45	61,755,966	29,187,557	67.14	71.08
9	low	43,709,854	41,160,864	94.17	60,579,514	30,008,517	68.65	72.91
10	DMSO	35,973,536	33,896,850	94.23	49,846,278	24,989,167	69.47	73.72
11	high	28,230,320	26,304,930	93.18	37,954,754	19,560,894	69.29	74.36
12	low	29,433,220	28,025,862	95.22	41,707,564	20,030,657	68.05	71.47
13	water	39,203,248	36,341,816	92.70	52,733,382	27,635,028	70.49	76.04
14	low	63,776,598	60,025,432	94.12	85,328,040	45,804,318	71.82	76.31
15	low	65,079,992	61,901,314	95.12	91,238,284	45,178,397	69.42	72.98
16	high	35,014,620	33,297,084	95.09	50,451,594	23,840,798	68.09	71.60
17	DMSO	39,428,424	37,792,988	95.85	55,874,152	27,389,566	69.47	72.47
18	water	52,533,504	49,327,384	93.90	72,432,912	36,462,701	69.41	73.92
19	water	58,565,430	54,933,806	93.80	80,230,594	40,944,996	69.91	74.54
20	high	38,981,036	36,706,200	94.16	54,189,878	26,745,441	68.61	72.86
21	DMSO	38,702,598	37,192,566	96.10	56,776,242	26,016,757	67.22	69.95
22	DMSO	37,677,664	35,859,700	95.17	52,838,662	26,273,738	69.73	73.27
23	high	26,744,744	25,219,084	94.30	36,257,074	18,961,647	70.90	75.19
24	low	37,499,686	35,636,388	95.03	52,651,544	25,816,288	68.84	72.44
25	DMSO	32,257,462	31,104,776	96.43	46,975,346	22,100,413	68.51	71.05

26	water	43,007,104	40,936,332	95.19	60,910,762	29,604,253	68.84	72.32
27	water	34,217,002	31,700,266	92.64	46,029,848	23,955,635	70.01	75.57
28	low	43,805,868	41,437,066	94.59	61,875,764	29,973,172	68.42	72.33
29	water	32,600,568	30,987,834	95.05	45,659,546	22,569,765	69.23	72.83
30	water	38,364,790	36,903,484	96.19	54,680,470	26,596,424	69.33	72.07
31	DMSO	30,440,606	29,446,940	96.74	45,207,270	20,233,804	66.47	68.71
32	high	36,037,706	34,342,716	95.30	51,598,372	24,654,776	68.41	71.79
33	DMSO	45,754,756	43,770,602	95.66	66,152,026	31,080,604	67.93	71.01
34	water	32,877,826	31,427,486	95.59	46,725,488	22,736,280	69.15	72.35
35	high	31,701,704	30,470,952	96.12	45,387,846	21,873,404	69.00	71.78
36	high	28,296,630	27,185,114	96.07	40,541,694	19,366,933	68.44	71.24
37	water	22,987,042	21,881,980	95.19	31,462,580	16,616,358	72.29	75.94
38	high	36,318,806	34,976,864	96.31	53,114,016	24,678,636	67.95	70.56
39	water	32,874,574	31,376,030	95.44	46,693,730	22,796,292	69.34	72.66
40	water	21,305,308	20,303,120	95.30	30,468,102	14,517,787	68.14	71.51
41	water	28,545,900	27,438,164	96.12	41,665,210	19,260,109	67.47	70.19
42	low	29,125,062	27,867,122	95.68	42,000,128	19,757,655	67.84	70.90
43	water	25,006,472	23,948,084	95.77	35,329,690	17,311,313	69.23	72.29
44	DMSO	26,048,126	24,313,206	93.34	35,482,884	17,920,900	68.80	73.71
45	low	38,438,124	36,608,946	95.24	54,487,298	26,115,517	67.94	71.34
46	low	39,976,674	38,287,674	95.78	58,212,496	26,829,398	67.11	70.07
47	DMSO	35,373,872	33,772,764	95.47	51,438,670	23,840,770	67.40	70.59
48	DMSO	34,040,346	32,435,878	95.29	49,241,686	22,719,156	66.74	70.04
49	low	38,126,574	35,946,182	94.28	52,890,314	26,275,643	68.92	73.10
50	low	32,346,608	30,768,784	95.12	46,715,012	21,811,313	67.43	70.89
51	high	31,933,598	30,460,620	95.39	46,314,106	21,594,175	67.62	70.89
52	high	35,180,150	33,455,112	95.10	50,202,962	23,812,598	67.69	71.18
53	water	29,334,058	28,191,686	96.11	42,444,174	19,943,165	67.99	70.74
54	low	38,371,786	36,799,228	95.90	54,848,428	26,156,217	68.17	71.08
55	high	36,221,064	34,091,048	94.12	50,027,088	25,133,205	69.39	73.72
56	low	20,950,978	19,997,362	95.45	30,237,116	14,096,291	67.28	70.49
57	high	39,361,098	37,476,884	95.21	56,630,282	26,499,770	67.32	70.71
58	water	29,706,856	28,032,714	94.36	41,729,320	20,370,469	68.57	72.67
59	DMSO	40,946,892	39,231,642	95.81	59,810,494	27,546,919	67.27	70.22

60	high	27,910,182	26,677,934	95.58	40,714,560	18,502,238	66.29	69.35
61	low	26,755,496	25,640,246	95.83	39,204,916	17,755,336	66.36	69.25
62	low	25,983,956	24,622,534	94.76	38,058,160	17,048,741	65.61	69.24
63	DMSO	33,235,704	31,198,978	93.87	46,053,836	23,095,418	69.49	74.03
64	DMSO	18,817,392	17,791,292	94.55	27,052,300	12,422,219	66.01	69.82

Supplementary Table 5 – Gene ontology (GO) categories enriched in each of the gene co-expression networks associated with clozapine exposure. ‘Expressed genes in GO’ shows how many genes expressed in our dataset are in that GO term and ‘Module gene in GO’ shows how many module genes are in that GO term.

