

Gene Sets Down-regulated in Wnt1
Dormant Residual Tumor Cells

	SP_PIR_KEYWORDS	# Down-regulated		
		Genes in Cluster	p-value	FDR (Benjamini)
Cluster 1	<u>Enrichment Score: 38.87</u>			
	cell cycle	132	1.80E-49	4.30E-47
	mitosis	74	1.10E-38	1.40E-36
	cell division	88	1.50E-38	1.50E-36
Cluster 2	<u>Enrichment Score: 24.81</u>			
	kinetochore	36	1.60E-25	1.10E-23
	chromosomal protein	42	1.00E-16	4.10E-15
Cluster 3	<u>Enrichment Score: 17.26</u>			
	ribonucleoprotein	71	1.00E-23	6.10E-22
	ribosomal protein	52	1.70E-19	9.20E-18
Cluster 4	<u>Enrichment Score: 16.28</u>			
	dna replication	34	2.00E-17	8.90E-16
Cluster 6	<u>Enrichment Score: 11.13</u>			
	DNA damage	38	8.40E-09	2.30E-07
	dna repair	34	5.30E-08	1.40E-06
Cluster 7	<u>Enrichment Score: 11</u>			
	atp-binding	152	9.10E-12	2.90E-10
	nucleotide-binding	176	3.00E-10	9.10E-09
Cluster 8	<u>Enrichment Score: 7.67</u>			
	ubl conjugation	83	7.20E-13	2.50E-11
	isopeptide bond	42	1.90E-06	3.80E-05
Cluster 9	<u>Enrichment Score: 6.33</u>			
	ribosome biogenesis	15	9.10E-07	1.90E-05
	rrna processing	15	3.00E-05	5.00E-04
Cluster 10	<u>Enrichment Score: 6.03</u>			
	cytoskeleton	71	2.00E-06	4.00E-05
	microtubule	34	1.50E-05	2.80E-04
Cluster 12	<u>Enrichment Score: 5.62</u>			
	chromosomal protein	42	1.00E-16	4.10E-15
Cluster 15	<u>Enrichment Score: 4.79</u>			
	molecular chaperone	7	1.80E-04	2.50E-03
Cluster 20	<u>Enrichment Score: 3.52</u>			
	mitochondrion	78	7.80E-04	1.00E-02
	transit peptide	47	4.60E-03	4.40E-02

Gene Sets Down-regulated in HER2/neu
Dormant Residual Tumor Cells

	SP_PIR_KEYWORDS	# Down-regulated		
		Genes in Cluster	p-value	FDR (Benjamini)
Cluster 1	<u>Enrichment Score: 25.71</u>			
	ribonucleoprotein	85	3.90E-31	6.20E-29
	ribosomal protein	67	1.70E-29	2.10E-27
Cluster 2	<u>Enrichment Score: 24.79</u>			
	cell division	79	7.80E-28	7.40E-26
	cell cycle	107	3.10E-27	2.40E-25
	mitosis	62	6.50E-25	3.40E-23
Cluster 4	<u>Enrichment Score: 12.94</u>			
	mitochondrion	149	4.70E-26	2.80E-24
	transit peptide	85	1.50E-14	5.80E-13
Cluster 5	<u>Enrichment Score: 11.29</u>			
	chromosomal protein	33	5.30E-09	1.30E-07
Cluster 6	<u>Enrichment Score: 9.67</u>			
	kinetochore	26	4.40E-13	1.60E-11
Cluster 7	<u>Enrichment Score: 9.26</u>			
	ubl conjugation	88	1.90E-12	6.40E-11
	isopeptide bond	51	6.30E-09	1.40E-07
Cluster 8	<u>Enrichment Score: 9.1</u>			
	rrna processing	22	7.50E-10	2.10E-08
	ribosome biogenesis	16	5.40E-07	9.50E-06
Cluster 9	<u>Enrichment Score: 7.04</u>			
	dna replication	27	3.40E-10	1.00E-08
Cluster 10	<u>Enrichment Score: 6.69</u>			
	nucleotide-binding	189	1.20E-09	3.30E-08
	atp-binding	152	2.10E-08	4.10E-07
Cluster 11	<u>Enrichment Score: 6.44</u>			
	dna repair	33	1.90E-06	3.00E-05
	DNA damage	35	3.20E-06	4.60E-05
Cluster 14	<u>Enrichment Score: 5.85</u>			
	cytoskeleton	67	6.10E-04	6.30E-03
Cluster 19	<u>Enrichment Score: 4.99</u>			
	molecular chaperone	6	2.70E-03	2.30E-02
Cluster 25	<u>Enrichment Score: 3.72</u>			
	microtubule	28	9.00E-03	6.70E-02