

Figure S1 Fluorescence in situ hybridization analysis of *HER-2* expression in HRNBC patients. (A,B) *HER-2* negative expression in TNBC patient tumor tissue; (C,D) *HER-2* positive expression in *HER-2* overexpression patient tumor tissue (400 \times).

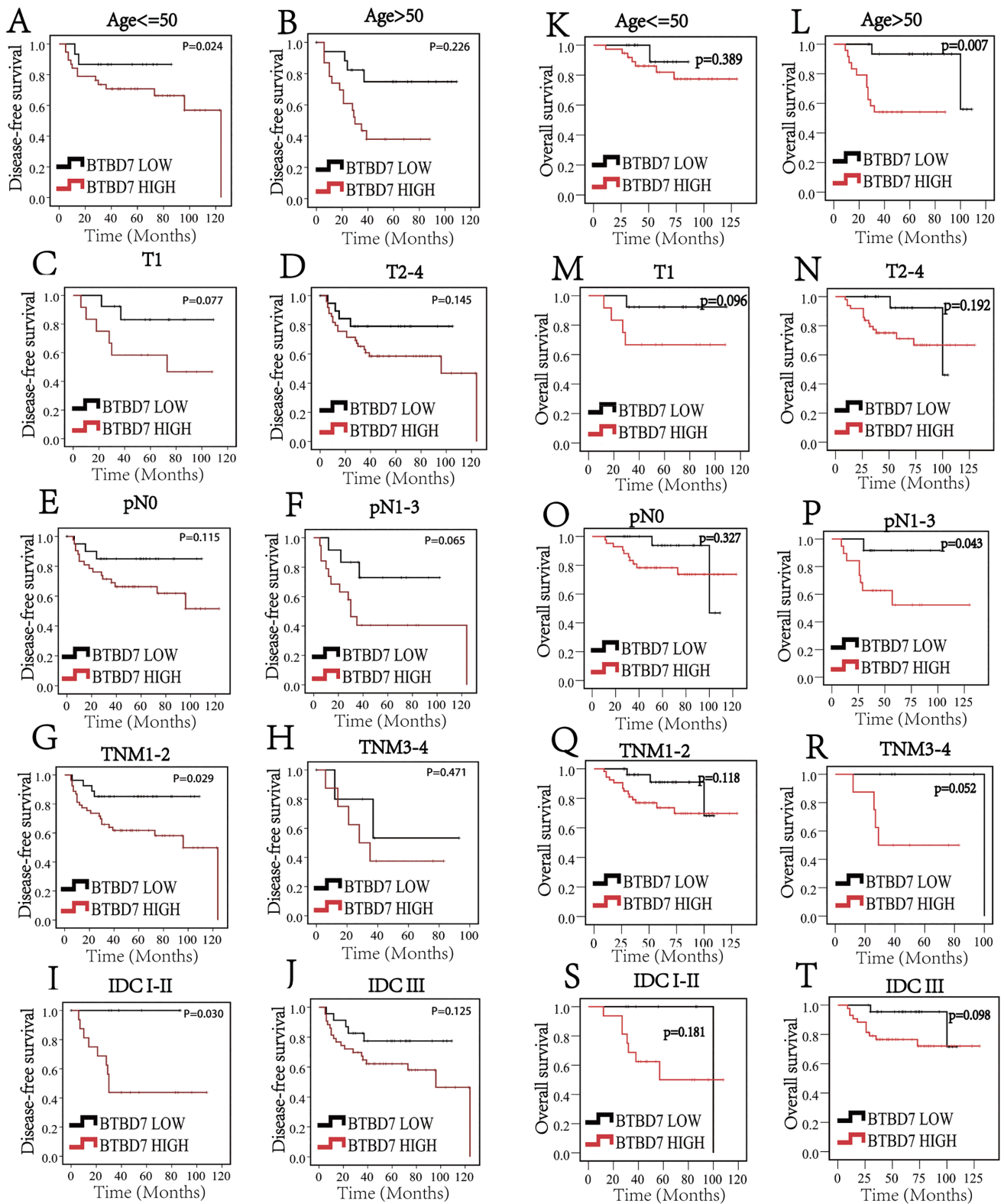


Figure S2 Subgroup analysis of DFS and OS in TNBC patients according to BTBD7 expression using Kaplan-Meier curves. (A-I) Kaplan-Meier curves of DFS according to BTBD7 expression differed by age, tumor volume, lymph node metastasis, TNM stage, and IDC differentiated degree; (K-T) Kaplan-Meier curves of OS according to BTBD7 differed by age, tumor volume, lymph node metastasis, TNM stage, and IDC differentiated degree. DFS, disease-free survival; IDC, invasive ductal carcinoma; OS, overall survival.

