**Supplementary Material**

1. **Supplementary Figures**



**Figure S1: X-tile plots of mRNAsi-related lncRNA signature for optimal cut-off determination in the training cohort.** (A-B) The cut-off (IRS= 0.97) was optimized to separate low mRNAsi-related lncRNA signature (blue) from high mRNAsi-related lncRNA signature (gray) in the frequency histogram of the training cohort. (C) Kaplan-Meier curve for testing the survival of sample subsets defined by the optimized cutoff value of mRNAsi-related lncRNA signature.

1. **Supplementary Tables**

**Table S1.** List of TCGA IDs for randomly grouped training and validation cohort

|  |  |
| --- | --- |
| **ID for training cohort** | **ID for validation cohort** |
| TCGA-F5-6864-01 | TCGA-AM-5820-01 |
| TCGA-AM-5821-01 | TCGA-F4-6854-01 |
| TCGA-AA-3543-01 | TCGA-AA-3672-01 |
| TCGA-AG-3878-01 | TCGA-AA-A02O-01 |
| TCGA-AA-3496-01 | TCGA-AA-3856-01 |
| TCGA-AA-3518-01 | TCGA-AA-A00R-01 |
| TCGA-AA-A01S-01 | TCGA-AG-3742-01 |
| TCGA-AG-3883-01 | TCGA-AA-3494-01 |
| TCGA-AG-A020-01 | TCGA-AA-3514-01 |
| TCGA-F4-6704-01 | TCGA-AA-3821-01 |
| TCGA-AA-3966-01 | TCGA-AA-A01Q-01 |
| TCGA-A6-6141-01 | TCGA-AA-A01V-01 |
| TCGA-CI-6619-01 | TCGA-AG-3896-01 |
| TCGA-AA-3525-01 | TCGA-AG-4007-01 |
| TCGA-G4-6295-01 | TCGA-AG-A01J-01 |
| TCGA-AA-3519-01 | TCGA-CK-6748-01 |
| TCGA-A6-A5ZU-01 | TCGA-EF-5830-01 |
| TCGA-CK-5914-01 | TCGA-EF-5831-01 |
| TCGA-D5-7000-01 | TCGA-4N-A93T-01 |
| TCGA-EI-6884-01 | TCGA-AA-3681-01 |
| TCGA-CM-6678-01 | TCGA-AG-A00C-01 |
| TCGA-CM-6676-01 | TCGA-AA-3662-01 |
| TCGA-D5-6932-01 | TCGA-AA-3511-01 |
| TCGA-D5-6928-01 | TCGA-AA-3663-01 |
| TCGA-AA-A01G-01 | TCGA-CL-5918-01 |
| TCGA-D5-6931-01 | TCGA-D5-6898-01 |
| TCGA-AD-5900-01 | TCGA-AG-3726-01 |
| TCGA-CA-5255-01 | TCGA-EI-6882-01 |
| TCGA-CA-5796-01 | TCGA-D5-6926-01 |
| TCGA-D5-6920-01 | TCGA-AG-A016-01 |
| TCGA-CA-5797-01 | TCGA-CM-6679-01 |
| TCGA-4T-AA8H-01 | TCGA-D5-6922-01 |
| TCGA-CA-5254-01 | TCGA-CM-6172-01 |
| TCGA-CA-6717-01 | TCGA-CM-6677-01 |
| TCGA-AA-3542-01 | TCGA-EI-6883-01 |
| TCGA-AA-3939-01 | TCGA-T9-A92H-01 |
| TCGA-CM-4752-01 | TCGA-EI-7002-01 |
| TCGA-CM-6169-01 | TCGA-AG-3575-01 |
| TCGA-CM-6675-01 | TCGA-CM-6162-01 |
| TCGA-D5-6930-01 | TCGA-CM-6680-01 |
| TCGA-EI-6885-01 | TCGA-CA-6716-01 |
| TCGA-CI-6621-01 | TCGA-D5-6923-01 |
| TCGA-G4-6323-01 | TCGA-CA-5256-01 |
| TCGA-AG-A008-01 | TCGA-D5-6539-01 |
| TCGA-D5-6924-01 | TCGA-CA-6715-01 |
| TCGA-CM-6167-01 | TCGA-DT-5265-01 |
| TCGA-AA-3679-01 | TCGA-NH-A6GC-01 |
| TCGA-AA-A017-01 | TCGA-CM-6674-01 |
| TCGA-AA-A01C-01 | TCGA-CM-6168-01 |
| TCGA-CM-5864-01 | TCGA-AG-3892-01 |
| TCGA-CM-6170-01 | TCGA-AA-3973-01 |
| TCGA-CK-4952-01 | TCGA-D5-6929-01 |
| TCGA-CM-6165-01 | TCGA-AF-2692-01 |
| TCGA-EI-6514-01 | TCGA-AA-3561-01 |
| TCGA-EI-6513-01 | TCGA-AA-A004-01 |
| TCGA-AD-A5EK-01 | TCGA-AA-3544-01 |
| TCGA-EI-6509-01 | TCGA-AA-3667-01 |
| TCGA-AA-3846-01 | TCGA-AG-3894-01 |
| TCGA-AG-3890-01 | TCGA-AG-4005-01 |
| TCGA-CM-5868-01 | TCGA-CM-6163-01 |
| TCGA-AY-A54L-01 | TCGA-CM-6171-01 |
| TCGA-CK-4947-01 | TCGA-CA-6719-01 |
| TCGA-EI-6512-01 | TCGA-AA-3844-01 |
| TCGA-AY-6386-01 | TCGA-AA-A00W-01 |
| TCGA-AY-A69D-01 | TCGA-CM-5861-01 |
| TCGA-D5-6536-01 | TCGA-CM-5863-01 |
| TCGA-AA-A00J-01 | TCGA-CM-6161-01 |
| TCGA-AA-A00K-01 | TCGA-D5-6535-01 |
| TCGA-NH-A50T-01 | TCGA-D5-6541-01 |
| TCGA-D5-6532-01 | TCGA-3L-AA1B-01 |
| TCGA-AY-A8YK-01 | TCGA-NH-A6GB-01 |
| TCGA-AA-3530-01 | TCGA-EI-6511-01 |
| TCGA-AY-A71X-01 | TCGA-AA-3833-01 |
| TCGA-A6-6781-01 | TCGA-AG-3608-01 |
| TCGA-AA-3560-01 | TCGA-AG-A014-01 |
| TCGA-AA-3562-01 | TCGA-AA-3971-01 |
| TCGA-AG-3882-01 | TCGA-D5-6540-01 |
| TCGA-CM-4744-01 | TCGA-EI-6881-01 |
| TCGA-D5-6529-01 | TCGA-AA-3866-01 |
| TCGA-A6-6782-01 | TCGA-AA-A00U-01 |
| TCGA-EI-6506-01 | TCGA-AG-4008-01 |
| TCGA-A6-6650-01 | TCGA-D5-6538-01 |
| TCGA-EI-6508-01 | TCGA-EI-6917-01 |
| TCGA-AG-A002-01 | TCGA-AH-6549-01 |
| TCGA-AA-3549-01 | TCGA-D5-6531-01 |
| TCGA-BM-6198-01 | TCGA-NH-A8F7-01 |
| TCGA-AY-6197-01 | TCGA-AA-3554-01 |
| TCGA-AA-3968-01 | TCGA-AG-3885-01 |
| TCGA-CM-6166-01 | TCGA-AA-3831-01 |
| TCGA-A6-5665-01 | TCGA-AA-3875-01 |
| TCGA-A6-5664-01 | TCGA-EI-6510-01 |
| TCGA-A6-6138-01 | TCGA-AA-3688-01 |
| TCGA-CM-5348-01 | TCGA-AA-A00D-01 |
| TCGA-AA-3556-01 | TCGA-AA-3713-01 |
| TCGA-AG-A00Y-01 | TCGA-AA-3526-01 |
| TCGA-A6-5662-01 | TCGA-AA-3986-01 |
| TCGA-AA-3553-01 | TCGA-NH-A50V-01 |
| TCGA-AA-3979-01 | TCGA-NH-A5IV-01 |
| TCGA-AA-3867-01 | TCGA-D5-5539-01 |
| TCGA-A6-6140-01 | TCGA-EI-6507-01 |
| TCGA-A6-6649-01 | TCGA-AG-3612-01 |
| TCGA-A6-6653-01 | TCGA-A6-6780-01 |
| TCGA-A6-6652-01 | TCGA-D5-6530-01 |
| TCGA-AA-3819-01 | TCGA-AA-3955-01 |
| TCGA-CM-4747-01 | TCGA-AD-6548-01 |
| TCGA-A6-6142-01 | TCGA-A6-6651-01 |
| TCGA-D5-6533-01 | TCGA-QL-A97D-01 |
| TCGA-AA-3538-01 | TCGA-AA-A00Z-01 |
| TCGA-AA-A01X-01 | TCGA-CM-5344-01 |
| TCGA-G4-6322-01 | TCGA-G4-6321-01 |
| TCGA-G4-6320-01 | TCGA-CM-4743-01 |
| TCGA-AD-6965-01 | TCGA-A6-6654-01 |
| TCGA-AA-3980-01 | TCGA-AA-3941-01 |
| TCGA-AA-A00O-01 | TCGA-AA-3950-01 |
| TCGA-AU-6004-01 | TCGA-AA-3520-01 |
| TCGA-AD-6963-01 | TCGA-AD-6890-01 |
| TCGA-CM-5341-01 | TCGA-AA-3977-01 |
| TCGA-A6-5667-01 | TCGA-AD-6895-01 |
| TCGA-QG-A5YW-01 | TCGA-A6-6648-01 |
| TCGA-AG-3728-01 | TCGA-AG-A00H-01 |
| TCGA-AA-A00E-01 | TCGA-AA-3949-01 |
| TCGA-AA-3861-01 | TCGA-CM-4748-01 |
| TCGA-CM-5349-01 | TCGA-G4-6588-01 |
| TCGA-AA-A01K-01 | TCGA-AA-3710-01 |
| TCGA-AA-3858-01 | TCGA-AA-3982-01 |
| TCGA-AA-3860-01 | TCGA-AA-3994-01 |
| TCGA-QG-A5Z2-01 | TCGA-CM-4751-01 |
| TCGA-A6-5657-01 | TCGA-A6-6137-01 |
| TCGA-AA-A01F-01 | TCGA-AA-3532-01 |
| TCGA-CM-5860-01 | TCGA-AA-3534-01 |
| TCGA-A6-4107-01 | TCGA-CM-6164-01 |
| TCGA-A6-5666-01 | TCGA-A6-5660-01 |
| TCGA-AZ-4615-01 | TCGA-AA-3555-01 |
| TCGA-AY-5543-01 | TCGA-AA-3870-01 |
| TCGA-AA-A01T-01 | TCGA-AF-4110-01 |
| TCGA-AA-3851-01 | TCGA-AA-3862-01 |
| TCGA-A6-3808-01 | TCGA-A6-5659-01 |
| TCGA-A6-5661-01 | TCGA-AA-3877-01 |
| TCGA-AA-3548-01 | TCGA-AA-A01I-01 |
| TCGA-AA-3956-01 | TCGA-AG-A01N-01 |
| TCGA-AA-A00F-01 | TCGA-DC-5869-01 |
| TCGA-AA-3975-01 | TCGA-AA-3855-01 |
| TCGA-F4-6805-01 | TCGA-A6-3809-01 |
| TCGA-AA-3502-01 | TCGA-A6-5656-01 |
| TCGA-AA-A01R-01 | TCGA-QG-A5YX-01 |
| TCGA-AA-3812-01 | TCGA-AA-3947-01 |
| TCGA-A6-2680-01 | TCGA-AA-3815-01 |
| TCGA-F4-6463-01 | TCGA-CI-6620-01 |
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| TCGA-AA-3854-01 | TCGA-AA-3531-01 |
| TCGA-AA-3970-01 | TCGA-A6-3807-01 |
| TCGA-A6-3810-01 | TCGA-AA-A010-01 |
| TCGA-AA-3841-01 | TCGA-F4-6856-01 |
| TCGA-AG-3887-01 | TCGA-F4-6569-01 |
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| TCGA-AA-3522-01 | TCGA-CM-4746-01 |
| TCGA-AA-3685-01 | TCGA-A6-2684-01 |
| TCGA-F5-6814-01 | TCGA-AA-3495-01 |
| TCGA-A6-2685-01 | TCGA-AF-3911-01 |
| TCGA-AA-A00A-01 | TCGA-F5-6861-01 |
| TCGA-AA-A00L-01 | TCGA-AA-3517-01 |
| TCGA-AG-A032-01 | TCGA-AA-3837-01 |
| TCGA-RU-A8FL-01 | TCGA-5M-AATE-01 |
| TCGA-G4-6311-01 | TCGA-AA-A02F-01 |
| TCGA-AA-A02W-01 | TCGA-AA-A02Y-01 |
| TCGA-AG-A02X-01 | TCGA-AA-A03J-01 |
| TCGA-AA-A00Q-01 | TCGA-F4-6806-01 |
| TCGA-F5-6571-01 | TCGA-A6-2678-01 |
| TCGA-QG-A5YV-01 | TCGA-G4-6306-01 |
| TCGA-F4-6807-01 | TCGA-CI-6622-01 |
| TCGA-D5-6534-01 | TCGA-A6-2679-01 |
| TCGA-A6-2675-01 | TCGA-AG-3587-01 |
| TCGA-A6-2674-01 | TCGA-AA-3678-01 |
| TCGA-A6-2681-01 | TCGA-CI-6623-01 |
| TCGA-AG-4022-01 | TCGA-AG-3898-01 |
| TCGA-A6-2672-01 | TCGA-CI-6624-01 |
| TCGA-AA-3675-01 | TCGA-AG-A025-01 |
| TCGA-F4-6855-01 | TCGA-AA-3673-01 |
| TCGA-F4-6703-01 | TCGA-AA-3972-01 |
| TCGA-AA-3864-01 | TCGA-CK-5913-01 |
| TCGA-AA-3664-01 | TCGA-AA-A029-01 |
| TCGA-AA-3655-01 | TCGA-G4-6304-01 |
| TCGA-G4-6315-01 | TCGA-G4-6307-01 |
| TCGA-AG-A02N-01 | TCGA-D5-5541-01 |
| TCGA-WS-AB45-01 | TCGA-D5-5540-01 |
| TCGA-G4-6299-01 | TCGA-AA-3506-01 |
| TCGA-AZ-4313-01 | TCGA-AZ-4315-01 |
| TCGA-G4-6628-01 | TCGA-SS-A7HO-01 |
| TCGA-G4-6297-01 | TCGA-AA-3509-01 |
| TCGA-CK-4950-01 | TCGA-G4-6310-01 |
| TCGA-G4-6625-01 | TCGA-AA-3510-01 |
| TCGA-DM-A28K-01 | TCGA-G4-6627-01 |
| TCGA-AZ-4308-01 | TCGA-AA-3660-01 |
| TCGA-AG-A036-01 | TCGA-CK-6747-01 |
| TCGA-DM-A0X9-01 | TCGA-AA-3697-01 |
| TCGA-DM-A28E-01 | TCGA-G4-6309-01 |
| TCGA-DY-A1DE-01 | TCGA-AZ-5407-01 |
| TCGA-DM-A1D0-01 | TCGA-DM-A28M-01 |
| TCGA-G4-6293-01 | TCGA-DM-A28H-01 |
| TCGA-DM-A1HB-01 | TCGA-CK-6751-01 |
| TCGA-DM-A282-01 | TCGA-DM-A1HA-01 |
| TCGA-CK-4948-01 | TCGA-DM-A1D9-01 |
| TCGA-AA-3529-01 | TCGA-AA-3845-01 |
| TCGA-AY-4071-01 | TCGA-AA-3850-01 |
| TCGA-AZ-4323-01 | TCGA-AA-3852-01 |
| TCGA-AG-A026-01 | TCGA-AA-3818-01 |
| TCGA-AA-A02H-01 | TCGA-5M-AAT4-01 |
| TCGA-AA-A02E-01 | TCGA-AZ-6608-01 |
| TCGA-AG-4021-01 | TCGA-AA-3666-01 |
| TCGA-AA-A00N-01 | TCGA-AA-3930-01 |
| TCGA-D5-6537-01 | TCGA-AA-3952-01 |
| TCGA-AA-A02J-01 | TCGA-AA-3492-01 |
| TCGA-CM-5862-01 | TCGA-AZ-6607-01 |
| TCGA-AZ-4616-01 | TCGA-AA-3696-01 |
| TCGA-AZ-6605-01 | TCGA-AZ-4614-01 |
| TCGA-AD-6899-01 | TCGA-F4-6570-01 |
| TCGA-DM-A285-01 | TCGA-AA-3489-01 |
| TCGA-AZ-6599-01 | TCGA-DM-A1DA-01 |
| TCGA-AA-3989-01 | TCGA-DM-A280-01 |
| TCGA-F4-6459-01 | TCGA-NH-A6GA-01 |
| TCGA-5M-AAT6-01 | TCGA-AA-3848-01 |
| TCGA-AA-3811-01 | TCGA-AA-3680-01 |
| TCGA-CA-6718-01 | TCGA-F4-6461-01 |
| TCGA-AD-6964-01 | TCGA-F5-6863-01 |
| TCGA-DC-6158-01 | TCGA-DM-A1D8-01 |
| TCGA-NH-A50U-01 | TCGA-AA-3516-01 |
| TCGA-AZ-6606-01 | TCGA-A6-4105-01 |
| TCGA-AA-3552-01 | TCGA-AD-6888-01 |
| TCGA-F4-6809-01 | TCGA-AF-2690-01 |
| TCGA-DM-A1D7-01 | TCGA-G5-6233-01 |
| TCGA-A6-2682-01 | TCGA-AA-3715-01 |
| TCGA-AA-A02K-01 | TCGA-AD-6901-01 |
| TCGA-DM-A288-01 | TCGA-AG-3584-01 |
| TCGA-A6-A565-01 | TCGA-A6-2677-01 |
| TCGA-AY-4070-01 | TCGA-A6-A566-01 |
| TCGA-A6-2683-01 | TCGA-DM-A28A-01 |
| TCGA-NH-A8F8-01 | TCGA-G4-6294-01 |
| TCGA-AA-A03F-01 | TCGA-AZ-6603-01 |
| TCGA-CK-5916-01 | TCGA-AA-3692-01 |
| TCGA-AA-A02R-01 | TCGA-AG-3574-01 |
| TCGA-G4-6298-01 | TCGA-AG-3582-01 |
| TCGA-DM-A0XD-01 | TCGA-A6-2686-01 |
| TCGA-AA-3869-01 | TCGA-AA-A01P-01 |
| TCGA-F4-6460-01 | TCGA-DM-A0XF-01 |
| TCGA-DY-A1H8-01 | TCGA-AG-A02G-01 |
| TCGA-DM-A28F-01 | TCGA-AA-A024-01 |
| TCGA-A6-2671-01 | TCGA-A6-2676-01 |
| TCGA-D5-5537-01 | TCGA-DM-A1DB-01 |
| TCGA-CK-5912-01 | TCGA-G4-6626-01 |
| TCGA-DM-A1D6-01 | TCGA-AZ-6598-01 |
| TCGA-AG-A023-01 | TCGA-DY-A1DG-01 |
| TCGA-A6-A56B-01 | TCGA-D5-5538-01 |
| TCGA-DM-A28G-01 | TCGA-A6-A567-01 |
| TCGA-G4-6303-01 | TCGA-AZ-5403-01 |
| TCGA-G4-6302-01 | TCGA-CK-4951-01 |
| TCGA-DM-A28C-01 | TCGA-AD-6889-01 |
| TCGA-AZ-6601-01 | TCGA-DM-A1D4-01 |

