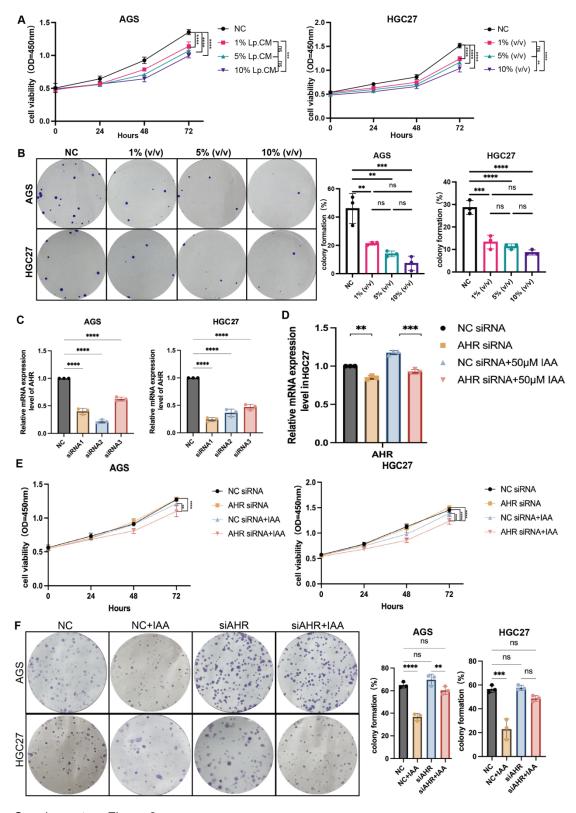


Supplementary Figure 1

- (A-C) The relative abundance of (A) *Lactobacillus* (B) *L. johnsonii* (C) *L. reuteri* in tumor tissues and normal tissues of GC patients. Data were analyzed by t tests; Means \pm SD. ns p \ge 0.05, *p < 0.05, ** p < 0.01, ****p < 0.001, *****p < 0.001.
- (D) PCR was used to determine the colonization of *L. paracasei* in both tumor or normal tissues of GC patients.
- (E) PCR was used to determine the colonization of *L. paracasei* in tumor tissues of HGC27 xenograft.
- (F) Beta-diversity by PCoA based on Binary-jaccard dissimilarity matrix in stomach samples of nude mice.
- (G) Heatmap of differential bacterial species (p<0.05) in nude mice, compared with control groups.

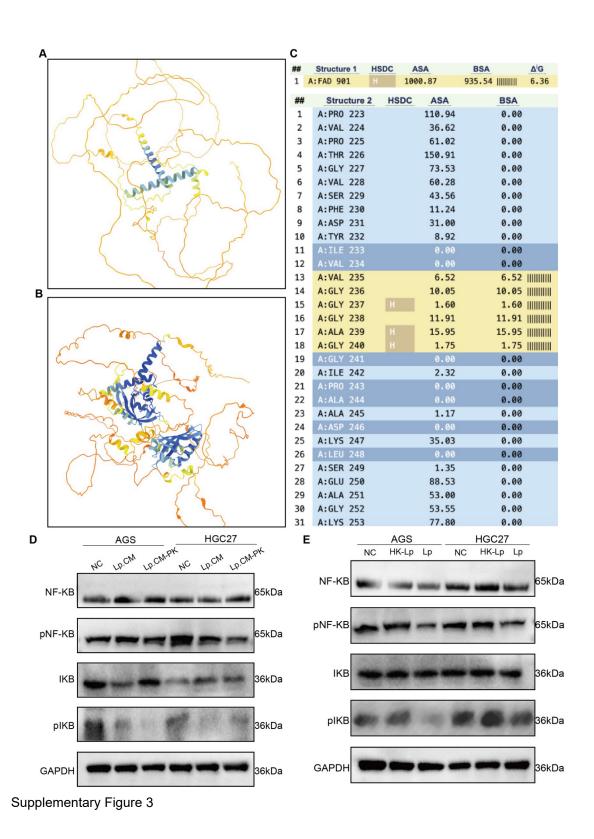
PCoA, principal coordinate analysis.



