

# Combined functional profiling of SNP association and copy number in luminal B tumours using GO Biological Process

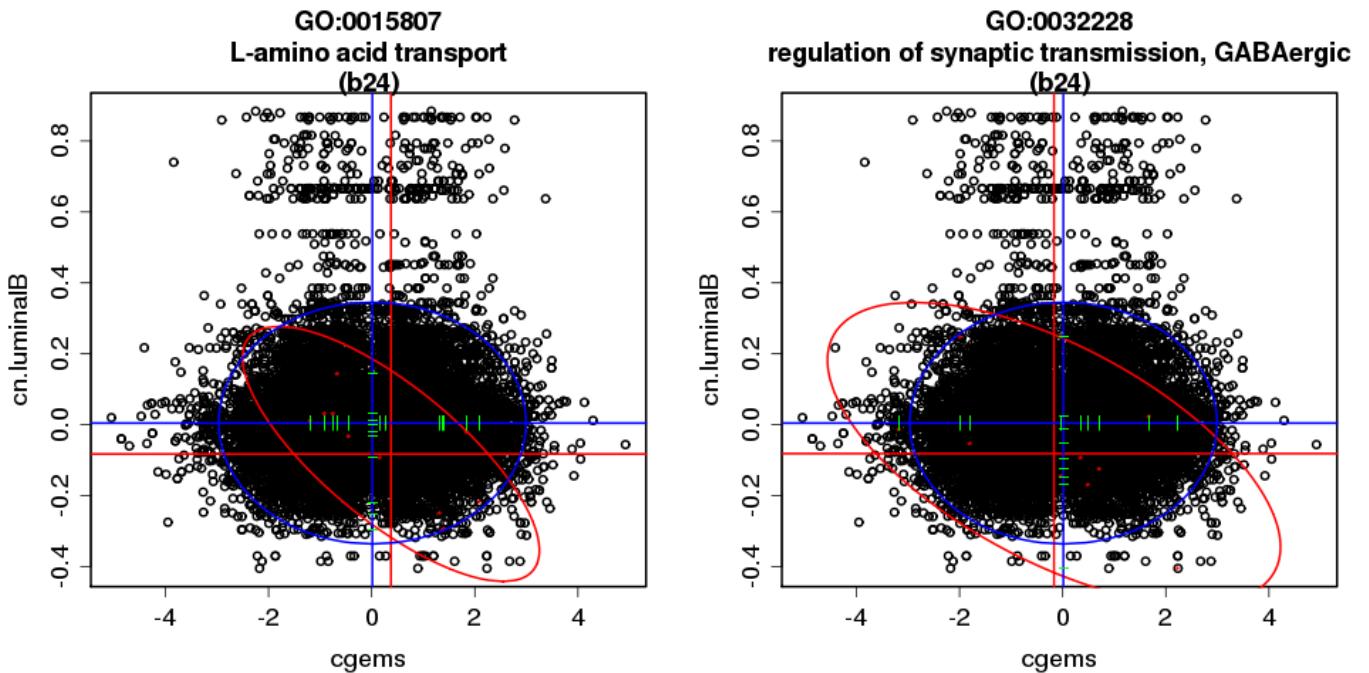
8 significant modules

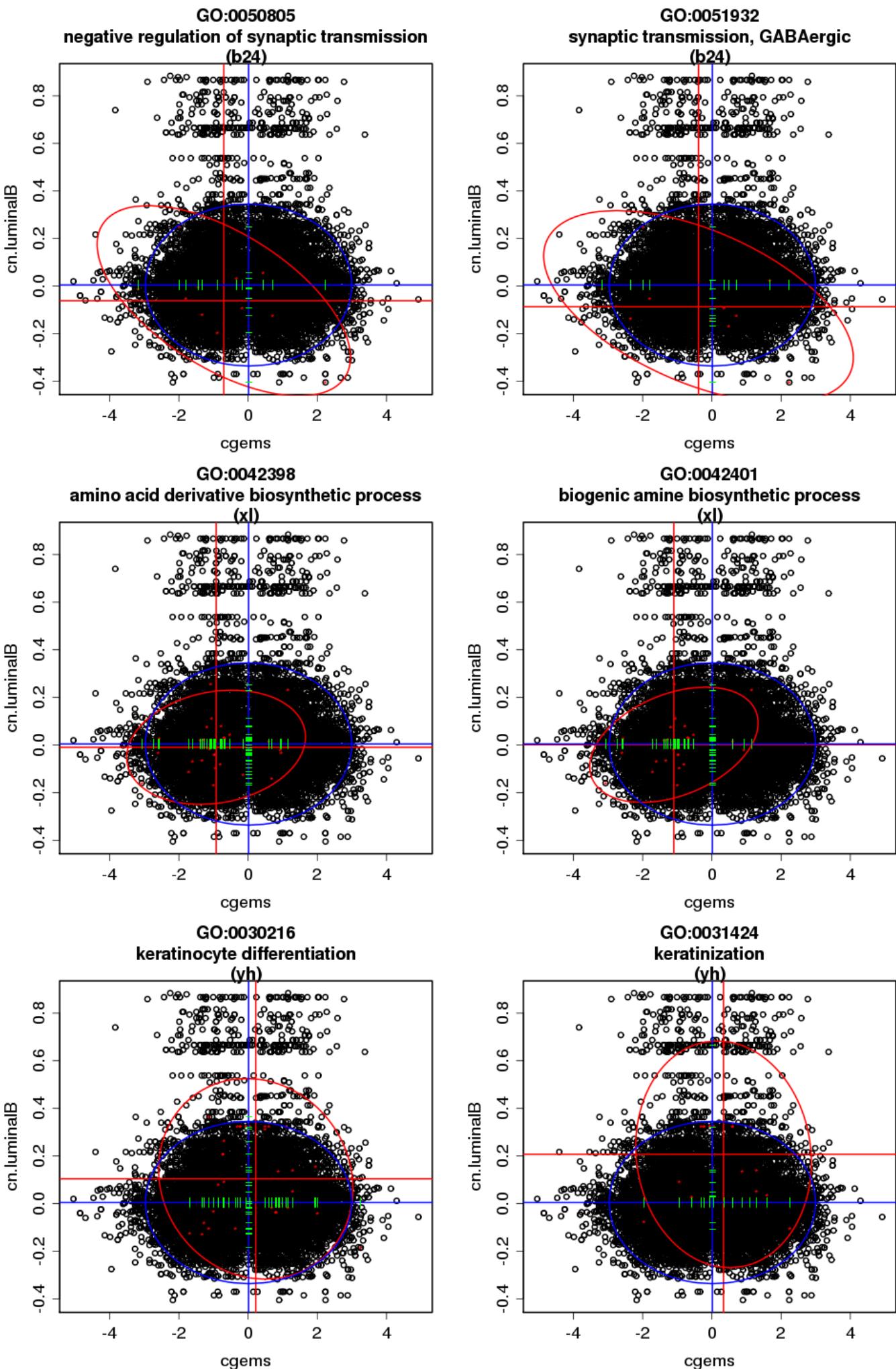
**LOR** indicates Log Odds Ratio of the coefficient or the interaction

**p** indicates FDR adjusted p-value

	LOR cgems	LOR cn.luminalB	In-ter	p cgems	p cn.luminalB	p Inter	pattern	name
GO:0015807	-0.09	-0.85	-0.59	0.98	0.46	0.04	b24	L-amino acid transport
GO:0032228	-0.63	-1.21	-0.68	0.65	0.24	0.01	b24	regulation of synaptic transmission, GABAergic
GO:0050805	-0.94	-1.24	-0.63	0.22	0.24	0.04	b24	negative regulation of synaptic transmission
GO:0051932	-0.82	-1.35	-0.67	0.49	0.17	0.02	b24	synaptic transmission, GABAergic
GO:0042398	-0.77	-0.02	0.12	0.04	0.99	1.00	xl	amino acid derivative biosynthetic process
GO:0042401	-0.93	0.12	0.20	0.01	0.98	1.00	xl	biogenic amine biosynthetic process
GO:0030216	0.20	0.41	-0.03	0.80	0.03	1.00	yh	keratinocyte differentiation
GO:0031424	0.29	0.59	-0.01	0.81	0.00	1.00	yh	keratinization

Table 1: LOR: log odds ratio; p: adjusted p-value FDR





# Combined functional profiling of SNP association and copy number in luminal B tumours using KEGG pathways

1 significant modules

**LOR** indicates Log Odds Ratio of the coefficient or the interaction

**p** indicates FDR adjusted p-value

	LOR cgems	LOR cn lumi-nalB	LOR Inter	p cgems	p cn lu-minalB	p Inter	pattern	name
hsa05217	-0.28	-0.11	0.56	0.59	0.89	0.01	b13	Basal cell carcinoma

Table 1: LOR: log odds ratio; p: adjusted p-value FDR