**Table S2.** The univariate screening of mRNAsi-related lncRNA for overall survival in the training cohort

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene symbol** | **HR** | **HR.95L** | **HR.95H** | **p value** |
| LINC02381 | 1.943200091 | 1.325145551 | 2.849518372 | 0.000670596 |
| AL391422.4 | 2.482626928 | 1.466161635 | 4.203790574 | 0.00071448 |
| AC005332.4 | 1.681989272 | 1.219787935 | 2.319327672 | 0.001514377 |
| AC068580.3 | 1.744941584 | 1.22439478 | 2.486796891 | 0.00207024 |
| CYTOR | 1.185398397 | 1.06361604 | 1.321124641 | 0.00210471 |
| LINC01503 | 1.313100955 | 1.095224677 | 1.574320004 | 0.003254928 |
| LINC01614 | 1.22429316 | 1.068591334 | 1.402681918 | 0.003546826 |
| AC068580.1 | 1.532587097 | 1.142816687 | 2.055293064 | 0.004350598 |
| AP001189.3 | 1.918749715 | 1.184290256 | 3.108697763 | 0.008120941 |
| LINC00926 | 1.284184763 | 1.065454336 | 1.547819037 | 0.008653057 |
| AC090559.1 | 1.402508796 | 1.080920729 | 1.819773522 | 0.010911109 |
| MIR4435-2HG | 1.242869805 | 1.040240912 | 1.48496885 | 0.016645477 |
| LINC01705 | 1.166847797 | 1.025268046 | 1.327978362 | 0.019383455 |
| AC104794.2 | 1.324915169 | 1.042259884 | 1.684225049 | 0.021559097 |
| PCED1B-AS1 | 1.412179563 | 1.042851042 | 1.91230678 | 0.025666876 |
| AC145098.1 | 1.542504176 | 1.049183768 | 2.267781111 | 0.02751475 |
| SMIM25 | 1.195884183 | 1.011450995 | 1.413947869 | 0.036331842 |
| AC138207.5 | 1.334616299 | 1.015279323 | 1.754394703 | 0.038579978 |
| AC036176.1 | 2.003273737 | 0.999013847 | 4.017067111 | 0.050325763 |
| AC139768.1 | 1.808135104 | 0.991128557 | 3.298616038 | 0.053493738 |
| SERPINB9P1 | 1.407534122 | 0.969356817 | 2.043780236 | 0.07242916 |
| AC080112.1 | 1.109211642 | 0.989547884 | 1.243346063 | 0.075146946 |
| FENDRR | 0.779972662 | 0.589676124 | 1.031680493 | 0.081613609 |
| AL139393.2 | 1.293435437 | 0.967733979 | 1.728755284 | 0.082144792 |
| HLA-DQB1-AS1 | 1.15751944 | 0.978008236 | 1.369979521 | 0.088881033 |
| AC147651.3 | 1.551421378 | 0.907994093 | 2.650797303 | 0.10809194 |
| MIR22HG | 1.090323141 | 0.974066021 | 1.220455827 | 0.132787741 |
| BX322234.1 | 1.260368356 | 0.929347952 | 1.709293479 | 0.136590375 |
| AC130371.2 | 1.654300734 | 0.849202594 | 3.222683183 | 0.138998789 |
| NKILA | 1.066351601 | 0.978626511 | 1.161940458 | 0.142456263 |
| PSMB8-AS1 | 1.072439874 | 0.976151488 | 1.178226226 | 0.145095491 |
| AC093278.2 | 1.605021398 | 0.835879856 | 3.081894685 | 0.155200656 |
| AC068768.1 | 1.526462856 | 0.828102298 | 2.813769332 | 0.175264823 |
| AL136084.3 | 1.237007747 | 0.908083956 | 1.685073452 | 0.177460937 |
| LINC01235 | 1.211388455 | 0.915176188 | 1.603474837 | 0.180114457 |
| AC009414.2 | 1.194663583 | 0.909550628 | 1.569149679 | 0.201072366 |
| LINC01436 | 1.140066082 | 0.929466643 | 1.398383343 | 0.208387848 |
| AL122035.1 | 1.325016762 | 0.8518819 | 2.060930535 | 0.211781676 |
| MEG3 | 1.096431692 | 0.938566727 | 1.280849214 | 0.245787174 |
| AC009065.2 | 0.981455632 | 0.949976482 | 1.0139779 | 0.260420081 |
| UBXN10-AS1 | 0.810318241 | 0.556525716 | 1.179847816 | 0.272550851 |
| MBNL1-AS1 | 0.681339072 | 0.338944941 | 1.369611627 | 0.281452609 |
| AC092535.4 | 1.069552645 | 0.936198786 | 1.221901672 | 0.322347891 |
| AL365203.2 | 1.164320712 | 0.846780756 | 1.60093709 | 0.34908848 |
| IGFL2-AS1 | 1.038399492 | 0.958477236 | 1.124986034 | 0.356466353 |
| AC084033.3 | 1.16076796 | 0.826869777 | 1.629497528 | 0.38899045 |
| AC012236.1 | 1.155838448 | 0.829266451 | 1.611017202 | 0.392618247 |
| WNT5A-AS1 | 1.191785352 | 0.788053858 | 1.802354384 | 0.405776174 |
| LINC01128 | 0.687964778 | 0.244475404 | 1.935963817 | 0.478616364 |
| AC009065.5 | 0.986886401 | 0.950788617 | 1.02435468 | 0.487487845 |
| AC104699.1 | 1.136279789 | 0.786258976 | 1.642120216 | 0.496489488 |
| TFAP2A-AS1 | 1.128958647 | 0.789124632 | 1.6151411 | 0.506799313 |
| AC015922.2 | 1.038020422 | 0.919592023 | 1.17170046 | 0.546019162 |
| C10orf25 | 1.241012641 | 0.614433419 | 2.506556981 | 0.547159843 |
| PGM5-AS1 | 0.928862841 | 0.709390056 | 1.216236639 | 0.591568435 |
| AP000759.1 | 1.046806128 | 0.877630718 | 1.24859243 | 0.611018356 |
| LINC01082 | 0.942653117 | 0.740396699 | 1.200160535 | 0.631746994 |
| AC116366.1 | 0.86268166 | 0.45776235 | 1.625777318 | 0.647777122 |
| C5orf56 | 0.905437364 | 0.58902559 | 1.391818682 | 0.650664926 |
| ZSCAN16-AS1 | 1.088313012 | 0.753131342 | 1.572667535 | 0.652310141 |
| SH3RF3-AS1 | 0.822736313 | 0.329398535 | 2.054942474 | 0.676103932 |
| SERTAD4-AS1 | 0.933485369 | 0.655956572 | 1.32843388 | 0.702202862 |
| AC027031.2 | 1.085775096 | 0.66992571 | 1.759758645 | 0.738362823 |
| AC104083.1 | 0.986427297 | 0.904461939 | 1.07582063 | 0.757508969 |
| ACTA2-AS1 | 1.043242711 | 0.790874741 | 1.376141247 | 0.764485733 |
| LINC02362 | 0.940818904 | 0.519323207 | 1.704411043 | 0.840530454 |
| AC012181.2 | 1.0442149 | 0.680823585 | 1.601567249 | 0.842843099 |
| CARD8-AS1 | 0.968829945 | 0.687675477 | 1.364933743 | 0.85631531 |
| LINC00578 | 1.021468126 | 0.734745979 | 1.420078726 | 0.899448265 |
| AC015922.3 | 0.992745408 | 0.865587191 | 1.138583676 | 0.917078525 |
| MIAT | 1.021281312 | 0.670050309 | 1.556622698 | 0.921989106 |
| AC009948.1 | 0.989316922 | 0.720324374 | 1.358760037 | 0.947105774 |
| AL034397.3 | 1.009817876 | 0.740130952 | 1.377772594 | 0.95085618 |
| AC010186.3 | 0.997995429 | 0.845558852 | 1.177913132 | 0.98107009 |
| MIR100HG | 1.00017009 | 0.777008641 | 1.287424819 | 0.998946551 |

**Table S3.** The univariate screening of mRNAsi-related lncRNA for overall survival in the training cohort

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **id** | **coef** | **HR** | **HR.95L** | **HR.95H** | **p value** |
| AC005332.4 | 0.511241633 | 1.667360159 | 1.135259003 | 2.448859595 | 0.009138489 |
| AC068580.1 | 0.325042967 | 1.384090114 | 1.033729826 | 1.853197417 | 0.029055658 |
| AC139768.1 | 0.555338087 | 1.742530011 | 0.960071135 | 3.162693606 | 0.06785288 |
| AL391422.4 | 0.825821319 | 2.283755688 | 1.353947232 | 3.852099932 | 0.001961501 |
| FENDRR | -0.185639292 | 0.830573135 | 0.643128397 | 1.072650091 | 0.154868418 |

**Table S4.** The univariate analysis of mRNAsi-related lncRNA signature for overall survival in the training cohort

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Parameters** | **HR** | **HR.95L** | **HR.95H** | **p value** |
| Gender (Male vs. Female) | 0.984923513 | 0.56134394 | 1.72812826 | 0.957765656 |
| Age | 1.035683915 | 1.01129759 | 1.060658288 | 0.003926049 |
| Location (RSCC vs. LSCRC) | 1.247464107 | 0.701930083 | 2.216982484 | 0.451060965 |
| Stage (stage II/III vs. stage I ) | 9.500405964 | 1.301206812 | 69.36461803 | 0.02645018 |
| Stage (stage IV vs. stage I ) | 22.25043073 | 2.886067144 | 171.5419783 | 0.002910406 |
| MSI status (MSS vs. MSI) | 0.779555896 | 0.387845171 | 1.566881428 | 0.484456287 |
| RCT (No vs. Yes) | 1.374611844 | 0.754864643 | 2.503174231 | 0.298153351 |
| LncRNA signature (high risk vs. low risk) | 3.439183168 | 1.84463035 | 6.412114415 | 0.000101768 |

**Table S5.** The univariate analysis of mRNAsi-related lncRNA signature for overall survival in the validation cohort

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Parameters** | **HR** | **HR.95L** | **HR.95H** | **p value** |
| Gender (Male vs. Female) | 1.142172401 | 0.652448554 | 1.999479936 | 0.641723064 |
| Age | 1.03111777 | 1.005916518 | 1.05695039 | 0.015214945 |
| Location (RSCC vs. LSCRC) | 1.991705141 | 1.126770265 | 3.520584001 | 0.017757614 |
| Stage (stage II/III vs. stage I ) | 1.266613307 | 0.439690003 | 3.648728105 | 0.661514471 |
| Stage (stage IV vs. stage I ) | 5.932599546 | 2.022085505 | 17.40566227 | 0.001186281 |
| MSI status (MSS vs. MSI) | 1.405556023 | 0.595010565 | 3.320256565 | 0.437625558 |
| RCT (No vs. Yes) | 1.11167422 | 0.636183666 | 1.942551559 | 0.710066821 |
| LncRNA signature (high risk vs. low risk) | 3.107946265 | 1.675208648 | 5.766045917 | 0.000322929 |