Supplementary Figure 2

- (A, B) (A)Cell viability at OD450nm (B) colony formation of human GC cells with PBS, 1% Lp.CM, 5% Lp.CM and 10% Lp.CM.
- (C) The knockdown effect of AHR of human GC cells through qPCR.

- (D) The mRNA level of AHR of HGC27 with siAHR and IAA.
- (E, F) (E)Cell viability at OD450nm (F) colony formation of human GC cells with PBS, IAA, siAHR and siAHR+IAA. Data were analyzed by two-way ANOVA; Means ± SD.



- (A, B) The 3D structure of (A)MTDH and (B)AHR using ChimeraX.
- (A) The receptor protein is located above, and the ligand protein is located below. Each row contains an amino acid residue, with the yellow region indicating the predicted binding region. HSDC is predicted for hydrogen bonding, BSA is the area of interaction encapsulation, and the more vertical lines there are, the higher the degree of encapsulation, indicating a tighter interaction.
- (D) Western blot analysis of the inhibition of NF-kB signaling pathway of AGS and HGC27 treated with Lp. CM and Lp. CM-PK.

Table 1 The proteins binding to AHR by COIP

JE High	n FE Master Accession Master Pri CON P13	Descriptio E	xp. q-val Su 0	56,701	verage # Pe	eptided # PSI	Ms # Un 83	ique (# /	AAs MV 593	V [kt ▼ c 59.5	alc. pl S 5,21	148.42	otide: Biological Cellular Cx Molecular Pfam IDs Entrez Gei Ensembl (Gene Sym Gene ID WikiPathw Reactome # Protein F Found in \$
JE High	Master Pri P04264	Keratin, ty	0	44.581	19	11	37	10	644	66	8.12	48.25	11 cell organi non-struct bone, tool P100038, [3848 ENSG000 KRT1 B2RA01; I Corticotro Formation 4 High
JE High JE High	Master Pri P35908 Master Pri CON P03	Keratin, ty		36.324 27.935	21	14	35	11	639	65.4	6.18	60.47 16.15	14 cell cycle (plasma m bone, tool P100038, f3849 ENSG000 KRT2 hsa:3849; Formation 2 High 10 stress rest non-struct nucleic ac P100273 *280717 ALB A5PJX3; b 0 High
JE High	Master Pri CON_PU	Keratin, ty		24.795	17	10	36	10	472	51.5	5.16	51.39	8 cell organi plasma mi cytoskelet P100038 3861 ENSG000 KRT14 hsa:3861: Corticotro Formation 4 High
JE High	Master Pri P16403	Histone H		21.438	24	5	16	5	213	21.4	10.93	31.89	5 cell organi nucleus; ot nucleic ac Pt00538 3006 ENSG000(H1-2 A8K4I2; h: Apoptosis 2 High
JE High	Master Pri CON_P35		0	20.05	13	8	14	8	623	62.1	5.3	11.88	8 0 High
JE High JE High	Master Pri Q7Z794 Master Pri P13647	Keratin, ty Keratin, ty	0	17.572 16.636	10	6	10	4	578 590	61.9 62.3	5.99 7.74	11.54 21.76	6 cell organi plasma mibone, toot P100038, f374454 ENSG000t KRT77 haa:37445 Formation 2 High 6 cell organi cytosoticy bone, toot P100038, f3852 ENSG000t KRT5 haa:3852; Formation 3 High