Module	GO category	Sub-ontology	Description	Over representation <i>P</i>	Expressed genes in GO	Module gene in GO
1	GO:0004930	MF	G protein-coupled receptor activity	1.56E-06	47	21
	GO:0007165	BP	signal transduction	8.58E-06	114	42
	GO:0007186	BP	G protein-coupled receptor signaling pathway	1.26E-05	60	23
4	GO:0015986	BP	ATP synthesis coupled proton transport	9.5944E-14	15	13
	GO:0046933	MF	proton-transporting ATP synthase activity, rotational mechanism	1.26096E-13	13	12
	GO:0005739	CC	mitochondrion	6.21472E-11	77	23
	GO:0005743	CC	mitochondrial inner membrane	4.96861E-10	32	15
	GO:0004129	MF	cytochrome-c oxidase activity	1.79586E-07	15	9
	GO:0005747	CC	mitochondrial respiratory chain complex I	6.59292E-07	17	9
	GO:0015078	MF	proton transmembrane transporter activity	2.78583E-06	11	7
	GO:0005751	CC	mitochondrial respiratory chain complex IV	2.58042E-05	10	6
5	GO:0002181	BP	cytoplasmic translation	< 2.93E-98	15	15
	GO:0022625	CC	cytosolic large ribosomal subunit	< 2.93E-98	39	39
	GO:0022627	CC	cytosolic small ribosomal subunit	< 2.93E-98	28	28
	GO:0005840	CC	ribosome	2.93E-98	81	80
	GO:0003735	MF	structural constituent of ribosome	5.09E-92	79	77
	GO:0006412	BP	translation	2.09E-86	93	79
	GO:0005622	CC	intracellular	2.32E-55	81	60
	GO:0043009	BP	chordate embryonic development	1.31E-15	34	19
	GO:0051726	BP	regulation of cell cycle	2.47E-08	17	11

	GO:0030218	BP	erythrocyte differentiation	2.90E-08	12	9
	GO:0003723	MF	RNA binding	4.00E-08	63	19
	GO:0006414	BP	translational elongation	4.86E-06	10	6
7	GO:0016020	CC	membrane	2.06E-05	580	36
	GO:0003676	MF	nucleic acid binding	1.32E-18	104	27
	GO:0003723	MF	RNA binding	1.49E-17	63	22
8	GO:0000381	BP	regulation of alternative mRNA splicing, via spliceosome	2.79E-12	12	9
	GO:0003729	MF	mRNA binding	3.83E-10	20	10
	GO:0008380	BP	RNA splicing	5.65E-08	13	7
	GO:0006397	BP	mRNA processing	1.97E-07	15	7
	GO:0009416	BP	response to light stimulus	8.22E-09	19	8
	GO:0000976	MF	transcription regulatory region sequence-specific DNA binding	1.49E-08	22	8
	GO:0008134	MF	transcription factor binding	4.63E-08	16	7
	GO:0032922	BP	circadian regulation of gene expression	2.26E-07	12	6
11	GO:0001078	MF	proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific	1.80E-06	16	6
	GO:0003700	MF	DNA-binding transcription factor activity	2.00E-06	110	13
	GO:0005634	CC	nucleus	1.24E-05	389	23
	GO:0000122	BP	negative regulation of transcription by RNA polymerase II	1.41E-05	24	6
	GO:0006351	BP	transcription, DNA-templated	1.43E-05	36	7
	GO:0005739	CC	mitochondrion	< 2.93E-98	77	19
	GO:0005743	CC	mitochondrial inner membrane	< 2.93E-98	32	13
13	GO:0070469	CC	respiratory chain	< 2.93E-98	19	14
	GO:0055114	BP	oxidation-reduction process	3.54E-10	77	15
	GO:0008137	MF	NADH dehydrogenase (ubiquinone) activity	5.43E-08	13	8
	GO:0016491	MF	oxidoreductase activity	6.70E-07	62	11

	GO:0005747	CC	mitochondrial respiratory chain complex I	1.48E-06	17	7
	GO:0006355	BP	regulation of transcription, DNA-templated	< 2.93E-98	185	19
	GO:0005634	CC	nucleus	2.65E-09	389	23
	GO:0007275	BP	multicellular organism development	1.79E-08	93	12
	GO:0003677	MF	DNA binding	2.37E-08	194	16
	GO:0043565	MF	sequence-specific DNA binding	3.43E-08	124	13
16	GO:0000981	MF	DNA-binding transcription factor activity, RNA polymerase II-specific	1.17E-07	54	9
	GO:0006357	BP	regulation of transcription by RNA polymerase II	2.61E-07	58	9
	GO:0003700	MF	DNA-binding transcription factor activity	8.56E-06	110	10
	GO:0000977	MF	RNA polymerase II regulatory region sequence-specific DNA binding	2.50E-05	37	6
	GO:0005198	MF	structural molecule activity	< 2.93E-98	31	11
19	GO:0005882	CC	intermediate filament	3.60E-07	15	6
	GO:0005509	MF	calcium ion binding	4.67E-06	75	7
	GO:0006357	BP	regulation of transcription by RNA polymerase II	6.03E-07	58	9
25	GO:0000978	MF	RNA polymerase II proximal promoter sequence-specific DNA binding	2.61E-06	24	6
	GO:0000981	MF	DNA-binding transcription factor activity, RNA polymerase II-specific	8.47E-06	54	8