**Table S6.** The correlation of each of five mRNAsi-related lncRNAs with mRNA from the same patients

|  |  |  |  |
| --- | --- | --- | --- |
| **LncRNAs** | **mRNAs** | **correlation coefficient**  | **p value** |
| AC005332.4 | CYTH4 | 0.504 | 1.89E-36 |
| AC005332.4 | SH2D1A | 0.504 | 1.70E-36 |
| AC005332.4 | IL10RA | 0.505 | 9.44E-37 |
| AC005332.4 | NCKAP1L | 0.505 | 1.10E-36 |
| AC005332.4 | STAT4 | 0.505 | 1.10E-36 |
| AC005332.4 | TRAF3IP3 | 0.505 | 1.22E-36 |
| AC005332.4 | TIGIT | 0.506 | 8.15E-37 |
| AC005332.4 | WAS | 0.506 | 6.84E-37 |
| AC005332.4 | ARHGAP9 | 0.507 | 4.99E-37 |
| AC005332.4 | PIK3CD | 0.507 | 5.66E-37 |
| AC005332.4 | GZMK | 0.508 | 3.78E-37 |
| AC005332.4 | CD86 | 0.51 | 1.91E-37 |
| AC005332.4 | IKZF1 | 0.511 | 1.36E-37 |
| AC005332.4 | IL2RB | 0.511 | 1.19E-37 |
| AC005332.4 | HCLS1 | 0.512 | 7.71E-38 |
| AC005332.4 | APOL3 | 0.513 | 6.69E-38 |
| AC005332.4 | LCP2 | 0.513 | 6.56E-38 |
| AC005332.4 | CD247 | 0.514 | 3.40E-38 |
| AC005332.4 | CYTIP | 0.514 | 3.59E-38 |
| AC005332.4 | HAVCR2 | 0.514 | 3.33E-38 |
| AC005332.4 | SCIMP | 0.517 | 1.16E-38 |
| AC005332.4 | CD72 | 0.518 | 7.57E-39 |
| AC005332.4 | CCR5 | 0.519 | 4.91E-39 |
| AC005332.4 | RASGRP1 | 0.519 | 5.82E-39 |
| AC005332.4 | FCGR3A | 0.52 | 3.91E-39 |
| AC005332.4 | ARHGAP25 | 0.525 | 4.89E-40 |
| AC005332.4 | IL2RA | 0.525 | 4.89E-40 |
| AC005332.4 | TNFSF13B | 0.526 | 3.30E-40 |
| AC005332.4 | DOCK2 | 0.527 | 2.24E-40 |
| AC005332.4 | FAM78A | 0.527 | 2.01E-40 |
| AC005332.4 | NLRC3 | 0.529 | 9.98E-41 |
| AC005332.4 | ITGAL | 0.53 | 6.40E-41 |
| AC005332.4 | CLEC2D | 0.532 | 3.77E-41 |
| AC005332.4 | CCL5 | 0.534 | 1.21E-41 |
| AC005332.4 | IKZF3 | 0.536 | 5.74E-42 |
| AC005332.4 | PTPRC | 0.536 | 7.35E-42 |
| AC005332.4 | CD53 | 0.537 | 4.83E-42 |
| AC005332.4 | STAT2 | 0.538 | 2.88E-42 |
| AC005332.4 | SLA | 0.54 | 1.41E-42 |
| AC005332.4 | SP140 | 0.545 | 1.25E-43 |
| AC005332.4 | RHOH | 0.546 | 9.75E-44 |
| AC005332.4 | SLA2 | 0.546 | 8.27E-44 |
| AC005332.4 | CD96 | 0.557 | 6.87E-46 |
| AC068580.1 | ITGAX | 0.502 | 3.81E-36 |
| AC068580.1 | MAP3K12 | 0.534 | 1.53E-41 |
| AC068580.1 | MYO9B | 0.503 | 2.70E-36 |
| AC068580.1 | RELT | 0.546 | 1.11E-43 |
| AC139768.1 | POU6F1 | 0.515 | 2.54E-38 |
| AL391422.4 | SEPT4 | 0.562 | 9.28E-47 |
| AL391422.4 | A2M | 0.548 | 3.64E-44 |
| AL391422.4 | ACKR1 | 0.53 | 7.40E-41 |
| AL391422.4 | ACTA2 | 0.518 | 7.12E-39 |
| AL391422.4 | ADAM12 | 0.534 | 1.34E-41 |
| AL391422.4 | ADAMTS1 | 0.505 | 1.22E-36 |
| AL391422.4 | ADAMTS10 | 0.507 | 5.95E-37 |
| AL391422.4 | ADGRA2 | 0.527 | 2.05E-40 |
| AL391422.4 | AEBP1 | 0.618 | 8.28E-59 |
| AL391422.4 | AFAP1L1 | 0.512 | 7.54E-38 |
| AL391422.4 | ALDH1A3 | 0.529 | 1.30E-40 |
| AL391422.4 | AMOTL1 | 0.559 | 2.81E-46 |
| AL391422.4 | ANGPTL2 | 0.564 | 4.11E-47 |
| AL391422.4 | ANTXR1 | 0.522 | 1.49E-39 |
| AL391422.4 | AOC3 | 0.546 | 8.27E-44 |
| AL391422.4 | ARHGAP31 | 0.524 | 6.73E-40 |
| AL391422.4 | ARHGEF15 | 0.581 | 1.30E-50 |
| AL391422.4 | ARHGEF17 | 0.555 | 2.07E-45 |
| AL391422.4 | ARHGEF25 | 0.539 | 1.74E-42 |
| AL391422.4 | ARHGEF6 | 0.509 | 2.97E-37 |
| AL391422.4 | ARMCX1 | 0.504 | 1.37E-36 |
| AL391422.4 | ATP10A | 0.514 | 3.21E-38 |
| AL391422.4 | ATP8B2 | 0.6 | 1.38E-54 |
| AL391422.4 | AXL | 0.521 | 2.24E-39 |
| AL391422.4 | BASP1 | 0.527 | 2.50E-40 |
| AL391422.4 | BCL6B | 0.549 | 2.18E-44 |
| AL391422.4 | BGN | 0.604 | 1.60E-55 |
| AL391422.4 | BOC | 0.585 | 2.00E-51 |
| AL391422.4 | C14orf132 | 0.53 | 5.99E-41 |
| AL391422.4 | C1R | 0.618 | 6.65E-59 |
| AL391422.4 | C1S | 0.615 | 5.26E-58 |
| AL391422.4 | C20orf194 | 0.537 | 4.96E-42 |
| AL391422.4 | C3 | 0.536 | 7.07E-42 |
| AL391422.4 | CALD1 | 0.502 | 3.20E-36 |
| AL391422.4 | CALHM5 | 0.531 | 5.79E-41 |
| AL391422.4 | CAVIN1 | 0.613 | 1.57E-57 |
| AL391422.4 | CCDC8 | 0.608 | 1.49E-56 |
| AL391422.4 | CCDC80 | 0.632 | 3.54E-62 |
| AL391422.4 | CCM2L | 0.508 | 4.07E-37 |
| AL391422.4 | CD34 | 0.555 | 2.13E-45 |
| AL391422.4 | CD93 | 0.509 | 2.29E-37 |
| AL391422.4 | CDH11 | 0.52 | 3.37E-39 |
| AL391422.4 | CERCAM | 0.525 | 5.97E-40 |
| AL391422.4 | CFH | 0.524 | 6.92E-40 |
| AL391422.4 | CHRD | 0.561 | 1.31E-46 |
| AL391422.4 | CLEC14A | 0.566 | 1.54E-47 |
| AL391422.4 | CLIP3 | 0.558 | 4.54E-46 |
| AL391422.4 | CLMP | 0.526 | 4.08E-40 |
| AL391422.4 | CMTM3 | 0.6 | 1.21E-54 |
| AL391422.4 | CNPY4 | 0.565 | 2.48E-47 |
| AL391422.4 | CNRIP1 | 0.561 | 1.27E-46 |
| AL391422.4 | COL14A1 | 0.542 | 5.82E-43 |
| AL391422.4 | COL16A1 | 0.554 | 3.12E-45 |
| AL391422.4 | COL18A1 | 0.527 | 2.71E-40 |
| AL391422.4 | COL1A1 | 0.529 | 1.03E-40 |
| AL391422.4 | COL1A2 | 0.551 | 1.14E-44 |
| AL391422.4 | COL3A1 | 0.539 | 1.63E-42 |
| AL391422.4 | COL4A2 | 0.53 | 8.54E-41 |
| AL391422.4 | COL5A1 | 0.538 | 2.48E-42 |
| AL391422.4 | COL5A2 | 0.52 | 3.17E-39 |
| AL391422.4 | COL6A3 | 0.526 | 4.04E-40 |
| AL391422.4 | COL8A1 | 0.576 | 1.38E-49 |
| AL391422.4 | COL8A2 | 0.602 | 3.17E-55 |
| AL391422.4 | COLEC12 | 0.524 | 6.92E-40 |
| AL391422.4 | COPZ2 | 0.609 | 9.53E-57 |
| AL391422.4 | CPXM2 | 0.503 | 2.76E-36 |
| AL391422.4 | CRISPLD2 | 0.562 | 9.70E-47 |
| AL391422.4 | CRYAB | 0.503 | 2.46E-36 |
| AL391422.4 | CTGF | 0.552 | 6.51E-45 |
| AL391422.4 | CTIF | 0.543 | 3.99E-43 |
| AL391422.4 | CXCL12 | 0.533 | 1.82E-41 |
| AL391422.4 | CXorf36 | 0.551 | 1.12E-44 |
| AL391422.4 | CYBRD1 | 0.531 | 4.13E-41 |
| AL391422.4 | CYR61 | 0.554 | 3.23E-45 |
| AL391422.4 | CYS1 | 0.614 | 6.44E-58 |
| AL391422.4 | CYYR1 | 0.541 | 8.59E-43 |
| AL391422.4 | DAAM2 | 0.557 | 9.14E-46 |
| AL391422.4 | DCN | 0.556 | 1.19E-45 |
| AL391422.4 | DLC1 | 0.517 | 1.06E-38 |
| AL391422.4 | DPYSL3 | 0.646 | 1.08E-65 |
| AL391422.4 | DZIP1 | 0.503 | 2.66E-36 |
| AL391422.4 | ECSCR | 0.511 | 1.07E-37 |
| AL391422.4 | EFEMP1 | 0.592 | 7.60E-53 |
| AL391422.4 | EFEMP2 | 0.524 | 6.56E-40 |
| AL391422.4 | EFS | 0.597 | 4.89E-54 |
| AL391422.4 | EGR2 | 0.554 | 2.87E-45 |
| AL391422.4 | EHD2 | 0.596 | 7.52E-54 |
| AL391422.4 | ELN | 0.53 | 7.04E-41 |
| AL391422.4 | EMILIN1 | 0.584 | 3.32E-51 |
| AL391422.4 | ENG | 0.542 | 4.25E-43 |
| AL391422.4 | ERG | 0.545 | 1.47E-43 |
| AL391422.4 | EVC | 0.574 | 3.45E-49 |
| AL391422.4 | FAM19A5 | 0.519 | 6.16E-39 |
| AL391422.4 | FBLN1 | 0.527 | 2.44E-40 |
| AL391422.4 | FBLN5 | 0.639 | 4.29E-64 |
| AL391422.4 | FBN1 | 0.586 | 1.25E-51 |
| AL391422.4 | FBXL7 | 0.611 | 3.12E-57 |
| AL391422.4 | FERMT2 | 0.536 | 7.62E-42 |
| AL391422.4 | FEZ1 | 0.601 | 7.23E-55 |
| AL391422.4 | FGFR1 | 0.577 | 8.18E-50 |
| AL391422.4 | FHL1 | 0.506 | 7.86E-37 |
| AL391422.4 | FIBIN | 0.531 | 5.83E-41 |
| AL391422.4 | FLI1 | 0.526 | 3.57E-40 |
| AL391422.4 | FLT4 | 0.513 | 5.02E-38 |
| AL391422.4 | FNDC1 | 0.565 | 2.26E-47 |
| AL391422.4 | FNDC4 | 0.558 | 6.14E-46 |
| AL391422.4 | FSTL1 | 0.589 | 2.38E-52 |
| AL391422.4 | FZD4 | 0.613 | 1.52E-57 |
| AL391422.4 | GABARAPL1 | 0.553 | 3.93E-45 |
| AL391422.4 | GALNT15 | 0.554 | 2.59E-45 |
| AL391422.4 | GAS7 | 0.563 | 5.26E-47 |
| AL391422.4 | GFPT2 | 0.518 | 8.43E-39 |
| AL391422.4 | GGT5 | 0.582 | 9.73E-51 |
| AL391422.4 | GIMAP1 | 0.501 | 4.98E-36 |
| AL391422.4 | GJA5 | 0.532 | 2.65E-41 |
| AL391422.4 | GLI2 | 0.522 | 1.42E-39 |
| AL391422.4 | GLI3 | 0.521 | 2.27E-39 |
| AL391422.4 | GLIS2 | 0.606 | 4.27E-56 |
| AL391422.4 | GLT8D2 | 0.57 | 2.35E-48 |
| AL391422.4 | GNG11 | 0.523 | 1.02E-39 |
| AL391422.4 | GRASP | 0.53 | 8.19E-41 |
| AL391422.4 | GUCY1B1 | 0.503 | 2.68E-36 |
| AL391422.4 | GYPC | 0.532 | 3.39E-41 |
| AL391422.4 | HEG1 | 0.569 | 3.63E-48 |
| AL391422.4 | HLX | 0.567 | 7.61E-48 |
| AL391422.4 | HSPA12B | 0.521 | 2.57E-39 |
| AL391422.4 | HTRA1 | 0.622 | 9.97E-60 |
| AL391422.4 | IGFBP5 | 0.545 | 1.37E-43 |
| AL391422.4 | IL1R1 | 0.602 | 3.75E-55 |
| AL391422.4 | ISLR | 0.508 | 3.85E-37 |
| AL391422.4 | ITGA11 | 0.529 | 1.22E-40 |
| AL391422.4 | JAM2 | 0.566 | 1.36E-47 |
| AL391422.4 | JAM3 | 0.558 | 4.35E-46 |
| AL391422.4 | JCAD | 0.525 | 6.33E-40 |
| AL391422.4 | KANK2 | 0.509 | 3.02E-37 |
| AL391422.4 | KCNE4 | 0.608 | 2.11E-56 |
| AL391422.4 | KIRREL1 | 0.513 | 6.66E-38 |
| AL391422.4 | LAMA4 | 0.567 | 7.85E-48 |
| AL391422.4 | LAMB2 | 0.52 | 4.39E-39 |
| AL391422.4 | LAMC1 | 0.502 | 3.96E-36 |
| AL391422.4 | LATS2 | 0.537 | 3.75E-42 |
| AL391422.4 | LAYN | 0.559 | 3.30E-46 |
| AL391422.4 | LDB2 | 0.56 | 1.98E-46 |
| AL391422.4 | LHFPL6 | 0.64 | 3.91E-64 |
| AL391422.4 | LMCD1 | 0.557 | 9.30E-46 |
| AL391422.4 | LMO2 | 0.51 | 1.44E-37 |
| AL391422.4 | LOXL4 | 0.558 | 6.25E-46 |
| AL391422.4 | LRRC32 | 0.546 | 9.76E-44 |
| AL391422.4 | LRRN4CL | 0.567 | 1.07E-47 |
| AL391422.4 | LTBP1 | 0.514 | 3.88E-38 |
| AL391422.4 | LTBP2 | 0.605 | 1.00E-55 |
| AL391422.4 | LUM | 0.545 | 1.43E-43 |
| AL391422.4 | LZTS1 | 0.562 | 9.89E-47 |
| AL391422.4 | MAFB | 0.542 | 4.64E-43 |
| AL391422.4 | MAN1C1 | 0.514 | 3.23E-38 |
| AL391422.4 | MAP1A | 0.559 | 2.96E-46 |
| AL391422.4 | MAP3K3 | 0.508 | 3.64E-37 |
| AL391422.4 | MCAM | 0.52 | 4.04E-39 |
| AL391422.4 | MEDAG | 0.574 | 3.31E-49 |
| AL391422.4 | MFAP5 | 0.515 | 2.54E-38 |
| AL391422.4 | MGP | 0.567 | 1.03E-47 |
| AL391422.4 | MMP19 | 0.553 | 5.41E-45 |
| AL391422.4 | MMP2 | 0.555 | 1.61E-45 |
| AL391422.4 | MMRN2 | 0.593 | 3.51E-53 |
| AL391422.4 | MN1 | 0.622 | 1.04E-59 |
| AL391422.4 | MOXD1 | 0.528 | 1.74E-40 |
| AL391422.4 | MPDZ | 0.525 | 5.58E-40 |
| AL391422.4 | MRAS | 0.647 | 3.75E-66 |
| AL391422.4 | MRC2 | 0.582 | 6.91E-51 |
| AL391422.4 | MRVI1 | 0.517 | 1.25E-38 |
| AL391422.4 | MSC | 0.535 | 9.93E-42 |
| AL391422.4 | MSN | 0.511 | 1.14E-37 |
| AL391422.4 | MSRB3 | 0.536 | 7.25E-42 |
| AL391422.4 | MXRA7 | 0.523 | 1.18E-39 |
| AL391422.4 | MXRA8 | 0.557 | 7.82E-46 |
| AL391422.4 | MYCT1 | 0.533 | 2.51E-41 |
| AL391422.4 | NGFR | 0.508 | 4.13E-37 |
| AL391422.4 | NKX3-2 | 0.519 | 5.87E-39 |
| AL391422.4 | NLGN2 | 0.506 | 7.04E-37 |
| AL391422.4 | NNMT | 0.512 | 9.33E-38 |
| AL391422.4 | NOTCH4 | 0.511 | 1.33E-37 |
| AL391422.4 | NPR1 | 0.594 | 2.49E-53 |
| AL391422.4 | NRP2 | 0.555 | 2.02E-45 |
| AL391422.4 | NTM | 0.514 | 3.79E-38 |
| AL391422.4 | NUAK1 | 0.558 | 5.80E-46 |
| AL391422.4 | NXN | 0.515 | 3.08E-38 |
| AL391422.4 | OLFML1 | 0.584 | 2.55E-51 |
| AL391422.4 | OLFML2B | 0.558 | 4.66E-46 |
| AL391422.4 | OSMR | 0.513 | 5.92E-38 |
| AL391422.4 | P4HA3 | 0.576 | 1.61E-49 |