JE High	Master Pri P16401	Histone H	0	14.931	11	3	10	3	226	22.6	10.92	26.73	3 cell organi nucleus; of nucleic ac Pf00538 73009 ENSG000(H1-5 hsa:3009; Apoptosis 2 High
JE High	Master Pri P49756	RNA-bindi	0	13.595	6	4	4	4	843	100.1	6.32	5.59	4 RNA meta nucleus;of nucleic ac Pf00078, \$88517 ENSG000(RBM25 A0PJL9; E mRNA Sp 1 High
JE High JE High	Master Pri P11387 Master Pri Q8NE71	DNA topoi	0	11.542 9.417	6	6	9	6	765 845	90.7	9.31 6.8	9.31	6 cell cycle (nucleus; of nucleic ac Pf01028, f7150 ENSG0001TOP1 A8KA78; f Ebola viru SUMOylat 3 High 3 protein me cytosol; tra translation Pf00005 23 ENSG0001ABCF1 A2BF75; h IL-18 sign ABC-famil 2 High
JE High	Master Pri Q9GZR7	ATP-depe	0	8.863	5	4	5	4	859	96.3	9.06	6.29	4 RNA meta nucleus other mok Pf00270, 157082 ENSG000 DDX24 E7EMJ4; 1 0 High
JE High	Master Pri Q9UQ88	Cyclin-des	0	8.835	4	3	4	3	783	91.3	5.36	4.27	3 cell cycle (nucleus;of kinase act Pf00069 728842 ENSG000(CDK11A hsa:728641p36 cop) Recruitme 2 High
JE High	Master Pri Q00839	Heterogen	0	8.673	5	4	7	4	825	90.5	6	4.28	4 cell cycle cytosol;cy cytoskelet Pf00622, [3192 ENSG000(HNRNPU hsa:3192; mRNA prc mRNA Sp 4 High
JE High JE High	Master Pri Q9NR30 Master Pri Q9H0A0	Nucleolar RNA cytid	0	8.537 8.402	6	4	5	4	783 1025	87.3 115.7	9.28 8.27	4.24 3.4	4 cell organi cytosotrmi enzyme re P100270, 19188 ENSG000 DDX21 B2RDL0; 110q11.21t Major path 3 High 4 protein mi nucleus; of nucleic ac P105127, 155226 ENSG000 NAT10 B4DFD5; I Metapathi rRNA mod 2 High
JE High	Master Pri Q9UHX1	Poly(U)-bit	0	8.336	3	3	3	3	559	59.8	5.29	6.48	3 cell organi nucleus:ot nucleic ac Pt00076 22827 ENSG000 PUF60 A8K8K8: F mRNA So 1 High
JE High	Master Prt Q07020	60S ribosc	0	7.426	19	3	4	3	188	21.6	11.72	3.39	3 protein mccytosot/EF nucleic ac Pf17135 6141 ENSG000(RPL18 F8VWC5; Cytoplasm Major path 14 High
JE High JE High	Master Pri CON_P12 Master Pri P46087	SWISS-PF Probable 2	0	7.4 7.257	7	2	4	2	359 812	38.4 89.2	5.5 9.23	5.16	2 stress rest non-struct enzyme re P100031 *280988 ENSBTAG AHSG A6QLF7; { Neutrophil 4 High 3 cell organi nucleus other mole P101189, f4839 ENSG0001 NOP2 A1A4Z3; Elmatinib ar RNA mod 3 High
JE High JE High	Master Pri P46087	Signal reci	0	6.753	4	2	2	2	671	74.6	9.23	25	2 other biolic cytosol;EF nucleic ac Pf08492, f6731 ENSG000 SRP72 G5E9Z8; f SRP-depe 1 High
E High	Master Pri 060524	Nuclear ex	0	6.223	3	3	5	3	1076	122.9	6.35	6.41	3 cell organi cytosot;tra translation P105670, f9147 ENSG000 NEMF AQULQ3; E 0 High
JE High	Master Pri P15924	Desmopla	0	6.15	- 1	4	5	4	2871	331.6	6.81	0	4 cell adhes plasma m cytoskelet Pf00681, 1832 ENSG000 DSP B2RTT2; [Arrhythmc Formation 9 High