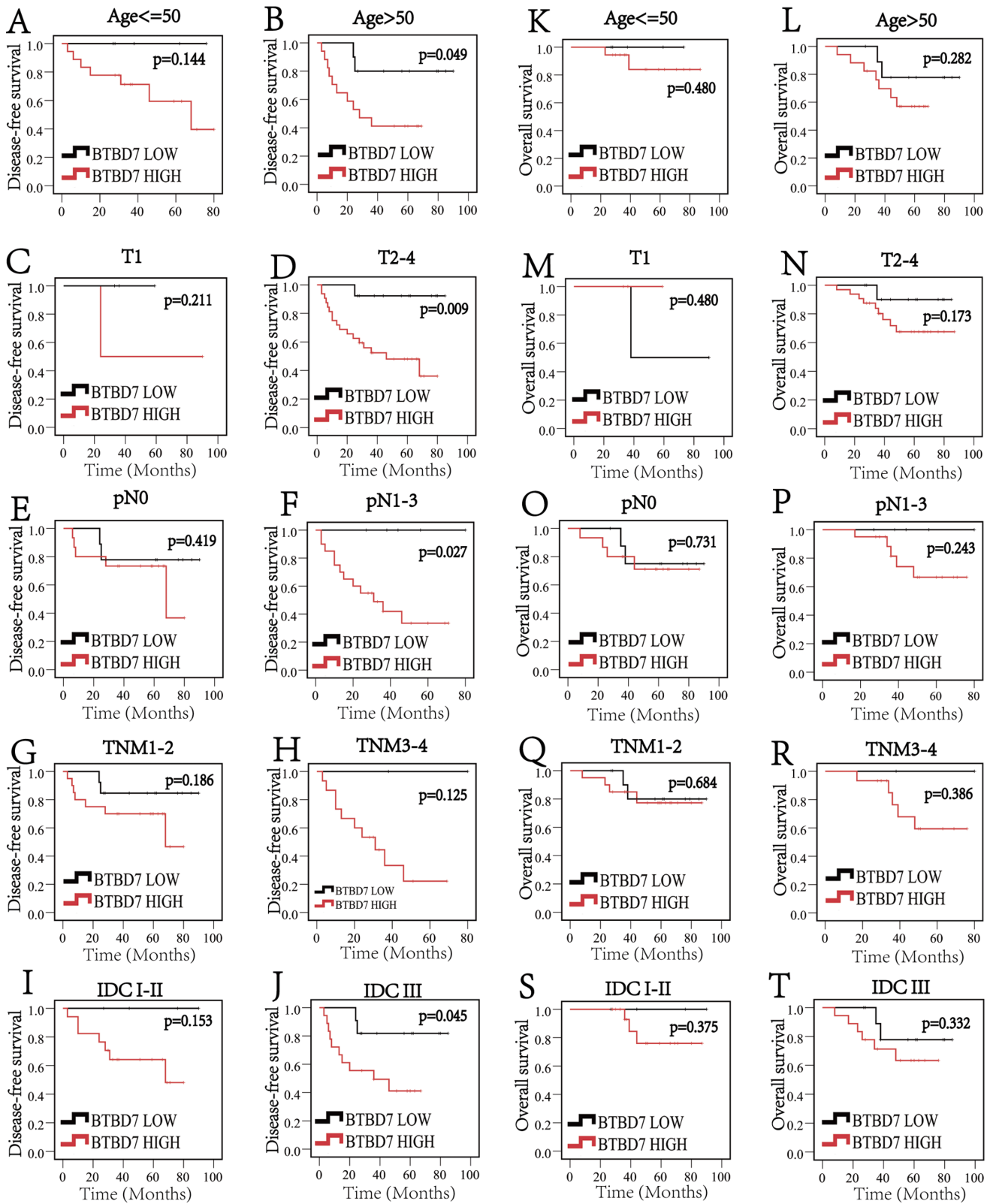


Figure S3 Subgroup analysis of DFS and OS in patients with HER-2 overexpression according to BTBD7 using Kaplan-Meier curves. (A-I) Kaplan-Meier curves of DFS according to BTBD7 differed by age, tumor volume, lymph node metastasis, TNM stage, and IDC differentiated degree; (K-T) Kaplan-Meier curves of OS according to BTBD7 differed by age, tumor volume, lymph node metastasis, TNM stage, and IDC differentiated degree. DFS, disease-free survival; IDC, invasive ductal carcinoma; OS, overall survival.

Table S1 Expression of Btbd7 and Slug protein in HRNBC tumor tissue

HRNBC tissue	Btbd7		P value
	Low	High	
Slug			
Low	28	26	0.001
High	20	70	

Table S2 30 GO terms enriched by DAVID

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
BP	GO:0006351 Transcription, DNA-templated	74	23.41772	1.52E-10	6670, 4293, 23528, 22913, 56252, 4090, 51042, 85457, 79618, 90317, 10499, 10773, 7638, 5978, 284370, 153222, 64324, 121274, 55252, 79088, 83744, 23093, 26122, 56980, 29994, 196528, 55814, 84671, 83463, 7768, 10589, 347344, 7586, 4793, 57680, 253461, 126231, 92285, 7182, 114803, 204851, 54891, 80264, 147687, 23186, 353274, 91748, 6248, 5439, 9575, 9774, 7750, 22869, 285267, 4287, 91664, 55193, 163049, 374879, 5170, 7592, 84614, 80854, 84458, 546, 55279, 7745, 54989, 9329, 11016, 152485, 904, 905, 58508	294	1955	16792	2.161922	2.03E-07	1.02E-07	1.01E-07
BP	GO:0006355 Regulation of transcription, DNA-templated	63	19.93671	1.07E-10	6670, 4293, 22913, 1385, 2033, 56252, 4090, 27125, 6667, 9736, 55206, 90317, 10499, 10773, 7638, 5978, 284370, 153222, 55252, 79088, 83744, 56980, 29994, 196528, 1386, 84671, 7768, 6239, 2957, 347344, 7586, 126231, 92285, 7182, 204851, 54891, 80264, 147687, 353274, 6248, 9439, 10114, 9575, 22869, 285267, 4287, 91664, 55193, 64864, 163049, 9252, 374879, 5170, 7592, 84614, 80854, 84458, 546, 55279, 7745, 11016, 152485, 58508	294	1504	16792	2.392477	1.43E-07	1.02E-07	1.01E-07