| AL391422.4 | PACS1 | 0.55 | 1.79E-44 |
| AL391422.4 | PALM | 0.557 | 6.57E-46 |
| AL391422.4 | PALMD | 0.573 | 6.72E-49 |
| AL391422.4 | PBXIP1 | 0.515 | 2.58E-38 |
| AL391422.4 | PCDH12 | 0.51 | 2.03E-37 |
| AL391422.4 | PDE1A | 0.532 | 3.39E-41 |
| AL391422.4 | PDE2A | 0.532 | 2.88E-41 |
| AL391422.4 | PDGFC | 0.501 | 5.39E-36 |
| AL391422.4 | PDGFRB | 0.577 | 7.35E-50 |
| AL391422.4 | PDGFRL | 0.536 | 7.57E-42 |
| AL391422.4 | PEA15 | 0.524 | 8.27E-40 |
| AL391422.4 | PECAM1 | 0.578 | 6.31E-50 |
| AL391422.4 | PLEKHO1 | 0.54 | 1.45E-42 |
| AL391422.4 | PLEKHO2 | 0.525 | 6.06E-40 |
| AL391422.4 | PLPP7 | 0.518 | 7.32E-39 |
| AL391422.4 | PODN | 0.56 | 2.17E-46 |
| AL391422.4 | PPP1R18 | 0.537 | 4.83E-42 |
| AL391422.4 | PRELP | 0.541 | 8.37E-43 |
| AL391422.4 | PTGIS | 0.585 | 1.77E-51 |
| AL391422.4 | PTPRM | 0.586 | 1.33E-51 |
| AL391422.4 | PXDC1 | 0.865 | 7.50E-165 |
| AL391422.4 | PXDN | 0.53 | 8.03E-41 |
| AL391422.4 | RAB31 | 0.501 | 4.32E-36 |
| AL391422.4 | RAB34 | 0.517 | 1.26E-38 |
| AL391422.4 | RAB7B | 0.509 | 2.74E-37 |
| AL391422.4 | RASSF2 | 0.533 | 2.08E-41 |
| AL391422.4 | RECK | 0.54 | 1.28E-42 |
| AL391422.4 | RFLNB | 0.52 | 3.83E-39 |
| AL391422.4 | RFTN1 | 0.578 | 4.72E-50 |
| AL391422.4 | RHOJ | 0.523 | 1.19E-39 |
| AL391422.4 | RTL8B | 0.553 | 5.73E-45 |
| AL391422.4 | S1PR1 | 0.57 | 2.84E-48 |
| AL391422.4 | SCN1B | 0.561 | 1.14E-46 |
| AL391422.4 | SEMA3G | 0.555 | 2.32E-45 |
| AL391422.4 | SERPINF1 | 0.613 | 1.38E-57 |
| AL391422.4 | SERPING1 | 0.596 | 7.02E-54 |
| AL391422.4 | SFRP2 | 0.527 | 2.02E-40 |
| AL391422.4 | SFRP4 | 0.557 | 7.24E-46 |
| AL391422.4 | SLC24A3 | 0.527 | 2.15E-40 |
| AL391422.4 | SLC9A9 | 0.527 | 2.38E-40 |
| AL391422.4 | SLIT2 | 0.554 | 2.76E-45 |
| AL391422.4 | SLIT3 | 0.61 | 4.80E-57 |
| AL391422.4 | SNX29 | 0.502 | 3.03E-36 |
| AL391422.4 | SPARC | 0.578 | 6.50E-50 |
| AL391422.4 | SPARCL1 | 0.524 | 8.95E-40 |
| AL391422.4 | SPART | 0.536 | 6.60E-42 |
| AL391422.4 | SPOCK1 | 0.505 | 1.03E-36 |
| AL391422.4 | SPSB1 | 0.536 | 6.07E-42 |
| AL391422.4 | SSC5D | 0.542 | 4.95E-43 |
| AL391422.4 | SSPN | 0.532 | 2.73E-41 |
| AL391422.4 | STARD8 | 0.539 | 2.01E-42 |
| AL391422.4 | STON1 | 0.514 | 3.74E-38 |
| AL391422.4 | SULF1 | 0.547 | 5.90E-44 |
| AL391422.4 | SVEP1 | 0.576 | 1.26E-49 |
| AL391422.4 | SYDE1 | 0.532 | 3.25E-41 |
| AL391422.4 | SYNC | 0.557 | 8.69E-46 |
| AL391422.4 | SYNPO | 0.589 | 2.18E-52 |
| AL391422.4 | SYT11 | 0.555 | 2.17E-45 |
| AL391422.4 | TCF7L1 | 0.554 | 3.37E-45 |
| AL391422.4 | TEK | 0.537 | 3.91E-42 |
| AL391422.4 | TGFB3 | 0.564 | 3.44E-47 |
| AL391422.4 | THBD | 0.506 | 6.47E-37 |
| AL391422.4 | THBS1 | 0.512 | 7.68E-38 |
| AL391422.4 | THBS2 | 0.564 | 3.62E-47 |
| AL391422.4 | THY1 | 0.56 | 2.61E-46 |
| AL391422.4 | TIE1 | 0.558 | 4.97E-46 |
| AL391422.4 | TIMP2 | 0.622 | 7.89E-60 |
| AL391422.4 | TMEM119 | 0.525 | 5.46E-40 |
| AL391422.4 | TMEM200B | 0.539 | 2.13E-42 |
| AL391422.4 | TNFSF12 | 0.589 | 2.45E-52 |
| AL391422.4 | TNXB | 0.51 | 1.73E-37 |
| AL391422.4 | TPST1 | 0.562 | 8.93E-47 |
| AL391422.4 | TSHZ3 | 0.56 | 1.74E-46 |
| AL391422.4 | TSPYL5 | 0.557 | 6.98E-46 |
| AL391422.4 | VASH1 | 0.543 | 3.11E-43 |
| AL391422.4 | VCAM1 | 0.527 | 2.73E-40 |
| AL391422.4 | VCAN | 0.516 | 2.04E-38 |
| AL391422.4 | VEGFC | 0.551 | 9.32E-45 |
| AL391422.4 | VIM | 0.608 | 2.02E-56 |
| AL391422.4 | VSTM4 | 0.588 | 4.93E-52 |
| AL391422.4 | WBP1L | 0.548 | 3.36E-44 |
| AL391422.4 | ZBTB47 | 0.505 | 1.18E-36 |
| AL391422.4 | ZNF512B | 0.517 | 1.13E-38 |
| AL391422.4 | ZNF521 | 0.595 | 1.32E-53 |
| FENDRR | A2M | 0.597 | 5.00E-54 |
| FENDRR | ACKR1 | 0.53 | 7.89E-41 |
| FENDRR | ACTA2 | 0.608 | 1.42E-56 |
| FENDRR | ACTG2 | 0.652 | 1.71E-67 |
| FENDRR | ADAM33 | 0.634 | 9.15E-63 |
| FENDRR | ADAMTS8 | 0.747 | 1.93E-98 |
| FENDRR | ADCY5 | 0.565 | 2.32E-47 |
| FENDRR | AMOTL1 | 0.553 | 4.97E-45 |
| FENDRR | ANGPTL1 | 0.559 | 2.85E-46 |
| FENDRR | AOC3 | 0.595 | 1.56E-53 |
| FENDRR | ARHGEF25 | 0.651 | 4.64E-67 |
| FENDRR | ARMCX1 | 0.529 | 9.85E-41 |
| FENDRR | ASB2 | 0.717 | 2.11E-87 |
| FENDRR | ATP1A2 | 0.68 | 3.09E-75 |
| FENDRR | ATP2B4 | 0.634 | 7.80E-63 |
| FENDRR | BOC | 0.527 | 2.33E-40 |
| FENDRR | C14orf132 | 0.593 | 3.42E-53 |
| FENDRR | C1QTNF2 | 0.529 | 1.16E-40 |
| FENDRR | C4B | 0.502 | 3.89E-36 |
| FENDRR | C8orf88 | 0.725 | 4.85E-90 |
| FENDRR | CACNA1H | 0.527 | 2.81E-40 |
| FENDRR | CACNA2D1 | 0.554 | 3.52E-45 |
| FENDRR | CALD1 | 0.573 | 5.14E-49 |
| FENDRR | CAP2 | 0.533 | 1.74E-41 |
| FENDRR | CASQ2 | 0.623 | 5.06E-60 |
| FENDRR | CAVIN2 | 0.733 | 3.15E-93 |
| FENDRR | CCDC69 | 0.596 | 9.32E-54 |
| FENDRR | CFL2 | 0.588 | 3.87E-52 |
| FENDRR | CH25H | 0.578 | 6.85E-50 |
| FENDRR | CHRDL1 | 0.566 | 1.28E-47 |
| FENDRR | CHRDL2 | 0.698 | 5.56E-81 |
| FENDRR | CHRNA3 | 0.532 | 2.68E-41 |
| FENDRR | CLIP3 | 0.645 | 1.13E-65 |
| FENDRR | CNN1 | 0.646 | 6.71E-66 |
| FENDRR | CNTNAP1 | 0.678 | 9.04E-75 |
| FENDRR | CSRP1 | 0.681 | 1.65E-75 |
| FENDRR | CYYR1 | 0.504 | 1.57E-36 |
| FENDRR | DAAM2 | 0.599 | 1.48E-54 |
| FENDRR | DACT3 | 0.693 | 3.51E-79 |
| FENDRR | DDR2 | 0.511 | 1.17E-37 |
| FENDRR | DES | 0.629 | 1.48E-61 |
| FENDRR | DIXDC1 | 0.563 | 4.57E-47 |
| FENDRR | DNAJB5 | 0.678 | 1.21E-74 |
| FENDRR | DZIP1 | 0.529 | 1.27E-40 |
| FENDRR | EDIL3 | 0.501 | 4.40E-36 |
| FENDRR | EDNRB | 0.542 | 6.05E-43 |
| FENDRR | ELN | 0.524 | 9.11E-40 |
| FENDRR | EMCN | 0.519 | 5.81E-39 |
| FENDRR | EML1 | 0.578 | 5.16E-50 |
| FENDRR | FAM129A | 0.547 | 5.25E-44 |
| FENDRR | FAT4 | 0.634 | 1.08E-62 |
| FENDRR | FBLN5 | 0.502 | 3.09E-36 |
| FENDRR | FBXL22 | 0.631 | 5.37E-62 |
| FENDRR | FBXL7 | 0.544 | 2.50E-43 |
| FENDRR | FBXO32 | 0.538 | 2.99E-42 |
| FENDRR | FERMT2 | 0.654 | 5.57E-68 |
| FENDRR | FEZ1 | 0.607 | 2.35E-56 |
| FENDRR | FHL1 | 0.59 | 2.04E-52 |
| FENDRR | FILIP1L | 0.607 | 2.83E-56 |
| FENDRR | FLNA | 0.535 | 9.24E-42 |
| FENDRR | FLNC | 0.58 | 2.68E-50 |
| FENDRR | FNBP1 | 0.558 | 4.34E-46 |
| FENDRR | FOXF1 | 0.849 | 1.20E-152 |
| FENDRR | FOXF2 | 0.76 | 6.72E-104 |
| FENDRR | FXYD6 | 0.674 | 1.45E-73 |
| FENDRR | GJC1 | 0.557 | 8.75E-46 |
| FENDRR | GNAO1 | 0.718 | 1.31E-87 |
| FENDRR | GPRASP1 | 0.584 | 2.63E-51 |
| FENDRR | GREM2 | 0.733 | 3.94E-93 |
| FENDRR | GUCY1A1 | 0.543 | 3.73E-43 |
| FENDRR | GUCY1B1 | 0.573 | 4.74E-49 |
| FENDRR | HAND2 | 0.654 | 8.29E-68 |
| FENDRR | HSD17B6 | 0.625 | 1.60E-60 |
| FENDRR | HSPB6 | 0.6 | 1.25E-54 |
| FENDRR | HSPB7 | 0.565 | 1.89E-47 |
| FENDRR | HSPB8 | 0.708 | 3.06E-84 |
| FENDRR | IGFBP5 | 0.513 | 6.40E-38 |
| FENDRR | ITGA7 | 0.531 | 5.40E-41 |
| FENDRR | ITGA8 | 0.528 | 1.80E-40 |
| FENDRR | ITGB3 | 0.531 | 4.54E-41 |
| FENDRR | ITIH5 | 0.59 | 1.53E-52 |
| FENDRR | ITPR1 | 0.556 | 1.05E-45 |
| FENDRR | JAM2 | 0.592 | 5.89E-53 |
| FENDRR | JAM3 | 0.64 | 2.70E-64 |
| FENDRR | JPH2 | 0.65 | 5.77E-67 |
| FENDRR | KANK2 | 0.695 | 6.70E-80 |
| FENDRR | KCND3 | 0.541 | 6.58E-43 |
| FENDRR | KCNMA1 | 0.686 | 3.76E-77 |
| FENDRR | KCNMB1 | 0.711 | 2.49E-85 |
| FENDRR | LDB2 | 0.529 | 1.25E-40 |
| FENDRR | LMOD1 | 0.719 | 5.00E-88 |
| FENDRR | LRRN4CL | 0.631 | 4.71E-62 |
| FENDRR | LSAMP | 0.501 | 4.80E-36 |
| FENDRR | LTBP1 | 0.504 | 1.87E-36 |
| FENDRR | MAB21L2 | 0.718 | 8.14E-88 |
| FENDRR | MAMDC2 | 0.708 | 4.25E-84 |
| FENDRR | MAN1C1 | 0.556 | 1.11E-45 |
| FENDRR | MCAM | 0.522 | 1.56E-39 |
| FENDRR | MEOX1 | 0.562 | 7.49E-47 |
| FENDRR | MFAP4 | 0.656 | 1.32E-68 |
| FENDRR | MOXD1 | 0.507 | 5.63E-37 |
| FENDRR | MPDZ | 0.527 | 2.35E-40 |
| FENDRR | MRGPRF | 0.724 | 7.30E-90 |
| FENDRR | MRVI1 | 0.738 | 3.52E-95 |
| FENDRR | MSRB3 | 0.65 | 7.19E-67 |
| FENDRR | MYH11 | 0.711 | 3.31E-85 |
| FENDRR | MYL9 | 0.676 | 3.64E-74 |
| FENDRR | MYLK | 0.749 | 2.18E-99 |
| FENDRR | MYOCD | 0.814 | 1.19E-130 |
| FENDRR | NDN | 0.55 | 2.04E-44 |
| FENDRR | NEXN | 0.549 | 2.43E-44 |
| FENDRR | NKX2-3 | 0.765 | 4.43E-106 |
| FENDRR | OGN | 0.503 | 2.44E-36 |
| FENDRR | OLFML2A | 0.597 | 5.27E-54 |
| FENDRR | OR51E2 | 0.623 | 5.12E-60 |
| FENDRR | P2RY14 | 0.66 | 1.85E-69 |
| FENDRR | PALLD | 0.53 | 6.23E-41 |
| FENDRR | PCDH18 | 0.703 | 1.11E-82 |
| FENDRR | PCP4L1 | 0.557 | 6.68E-46 |
| FENDRR | PDE2A | 0.594 | 2.02E-53 |
| FENDRR | PDLIM3 | 0.636 | 2.93E-63 |
| FENDRR | PGM5 | 0.642 | 8.20E-65 |
| FENDRR | PLN | 0.685 | 8.68E-77 |
| FENDRR | PLPP1 | 0.589 | 2.15E-52 |
| FENDRR | POPDC2 | 0.703 | 1.87E-82 |
| FENDRR | PPP1R12B | 0.683 | 2.72E-76 |
| FENDRR | PPP1R14A | 0.556 | 1.47E-45 |
| FENDRR | PPP1R3C | 0.589 | 3.04E-52 |
| FENDRR | PRIMA1 | 0.678 | 1.32E-74 |
| FENDRR | PSD | 0.647 | 5.69E-66 |
| FENDRR | PTGS1 | 0.566 | 1.46E-47 |
| FENDRR | PTN | 0.6 | 9.11E-55 |
| FENDRR | RASL12 | 0.764 | 9.90E-106 |
| FENDRR | RBPMS2 | 0.713 | 7.16E-86 |
| FENDRR | RCAN2 | 0.592 | 7.45E-53 |
| FENDRR | REEP2 | 0.569 | 3.34E-48 |
| FENDRR | RGMA | 0.699 | 3.56E-81 |
| FENDRR | RGS5 | 0.694 | 1.03E-79 |
| FENDRR | SAMD11 | 0.518 | 7.28E-39 |
| FENDRR | SELP | 0.512 | 7.06E-38 |
| FENDRR | SETBP1 | 0.514 | 3.70E-38 |
| FENDRR | SGCA | 0.645 | 1.34E-65 |
| FENDRR | SHISAL1 | 0.671 | 9.32E-73 |
| FENDRR | SLC24A3 | 0.534 | 1.65E-41 |
| FENDRR | SLC2A4 | 0.549 | 2.20E-44 |
| FENDRR | SLC9A9 | 0.519 | 5.46E-39 |
| FENDRR | SORBS1 | 0.615 | 4.19E-58 |
| FENDRR | SPARCL1 | 0.645 | 1.23E-65 |
| FENDRR | SPEG | 0.615 | 3.67E-58 |
| FENDRR | SVIL | 0.633 | 1.62E-62 |
| FENDRR | SYNM | 0.686 | 2.60E-77 |
| FENDRR | SYNPO2 | 0.676 | 4.33E-74 |
| FENDRR | SYT11 | 0.532 | 2.90E-41 |
| FENDRR | TACR2 | 0.642 | 6.92E-65 |
| FENDRR | TAGLN | 0.651 | 3.76E-67 |
| FENDRR | TCEAL2 | 0.685 | 5.46E-77 |
| FENDRR | TCEAL7 | 0.631 | 6.88E-62 |
| FENDRR | TCF21 | 0.697 | 9.88E-81 |
| FENDRR | TCF7L1 | 0.543 | 3.27E-43 |
| FENDRR | TEK | 0.514 | 3.25E-38 |
| FENDRR | TGFB1I1 | 0.538 | 2.51E-42 |
| FENDRR | TMEM100 | 0.522 | 1.84E-39 |
| FENDRR | TMEM200B | 0.717 | 2.04E-87 |
| FENDRR | TMEM35A | 0.629 | 2.20E-61 |
| FENDRR | TMOD1 | 0.502 | 3.70E-36 |
| FENDRR | TNS1 | 0.635 | 4.50E-63 |
| FENDRR | TPM2 | 0.613 | 1.50E-57 |
| FENDRR | TSPAN11 | 0.549 | 3.21E-44 |
| FENDRR | TSPYL5 | 0.531 | 5.14E-41 |
| FENDRR | VAT1L | 0.637 | 1.39E-63 |
| FENDRR | VSTM4 | 0.508 | 3.46E-37 |
| FENDRR | WFDC1 | 0.796 | 8.15E-121 |
| FENDRR | WNT2B | 0.502 | 2.98E-36 |
| FENDRR | ZCCHC24 | 0.574 | 3.46E-49 |
| FENDRR | ZEB1 | 0.575 | 2.68E-49 |

