



Correction to: Gene expression analyses on multi-target mode of action of black cohosh in menopausal complaints – a pilot study in rodents

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In the original article published, the table legends were erroneously incompletely transferred from the manuscript to the

published version. The correct table (Tables 1, 2, 3, 4) legends are given below.

Apart from this many typographical errors have been corrected.

The original article has been corrected.

Table 1 Number of differentially regulated genes

Hi Hy	PRAE	OVX	OVX + iCR	Compensation
PRAE		836	2401	213
OVX	943		2210	
OVX + iCR	1760	1759		
Compensation	349			

Selection, filtering, and compensation analysis of differentially regulated genes within the hippocampus and hypothalamus. The data are shown as a cross tabulation with the top right side showing the data for the hippocampus (Hi) and the bottom left side showing the data for the hypothalamus (Hy). The compensation analysis identified features in which treatment with black cohosh counteracted the effect of ovariectomy.

The original articles can be found online at <https://doi.org/10.1007/s00404-021-06105-8>.

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Table 2 Selected target genes for qPCR

No	Gene	Name
1. Target gene selection based on Table "GSEA compensation analysis" ($FC > 1.5$, $p < 0.2$; Filter: compensation). Question: Which OVX-induced changes are compensated by iCR?		
1	AVPR1A (Hi)	Arginine vasopressin receptor 1A
2	GAL (Hi)	Galanin and GMAP prepropeptide
3	CALCA (Hi)	Calcitonin related polypeptide alpha
4	HCRT (Hi)	Hypocretin neuropeptide precursor
5	PNOC (Hi)	Prepronociceptin
6	IL5 (Hi)	Interleukin 5
7	BCL2 (Hy)	BCL2, apoptosis regulator
8	IGFBP1 (Hy)	Insulin like growth factor binding protein 1
9	IGFBP5 (Hy)	Insulin like growth factor binding protein 5
10	IL3 (Hy)	Interleukin 3
11	TRPV3 (Hy)	Transient receptor potential cation channel subfamily V member 3
2. Target gene selection based on "GSEA iCR exclusive" ($FC > 1.5$, $p < 0.2$; Filter: iCR exclusive). Question: Which gene expression is exclusively changed by iCR?		
12	PRL7A3 (Hi)	Prolactin family 7, subfamily a, member 3
13	PLCB1 (Hy)	Phospholipase C beta 1
14	MAPK9 (Hy)	Mitogen-activated protein kinase 9
15	ADCY1 (Hy)	Adenylate cyclase 1
16	G6PC (Hy)	Glucose-6-phosphatase catalytic subunit
17	CACNA1A (Hy)	Calcium voltage-gated channel subunit alpha1 A
3. Generally important target genes not covered in above mentioned lists. Question: Which further genes are of general importance in regard to the present scientific work?		
18	ESR1	Estrogen receptor 1 (alpha)
19	ESR2	Estrogen receptor 2 (beta)
20	OPRM1	Opioid receptor mu 1
21	KISS1	KiSS-1 metastasis-suppressor
22	TAC3	Tachykinin 3

Overview of selected target genes. Hi = Hippocampus, Hy = Hypothalamus, OVX = bilateral ovariectomy, iCR = isopropanolic extract of *Cimicifuga racemosa* (black cohosh).

Table 3 qPCR values expressed as fold change, and intergroup comparisons (t test). **a** hippocampus, **b** hypothalamus