BP	GO:0045944 Positive regulation of transcription from RNA polymerase II promoter	32	10.12658	0.001015	6670, 7189, 4297, 6872, 57680, 1385, 2033, 253461, 54790, 7182, 114803, 23064, 6667, 659, 5216, 54778, 10499, 5978, 9575, 25836, 55252, 9252, 5926, 6938, 55870, 546, 1386, 5966, 904, 138474, 905, 7707	294	981	16792	1.8631	0.742558	0.193753	0.193318
BP	GO:0000122 Negative regulation of transcription from RNA polymerase II promoter	23	7.278481	0.007908	23405, 6670, 25836, 23528, 7189, 5494, 153222, 64324, 5663, 57680, 2033, 51042, 23186, 22890, 1386, 6239, 10499, 11016, 5966, 5978, 51547, 7707, 10589	294	720	16792	1.824528	0.999975	0.754623	0.752929
BP	GO:0006468 Protein phosphorylation	22	6.962025	5.40E-05	4293, 9113, 6792, 91754, 6872, 9578, 1385, 2241, 57551, 4090, 9252, 5170, 204851, 57448, 102, 10746, 2764, 10087, 10114, 138474, 904, 905	294	456	16792	2.755579	0.069649	0.014438	0.014406
BP	GO:0006366 Transcription from RNA polymerase II promoter	21	6.64557	7.10E-04	9575, 9321, 4297, 6872, 1385, 2033, 5926, 6938, 55870, 27125, 1386, 659, 6239, 5966, 138474, 904, 5978, 5439, 905, 2957, 7707	294	513	16792	2.338067	0.612902	0.158123	0.157768
BP	GO:0045893 Positive regulation of transcription, DNA-templated	20	6.329114	0.00182	9575, 6670, 23528, 5494, 4297, 64324, 5663, 1385, 57680, 4090, 6182, 10746, 80854, 6667, 79618, 54778, 6239, 80142, 138474, 5978	294	515	16792	2.218083	0.912319	0.270204	0.269597
BP	GO:0016567 Protein ubiquitination	16	5.063291	0.001679	51529, 122809, 9040, 130507, 57534, 331, 57448, 55148, 997, 84078, 197131, 9867, 54778, 10116, 8925, 8816	294	359	16792	2.545544	0.894143	0.270204	0.269597
BP	GO:0045892 Negative regulation of transcription, DNA-templated	16	5.063291	0.029275	9575, 6670, 25836, 9774, 23528, 7189, 57680, 253461, 9252, 5926, 23186, 85457, 79618, 83463, 5978, 7707	294	499	16792	1.831363	1	1	0.998502