**Table S7.** The GO analysis of the mRNAsi-related lncRNA signature

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **GOID** | **GOTerm** | **Corrected Term P Value**  | **Corrected Group P Value** | **GO Groups Name** | **% Associated Genes** | **No. Genes** | **Associated Genes Found** |
| GO:0048495 | Roundabout binding | 0.00 | 0.00 | Roundabout binding | 80.00 | 4.00 | [MYO9B, SLIT2, SLIT3, TGFB1I1] |
| GO:0048251 | elastic fiber assembly | 0.00 | 0.00 | extracellular matrix organization | 80.00 | 4.00 | [FBLN5, MFAP4, MYH11, TNXB] |
| GO:0048407 | platelet-derived growth factor binding | 0.00 | 0.00 | extracellular matrix organization | 45.45 | 5.00 | [COL1A1, COL1A2, COL3A1, COL5A1, PDGFRB] |
| GO:0030199 | collagen fibril organization | 0.00 | 0.00 | extracellular matrix organization | 41.18 | 7.00 | [AEBP1, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, PXDN] |
| GO:0033622 | integrin activation | 0.00 | 0.00 | integrin activation | 30.00 | 6.00 | [COL16A1, CXCL12, FERMT2, JAM3, RFTN1, SELP] |
| GO:0050431 | transforming growth factor beta binding | 0.01 | 0.00 | growth factor binding | 28.57 | 6.00 | [ENG, GPRASP1, LRRC32, LTBP1, LTBP2, TGFB3] |
| GO:0048592 | eye morphogenesis | 0.03 | 0.00 | animal organ development | 23.08 | 6.00 | [ANGPTL1, COL5A1, COL5A2, EFEMP1, FBN1, PTPRM] |
| GO:0048592 | eye morphogenesis | 0.03 | 0.00 | animal organ morphogenesis | 23.08 | 6.00 | [ANGPTL1, COL5A1, COL5A2, EFEMP1, FBN1, PTPRM] |
| GO:0003254 | regulation of membrane depolarization | 0.03 | 0.00 | membrane depolarization | 22.22 | 6.00 | [CFH, DCN, FHL1, GJA5, SCN1B, SLA] |
| GO:0035987 | endodermal cell differentiation | 0.02 | 0.00 | formation of primary germ layer | 20.00 | 7.00 | [COL4A2, COL5A1, COL5A2, COL8A1, ITGA7, LAMA4, MMP2] |
| GO:0019838 | growth factor binding | 0.00 | 0.00 | growth factor binding | 20.00 | 20.00 | [A2M, COL1A1, COL1A2, COL3A1, COL5A1, ENG, FGFR1, FLT4, GPRASP1, IGFBP5, IL1R1, IL2RB, ITGB3, LRRC32, LTBP1, LTBP2, OSMR, PDGFRB, TGFB3, THBS1] |
| GO:0051899 | membrane depolarization | 0.01 | 0.00 | membrane depolarization | 19.51 | 8.00 | [CACNA2D1, CFH, DCN, ERG, FHL1, GJA5, SCN1B, SLA] |
| GO:0001704 | formation of primary germ layer | 0.00 | 0.00 | formation of primary germ layer | 19.15 | 9.00 | [COL4A2, COL5A1, COL5A2, COL8A1, ITGA7, ITGA8, ITGB3, LAMA4, MMP2] |
| GO:0007492 | endoderm development | 0.02 | 0.00 | formation of primary germ layer | 18.92 | 7.00 | [COL4A2, COL5A1, COL5A2, COL8A1, ITGA7, LAMA4, MMP2] |
| GO:0001706 | endoderm formation | 0.02 | 0.00 | formation of primary germ layer | 18.92 | 7.00 | [COL4A2, COL5A1, COL5A2, COL8A1, ITGA7, LAMA4, MMP2] |
| GO:0005518 | collagen binding | 0.00 | 0.00 | collagen binding | 18.18 | 10.00 | [ADAM12, AEBP1, ANTXR1, DDR2, ITGA11, LUM, MRC2, PODN, SPARC, THBS1] |
| GO:0045123 | cellular extravasation | 0.03 | 0.00 | cell-substrate adhesion | 17.95 | 7.00 | [CXCL12, ITGAL, JAM2, PECAM1, SELP, THY1, VCAM1] |
| GO:0001937 | negative regulation of endothelial cell proliferation | 0.04 | 0.00 | circulatory system development | 17.50 | 7.00 | [ANGPTL1, NGFR, PTPRM, SPARC, SULF1, THBS1, VASH1] |
| GO:0043062 | extracellular structure organization | 0.00 | 0.00 | extracellular matrix organization | 17.11 | 13.00 | [AEBP1, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, FBLN5, LAMB2, LAMC1, MFAP4, MYH11, PXDN, TNXB] |
| GO:0030198 | extracellular matrix organization | 0.00 | 0.00 | extracellular matrix organization | 17.11 | 13.00 | [AEBP1, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, FBLN5, LAMB2, LAMC1, MFAP4, MYH11, PXDN, TNXB] |
| GO:0016525 | negative regulation of angiogenesis | 0.00 | 0.00 | circulatory system development | 16.49 | 16.00 | [ADAMTS1, ANGPTL1, ATP2B4, COL4A2, DCN, ECSCR, MMRN2, NGFR, PTPRM, SERPINF1, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:2000181 | negative regulation of blood vessel morphogenesis | 0.00 | 0.00 | circulatory system development | 16.16 | 16.00 | [ADAMTS1, ANGPTL1, ATP2B4, COL4A2, DCN, ECSCR, MMRN2, NGFR, PTPRM, SERPINF1, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:1901343 | negative regulation of vasculature development | 0.00 | 0.00 | circulatory system development | 14.55 | 16.00 | [ADAMTS1, ANGPTL1, ATP2B4, COL4A2, DCN, ECSCR, MMRN2, NGFR, PTPRM, SERPINF1, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0019955 | cytokine binding | 0.00 | 0.00 | growth factor binding | 14.43 | 14.00 | [A2M, ACKR1, CCR5, ENG, FZD4, GPRASP1, GYPC, IL1R1, IL2RB, ITGB3, LRRC32, LTBP1, LTBP2, TGFB3] |
| GO:0007369 | gastrulation | 0.01 | 0.00 | formation of primary germ layer | 14.29 | 10.00 | [COL4A2, COL5A1, COL5A2, COL8A1, IL1R1, ITGA7, ITGA8, ITGB3, LAMA4, MMP2] |
| GO:0048880 | sensory system development | 0.02 | 0.00 | animal organ morphogenesis | 14.06 | 9.00 | [ANGPTL1, CHRDL1, COL5A1, COL5A2, EFEMP1, FBN1, FZD4, MAB21L2, PTPRM] |
| GO:0150063 | visual system development | 0.02 | 0.00 | animal organ morphogenesis | 14.06 | 9.00 | [ANGPTL1, CHRDL1, COL5A1, COL5A2, EFEMP1, FBN1, FZD4, MAB21L2, PTPRM] |
| GO:0001654 | eye development | 0.02 | 0.00 | animal organ morphogenesis | 14.06 | 9.00 | [ANGPTL1, CHRDL1, COL5A1, COL5A2, EFEMP1, FBN1, FZD4, MAB21L2, PTPRM] |
| GO:0006909 | phagocytosis | 0.01 | 0.00 | phagocytosis | 12.00 | 12.00 | [ARHGAP25, AXL, C3, C4B, COLEC12, IL2RB, ITGB3, PECAM1, PTPRC, RAB34, RAB7B, THBS1] |
| GO:0005178 | integrin binding | 0.00 | 0.00 | cell-substrate adhesion | 11.71 | 13.00 | [ADAM12, COL16A1, COL3A1, CXCL12, EMILIN1, FBN1, ITGB3, JAM2, JAM3, PTN, THBS1, THY1, VCAM1] |
| GO:0048598 | embryonic morphogenesis | 0.00 | 0.00 | formation of primary germ layer | 11.57 | 14.00 | [ACKR1, COL4A2, COL5A1, COL5A2, COL8A1, EFEMP1, FBN1, FOXF1, IL1R1, ITGA7, ITGA8, ITGB3, LAMA4, MMP2] |
| GO:0045765 | regulation of angiogenesis | 0.00 | 0.00 | circulatory system development | 10.88 | 26.00 | [ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL4A2, DCN, ECSCR, FLI1, HSPB6, ITGAX, JCAD, MAP3K3, MMRN2, NGFR, PTGIS, PTPRM, RHOJ, SERPINF1, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0001568 | blood vessel development | 0.00 | 0.00 | circulatory system development | 10.80 | 38.00 | [ACTA2, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL1A1, COL1A2, COL4A2, DCN, ECSCR, ENG, FLI1, FOXF1, GJA5, HSPB6, ITGAX, JAM3, JCAD, MAP3K3, MCAM, MEOX1, MMRN2, MYLK, NGFR, PECAM1, PTGIS, PTPRM, RHOJ, SERPINF1, SLIT2, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0072358 | cardiovascular system development | 0.00 | 0.00 | circulatory system development | 10.53 | 40.00 | [ACTA2, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL1A1, COL1A2, COL4A2, DCN, ECSCR, ENG, FLI1, FLT4, FOXF1, FZD4, GJA5, HSPB6, ITGAX, JAM3, JCAD, MAP3K3, MCAM, MEOX1, MMRN2, MYLK, NGFR, PECAM1, PTGIS, PTPRM, RHOJ, SERPINF1, SLIT2, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0001944 | vasculature development | 0.00 | 0.00 | circulatory system development | 10.53 | 40.00 | [ACTA2, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL1A1, COL1A2, COL4A2, DCN, ECSCR, ENG, FLI1, FLT4, FOXF1, FZD4, GJA5, HSPB6, ITGAX, JAM3, JCAD, MAP3K3, MCAM, MEOX1, MMRN2, MYLK, NGFR, PECAM1, PTGIS, PTPRM, RHOJ, SERPINF1, SLIT2, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0001936 | regulation of endothelial cell proliferation | 0.03 | 0.00 | circulatory system development | 10.43 | 12.00 | [ANGPTL1, CDH11, FGFR1, FLT4, ITGB3, JCAD, NGFR, PTPRM, SPARC, SULF1, THBS1, VASH1] |
| GO:0001935 | endothelial cell proliferation | 0.02 | 0.00 | circulatory system development | 10.32 | 13.00 | [ANGPTL1, CD34, CDH11, FGFR1, FLT4, ITGB3, JCAD, NGFR, PTPRM, SPARC, SULF1, THBS1, VASH1] |
| GO:0048514 | blood vessel morphogenesis | 0.00 | 0.00 | circulatory system development | 10.06 | 34.00 | [ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL4A2, DCN, ECSCR, ENG, FLI1, FOXF1, GJA5, HSPB6, ITGAX, JAM3, JCAD, MAP3K3, MCAM, MEOX1, MMRN2, MYLK, NGFR, PTGIS, PTPRM, RHOJ, SERPINF1, SLIT2, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:1901342 | regulation of vasculature development | 0.00 | 0.00 | circulatory system development | 9.96 | 26.00 | [ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL4A2, DCN, ECSCR, FLI1, HSPB6, ITGAX, JCAD, MAP3K3, MMRN2, NGFR, PTGIS, PTPRM, RHOJ, SERPINF1, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0001525 | angiogenesis | 0.00 | 0.00 | circulatory system development | 9.78 | 31.00 | [ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL4A2, DCN, ECSCR, FLI1, GJA5, HSPB6, ITGAX, JAM3, JCAD, MAP3K3, MCAM, MEOX1, MMRN2, NGFR, PTGIS, PTPRM, RHOJ, SERPINF1, SLIT2, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0009887 | animal organ morphogenesis | 0.00 | 0.00 | animal organ development | 9.77 | 21.00 | [ANGPTL1, CD34, CNRIP1, COL1A1, COL1A2, COL5A1, COL5A2, CSRP1, EFEMP1, ELN, FBN1, FOXF1, GJA5, MSN, MYL9, MYLK, PTPRM, RELT, SFRP2, SFRP4, TGFB3] |
| GO:0009887 | animal organ morphogenesis | 0.00 | 0.00 | animal organ morphogenesis | 9.77 | 21.00 | [ANGPTL1, CD34, CNRIP1, COL1A1, COL1A2, COL5A1, COL5A2, CSRP1, EFEMP1, ELN, FBN1, FOXF1, GJA5, MSN, MYL9, MYLK, PTPRM, RELT, SFRP2, SFRP4, TGFB3] |
| GO:0009887 | animal organ morphogenesis | 0.00 | 0.00 | multicellular organism development | 9.77 | 21.00 | [ANGPTL1, CD34, CNRIP1, COL1A1, COL1A2, COL5A1, COL5A2, CSRP1, EFEMP1, ELN, FBN1, FOXF1, GJA5, MSN, MYL9, MYLK, PTPRM, RELT, SFRP2, SFRP4, TGFB3] |
| GO:0007160 | cell-matrix adhesion | 0.00 | 0.00 | cell-substrate adhesion | 9.76 | 16.00 | [ADAM12, CD96, COL16A1, COL3A1, DLC1, EMILIN1, FERMT2, ITGA11, ITGA8, ITGAL, ITGB3, RFTN1, TEK, THBS1, THY1, VCAM1] |
| GO:0072359 | circulatory system development | 0.00 | 0.00 | circulatory system development | 9.62 | 48.00 | [ACTA2, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL1A1, COL1A2, COL3A1, COL4A2, DCN, ECSCR, ELN, ENG, FBN1, FLI1, FLT4, FOXF1, FZD4, GJA5, HAND2, HSPB6, ITGAX, JAM3, JCAD, MAP3K3, MCAM, MEOX1, MMRN2, MYH11, MYL9, MYLK, MYOCD, NGFR, PECAM1, PTGIS, PTPRM, RHOJ, SERPINF1, SFRP2, SLIT2, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0010594 | regulation of endothelial cell migration | 0.00 | 0.00 | circulatory system development | 9.50 | 17.00 | [ANGPTL1, ATP2B4, DCN, FGFR1, FLI1, FLT4, ITGB3, JCAD, MAP3K3, MMRN2, PTPRM, RHOJ, SLIT2, SPARC, TEK, THBS1, VASH1] |
| GO:0048646 | anatomical structure formation involved in morphogenesis | 0.00 | 0.00 | circulatory system development | 9.37 | 43.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, CNTNAP1, COL4A2, COL5A1, COL5A2, COL8A1, DCN, ECSCR, FLI1, FLT4, GJA5, HSPB6, ITGA7, ITGA8, ITGAX, ITGB3, JAM3, JCAD, LAMA4, MAP3K3, MCAM, MEOX1, MMP2, MMRN2, NGFR, PTGIS, PTPRM, RELT, RHOJ, SERPINF1, SLIT2, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0007179 | transforming growth factor beta receptor signaling pathway | 0.04 | 0.00 | growth factor binding | 9.35 | 13.00 | [ADAM12, COL1A2, COL3A1, ENG, FERMT2, GPRASP1, LRRC32, LTBP1, PXDN, RFTN1, TGFB1I1, TGFB3, THBS1] |
| GO:0031589 | cell-substrate adhesion | 0.00 | 0.00 | cell-substrate adhesion | 9.35 | 23.00 | [ADAM12, ANTXR1, CD96, COL16A1, COL3A1, DLC1, EMILIN1, FBLN1, FERMT2, FLNA, FZD4, ITGA11, ITGA8, ITGAL, ITGB3, LAMB2, LAMC1, RFTN1, SPOCK1, TEK, THBS1, THY1, VCAM1] |