JE High JE High	Master Pri CON_P00 Master Pri Q02878	Trypsin - 5 60S ribosc	0	6.024 5.59	10	2	124	2	231 288	24.4 32.7	7.18	103.2	2 protein me non-struct other mole P100089 0 High 3 cell organi cytosot EF nucleic ac P101159, [6128 ENSG000 RPL6 hsa:6128; Cytoplasn SRP-depe 14 High
JE High	Master Pri Q02878 Master Pri P50914	60S ribosc	0	5.59	10	3	3	3	288	23.4	10.58	5.39	2 protein micrytosot;Er nucleic ac P101159, 16128 ENSG000I HPL6 hsa:6128; Cytoplash SHP-depe 14 High ENSG000I RPL14 hsa:9045; Cytoplash SRP-depe 14 High
E High	Master Pri P36578	60S ribosc	0	5.454	10	4	4	4	427	47.7	11.06	0.00	4 protein mi cytosot;EF other moli P100573, 76124 ENSG000 RPL4 A8K502; r Cytoplasm SRP-depe 14 High
E High	Master Prt P31944	Caspase-	0	5.397	9	2	3	2	242	27.7	5.58	6.08	2 protein me plasma meother mole P100656 23581 ENSG000 CASP14 hsa: 23581 Vitamin D Formation 2 High
E High	Master Pri Q7RTS7 Master Pri Q60841	Keratin, ty	0	5.197	4	2	3	1	529 1220	57.8 138.7	7.71 5.49	3.91	2 cell organi cytosotcy bone, toot P100038, f121391 ENSG000 KRT74 B5MD61; Formation 2 High 1 cell organi cytosototl nucleic ac P100009, f9669 ENSG000 EIF5B hsa:9669; Translatior GTP hydro 3 High
E High	Master Pri 060841 Master Pri Q5SSJ5	Eukaryotic Heteroche	0	5.058 4.933	4	2	3	2	1220 553	138.7 61.2	5.49 9.67	4.59 1.95	1 cell organi cytosol;oti nucleic ac P100009, f9669 ENSG000! EIF5B hsa:9669; Translatior GTP hydro 3 High 2 cell organi nucleus;ot nucleic ac P100538 **[50809] ENSG000! HP1BP3 A6NI71; A 0 High
High	Master Pri CON_EN	(Bos tauru	0	4.816	6	2	3	2	401	43.9	5.35	5.29	2 0 High
High	Master Pri Q13435	Splicing fa	0	4.414	2	2	3	2	895	100.2	5.67	0	2 cell organi nucleus P102037, [10992 ENSG000/SF3B2 A8K485; EmRNA prc mRNA Sp 3 High
High	Master Pri Q9Y5B9 Master Pri Q75339	FACT corr	0	4.389	2	2	2	2	1047	119.8	5.66	2.57	2 cell organi nucleus other mole Pf00557, 11198 ENSG000 SUPT16H has:11198 Formation 12 High 1 other biolic non-struct Pf00090, (8483 ENSG000 CILP B2R8F7:1 Signaling 1 High
High High	Master Pri 075339 Master Pri P62805	Cartilage i Histone H	0	4.334	21	2	2	2	1184	132.5	8.41 11.36	8.3 1.83	2 cell organi non-struct nucleic ac Pf15511 121504: 5 ENSG000(H4C1: H4/A2VCL0: f Gastric ca RMTs met 52 High
High	Master Pri P62424	60S ribosc	0	4.237	9	2	2	2	266	30	10.61	1.82	2 protein my other mem other mole Pf01248 6130 ENSG000 RPL7A hsa:6130; Cytoplasm Major path 14 High
High	Master Pri Q9UKV3	Apoptotic	0	4.185	2	2	2	2	1341	151.8	6.43	0	2 cell organi plasma mi nucleic ac P102037, [22985 ENSG000i ACIN1 B2RTT4; [mRNA Sp 2 High