BP	GO:0006974 Cellular response to DNA damage stimulus	15	4.746835	1.79E-05	25836, 259282, 7189, 9766, 6872, 5663, 253461, 57551, 331, 257218, 80854, 324, 23064, 22890, 1386	294	208	16792	4.118917	0.023665	0.007983	0.007965
CC	GO:0016021 Integral component of membrane	61	36.52695	0.009806	389762, 58473, 389761, 55161, 80762, 10975, 146894, 115286, 433, 5018, 93109, 9934, 8608, 10058, 90550, 6048, 149466, 729515, 1468, 26001, 54600, 368, 283951, 140885, 10462, 526, 6834, 8992, 92840, 114926, 9766, 374882, 4233, 113235, 56670, 9120, 147007, 54577, 54576, 55423, 54575, 117247, 5159, 11001, 54658, 537, 1317, 10434, 2180, 91663, 5770, 6302, 10326, 861, 283578, 389763, 9528, 6337, 7109, 93517, 4712	163	5163	18224	1.320942	0.846225	0.208557	0.206362
CC	GO:0070062 Extracellular exosome	45	26.94611	8.52E-05	7263, 6036, 374882, 6696, 6037, 23365, 56670, 84617, 55020, 55161, 4507, 550, 146894, 56954, 8802, 5159, 11001, 537, 759, 10058, 10434, 91663, 10380, 39, 93100, 94056, 4060, 5590, 483, 10965, 10326, 84836, 10747, 388, 54600, 6337, 11331, 5269, 140885, 9528, 966, 526, 64081, 89941, 4832	163	2811	18224	1.789813	0.016059	0.003238	0.003204
CC	GO:0005739 Mitochondrion	35	20.95808	1.73E-08	7384, 7263, 27349, 64928, 4728, 4729, 51263, 115286, 56954, 58510, 84105, 5830, 51027, 8802, 11001, 4720, 5018, 10058, 10434, 4704, 2180, 90550, 35, 37, 39, 10965, 339229, 10469, 27034, 11331, 4731, 4832, 10587, 4712, 4713	163	1331	18224	2.939992	3.28E-06	1.09E-06	1.08E-06
CC	GO:0005743 Mitochondrial inner membrane	24	14.37126	8.51E-12	90550, 7384, 7263, 37, 64928, 4705, 10469, 10975, 4729, 1468, 51263, 115286, 58510, 8802, 11331, 4731, 55967, 6834, 5018, 4712, 4723, 374291, 4713, 10058	163	441	18224	6.084554	1.62E-09	1.35E-09	1.34E-09
CC	GO:0005789 Endoplasmic reticulum membrane	18	10.77844	0.001755	2180, 92840, 113655, 6048, 55161, 54600, 368, 54577, 54884, 54576, 54575, 11001, 54658, 966, 51128, 5833, 8608, 10058	163	862	18224	2.334648	0.283733	0.055568	0.054983