| GO:0035239 | tube morphogenesis | 0.00 | 0.00 | circulatory system development | 9.26 | 35.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL4A2, DCN, ECSCR, ENG, FLI1, FOXF1, GJA5, HSPB6, ITGAX, JAM3, JCAD, MAP3K3, MCAM, MEOX1, MMRN2, MYLK, NGFR, PTGIS, PTPRM, RHOJ, SERPINF1, SLIT2, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0050839 | cell adhesion molecule binding | 0.01 | 0.00 | cell-substrate adhesion | 9.09 | 16.00 | [ADAM12, COL16A1, COL3A1, CXCL12, EMILIN1, FBN1, ITGAL, ITGB3, JAM2, JAM3, MSN, PTN, PTPRM, THBS1, THY1, VCAM1] |
| GO:0071559 | response to transforming growth factor beta | 0.01 | 0.00 | growth factor binding | 8.99 | 16.00 | [ADAM12, COL1A2, COL3A1, ENG, FERMT2, FNDC4, FSTL1, GPRASP1, LRRC32, LTBP1, PDE2A, PXDN, RFTN1, TGFB1I1, TGFB3, THBS1] |
| GO:0035295 | tube development | 0.00 | 0.00 | circulatory system development | 8.72 | 36.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, CLMP, COL4A2, DCN, ECSCR, ENG, FLI1, FOXF1, GJA5, HSPB6, ITGAX, JAM3, JCAD, MAP3K3, MCAM, MEOX1, MMRN2, MYLK, NGFR, PTGIS, PTPRM, RHOJ, SERPINF1, SLIT2, SPARC, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0071560 | cellular response to transforming growth factor beta stimulus | 0.03 | 0.00 | growth factor binding | 8.62 | 15.00 | [ADAM12, COL1A2, COL3A1, ENG, FERMT2, FSTL1, GPRASP1, LRRC32, LTBP1, PDE2A, PXDN, RFTN1, TGFB1I1, TGFB3, THBS1] |
| GO:0043542 | endothelial cell migration | 0.01 | 0.00 | circulatory system development | 8.33 | 18.00 | [ANGPTL1, ATP2B4, DCN, FGFR1, FLI1, FLT4, ITGB3, JCAD, MAP3K3, MMRN2, PTPRM, PXDN, RHOJ, SLIT2, SPARC, TEK, THBS1, VASH1] |
| GO:0010632 | regulation of epithelial cell migration | 0.02 | 0.00 | circulatory system development | 7.79 | 18.00 | [ADAM12, ANGPTL1, ATP2B4, DCN, FGFR1, FLI1, FLT4, ITGB3, JCAD, MAP3K3, MMRN2, PTPRM, RHOJ, SLIT2, SPARC, TEK, THBS1, VASH1] |
| GO:0051093 | negative regulation of developmental process | 0.00 | 0.00 | circulatory system development | 7.73 | 33.00 | [ADAMTS1, ANGPTL1, ATP2B4, CHRD, COL4A2, COL5A1, COL5A2, CSRP1, DCN, ECSCR, EFEMP1, FBLN1, FBN1, FSTL1, ITGB3, MAFB, MAP3K3, MMRN2, MYOCD, NGFR, PTPRM, RBPMS2, SERPINF1, SFRP2, SLIT2, SPARC, SPOCK1, SULF1, TEK, THBS1, THBS2, VASH1, ZEB1] |
| GO:2000146 | negative regulation of cell motility | 0.01 | 0.00 | circulatory system development | 7.69 | 20.00 | [ACKR1, ANGPTL1, ATP2B4, CHRD, CXCL12, DCN, DLC1, ENG, FBLN1, FSTL1, IGFBP5, MMRN2, PODN, PTPRM, RECK, SLIT2, SULF1, THBS1, VASH1, WAS] |
| GO:0051271 | negative regulation of cellular component movement | 0.01 | 0.00 | circulatory system development | 7.58 | 20.00 | [ACKR1, ANGPTL1, ATP2B4, CHRD, CXCL12, DCN, DLC1, ENG, FBLN1, FSTL1, IGFBP5, MMRN2, PODN, PTPRM, RECK, SLIT2, SULF1, THBS1, VASH1, WAS] |
| GO:0040013 | negative regulation of locomotion | 0.03 | 0.00 | circulatory system development | 7.22 | 20.00 | [ACKR1, ANGPTL1, ATP2B4, CHRD, CXCL12, DCN, DLC1, ENG, FBLN1, FSTL1, IGFBP5, MMRN2, PODN, PTPRM, RECK, SLIT2, SULF1, THBS1, VASH1, WAS] |
| GO:0009653 | anatomical structure morphogenesis | 0.00 | 0.00 | circulatory system development | 7.08 | 72.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ANTXR1, ATP2B4, CCN1, CD34, CDH11, CNRIP1, CNTNAP1, COL1A1, COL1A2, COL4A2, COL5A1, COL5A2, COL8A1, CRISPLD2, CSRP1, DCN, DLC1, ECSCR, EFEMP1, ELN, ENG, FBLN1, FBN1, FLI1, FLNA, FLT4, FOXF1, FZD4, GJA5, GLI2, GLI3, HSPB6, IL1R1, ITGA7, ITGA8, ITGAX, ITGB3, JAM3, JCAD, LAMA4, LAMB2, LAMC1, MAP3K3, MCAM, MEOX1, MMP2, MMRN2, MSN, MYL9, MYLK, NGFR, PTGIS, PTPRM, RELT, RHOJ, SERPINF1, SFRP2, SFRP4, SLIT2, SLIT3, SPARC, STAT2, SULF1, TEK, TGFB3, THBS1, THBS2, VASH1] |
| GO:0090132 | epithelium migration | 0.04 | 0.00 | circulatory system development | 6.99 | 20.00 | [ADAM12, ANGPTL1, ATP2B4, DCN, FGFR1, FLI1, FLT4, ITGB3, JCAD, KANK2, MAP3K3, MMRN2, PTPRM, PXDN, RHOJ, SLIT2, SPARC, TEK, THBS1, VASH1] |
| GO:0010631 | epithelial cell migration | 0.04 | 0.00 | circulatory system development | 6.99 | 20.00 | [ADAM12, ANGPTL1, ATP2B4, DCN, FGFR1, FLI1, FLT4, ITGB3, JCAD, KANK2, MAP3K3, MMRN2, PTPRM, PXDN, RHOJ, SLIT2, SPARC, TEK, THBS1, VASH1] |
| GO:0070848 | response to growth factor | 0.00 | 0.00 | growth factor binding | 6.71 | 30.00 | [ADAM12, ATP2B4, CCL5, CCN1, CHRD, COL1A2, COL3A1, DCN, ENG, FERMT2, FGFR1, FLT4, FNDC4, FSTL1, GPRASP1, JCAD, LRRC32, LTBP1, MMRN2, PDE2A, PDGFRB, PXDN, RFTN1, SLA2, SLIT2, SULF1, TGFB1I1, TGFB3, THBS1, TMEM100] |
| GO:0001667 | ameboidal-type cell migration | 0.05 | 0.00 | circulatory system development | 6.71 | 21.00 | [ADAM12, ANGPTL1, ATP2B4, DCN, FGFR1, FLI1, FLT4, ITGB3, JCAD, KANK2, MAP3K3, MMRN2, PTPRM, PXDN, RHOJ, SLIT2, SPARC, SYDE1, TEK, THBS1, VASH1] |
| GO:0071363 | cellular response to growth factor stimulus | 0.00 | 0.00 | growth factor binding | 6.67 | 29.00 | [ADAM12, ATP2B4, CCL5, CCN1, CHRD, COL1A2, COL3A1, DCN, ENG, FERMT2, FGFR1, FLT4, FSTL1, GPRASP1, JCAD, LRRC32, LTBP1, MMRN2, PDE2A, PDGFRB, PXDN, RFTN1, SLA2, SLIT2, SULF1, TGFB1I1, TGFB3, THBS1, TMEM100] |
| GO:2000145 | regulation of cell motility | 0.00 | 0.00 | circulatory system development | 6.48 | 49.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CCL5, CCN1, CHRD, COL1A1, CXCL12, DCN, DLC1, ENG, FBLN1, FGFR1, FLI1, FLNA, FLT4, FSTL1, IGFBP5, ITGAX, ITGB3, JAM2, JAM3, JCAD, MAP3K3, MMRN2, MSN, MYLK, NEXN, PDGFRB, PECAM1, PIK3CD, PODN, PTPRC, PTPRM, RECK, RHOJ, SLIT2, SPARC, SULF1, SYDE1, TACR2, TEK, THBS1, THY1, VASH1, VEGFC, WAS] |
| GO:0022603 | regulation of anatomical structure morphogenesis | 0.00 | 0.00 | circulatory system development | 6.47 | 35.00 | [ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CD34, CDH11, COL4A2, COL5A1, COL5A2, DCN, DLC1, ECSCR, FBLN1, FLI1, FLNA, HSPB6, IL1R1, ITGAX, JCAD, MAP3K3, MMRN2, MSN, NGFR, PTGIS, PTPRM, RHOJ, SERPINF1, SLIT2, SPARC, STAT2, SULF1, TEK, THBS1, THBS2, VASH1] |
| GO:0097435 | supramolecular fiber organization | 0.02 | 0.00 | extracellular matrix organization | 6.40 | 27.00 | [AEBP1, ANGPTL2, ARHGAP25, CCN2, CFL2, CLIP3, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, CRYAB, DES, DLC1, FBLN5, FLNA, HCLS1, LMOD1, LTBP2, MFAP4, MYH11, NCKAP1L, PXDN, SLIT2, TGFB3, TNXB, WAS] |
| GO:0030334 | regulation of cell migration | 0.00 | 0.00 | circulatory system development | 6.38 | 46.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CCL5, CCN1, CHRD, COL1A1, CXCL12, DCN, DLC1, ENG, FGFR1, FLI1, FLNA, FLT4, FSTL1, IGFBP5, ITGAX, ITGB3, JAM2, JAM3, JCAD, MAP3K3, MMRN2, MSN, MYLK, NEXN, PDGFRB, PECAM1, PIK3CD, PODN, PTPRC, PTPRM, RECK, RHOJ, SLIT2, SPARC, SULF1, SYDE1, TEK, THBS1, THY1, VASH1, VEGFC] |
| GO:0051270 | regulation of cellular component movement | 0.00 | 0.00 | circulatory system development | 6.30 | 50.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CCL5, CCN1, CHRD, COL1A1, CXCL12, DCN, DLC1, ENG, FBLN1, FGFR1, FLI1, FLNA, FLT4, FSTL1, GJA5, IGFBP5, ITGAX, ITGB3, JAM2, JAM3, JCAD, MAP3K3, MMRN2, MSN, MYLK, NEXN, PDGFRB, PECAM1, PIK3CD, PODN, PTPRC, PTPRM, RECK, RHOJ, SLIT2, SPARC, SULF1, SYDE1, TACR2, TEK, THBS1, THY1, VASH1, VEGFC, WAS] |
| GO:0016477 | cell migration | 0.00 | 0.00 | circulatory system development | 6.26 | 61.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CCL5, CCN1, CHRD, COL1A1, COL5A1, CXCL12, DCN, DLC1, EDNRB, EMILIN1, ENG, FGFR1, FLI1, FLNA, FLT4, FSTL1, IGFBP5, ITGA11, ITGAL, ITGAX, ITGB3, JAM2, JAM3, JCAD, KANK2, LAMB2, LAMC1, MAP3K3, MEOX1, MMRN2, MSN, MYLK, NCKAP1L, NEXN, OR51E2, PDGFRB, PECAM1, PIK3CD, PODN, PTPRC, PTPRM, PXDN, RECK, RHOJ, SAMD11, SELP, SLIT2, SPARC, SULF1, SYDE1, TEK, THBS1, THY1, VASH1, VCAM1, VEGFC] |
| GO:2000147 | positive regulation of cell motility | 0.01 | 0.00 | circulatory system development | 6.25 | 29.00 | [ADAM12, ADAMTS1, ANGPTL1, CCL5, CCN1, COL1A1, CXCL12, FGFR1, FLI1, FLT4, IGFBP5, ITGAX, ITGB3, JAM2, JCAD, MAP3K3, MYLK, PDGFRB, PECAM1, PIK3CD, PTPRC, RHOJ, SPARC, SYDE1, TACR2, TEK, THBS1, THY1, VEGFC] |
| GO:0030335 | positive regulation of cell migration | 0.02 | 0.00 | circulatory system development | 6.22 | 28.00 | [ADAM12, ADAMTS1, ANGPTL1, CCL5, CCN1, COL1A1, CXCL12, FGFR1, FLI1, FLT4, IGFBP5, ITGAX, ITGB3, JAM2, JCAD, MAP3K3, MYLK, PDGFRB, PECAM1, PIK3CD, PTPRC, RHOJ, SPARC, SYDE1, TEK, THBS1, THY1, VEGFC] |
| GO:0048870 | cell motility | 0.00 | 0.00 | circulatory system development | 6.22 | 65.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CCL5, CCN1, CD34, CHRD, COL1A1, COL5A1, CXCL12, DCN, DLC1, EDNRB, EMILIN1, ENG, FBLN1, FGFR1, FLI1, FLNA, FLT4, FSTL1, IGFBP5, ITGA11, ITGAL, ITGAX, ITGB3, JAM2, JAM3, JCAD, KANK2, LAMB2, LAMC1, MAP3K3, MEOX1, MMRN2, MSN, MYLK, NCKAP1L, NEXN, OR51E2, PDGFRB, PECAM1, PIK3CD, PODN, PTPRC, PTPRM, PXDN, RECK, RHOJ, SAMD11, SELP, SLIT2, SPARC, SULF1, SYDE1, TACR2, TEK, THBS1, THY1, VASH1, VCAM1, VEGFC, WAS] |
| GO:0051272 | positive regulation of cellular component movement | 0.01 | 0.00 | circulatory system development | 6.20 | 29.00 | [ADAM12, ADAMTS1, ANGPTL1, CCL5, CCN1, COL1A1, CXCL12, FGFR1, FLI1, FLT4, IGFBP5, ITGAX, ITGB3, JAM2, JCAD, MAP3K3, MYLK, PDGFRB, PECAM1, PIK3CD, PTPRC, RHOJ, SPARC, SYDE1, TACR2, TEK, THBS1, THY1, VEGFC] |
| GO:0009888 | tissue development | 0.00 | 0.00 | multicellular organism development | 6.19 | 44.00 | [ACKR1, ACTA2, ADAM12, ANGPTL1, CCN1, CD34, CNRIP1, COL1A1, COL4A2, COL5A1, COL5A2, COL8A1, CSRP1, DDR2, EFEMP1, ENG, FLNA, FOXF1, FSTL1, GLI2, ITGA7, ITGA8, ITGAX, ITGB3, KANK2, LAMA4, MMP2, MSN, MYH11, MYL9, MYLK, MYOCD, PECAM1, PTPRC, SFRP2, SFRP4, SLIT2, SVIL, TAGLN, TGFB1I1, TGFB3, TMEM119, WNT2B, ZEB1] |
| GO:0040017 | positive regulation of locomotion | 0.01 | 0.00 | circulatory system development | 6.16 | 30.00 | [ADAM12, ADAMTS1, ANGPTL1, CCL5, CCN1, COL1A1, CXCL12, FGFR1, FLI1, FLT4, IGFBP5, ITGAX, ITGB3, JAM2, JCAD, MAP3K3, MYLK, PDGFRB, PECAM1, PIK3CD, PTPRC, RHOJ, SLIT2, SPARC, SYDE1, TACR2, TEK, THBS1, THY1, VEGFC] |
| GO:0040012 | regulation of locomotion | 0.00 | 0.00 | circulatory system development | 6.11 | 49.00 | [ACKR1, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, CCL5, CCN1, CHRD, COL1A1, CXCL12, DCN, DLC1, ENG, FBLN1, FGFR1, FLI1, FLNA, FLT4, FSTL1, IGFBP5, ITGAX, ITGB3, JAM2, JAM3, JCAD, MAP3K3, MMRN2, MSN, MYLK, NEXN, PDGFRB, PECAM1, PIK3CD, PODN, PTPRC, PTPRM, RECK, RHOJ, SLIT2, SPARC, SULF1, SYDE1, TACR2, TEK, THBS1, THY1, VASH1, VEGFC, WAS] |
| GO:0051241 | negative regulation of multicellular organismal process | 0.00 | 0.00 | circulatory system development | 6.04 | 35.00 | [ADAMTS1, ANGPTL1, ATP2B4, AXL, CD34, CHRD, COL4A2, COL5A1, COL5A2, DCN, ECSCR, EFEMP1, FBN1, FSTL1, HAVCR2, MAFB, MMRN2, MYOCD, NGFR, NLRC3, PLN, POPDC2, PTPRM, SERPINF1, SFRP2, SLIT2, SPARC, SPOCK1, SULF1, TEK, TGFB3, THBS1, THBS2, TIGIT, VASH1] |
| GO:2000026 | regulation of multicellular organismal development | 0.00 | 0.00 | circulatory system development | 5.93 | 54.00 | [ADAM12, ADAMTS1, ANGPTL1, ATP2B4, AXL, CCN1, CD34, CDH11, COL1A1, COL4A2, COL5A1, COL5A2, DCN, DDR2, ECSCR, EFEMP1, FBN1, FGFR1, FLI1, FSTL1, HCLS1, HSPB6, IL1R1, IL2RA, ITGAX, JCAD, MAFB, MAP3K3, MMRN2, MYOCD, NGFR, PTGIS, PTN, PTPRM, RAB7B, RHOH, RHOJ, S1PR1, SERPINF1, SFRP2, SFRP4, SLIT2, SPARC, SPOCK1, SULF1, SYDE1, TEK, TGFB1I1, TGFB3, THBS1, THBS2, TMEM119, VASH1, ZEB1] |