High High	Master Pri 076021 Master Pri P62241	Ribosoma 40S ribosc	0	4.15	5 11	2	2	2	490 208	54.9 24.2	10.13	1.92	2 RNA meta cytosottra nucleic ac P100687 26156 ENSG000/RSL1D1 B4DJ58; [0 High 2 protein mr cytosot EF other mole P101201 6202 ENSG000/RPS8 hsa:6202; Cytoplasm SRP-depe 19 High
High	Master Pri P47914	60S ribosc	0	4.114	9	1	3	1	159	17.7	11.66	7.09	1 protein micrytosoc;E- other moit P101201 6202 ENSG000(RPL29 A8K0H3; ECytoplasin SHP-Gepe 19 High 1 protein micrytosoc;tra other moit P101779 6159 ENSG000(RPL29 A8K0H3; ECytoplasin Regulation 14 High
High	Master Prt Q96GQ7	Probable /	0	3.824	4	3	3	3	796	89.8	9.28	0	3 RNA meta nucleus:of other mole Pf00270, 155661 DDX27 A0AVB6; E 0 High
High	Master Pri P23246	Splicing fa	0	3.737	4	2	2	2	707	76.1	9.44	2.12	2 cell organi cytosotnu nucleic ac P100076, f6421 ENSG000(SFPQ hsa:6421; mRNA prc Suppressi 4 High
High High	Master Pri Q6UWP8 Master Pri P49848	Suprabasi Transcript	0	3.324	3	1	2	1	590 677	60.5 72.6	7.01 8.6	2.01	1 PM21009 374897 ENSG0001SBSN A8K5J0; E 0 High 1 cell organi cytosobnu signal tran Pf02969, f6878 ENSG0001TAF6 A4D282; / Eukaryotic RNA Polyr 11 High
High	Master Pri 096SB4	SRSF prot	0	3.194	2	1	2	1	655	74.3	6,16	3.71	1 cell cycle (plasma m kinase act P100069 6732 ENSG000 SRPK1 B4D861; I VEGFA-VE Replacem 4 High
High	Master Pri Q8IWX8	Calcium h	0	3.175	1	1	1	1	916	103.6	9.04	0	1 RNA meta other men other mole Pf01585, 10523 ENSG000/ CHERP hsa:10523 mRNA Sp 1 High
High	Master Pri Q9NVP1	ATP-depe	0	2.978	1	1	-1	1	670	75.4	9.5	2.53	1 RNA meta nucleus;ot other mole Pf00270, 18886 ENSG000(DDX18 hsa:8886; 0 High
High High	Master Pri Q13428 Master Pri Q9NW13	Treacle pr	0	2.893	2	2	2	2	1488 759	152 85.7	9.04	0	2 RNA meta cytosolynu other molic Pf03546 *6949 ENSG0001TCOF1 A0JLU0; E 0 High 1 RNA meta nucleus Pf00076 *55131 ENSG0001RBM28 A4D100; E Major patr 1 High
High	Master Pri Cerviv 13	40S ribosc	0	2.728	3	1	1	1	249	28.7	10.84	1.76	1 cell cycle (cytosotEF other moli P101092 6194 ENSG000(RPS6 hsa:6194; IL-5 signal SRP-depe 49 High
High	Master Pri P62851	40S ribosc	0	2.527	8	1	5	1	125	13.7	10.11	10.18	1 protein mi cytosol;tra other mole P103297 6230 ENSG000/ RPS25 B2R4M7; Cytoplasn Mejor path 19 High
High	Master Pri Q8WUA2		0	2.295	2	1	1	1	492	57.2	5.92	0	1 cytosotnu other moli Pf00078, f85313 ENSG000 PPIL4 B2RD34; mRNA Sp 1 High
E High	Master Pri Q8TDD1 Master Pri P04406	ATP-depe Glyceralde	0	2.164 1.987	- 1	1	1	1	881	98.5	10.02 8.46	0	1 RNA meta ER/Golgi.r signal tran P100270, 179039 ENSG000 DDX54 hsa:79039 0 High 1 cell organi plasma mienzyme re P100044, 12597 ENSG000 GAPDH E7EUT4; ir Cori cycle Glycolysis 16 High
E High	Master Pri P04406	Transcript	0	1.969	1	1	1	1	1098	123.8	8.65	0	1 RNA meta nucleus other mole P100397, [10915 ENSG000/TCERG1 hsa:10915 mRNA Sp 1 High