CC	GO:0005759 Mitochondrial matrix	15	8.982036	1.38E-06	7263, 35, 37, 4705, 10965, 10469, 4728, 27034, 8802, 54988, 4720, 84693, 374291, 10587, 4704	163	327	18224	5.128609	2.62E-04	6.54E-05	6.47E-05
CC	GO:0005747 Mitochondrial respiratory chain complex I	11	6.586826	1.42E-11	4705, 4728, 4729, 4720, 4731, 55967, 4723, 374291, 4712, 4713, 4704	163	49	18224	25.09879	2.70E-09	1.35E-09	1.34E-09
CC	GO:0016324 Apical plasma membrane	8	4.790419	0.015444	146894, 368, 113235, 6337, 5159, 6712, 2030, 5590	163	291	18224	3.073641	0.948039	0.266761	0.263953
CC	GO:0031966 Mitochondrial membrane	5	2.994012	0.009879	1468, 6048, 5018, 4712, 4704	163	94	18224	5.947004	0.848376	0.208557	0.206362
CC	GO:0043209 Myelin sheath	5	2.994012	0.046858	4705, 22933, 7384, 4729, 526	163	152	18224	3.677753	0.99989	0.741917	0.734107
MF	GO:0008137 NADH dehydrogenase (ubiquinone) activity	11	6.586826	1.19E-11	4705, 4728, 4729, 4720, 4731, 55967, 4723, 374291, 4712, 4713, 4704	152	48	16881	25.45107	3.50E-09	3.50E-09	3.43E-09
MF	GO:0046982 Protein heterodimerization activity	11	6.586826	0.009087	7164, 5154, 861, 6256, 54600, 54577, 64321, 54576, 54575, 54658, 150	152	465	16881	2.627207	0.932313	0.243691	0.238735
MF	GO:0019899 Enzyme binding	10	5.988024	0.003096	5770, 6256, 54600, 54577, 54576, 54575, 5830, 5159, 11001, 54658	152	333	16881	3.335111	0.599397	0.101485	0.099421
MF	GO:0009055 Electron carrier activity	8	4.790419	1.60E-05	10975, 35, 4729, 37, 27034, 4720, 55967, 8608	152	90	16881	9.87193	0.004711	0.001574	0.001542
MF	GO:0005525 GTP binding	8	4.790419	0.057379	388, 8802, 54988, 387496, 89941, 51128, 4337, 84617	152	384	16881	2.313734	1	0.995696	0.975445
MF	GO:0003824 Catalytic activity	6	3.592814	0.02702	2180, 4507, 54988, 64081, 4337, 5833	152	188	16881	3.544443	0.99969	0.569341	0.557761
MF	GO:0003954 NADH dehydrogenase activity	5	2.994012	4.19E-07	4728, 4720, 4723, 374291, 4704	152	8	16881	69.41201	1.24E-04	6.18E-05	6.05E-05
MF	GO:0001972 Retinoic acid binding	5	2.994012	4.77E-05	54600, 54577, 54576, 54575, 54658	152	23	16881	24.14331	0.013979	0.003519	0.003448