Hippocampus		AVPR1A	GAL	CALCA	HCRT	PNOC	IL5	BCL2	IGFBP1	IGFBP5	IL3	TRPV3
Fold change	PRAE	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	OVX	1.125	1.653	1.434	2.780	1.206	0.622	1.591	1.117	0.959	0.832	1.149
	OVX + iCR	0.468	0.927	0.676	0.572	0.543	0.159	1.227	0.657	0.644	0.530	0.611
Inbetween group comparisons	PRAE-OVX	0.270	0.001	0.087	0.135	0.190	0.000	0.011	0.502	0.607	0.073	0.024
	OVX-(OVX + iCR)	0.029	0.021	0.069	0.128	0.026	0.009	0.055	0.029	0.004	0.002	0.002
	PRAE-(OVX + iCR)	0.002	0.458	0.046	0.099	0.000	0.002	0.220	0.117	0.026	0.016	0.016
a												
Hippocampus		PRL7A3	PLCB1	MAPK9	ADCY1	G6PC	CACNA1A	ESR1	ESR2	OPRM1	KISS1	TAC3
Fold change	PRAE	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	OVX	1.087	1.181	1.223	0.707	2.056	0.946	1.564	1.586	1.017	1.046	1.429
	OVX + iCR	0.493	0.642	0.555	0.511	0.722	0.920	0.838	0.949	0.920	0.483	0.637
Inbetween group comparisons	PRAE-OVX	0.034	0.070	0.090	0.005	0.016	0.065	0.016	0.050	0.812	0.359	0.011
	OVX-(OVX + iCR)	0.003	0.003	0.005	0.001	0.033	0.995	0.039	0.076	0.705	0.005	0.006
	PRAE-(OVX + iCR)	0.001	0.003	0.003	0.001	0.125	0.734	0.158	0.409	0.976	0.023	0.002
b												
Hypothalamus		AVPR1A	GAL	CALCA	HCRT	PNOC	IL5	BCL2	IGFBP1	IGFBP5	IL3	TRPV3
Fold change	PRAE	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	OVX	1.233	0.974	0.890	0.783	0.928	1.033	0.878	0.721	0.682	0.647	1.299
	OVX + iCR	0.759	0.696	0.691	0.492	0.610	3.199	0.645	0.762	0.691	0.897	0.991
Inbetween group comparisons	PRAE-OVX	0.001	0.370	0.104	0.172	0.281	0.325	0.139	0.002	0.025	0.110	0.009
	OVX-(OVX + iCR)	0.035	0.151	0.081	0.013	0.037	0.178	0.017	0.524	0.460	0.047	0.064
	PRAE-(OVX + iCR)	0.147	0.172	0.089	0.025	0.073	0.180	0.005	0.048	0.037	0.285	0.970
b												
Hypothalamus		PRL7A3	PLCB1	MAPK9	ADCY1	G6PC	CACNA1A	ESR1	ESR2	OPRM1	KISS1	TAC3
Fold change	PRAE	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	OVX	0.884	1.070	1.540	0.961	1.487	0.791	1.179	0.922	0.900	2.096	1.131
	OVX + iCR	0.968	0.822	1.055	0.632	1.834	0.492	0.713	0.854	0.600	2.383	0.875
Inbetween group comparisons	PRAE-OVX	0.026	0.400	0.001	0.604	0.143	0.027	0.031	0.007	0.034	0.019	0.024
	OVX-(OVX + iCR)	0.348	0.094	0.046	0.025	0.290	0.007	0.038	0.002	0.001	0.009	0.080
	PRAE-(OVX + iCR)	0.838	0.403	0.504	0.085	n.a	0.001	0.161	0.001	0.001	0.016	0.351

qPCR values expressed as fold change and intergroup comparisons (t-test). **a** hippocampus, **b** hypothalamus; PRAE = intact animals, OVX = bilateral ovariectomy, OVX+iCR = treatment with isopropanolic extract of *Cimicifuga racemosa* (black cohosh) after OVX.

Table 4 Comparison of microarray and qPCR results

Gene	Question for selecting this gene (details see text)	Hippocampus	Hypothalamus
AVPR1A	Compensation (Hi)	# ²	XX ³
GAL	Compensation (Hi)	XX	O
CALCA	Compensation (Hi)	XX	O
HCRT	Compensation (Hi)	XX	X
PNOC	Compensation (Hi)	# ²	<>
IL5	Compensation (Hi)	<>	<>
BCL2	Compensation (Hy)	<>	<>
IGFBP1	Compensation (Hy)	xx ³	<>
IGFBP5	Compensation (Hy)	<>	<>
IL3	Compensation (Hy)	<>	<>
TRPV3	Compensation (Hy)	<>	<>
PRL7A3	iCR exclusive (Hi)	<>	XX ³
PLCB1	iCR exclusive (Hy)	<>	<>
MAPK9	iCR exclusive (Hy)	<>	<>
ADCY1	iCR exclusive (Hy)	<>	<>
G6PC	iCR exclusive (Hy)	<>	<>
CACNA1A	iCR exclusive (Hy)	<>	<>
ESR1	General interest	# ¹	# ¹
ESR2	General interest	# ¹	O
OPRM1	General interest	O	# ²
KISS1	General interest	<>	O
TAC3	General interest	# ¹	XX ³

“XX” = qPCR and microarray mutually show ‘compensation of OVX-induced effect by iCR’

“X” = qPCR and microarray mutually show ‘exclusive effect of iCR’

“O” = qPCR and microarray show ‘no relevant effect of iCR’

“<>” = qPCR and microarray results are not consistent with each other “#” = target genes, which do not show similar patterns at the two techniques but are worth to be discussed

1 compensation in qPCR, but no such effect found in the microarray

2 compensation in microarray, but in qPCR only a trend of an OVX-effect and a significant iCR-effect was found

3 compensation in qPCR, but in microarray only a trend was seen which did not meet the FC threshold criteria.