High	Master Pri P04040	Catalase (0	1.961	2	1	-1	1	527	59.7	7.39	0	1 protein me non-struct other mole P100199, f847 ENSG000 CAT A8K6C0; ESelenium Peroxisom 12 High
High	Master Pri Q12906	Interleukin	0	1.941	- 1	1	1	1	894 549	95.3	8.76	1.81	1 protein me mitochone nucleic ac P100035, 73609 ENSG000 ILF3 A8K6F2; C PKR-medi 2 High
High High	Master Pri Q9BVP2 Master Pri Q13823	Guanine n Nucleolar	0	1.903	2	1	1	1	549 731	62 83.6	9.16 9.25	0	1 other blok nucleus; of nucleic ac Pf01926, 126354 ENSG000 GNL3 B2RDC1; Major patr 1 High 1 other blok nucleus other mole Pf01926, 129889 ENSG000 GNL2 hsa:29885 0 High
High	Master Pri Q13623	Translocat	0	1.892	2	1	1	1	399	45.8	7.12	0	1 transport; other mem other mole Pf03839 7095 ENSG000 SEC62 D3DNQ0; 0 High
High	Master Pri P01040	Cystatin-A	0	1.888	12	1	1	1	98	11	5.5	0	1 cell adhes non-structenzyme re P100031 1475 ENSG000 CSTA hsa:1475; 8p23.1 co Formation 2 High
High High	Master Pri Q9BZE4	GTP-bindi	0	1.864	2	1	1	1	634	73.9	9.5	1.72	1 RNA meta other men other mole Pf06858, [23560 ENSG000 GTPBP4 B3KMC5; 0 High
High High	Master Pri B9A064 Master Pri Q9UGP8	Immunogli Translassi	0	1.862 1.842	4	1	1	1	214 760	23 87.9	8.84 5.31	0	1 other biolc other cell cother mole P107654 *10042306 ENSG0001 (GLL5 B9A064; t 0 High 1 other met transporte P100226, (*11231 ENSG0001 SEC63 hsa:11231 0 High
High	Master Pri Q6PJE2	POM121 a	0	1.793	8	1	1	1	187	20.6	7.18	0	1 other men P100100 22932 ENSG000 POMZP3 F6STJ3; h 0 High
High High	Master Prt 014744	Protein are	0	1.785	2	1	2	1	637	72.6	6.29	0	1 cell organi cytosot;EF nucleic ac P105185, 110419 ENSG000 PRMT5 A8MTP3; Transcript snRNP As 5 High
High	Master Pri P13639	Elongation	0	1.758	- 1	1	1	1	858	95.3	6.83	0	1 protein mi non-struct translation P100009, 1938 ENSG000(EEF2 A0A384N(Translation Neutrophil 9 High
High High	Master Pri Q99575 Master Pri P48741	Ribonucle Putative h	0	1.719	1	1	1	1	1024 367	114.6 40.2	9.22 7.87	1.8	1 RNA meta nucleus; of nucleic ac Pf06978, 10940 ENSG000 POP1 A8KSW9; tRNA proc 1 High 1 protein menucleus; of other mole Pf00012 HSPA7 P19790; F Regulatior 1 High
High	Master Pri P02100	Hemoglob	0	1.69	7	1	2	1	147	16.2	8.63	0	1 other metr cytosol;otl other mole Pf00042 3046 ENSG000/ HBE1 hsa:3046; Factors in 1 High
High	Master Pri 015446	DNA-direc	0	1.675	3	1	1	1	510	55	8.51	0	1 RNA meta cytosol;ml Pf08208 10849 ENSG000 POLR1G hsa:10849 2q13 cop; B-WICH c 6 High
High	Master Pri P20930	Filaggrin C	0	1.611	0	1	1	1	4061	434.9	9.25	0	1 protein me plasma mi bone, tool Pl01023, 12312 ENSG000 FLG hsa:2312; Formation 1 High