MF	GO:0015020 Glucuronosyltransferase activity	5	2.994012	1.23E-04	54600, 54577, 54576, 54575, 54658	152	29	16881	19.14814	0.035569	0.007243	0.007096
MF	GO:0051539 4 iron, 4 sulfur cluster binding	5	2.994012	5.29E-04	4728, 4720, 4337, 4723, 374291	152	42	16881	13.22133	0.144432	0.025991	0.025463

Table S3 25 KEGG terms enriched by KOBAS 3.0

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
R-HSA-73857	RNA Polymerase II Transcription	52	1316	7.16E-28	1.61E-24	1.61E-24	ZNF699 MED23 BAX HIPK1 PRELID1 GTF2A1 CCNT1 CCNT2 CPSF2 ZNF426 PPM1A AFF4 RNF111 NR2C2AP LSM10 ZNF585B ZNF347 ZNF430 PHC3 ARID2 ZNF417 ZNF510 ZNF641 KMT2C ZNF221 KMT2A ZNF41 SOCS4 SP1 TCF12 CREB1 NR2C2 ZNF573 PDPK1 EP300 PAPOLA POLR2J ZNF445 TJP1 ZNF615 TAF1 ZNF616 ZNF619 ZNF484 TAF1L ZKSCAN1 ZNF791 PBRM1 ZKSCAN8 ATXN3 ZNF770 ATF2	52
R-HSA-162582	Signal Transduction	52	2689	9.21E-15	5.19E-12	5.19E-12	ATP6V1F SMAD5 SEL1L BAX UHMK1 ADAM10 LATS1 GTF2A1 SP1 CCNT1 ARHGAP5 CCNT2 KBTBD7 EP300 PPM1A CHD8 PSEN1 MIB1 NF1 PHC3 DRAP1 RPS6KA5 RANBP2 NCOA2 ARHGEF12 ZNF225 TRAF6 STAG2 DAAM1 RNF111 REST FER CREB1 NUMB DYNC1H1 PPP2R5E USP34 TAOK1 POLR2J PRKAR2A TJP1 UBE2M SOS2 BDP1 XIAP RCOR1 PFN1 BMPR2 MYO9A PDPK1 STAM2 ATF2	52
R-HSA-392499	Metabolism of proteins	49	2012	1.02E-17	1.15E-14	1.15E-14	RAD23A SEL1L NCOA2 ADAM10 MRPS12 SHPRH EXOSC4 KBTBD7 GPS1 STAM2 ASXL2 CDC34 ARF5 PHC3 CREBRF ADRM1 RANBP2 TLL5 KLHL11 MRPL12 PFDN2 WDR20 TRAF6 COPE STAG2 SP3 MRPL38 EIF5 USP12 MRPL4 MGAT5 MYSM1 DYNC1H1 INO80D EP300 USP34 MAN1A2 RAB27B UBE2M EXOC5 FEM1B MRPS24 RAB33B MAN2A1 GADD45GIP1 DCAF5 APC UBE2S ATXN3	49
R-HSA-212436	Generic Transcription Pathway	47	1193	3.65E-25	5.48E-22	5.48E-22	ZNF699 MED23 BAX HIPK1 PRELID1 CCNT1 CCNT2 ZNF426 PPM1A RNF111 NR2C2AP ZNF585B ZNF347 ZNF430 PHC3 ARID2 ZNF417 ZNF510 ZNF641 KMT2C ZNF221 KMT2A ZNF41 SOCS4 SP1 TCF12 CREB1 NR2C2 ZNF573 PDPK1 EP300 POLR2J ZNF445 TJP1 ZNF615 TAF1 ZNF616 ZNF619 ZNF484 TAF1L ZKSCAN1 ZNF791 PBRM1 ZKSCAN8 ATXN3 ZNF770 ATF2	47
