

**S6 Table Summary of GO term enrichment analysis of 60 genes showing pattern D.**

GO-BP term	Gene	Count	Fold Enrichment	P value	FDR
<u>Overrepresented</u>					
peptide biosynthetic process (GO:0043043)	<i>RPS6,RPL36,RPL8,RPS20,RPL37, RPL15,RPS16,RPSA,RPL5,RPS7</i>	10	11.16	2.3E-08	0.0002
translation (GO:0006412)	<i>RPS6,RPL36,RPL8,RPS20,RPL37, RPL15,RPS16,RPSA,RPL5,RPS7</i>	10	11.59	1.6E-08	0.0002
peptide metabolic process (GO:0006518)	<i>RPS6,RPL36,RPL8,RPS20,RPL37, RPL15,RPS16,RPSA,RPL5,RPS7</i>	10	8.61	2.4E-07	0.0008
amide biosynthetic process (GO:0043604)	<i>RPS6,RPL36,RPL8,RPS20,RPL37, RPL15,RPS16,RPSA,RPL5,RPS7</i>	10	8.68	2.2E-07	0.0010
ribosomal small subunit biogenesis (GO:0042274)	<i>RPS6,RPS10,RPS16,RPSA,RPS7</i>	5	25.31	2.2E-06	0.0051
positive regulation of sprouting angiogenesis (GO:1903672)	<i>KDR,DLL1,BMPER,APLNR</i>	4	50.63	1.9E-06	0.0054
cellular amide metabolic process (GO:0043603)	<i>RPS6,RPL36,RPL8,RPS20,RPL37, RPL15,RPS16,RPSA,RPL5,RPS7</i>	10	5.94	6.3E-06	0.0110
cellular nitrogen compound biosynthetic process (GO:0044271)	<i>RPS6,RPL36,RPL8,RPS20,RPL37, RPL15,RPS16,RPSA,RPL5,RPS7, POLR3H,MOXD1</i>	12	4.39	5.7E-06	0.0113
cell population proliferation (GO:0008283)	<i>RPS6,CEBPB,BMPER,IRF2,LMB R1L,WNT3A,CD151,FAM83B</i>	8	7.84	8.5E-06	0.0131
ribosome biogenesis (GO:0042254)	<i>RPS6,RPS10,RPS16,RPSA,RPL5, NIP7,RPS7</i>	7	9.48	9.9E-06	0.0138
regulation of sprouting angiogenesis (GO:1903670)	<i>KDR,DLL1,BMPER,APLNR</i>	4	28.62	1.6E-05	0.0197
ribosome assembly (GO:0042255)	<i>RPS10,RPSA,RPL5,NIP7</i>	4	24.84	2.6E-05	0.0305
organonitrogen compound biosynthetic process (GO:1901566)	<i>RPS6,RPL36,RPL8,RPS20,RPL37, RPL15,RPS16,RPSA,RPL5,RPS7, MOXD1</i>	11	4.03	3.2E-05	0.0345
cytoplasmic translation (GO:0002181)	<i>RPL36,RPL8,RPL15,RPSA</i>	4	21.58	4.4E-05	0.0440
<u>Primitive streak formation-related</u>					
gastrulation (GO:0007369)	<i>RPS6, WNT3A, CRB2</i>	3	8.37	5.9E-03	0.8910
anterior/posterior pattern specification (GO:0009952)	<i>DLL1, WNT3A, CRB2</i>	3	5.2	2.1E-02	1.0000
anatomical structure formation involved in morphogenesis (GO:0048646)	<i>DLL1, BMPER, WNT3A, CRB2, RPS7</i>	5	2.67	4.0E-02	1.0000
gastrulation with mouth forming second (GO:0001702)	<i>CRB2</i>	1	16.45	6.2E-02	1.0000
axis specification (GO:0009798)	<i>DLL1</i>	1	5.31	1.7E-01	1.0000
<u>Chromosome segregation-related</u>					
nuclear chromosome segregation (GO:0098813)	<i>HORMAD2</i>	1	0.438	1.8E+00	1.0000
chromosome segregation (GO:0007059)	<i>HORMAD2</i>	1	0.502	1.5E+00	1.0000

Overrepresented GO-BP terms and GO-BP terms related to primitive streak formation and chromosome segregation are shown. Processes that involve many ribosomal protein genes are indicated in gray.