High High	Master Pri Q5C9Z4 Master Pri Q9Y3U8	60S ribosc	0	1.599	10	1	1	1	860 105	96.2	8.1 11.59	0	1 other biolc nucleus Pf02847, f64434 ENSG000i NOM1 haa:64434 0 High 1 protein mic cytosol;tra other mole Pf01158 "25873 ENSG000i RPL36 B2R4Y1; (Cytoplasn SRP-depe 14 High
High	Master Pri Q02413	Desmogle	0	1.566	1	1	1	1	1049	113.7	5.03	0	1 cell adhes plasma m other mole P100028, 1828 ENSG000 DSG1 B7Z845; h Formation 6 High
High	Master Pri Q9BRD0	BUD13 hc	0	1.536	2	1	1	1	619	70.5	9.86	0	1 cell organi nucleus Pf09736 84811 ENSG000(BUD13 A8K0S0; F mRNA Sp 1 High
High High	Master Pri Q96GA3 Master Pri Q00268	Protein LT Transcript	0	1.508	3	1	1	1	475 1085	54.8 110	4.91 9.94	0	1 transport; cytosol;nu P104180 *84946 ENSG000LTV1 hsa: 84946 Major patr 1 High 1 cell organi cytosol;nu signal tran P105236, *16874 ENSG000 TAF4 A6NGD9: RNA Polyr 9 High
High High	Master Pri 000268 Master Pri Q969Q0	Transcript 60S ribosc	0	1.499	8	1	1	1	1085	110	9.94	0	1 cell organi cytosot;nu signal tran P105238, 16874 ENSG0001TAF4 A6NGD9; RNA Polyr 9 High 1 protein ms plasma ms other mols P100935 6166 ENSG0001 RPL36AL hsa:6166; Major path 13 High
High	Master Pri Q14684	Ribosoma	0	1.481	1	1	1	1	758	84.4	9.76	1.61	1 RNA meta nucleus;ot other moli P105997 23076 ENSG000 (RRP1B hsa:2307€ 0 High
High	Master Pri Q8TD19	Serine/thre	0	1.46	1	1	1	1	979	107.1	5.74	0	1 cell cycle (cytosot;nu enzyme re Pf00069, f91754 ENSG000/NEK9 hsa:91754 Ciliopathie EML4 and 4 High
High High	Master Pri Q9H307 Master Pri Q92841	Pinin OS=	0	1.435	1	1	1	1	717 729	81.6 80.2	7.14 8.27	0	1 cell adhes plasma minucieic ac P104696, f5411 ENSG000 PNN B4DZX8; mRNA Sp 1 High 1 RNA meta cytosotinu nucieic ac P100270, f10521 ENSG000 DDX17 B1AHM0; Novel intri SUMOyiat 2 High
High	Master Pri Q9/2841 Master Pri Q9/WH9		0	1.43	1	1	1	1	1034	117,1	7.87	0	1 other biolc nucleus nucleic ac P100276, 179811 ENSG000 SLTM A8K5V8; E 0 High
High	Master Pri P35499	Sodium ch	0	1.406	0	1	1	1	1836	207.9	5.1	0	1 transport; cplasma m transporte P100520, f6329 ENSG000/SCN4A hsa:6329; Interaction 2 High
High High	Master Pri Q13885	Tubulin be	0	1.395	2	1	1	1	445	49.9	4.89	0	1 cell cycle (cytoskelet cytoskelet Pf00091, 7280 ENSG000/TUBB2A hsa:7280; Alzheimer Recycling 35 High
High High	Master Pri P21810 Master Pri P35579	Biglycan C Myosin-9	0	1.364	3	1	1	1	368 1960	41.6 226.4	7.52 5.6	0	1 developm non-struc extracellul P101462, f633 ENSG000/BGN D3DWU3; ECM prot 11 High 1 cell cycle (plasma m signal tran P100063, f4627 ENSG000/MYH9 A8K6E4.); Primary fo Regulation 16 High
High High	Master Prt P02452	Collagen a	0.005	1.342	1	1	1	1	1464	138.9	5.8	0	1 0 High