R-HSA-597592	Post-translational protein modification	38	1412	3.20E-15	2.89E-12	2.89E-12	RAD23A NCOA2 ADAM10 SHPRH KBTBD7 GPS1 STAM2 ASXL2 CDC34 ARF5 PHC3 FEM1B RANBP2 TLL5 KLHL11 SEL1L WDR20 TRAF6 COPE STAG2 SP3 MAN2A1 USP12 MGAT5 MYSM1 DYNC1H1 INO80D EP300 USP34 MAN1A2 RAB27B UBE2M RAB33B ADRM1 DCAF5 APC UBE2S ATXN3	38
R-HSA-168256	Immune System	36	2096	3.89E-09	3.58E-07	3.58E-07	HECTD1 NFKBIB ANAPC11 ADAM10 ATP6V1F REL ATP7A KBTBD7 EEA1 PSEN1 CDC34 LTN1 PDPK1 NF1 RNF111 PJA2 RANBP2 KLHL11 ZNF225 TRAF6 BDP1 CREB1 HERC1 DYNC1H1 UBR1 EP300 SOS2 PDAP1 UBE2M RPS6KA5 PTGES2 LNPEP PPP2R5E UBE2S BOLA2 ATF2	36
hsa05168	Herpes simplex virus 1 infection	19	492	1.14E-10	1.77E-08	1.77E-08	ZNF699 ZNF221 ZNF615 TRAF6 ZNF41 ZNF616 ZNF619 ZNF81 ZNF484 ZNF845 BAX ZNF426 ZNF585B ZNF347 ZNF430 ZNF417 ZNF510 ZNF641 ZNF791	19
R-HSA-8953854	Metabolism of RNA	19	667	1.41E-08	1.2E-06	1.2E-06	DDX49 HSD17B10 TNPO1 SMG1 WDR36 RPP21 SNRPA LSM7 LSM10 CPSF2 LSM4 UTP14C POP7 BUD31 TTC37 RANBP2 PAPOLA EXOSC4 POLR2J	19
R-HSA-1280218	Adaptive Immune System	19	748	8.05E-08	5.04E-06	5.04E-06	KBTBD7 KLHL11 HECTD1 UBE2M TRAF6 NFKBIB ANAPC11 DYNC1H1 CDC34 LTN1 HERC1 REL PDPK1 LNPEP PPP2R5E UBE2S PJA2 UBR1 RNF111	19
R-HSA-199991	Membrane Trafficking	18	631	3.33E-08	2.68E-06	2.68E-06	GPS1 RAB27B TJP1 RAB33B STAM2 EXOC5 NAA30 FCHO2 ARF5 MAN2A1 PIK3C2A GCC2 COPE DYNC1H1 LNPEP TRIP11 DENND4C MAN1A2	18
R-HSA-5653656	Vesicle-mediated transport	18	669	7.78E-08	4.94E-06	4.94E-06	GPS1 RAB27B TJP1 RAB33B STAM2 EXOC5 NAA30 FCHO2 ARF5 MAN2A1 PIK3C2A GCC2 COPE DYNC1H1 LNPEP TRIP11 DENND4C MAN1A2	18
hsa01100	Metabolic pathways	18	1433	0.001393	0.013797	0.013797	ACER2 HSD17B10 ATP6V1F PIKFYVE INDUFB7 PTGES2 ALDH6A1 INDUFB1 SRM MAN2A1 PIK3C2A SPTLC2 MGAT5 GALC B3GAT3 ENTPD5 MAN1A2 INDUFA11	18
R-HSA-168249	Innate Immune System	17	1043	0.000107	0.002123	0.002123	PDAP1 ATP6V1F UBE2M RPS6KA5 TRAF6 EEA1 PTGES2 PSEN1 CDC34 CREB1 ADAM10 NFKBIB DYNC1H1 PDPK1 EP300 ATP7A ATF2	17