| GO:0071495 | cellular response to endogenous stimulus | 0.00 | 0.00 | growth factor binding | 5.92 | 46.00 | [ADAM12, ATP1A2, ATP2B4, CACNA1H, CACNA2D1, CASQ2, CCL5, CCN1, CDH11, CHRD, COL1A2, COL3A1, ENG, FERMT2, FGFR1, FLNA, FSTL1, GPRASP1, IGFBP5, KANK2, LATS2, LMO2, LRRC32, LTBP1, MRGPRF, MSN, NGFR, OR51E2, PALM, PDE2A, PDGFRB, PXDN, RAB31, RFTN1, SAMD11, SLA2, SLC2A4, SLIT2, SLIT3, SULF1, TGFB1I1, TGFB3, THBS1, TMEM100, VCAM1, VIM] |
| GO:0007275 | multicellular organism development | 0.00 | 0.00 | multicellular organism development | 5.84 | 104.00 | [ACKR1, ACTA2, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, AXL, CCN1, CD34, CDH11, CHRD, CHRDL1, CHRNA3, CLMP, CNRIP1, CNTNAP1, COL1A1, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL8A1, COLEC12, CSRP1, DCN, DDR2, ECSCR, EFEMP1, ELN, EML1, ENG, FBN1, FGFR1, FLI1, FLT4, FOXF1, FOXF2, FSTL1, FZD4, GJA5, GLI2, GLI3, HAND2, HAVCR2, HCLS1, HSPB6, IKZF1, IL1R1, IL2RA, ITGA7, ITGA8, ITGAX, ITGB3, JAM3, JCAD, KANK2, LAMA4, MAB21L2, MAFB, MAP3K3, MCAM, MEOX1, MMP2, MMRN2, MSN, MYH11, MYL9, MYLK, MYOCD, NCKAP1L, NGFR, NOTCH4, PECAM1, PTGIS, PTN, PTPRC, PTPRM, RAB7B, RELT, RHOH, RHOJ, S1PR1, SERPINF1, SFRP2, SFRP4, SLIT2, SLIT3, SPARC, SPART, SPOCK1, SULF1, SVIL, SYDE1, TCF7L1, TEK, TGFB1I1, TGFB3, THBS1, THBS2, TMEM119, VASH1, WNT2B, ZEB1] |
| GO:0007275 | multicellular organism development | 0.00 | 0.00 | circulatory system development | 5.84 | 104.00 | [ACKR1, ACTA2, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, AXL, CCN1, CD34, CDH11, CHRD, CHRDL1, CHRNA3, CLMP, CNRIP1, CNTNAP1, COL1A1, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL8A1, COLEC12, CSRP1, DCN, DDR2, ECSCR, EFEMP1, ELN, EML1, ENG, FBN1, FGFR1, FLI1, FLT4, FOXF1, FOXF2, FSTL1, FZD4, GJA5, GLI2, GLI3, HAND2, HAVCR2, HCLS1, HSPB6, IKZF1, IL1R1, IL2RA, ITGA7, ITGA8, ITGAX, ITGB3, JAM3, JCAD, KANK2, LAMA4, MAB21L2, MAFB, MAP3K3, MCAM, MEOX1, MMP2, MMRN2, MSN, MYH11, MYL9, MYLK, MYOCD, NCKAP1L, NGFR, NOTCH4, PECAM1, PTGIS, PTN, PTPRC, PTPRM, RAB7B, RELT, RHOH, RHOJ, S1PR1, SERPINF1, SFRP2, SFRP4, SLIT2, SLIT3, SPARC, SPART, SPOCK1, SULF1, SVIL, SYDE1, TCF7L1, TEK, TGFB1I1, TGFB3, THBS1, THBS2, TMEM119, VASH1, WNT2B, ZEB1] |
| GO:0007167 | enzyme linked receptor protein signaling pathway | 0.02 | 0.00 | growth factor binding | 5.80 | 32.00 | [ADAM12, ANGPTL1, CCN1, CHRD, COL1A2, COL3A1, DCN, DDR2, EFEMP1, ENG, FERMT2, FGFR1, FLT4, GPRASP1, IGFBP5, JCAD, LRRC32, LTBP1, MMRN2, NPR1, PDGFC, PDGFRB, PXDN, RAB7B, RFTN1, SULF1, TEK, TGFB1I1, TGFB3, THBS1, TMEM100, VEGFC] |
| GO:0048731 | system development | 0.00 | 0.00 | multicellular organism development | 5.65 | 94.00 | [ACKR1, ACTA2, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, AXL, CCN1, CD34, CDH11, CHRD, CHRDL1, CHRNA3, CLMP, CNRIP1, CNTNAP1, COL1A1, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COLEC12, CSRP1, DCN, DDR2, ECSCR, EFEMP1, ELN, EML1, ENG, FBN1, FGFR1, FLI1, FLT4, FOXF1, FOXF2, FSTL1, FZD4, GJA5, GLI2, HAND2, HAVCR2, HCLS1, HSPB6, IKZF1, IL2RA, ITGA8, ITGAX, JAM3, JCAD, KANK2, MAB21L2, MAFB, MAP3K3, MCAM, MEOX1, MMRN2, MSN, MYH11, MYL9, MYLK, MYOCD, NCKAP1L, NGFR, NOTCH4, PECAM1, PTGIS, PTN, PTPRC, PTPRM, RAB7B, RELT, RHOH, RHOJ, S1PR1, SERPINF1, SFRP2, SFRP4, SLIT2, SLIT3, SPARC, SPOCK1, SULF1, SVIL, TCF7L1, TEK, TGFB1I1, TGFB3, THBS1, THBS2, TMEM119, VASH1, WNT2B] |
| GO:0048731 | system development | 0.00 | 0.00 | circulatory system development | 5.65 | 94.00 | [ACKR1, ACTA2, ADAM12, ADAMTS1, ANGPTL1, ATP2B4, AXL, CCN1, CD34, CDH11, CHRD, CHRDL1, CHRNA3, CLMP, CNRIP1, CNTNAP1, COL1A1, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COLEC12, CSRP1, DCN, DDR2, ECSCR, EFEMP1, ELN, EML1, ENG, FBN1, FGFR1, FLI1, FLT4, FOXF1, FOXF2, FSTL1, FZD4, GJA5, GLI2, HAND2, HAVCR2, HCLS1, HSPB6, IKZF1, IL2RA, ITGA8, ITGAX, JAM3, JCAD, KANK2, MAB21L2, MAFB, MAP3K3, MCAM, MEOX1, MMRN2, MSN, MYH11, MYL9, MYLK, MYOCD, NCKAP1L, NGFR, NOTCH4, PECAM1, PTGIS, PTN, PTPRC, PTPRM, RAB7B, RELT, RHOH, RHOJ, S1PR1, SERPINF1, SFRP2, SFRP4, SLIT2, SLIT3, SPARC, SPOCK1, SULF1, SVIL, TCF7L1, TEK, TGFB1I1, TGFB3, THBS1, THBS2, TMEM119, VASH1, WNT2B] |
| GO:0048513 | animal organ development | 0.00 | 0.00 | animal organ development | 5.57 | 59.00 | [ACTA2, ADAM12, ANGPTL1, AXL, CCN1, CD34, CDH11, CHRD, CHRDL1, CNRIP1, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, COLEC12, CSRP1, DDR2, EFEMP1, ELN, EML1, FBN1, FGFR1, FLI1, FOXF1, FOXF2, FSTL1, FZD4, GJA5, GLI2, HAND2, HCLS1, IKZF1, ITGA8, KANK2, MAB21L2, MAFB, MSN, MYH11, MYL9, MYLK, MYOCD, NCKAP1L, NOTCH4, PECAM1, PTPRC, PTPRM, RAB7B, RELT, RHOH, SFRP2, SFRP4, SLIT2, SLIT3, SVIL, TGFB1I1, TGFB3, TMEM119, WNT2B] |
| GO:0048513 | animal organ development | 0.00 | 0.00 | multicellular organism development | 5.57 | 59.00 | [ACTA2, ADAM12, ANGPTL1, AXL, CCN1, CD34, CDH11, CHRD, CHRDL1, CNRIP1, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, COLEC12, CSRP1, DDR2, EFEMP1, ELN, EML1, FBN1, FGFR1, FLI1, FOXF1, FOXF2, FSTL1, FZD4, GJA5, GLI2, HAND2, HCLS1, IKZF1, ITGA8, KANK2, MAB21L2, MAFB, MSN, MYH11, MYL9, MYLK, MYOCD, NCKAP1L, NOTCH4, PECAM1, PTPRC, PTPRM, RAB7B, RELT, RHOH, SFRP2, SFRP4, SLIT2, SLIT3, SVIL, TGFB1I1, TGFB3, TMEM119, WNT2B] |
| GO:0048513 | animal organ development | 0.00 | 0.00 | circulatory system development | 5.57 | 59.00 | [ACTA2, ADAM12, ANGPTL1, AXL, CCN1, CD34, CDH11, CHRD, CHRDL1, CNRIP1, COL1A1, COL1A2, COL3A1, COL5A1, COL5A2, COLEC12, CSRP1, DDR2, EFEMP1, ELN, EML1, FBN1, FGFR1, FLI1, FOXF1, FOXF2, FSTL1, FZD4, GJA5, GLI2, HAND2, HCLS1, IKZF1, ITGA8, KANK2, MAB21L2, MAFB, MSN, MYH11, MYL9, MYLK, MYOCD, NCKAP1L, NOTCH4, PECAM1, PTPRC, PTPRM, RAB7B, RELT, RHOH, SFRP2, SFRP4, SLIT2, SLIT3, SVIL, TGFB1I1, TGFB3, TMEM119, WNT2B] |
| GO:0050793 | regulation of developmental process | 0.00 | 0.00 | multicellular organism development | 5.30 | 66.00 | [ADAM12, ADAMTS1, ANGPTL1, ATP2B4, AXL, CCN1, CCN2, CD34, CDH11, CHRD, COL1A1, COL4A2, COL5A1, COL5A2, CSRP1, DCN, DDR2, DLC1, ECSCR, EFEMP1, FBLN1, FBN1, FGFR1, FLI1, FLNA, FSTL1, HCLS1, HSPB6, IL1R1, IL2RA, ITGAX, ITGB3, JCAD, LTBP2, MAFB, MAP3K3, MMRN2, MSN, MYOCD, NGFR, NUAK1, PTGIS, PTN, PTPRM, RAB7B, RBPMS2, RHOH, RHOJ, S1PR1, SERPINF1, SFRP2, SFRP4, SLIT2, SPARC, SPOCK1, STAT2, SULF1, SYDE1, TEK, TGFB1I1, TGFB3, THBS1, THBS2, TMEM119, VASH1, ZEB1] |
| GO:0050793 | regulation of developmental process | 0.00 | 0.00 | circulatory system development | 5.30 | 66.00 | [ADAM12, ADAMTS1, ANGPTL1, ATP2B4, AXL, CCN1, CCN2, CD34, CDH11, CHRD, COL1A1, COL4A2, COL5A1, COL5A2, CSRP1, DCN, DDR2, DLC1, ECSCR, EFEMP1, FBLN1, FBN1, FGFR1, FLI1, FLNA, FSTL1, HCLS1, HSPB6, IL1R1, IL2RA, ITGAX, ITGB3, JCAD, LTBP2, MAFB, MAP3K3, MMRN2, MSN, MYOCD, NGFR, NUAK1, PTGIS, PTN, PTPRM, RAB7B, RBPMS2, RHOH, RHOJ, S1PR1, SERPINF1, SFRP2, SFRP4, SLIT2, SPARC, SPOCK1, STAT2, SULF1, SYDE1, TEK, TGFB1I1, TGFB3, THBS1, THBS2, TMEM119, VASH1, ZEB1] |
| GO:0002682 | regulation of immune system process | 0.02 | 0.00 | regulation of immune system process | 5.06 | 43.00 | [A2M, AXL, C3, C4B, CCL5, CDH11, CFH, COL3A1, COLEC12, CXCL12, FBN1, FERMT2, FLI1, FSTL1, HAVCR2, HCLS1, IKZF1, IL1R1, IL2RA, JAM2, JAM3, KANK2, LCP2, MAFB, MSN, NCKAP1L, PIK3CD, PTPRC, RAB7B, RASGRP1, RFTN1, RHOH, S1PR1, SERPING1, SLIT2, TGFB3, THBS1, THY1, TIGIT, TNFSF13B, VCAM1, VEGFC, WAS] |
| GO:0030154 | cell differentiation | 0.00 | 0.00 | multicellular organism development | 4.87 | 64.00 | [ACTA2, ADAM12, ANGPTL1, ANTXR1, ATP2B4, AXL, CCN1, CCN2, CD34, CHRD, CNTNAP1, COL1A1, COL4A2, COL5A1, COL5A2, COL8A1, CSRP1, DDR2, DZIP1, EFEMP1, ENG, FBLN1, FBN1, FGFR1, FLI1, FLNA, FSTL1, GALNT15, HCLS1, IKZF1, ITGA7, ITGA8, ITGB3, LAMA4, LAMB2, LAMC1, LTBP2, MAFB, MMP2, MSN, MYH11, MYOCD, NCKAP1L, OR51E2, PECAM1, PTN, PTPRC, PTPRM, RAB7B, RBPMS2, RHOH, SERPINF1, SFRP2, SFRP4, SLIT2, SLIT3, SPOCK1, TAGLN, TEK, TGFB1I1, TGFB3, TMEM119, WNT2B, ZEB1] |
| GO:0030154 | cell differentiation | 0.00 | 0.00 | circulatory system development | 4.87 | 64.00 | [ACTA2, ADAM12, ANGPTL1, ANTXR1, ATP2B4, AXL, CCN1, CCN2, CD34, CHRD, CNTNAP1, COL1A1, COL4A2, COL5A1, COL5A2, COL8A1, CSRP1, DDR2, DZIP1, EFEMP1, ENG, FBLN1, FBN1, FGFR1, FLI1, FLNA, FSTL1, GALNT15, HCLS1, IKZF1, ITGA7, ITGA8, ITGB3, LAMA4, LAMB2, LAMC1, LTBP2, MAFB, MMP2, MSN, MYH11, MYOCD, NCKAP1L, OR51E2, PECAM1, PTN, PTPRC, PTPRM, RAB7B, RBPMS2, RHOH, SERPINF1, SFRP2, SFRP4, SLIT2, SLIT3, SPOCK1, TAGLN, TEK, TGFB1I1, TGFB3, TMEM119, WNT2B, ZEB1] |
| GO:0051239 | regulation of multicellular organismal process | 0.00 | 0.00 | circulatory system development | 4.87 | 77.00 | [ADAM12, ADAMTS1, ANGPTL1, ATP2B4, AXL, C3, CACNA2D1, CASQ2, CCN1, CD34, CDH11, CHRD, COL1A1, COL4A2, COL5A1, COL5A2, CSRP1, DCN, DDR2, ECSCR, EFEMP1, ERG, FBN1, FGFR1, FLI1, FLT4, FSTL1, GJA5, HAND2, HAVCR2, HCLS1, HSPB6, IL1R1, IL2RA, ITGAX, ITGB3, JCAD, KCND3, LMCD1, LRRC32, LTBP1, MAFB, MAP3K3, MEOX1, MMRN2, MYOCD, NGFR, NLRC3, PLN, POPDC2, PTGIS, PTN, PTPRC, PTPRM, RAB7B, RASGRP1, RHOH, RHOJ, S1PR1, SCN1B, SERPINF1, SFRP2, SFRP4, SLIT2, SPARC, SPOCK1, SULF1, SYDE1, TEK, TGFB1I1, TGFB3, THBS1, THBS2, TIGIT, TMEM119, VASH1, ZEB1] |
| GO:0071310 | cellular response to organic substance | 0.00 | 0.00 | growth factor binding | 4.81 | 66.00 | [ADAM12, ADCY5, ATP1A2, ATP2B4, AXL, CACNA1H, CACNA2D1, CASQ2, CCL5, CCN1, CCR5, CDH11, CHRD, COL1A2, COL3A1, COLEC12, CXCL12, DCN, ENG, FERMT2, FGFR1, FLNA, FLT4, FSTL1, FZD4, GPRASP1, HCLS1, HSPB8, IGFBP5, IL1R1, IL2RA, IL2RB, JCAD, KANK2, LATS2, LMO2, LRRC32, LTBP1, MMRN2, MRGPRF, MSN, MYLK, NGFR, OR51E2, OSMR, PALM, PDE2A, PDGFRB, POPDC2, PTGIS, PXDN, RAB31, RFTN1, SAMD11, SLA2, SLC2A4, SLIT2, SLIT3, STAT2, SULF1, TGFB1I1, TGFB3, THBS1, TMEM100, VCAM1, VIM] |
| GO:0007166 | cell surface receptor signaling pathway | 0.00 | 0.00 | growth factor binding | 4.72 | 72.00 | [ADAM12, ADGRA2, ANGPTL1, AXL, CCL5, CCN1, CCR5, CDH11, CHRD, CHRNA3, COL1A1, COL1A2, COL3A1, CXCL12, DACT3, DCN, DDR2, DIXDC1, EFEMP1, ENG, FERMT2, FGFR1, FLNA, FLT4, FSTL1, FZD4, GLI2, GLI3, GPRASP1, IGFBP5, IKZF1, IL10RA, IL1R1, IL2RA, IL2RB, ITGA11, ITGB3, JCAD, LATS2, LCP2, LRRC32, LTBP1, MAP3K12, MMRN2, MYO9B, NCKAP1L, NPR1, OSMR, PDGFC, PDGFRB, PEA15, POPDC2, PTN, PTPRC, PXDN, RAB7B, RFTN1, SFRP2, SFRP4, SLIT2, SLIT3, STAT2, SULF1, TEK, TGFB1I1, TGFB3, THBS1, THY1, TMEM100, TNFSF12, VEGFC, WNT2B] |
| GO:0032879 | regulation of localization | 0.00 | 0.00 | circulatory system development | 4.41 | 83.00 | [ACKR1, ADAM12, ADAMTS1, ADCY5, ANGPTL1, ATP2B4, AXL, C3, C4B, CACNA2D1, CASQ2, CCL5, CCN1, CCR5, CD34, CDH11, CFH, CHRD, CLIP3, CNPY4, COL1A1, CRYAB, CSRP1, CXCL12, DCN, DLC1, ENG, ERG, FBLN1, FGFR1, FHL1, FLI1, FLNA, FLT4, FSTL1, GJA5, HAVCR2, HCLS1, IGFBP5, IL2RB, ITGAX, ITGB3, JAM2, JAM3, JCAD, JPH2, MAP3K3, MEOX1, MMRN2, MSN, MYLK, NEXN, NGFR, NLGN2, PDGFRB, PEA15, PECAM1, PIK3CD, PLN, PODN, POPDC2, PTPRC, PTPRM, RAB7B, RASGRP1, RECK, RHOJ, SCN1B, SFRP4, SLA, SLIT2, SPARC, STON1, SULF1, SYDE1, TACR2, TEK, TGFB3, THBS1, THY1, VASH1, VEGFC, WAS] |
| GO:0010033 | response to organic substance | 0.01 | 0.00 | growth factor binding | 4.36 | 72.00 | [ADAM12, ADCY5, ATP1A2, ATP2B4, AXL, C4B, CACNA1H, CACNA2D1, CASQ2, CCL5, CCN1, CCR5, CDH11, CHRD, CNRIP1, COL1A2, COL3A1, COLEC12, CSRP1, CXCL12, DCN, DNAJB5, ENG, FERMT2, FGFR1, FLNA, FLT4, FNDC4, FSTL1, FZD4, GPRASP1, HCLS1, HSPB8, IGFBP5, IL1R1, IL2RA, IL2RB, JCAD, KANK2, KCNMA1, LATS2, LMO2, LRRC32, LTBP1, MMRN2, MRGPRF, MSN, MYLK, NGFR, OR51E2, OSMR, PALM, PDE2A, PDGFRB, POPDC2, PTGIS, PXDN, RAB31, RFTN1, SAMD11, SLA2, SLC2A4, SLIT2, SLIT3, STAT2, SULF1, TGFB1I1, TGFB3, THBS1, TMEM100, VCAM1, VIM] |