High	Master Prt P12111	Collagen a	0.005	1.327	1	1	2	1	3177	343.5	6.68	0	1 cell adhes extracellul enzyme re P100014, [1293 ENSG000 COL6A3 A8MT30; ImiRNA tar Collagen c 11 High
High	Master Pri Q7L014	Probable /	0.005	1.304	1	1	1	1	1031	117.3	9.29	0	1 cell organi other men other moli P100270, 19879 ENSG000 DDX46 hsa:9879; mRNA Sp 1 High
High High	Master Pri Q9UHB9 Master Pri Q4G0W2	Signal rec	0.005	1.286	- 1	1	1	1	627 176	70.7	8.56 8.28	0	1 other bloic cytosot;EF nucleic ac P116969 16730 ENSG000/SRP68 B3KUU5; SRP-depe 1 High 1 other metr other mok P100782 1285193 ENSG000/DUSP28 hsa:265152q37 cop 1 High
High	Master Pri Q4G0W2 Master Pri Q01518	Adenylyl c	0.005	1.263	3	1	1	1	475	51.9	8.28	0	1 cell organi non-struct cytoskelet Pf01213, 10487 ENSG000 CAP1 hsa:10487 Angiopole Neutrophil 7 High
High	Master Pri 000567	Nucleolar	0.005	1.262	1	1	1	1	594	66	9.19	0	1 RNA meta nucleus;ot nucleic ac P101798, \$\infty\$10528 ENSG000(NOP56 hsa:10526 Major patt 3 High
High	Master Pri Q86UE4	Protein LY	0.005	1.234	2	1	1	1	582	63.8	9.32	0	1 signal tran plasma m nucleic ac Pf15686 92140 ENSG000 MTDH hsa:9214C Gastric ca 3 High
High High	Master Pri P26373 Master Pri P08670	60S ribosc Vimentin (0.004	1.232	5	1	1	1	211 466	24.2 53.6	11.65 5.12	0	1 protein mic cytosol;EF other mole Pf01294 "6137 ENSG000 RPL13 B4DLX3; f Cytoplasm SRP-depe 14 High 1 cell organi plasma mi cytoskelet Pf00038, f7431 ENSG000 VIM B0YJC2; f Allograft n Aggrepha; 21 High
High High	Master Pri P08670 Master Pri O60832	H/ACA rib	0.004	1.206	2	1	1	1	466 514	57.6	9.42	0	1 cell organi plasma mi cytoskelet P100038, f7431 ENSG0001VIM B0YJC2; (Allograft rt Aggrepha; 21 High 1 cell organi nucleus; ot nucleic ac P101472, f1736 ENSG0001DKC1 F5BSB3; rRNA mod 2 High
High	Master Pri P46776	60S ribosc	0.004	1.202	7	1	1	1	148	16.6	11	0	1 protein mic cytosol;EF other moli Pf00828 6157 ENSG000 RPL27A B2R4B3; i Cytoplasin Regulation 15 High
High	Master Pri CON_Q3		0.004	1.201	2	1	1	1	484	54.1	6.16	0	1 0 High
E High	Master Pri P42766 Master Pri P41214	60S ribosc Eukaryotic	0.004	1.198	8	1	1	1	123	14.5 64.7	11.05 7.65	0	1 protein mx cytosol;tra nucleic ac P100831 [*] 11224 ENSG000 RPL35 A8K4V7; l' Cytoplasm SRP-depe 14 High 1 cell organi cytosol;nu nucleic ac P101253, [*] 1939 ENSG000 EIF2D hsa:1939; 0 High
	Master Pri P41214 Master Pri Q6NZI2	Caveolae-	0.004	1.192	2	1	1	1	390	64.7 43.5	7.65 5.6	0	1 cell organi cytosotnu nucleic ac P101253, [1939 ENSG000 EIF2D hsa:1939; 0 High 1 RNA meta plasma mi nucleic ac P115237
High		Protein SI	0.004	1.181	-			-	687	79.8	9.25		1 transport; nucleus Pf05285, 155153 ENSG000 SDAD1 hsa:55153 0 High