R-HSA-1266738	Developmental Biology	17	1082	0.000164	0.002906	0.002906	NCOA2 PRKAR2A ARHGEF12 RPS6KA5 SOS2 PSEN1 DRAP1 KMT2A CREB1 ADAM10 PFN1 KMT2C NUMB TCF12 EP300 MED23 POLR2J	17
R-HSA-1280215	Cytokine Signaling in Immune system	15	836	0.000098	0.001962	0.001962	KBTBD7 ZNF225 RPS6KA5 UBE2M SOS2 TRAF6 NFKBIB BDP1 CREB1 BOLA2 NF1 PDPK1 PPP2R5E RANBP2 ATF2	15
R-HSA-4839726	Chromatin organization	14	273	1.07E-09	1.17E-07	1.17E-07	NCOA2 KMT2C ASH1L CLOCK ARID2 KMT2A REST RCOR1 PBRM1 NSD1 ARID4A EP300 SETD7 ATF2	14
R-HSA-3247509	Chromatin modifying enzymes	14	273	1.07E-09	1.17E-07	1.17E-07	NCOA2 KMT2C ASH1L CLOCK ARID2 KMT2A REST RCOR1 PBRM1 NSD1 ARID4A EP300 SETD7 ATF2	14
R-HSA-983168	Antigen processing: Ubiquitination & Proteasome degradation	13	308	3.82E-08	3.02E-06	3.02E-06	KBTBD7 KLHL11 HECTD1 UBE2M ANAPC11 CDC34 LTN1 HERC1 RNF111 LNPEP UBE2S PJA2 UBR1	13
R-HSA-983169	Class I MHC mediated antigen processing & presentation	13	370	2.91E-07	1.56E-05	1.56E-05	KBTBD7 KLHL11 HECTD1 UBE2M ANAPC11 CDC34 LTN1 HERC1 RNF111 LNPEP UBE2S PJA2 UBR1	13
R-HSA-5688426	Deubiquitination	12	296	1.94E-07	1.15E-05	1.15E-05	WDR20 TRAF6 RAD23A USP34 STAM2 ASXL2 USP12 MYSM1 INO80D EP300 ADRM1 ATXN3	12
R-HSA-194315	Signaling by Rho GTPases	12	449	1.25E-05	0.000347	0.000347	NCOA2 ARHGEF12 SOS2 DAAM1 PFN1 PDPK1 MYO9A DYNC1H1 ARHGAP5 PPP2R5E TAOK1 RANBP2	12
R-HSA-449147	Signaling by Interleukins	12	619	0.000244	0.003821	0.003821	KBTBD7 RPS6KA5 SOS2 TRAF6 NFKBIB BDP1 CREB1 NF1 PDPK1 PPP2R5E BOLA2 ATF2	12
R-HSA-8939211	ESR-mediated signaling	11	221	8.88E-08	5.48E-06	5.48E-06	NCOA2 EP300 STAG2 SP1 UHMK1 CREB1 GTF2A1 CCNT1 PDPK1 ATF2 POLR2J	11
R-HSA-9006931	Signaling by Nuclear Receptors	11	264	4.85E-07	0.000025	0.000025	NCOA2 EP300 STAG2 SP1 UHMK1 CREB1 GTF2A1 CCNT1 PDPK1 ATF2 POLR2J	11
R-HSA-9006925	Intracellular signaling by second messengers	11	288	1.1E-06	4.47E-05	4.47E-05	ZNF225 TRAF6 XIAP REST PRKAR2A RCOR1 CREB1 PHC3 PDPK1 PPP2R5E ATF2	11