**Table S8.** The KEGG pathway analysis of the mRNAsi-related lncRNA signature

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **GO ID** | **GOTerm** | **Corrected Term P Value** | **Corrected Group P Value** | **GO Groups** | **% Associated Genes** | **No. Genes** | **Associated Genes Found** |
| KEGG:04530 | Tight junction | 0.03 | 0.01 | Tight junction | 5.92 | 10.00 | [AMOTL1, HCLS1, JAM2, JAM3, MPDZ, MSN, MYH11, MYL9, SYNPO, WAS] |
| KEGG:05200 | Pathways in cancer | 0.00 | 0.00 | Pathways in cancer | 4.90 | 26.00 | [ADCY5, COL4A2, CXCL12, EDNRB, FGFR1, FLT4, FZD4, GLI2, GLI3, GNG11, IL2RA, IL2RB, LAMA4, LAMB2, LAMC1, MMP2, NOTCH4, PDGFRB, PIK3CD, RASGRP1, STAT2, STAT4, TCF7L1, TGFB3, VEGFC, WNT2B] |
| KEGG:04145 | Phagosome | 0.04 | 0.01 | Phagosome | 5.92 | 9.00 | [C1R, C3, COLEC12, FCGR3A, ITGB3, MRC2, RAB7B, THBS1, THBS2] |
| KEGG:05205 | Proteoglycans in cancer | 0.00 | 0.00 | Proteoglycans in cancer | 8.82 | 18.00 | [COL1A1, COL1A2, DCN, FGFR1, FLNA, FLNC, FZD4, HCLS1, ITGB3, ITPR1, LUM, MMP2, MRAS, MSN, PIK3CD, PPP1R12B, THBS1, WNT2B] |
| KEGG:05215 | Prostate cancer | 0.03 | 0.01 | Prostate cancer | 7.22 | 7.00 | [ERG, FGFR1, PDGFC, PDGFRB, PIK3CD, TCF7L1, ZEB1] |
| KEGG:05323 | Rheumatoid arthritis | 0.03 | 0.01 | Rheumatoid arthritis | 7.53 | 7.00 | [CCL5, CD86, CXCL12, ITGAL, TEK, TGFB3, TNFSF13B] |
| KEGG:04350 | TGF-beta signaling pathway | 0.01 | 0.00 | TGF-beta signaling pathway | 8.51 | 8.00 | [CHRD, DCN, FBN1, GREM2, LTBP1, RGMA, TGFB3, THBS1] |
| KEGG:04514 | Cell adhesion molecules (CAMs) | 0.00 | 0.00 | Cell adhesion molecules (CAMs) | 10.20 | 15.00 | [CD34, CD86, CNTNAP1, ITGA8, ITGAL, JAM2, JAM3, NLGN2, PECAM1, PTPRC, PTPRM, SELP, TIGIT, VCAM1, VCAN] |
| KEGG:04611 | Platelet activation | 0.00 | 0.00 | Platelet activation | 10.48 | 13.00 | [ADCY5, COL1A1, COL1A2, COL3A1, GUCY1A1, GUCY1B1, ITGB3, ITPR1, LCP2, MYLK, PIK3CD, PTGS1, RASGRP1] |
| KEGG:04666 | Fc gamma R-mediated phagocytosis | 0.03 | 0.01 | Fc gamma R-mediated phagocytosis | 7.53 | 7.00 | [CFL2, DOCK2, FCGR3A, PIK3CD, PLPP1, PTPRC, WAS] |
| KEGG:04670 | Leukocyte transendothelial migration | 0.00 | 0.00 | Leukocyte transendothelial migration | 10.71 | 12.00 | [CXCL12, ITGAL, JAM2, JAM3, MMP2, MSN, MYL9, PECAM1, PIK3CD, RHOH, THY1, VCAM1] |
| KEGG:04810 | Regulation of actin cytoskeleton | 0.00 | 0.00 | Regulation of actin cytoskeleton | 8.92 | 19.00 | [ARHGEF6, CFL2, CXCL12, FGFR1, ITGA11, ITGA7, ITGA8, ITGAL, ITGAX, ITGB3, MRAS, MSN, MYL9, MYLK, NCKAP1L, PDGFC, PDGFRB, PIK3CD, PPP1R12B] |
| KEGG:04974 | Protein digestion and absorption | 0.00 | 0.00 | Protein digestion and absorption | 11.58 | 11.00 | [ATP1A2, COL14A1, COL18A1, COL1A1, COL1A2, COL3A1, COL4A2, COL5A1, COL5A2, COL6A3, ELN] |
| KEGG:05144 | Malaria | 0.00 | 0.00 | Malaria | 18.00 | 9.00 | [ACKR1, GYPC, ITGAL, PECAM1, SELP, TGFB3, THBS1, THBS2, VCAM1] |
| KEGG:04010 | MAPK signaling pathway | 0.00 | 0.00 | PI3K-Akt signaling pathway | 5.76 | 17.00 | [CACNA1H, CACNA2D1, FGFR1, FLNA, FLNC, FLT4, IL1R1, MAP3K12, MAP3K3, MRAS, NGFR, PDGFC, PDGFRB, RASGRP1, TEK, TGFB3, VEGFC] |
| KEGG:04015 | Rap1 signaling pathway | 0.00 | 0.00 | PI3K-Akt signaling pathway | 7.14 | 15.00 | [ADCY5, FGFR1, FLT4, GNAO1, ITGAL, ITGB3, LCP2, MRAS, NGFR, PDGFC, PDGFRB, PIK3CD, TEK, THBS1, VEGFC] |
| KEGG:04151 | PI3K-Akt signaling pathway | 0.00 | 0.00 | PI3K-Akt signaling pathway | 7.34 | 26.00 | [COL1A1, COL1A2, COL4A2, COL6A3, FGFR1, FLT4, GNG11, IL2RA, IL2RB, ITGA11, ITGA7, ITGA8, ITGB3, LAMA4, LAMB2, LAMC1, NGFR, OSMR, PDGFC, PDGFRB, PIK3CD, TEK, THBS1, THBS2, TNXB, VEGFC] |
| KEGG:05410 | Hypertrophic cardiomyopathy (HCM) | 0.00 | 0.00 | Dilated cardiomyopathy (DCM) | 10.00 | 9.00 | [CACNA2D1, DES, ITGA11, ITGA7, ITGA8, ITGB3, SGCA, TGFB3, TPM2] |
| KEGG:05412 | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 0.00 | 0.00 | Dilated cardiomyopathy (DCM) | 10.39 | 8.00 | [CACNA2D1, DES, ITGA11, ITGA7, ITGA8, ITGB3, SGCA, TCF7L1] |
| KEGG:05414 | Dilated cardiomyopathy (DCM) | 0.00 | 0.00 | Dilated cardiomyopathy (DCM) | 11.46 | 11.00 | [ADCY5, CACNA2D1, DES, ITGA11, ITGA7, ITGA8, ITGB3, PLN, SGCA, TGFB3, TPM2] |
| KEGG:04610 | Complement and coagulation cascades | 0.00 | 0.00 | Complement and coagulation cascades | 10.59 | 9.00 | [A2M, C1R, C1S, C3, C4B, CFH, ITGAX, SERPING1, THBD] |
| KEGG:05133 | Pertussis | 0.03 | 0.00 | Complement and coagulation cascades | 7.89 | 6.00 | [C1R, C1S, C3, C4B, CFL2, SERPING1] |
| KEGG:05150 | Staphylococcus aureus infection | 0.01 | 0.00 | Complement and coagulation cascades | 8.33 | 8.00 | [C1R, C1S, C3, C4B, CFH, FCGR3A, ITGAL, SELP] |
| KEGG:04512 | ECM-receptor interaction | 0.00 | 0.00 | ECM-receptor interaction | 15.91 | 14.00 | [COL1A1, COL1A2, COL4A2, COL6A3, ITGA11, ITGA7, ITGA8, ITGB3, LAMA4, LAMB2, LAMC1, THBS1, THBS2, TNXB] |
| KEGG:04926 | Relaxin signaling pathway | 0.00 | 0.00 | ECM-receptor interaction | 9.30 | 12.00 | [ACTA2, ADCY5, COL1A1, COL1A2, COL3A1, COL4A2, EDNRB, GNAO1, GNG11, MMP2, PIK3CD, VEGFC] |
| KEGG:04933 | AGE-RAGE signaling pathway in diabetic complications | 0.00 | 0.00 | ECM-receptor interaction | 10.00 | 10.00 | [COL1A1, COL1A2, COL3A1, COL4A2, MMP2, PIK3CD, TGFB3, THBD, VCAM1, VEGFC] |
| KEGG:05146 | Amoebiasis | 0.00 | 0.00 | ECM-receptor interaction | 10.78 | 11.00 | [COL1A1, COL1A2, COL3A1, COL4A2, IL1R1, LAMA4, LAMB2, LAMC1, PIK3CD, RAB7B, TGFB3] |
| KEGG:04015 | Rap1 signaling pathway | 0.00 | 0.00 | Focal adhesion | 7.14 | 15.00 | [ADCY5, FGFR1, FLT4, GNAO1, ITGAL, ITGB3, LCP2, MRAS, NGFR, PDGFC, PDGFRB, PIK3CD, TEK, THBS1, VEGFC] |
| KEGG:04151 | PI3K-Akt signaling pathway | 0.00 | 0.00 | Focal adhesion | 7.34 | 26.00 | [COL1A1, COL1A2, COL4A2, COL6A3, FGFR1, FLT4, GNG11, IL2RA, IL2RB, ITGA11, ITGA7, ITGA8, ITGB3, LAMA4, LAMB2, LAMC1, NGFR, OSMR, PDGFC, PDGFRB, PIK3CD, TEK, THBS1, THBS2, TNXB, VEGFC] |
| KEGG:04510 | Focal adhesion | 0.00 | 0.00 | Focal adhesion | 12.06 | 24.00 | [COL1A1, COL1A2, COL4A2, COL6A3, FLNA, FLNC, FLT4, ITGA11, ITGA7, ITGA8, ITGB3, LAMA4, LAMB2, LAMC1, MYL9, MYLK, PDGFC, PDGFRB, PIK3CD, PPP1R12B, THBS1, THBS2, TNXB, VEGFC] |
| KEGG:04512 | ECM-receptor interaction | 0.00 | 0.00 | Focal adhesion | 15.91 | 14.00 | [COL1A1, COL1A2, COL4A2, COL6A3, ITGA11, ITGA7, ITGA8, ITGB3, LAMA4, LAMB2, LAMC1, THBS1, THBS2, TNXB] |
| KEGG:05146 | Amoebiasis | 0.00 | 0.00 | Focal adhesion | 10.78 | 11.00 | [COL1A1, COL1A2, COL3A1, COL4A2, IL1R1, LAMA4, LAMB2, LAMC1, PIK3CD, RAB7B, TGFB3] |
| KEGG:05165 | Human papillomavirus infection | 0.00 | 0.00 | Focal adhesion | 6.36 | 21.00 | [COL1A1, COL1A2, COL4A2, COL6A3, FZD4, ITGA11, ITGA7, ITGA8, ITGB3, LAMA4, LAMB2, LAMC1, NOTCH4, PDGFRB, PIK3CD, STAT2, TCF7L1, THBS1, THBS2, TNXB, WNT2B] |
| KEGG:04022 | cGMP-PKG signaling pathway | 0.00 | 0.00 | Vascular smooth muscle contraction | 8.98 | 15.00 | [ADCY5, ATP1A2, ATP2B4, EDNRB, GUCY1A1, GUCY1B1, ITPR1, KCNMA1, KCNMB1, MRVI1, MYL9, MYLK, NPR1, PDE2A, PLN] |
| KEGG:04270 | Vascular smooth muscle contraction | 0.00 | 0.00 | Vascular smooth muscle contraction | 12.12 | 16.00 | [ACTA2, ACTG2, ADCY5, CALD1, GUCY1A1, GUCY1B1, ITPR1, KCNMA1, KCNMB1, MRVI1, MYH11, MYL9, MYLK, NPR1, PPP1R12B, PPP1R14A] |
| KEGG:04713 | Circadian entrainment | 0.03 | 0.00 | Vascular smooth muscle contraction | 7.22 | 7.00 | [ADCY5, CACNA1H, GNAO1, GNG11, GUCY1A1, GUCY1B1, ITPR1] |
| KEGG:04921 | Oxytocin signaling pathway | 0.02 | 0.00 | Vascular smooth muscle contraction | 6.54 | 10.00 | [ADCY5, CACNA2D1, GNAO1, GUCY1A1, GUCY1B1, ITPR1, MYL9, MYLK, NPR1, PPP1R12B] |
| KEGG:04924 | Renin secretion | 0.01 | 0.00 | Vascular smooth muscle contraction | 10.14 | 7.00 | [ADCY5, GUCY1A1, GUCY1B1, ITPR1, KCNMA1, NPR1, PDE1A] |
| KEGG:04925 | Aldosterone synthesis and secretion | 0.03 | 0.00 | Vascular smooth muscle contraction | 7.14 | 7.00 | [ADCY5, ATP1A2, ATP2B4, CACNA1H, ITPR1, NPR1, PDE2A] |
| KEGG:04970 | Salivary secretion | 0.02 | 0.00 | Vascular smooth muscle contraction | 7.78 | 7.00 | [ADCY5, ATP1A2, ATP2B4, GUCY1A1, GUCY1B1, ITPR1, KCNMA1] |