

| GeneName | Probe Name | CORTEX | | | HIPPOCAMPUS | | |
|---------------|---------------|--------|-------|-------|-------------|-------|-------|
| | | M4 | M6 | M9 | M4 | M6 | M9 |
| Dhx36 | A_51_P148959 | -1.60 | -1.54 | -1.75 | -1.70 | -1.45 | -1.64 |
| Gmps | A_55_P2185323 | -1.86 | -2.26 | -2.08 | -2.19 | -1.67 | -2.79 |
| Rec8 | A_51_P246677 | -1.97 | -2.38 | -2.45 | -1.95 | -2.14 | -2.05 |
| 5430435G22Rik | A_55_P2082989 | 2.00 | 1.65 | 4.41 | 2.88 | 2.61 | 4.12 |
| 5730416F02Rik | A_52_P110070 | 2.03 | 1.83 | 1.77 | 1.90 | 1.51 | 1.81 |
| Abi3 | A_51_P185906 | 2.32 | 2.75 | 3.23 | 2.65 | 2.95 | 3.09 |
| Adora3 | A_55_P1972605 | 1.66 | 1.89 | 1.47 | 2.19 | 1.95 | 2.60 |
| Agpat2 | A_55_P1970810 | 1.45 | 1.60 | 1.47 | 1.48 | 1.62 | 1.94 |
| AI646519 | A_55_P2359610 | 1.71 | 1.66 | 1.78 | 1.92 | 1.61 | 2.07 |
| Aif1 | A_51_P400543 | 2.15 | 2.44 | 2.18 | 2.46 | 2.28 | 2.91 |
| Ang | A_51_P391159 | 1.53 | 1.45 | 1.74 | 1.98 | 2.27 | 1.49 |
| Anxa3 | A_55_P2056325 | 1.83 | 1.63 | 1.75 | 1.80 | 1.57 | 2.43 |
| Apbb1ip | A_55_P1961009 | 1.83 | 1.79 | 2.11 | 2.72 | 2.71 | 2.91 |
| Arhgap9 | A_55_P2091551 | 2.00 | 2.52 | 2.14 | 2.37 | 2.70 | 3.27 |
| Arpc1b | A_55_P2023076 | 1.78 | 2.07 | 2.57 | 1.88 | 1.55 | 3.86 |
| Asb10 | A_55_P2044710 | 2.25 | 1.52 | 2.80 | 2.64 | 4.01 | 2.32 |
| Aspg | A_52_P338956 | 2.00 | 2.96 | 2.85 | 3.25 | 4.34 | 5.23 |
| Atf3 | A_52_P452689 | 2.24 | 2.62 | 2.08 | 1.81 | 3.84 | 2.45 |
| B2m | A_51_P129012 | 1.74 | 1.63 | 2.54 | 1.78 | 2.45 | 2.45 |
| B2m | A_51_P129012 | 1.66 | 1.66 | 2.74 | 1.64 | 2.75 | 2.53 |
| Bcl3 | A_55_P2066116 | 2.10 | 3.05 | 3.70 | 2.87 | 3.73 | 5.85 |
| Bcl2a1c | A_52_P299771 | 2.78 | 2.48 | 3.21 | 2.43 | 4.43 | 3.64 |
| Bst2 | A_51_P169693 | 2.45 | 2.47 | 3.59 | 1.59 | 2.67 | 3.92 |
| C1qa | A_51_P181451 | 2.65 | 3.25 | 3.98 | 3.02 | 3.84 | 4.68 |
| C1qb | A_51_P351860 | 2.32 | 2.95 | 3.20 | 2.63 | 5.14 | 2.92 |
| C1qc | A_51_P102789 | 2.83 | 2.00 | 5.67 | 3.03 | 4.58 | 4.20 |
| C1qc | A_51_P102789 | 2.60 | 2.12 | 5.66 | 2.86 | 4.22 | 4.16 |
| C1qc | A_51_P102789 | 2.56 | 2.07 | 5.52 | 2.82 | 4.47 | 4.27 |
| C1qc | A_51_P102789 | 2.53 | 2.30 | 5.50 | 2.88 | 4.52 | 4.74 |
| C1qc | A_51_P102789 | 2.60 | 2.21 | 5.66 | 2.85 | 4.13 | 4.63 |
| C1qc | A_51_P102789 | 2.52 | 2.22 | 5.59 | 3.06 | 4.00 | 4.52 |
| C1qc | A_51_P102789 | 2.55 | 2.32 | 5.58 | 2.91 | 4.12 | 4.51 |
| C1qc | A_51_P102789 | 2.53 | 2.18 | 5.47 | 2.99 | 3.97 | 4.29 |
| C1qc | A_51_P102789 | 2.58 | 1.97 | 5.75 | 2.97 | 5.40 | 4.12 |
| C1qc | A_51_P102789 | 2.64 | 2.03 | 5.53 | 2.89 | 4.20 | 4.12 |
| C3ar1 | A_51_P282557 | 2.15 | 1.96 | 2.88 | 2.13 | 5.69 | 2.96 |
| Capg | A_55_P1998631 | 2.57 | 2.15 | 3.66 | 2.78 | 2.71 | 3.85 |
| Ccl4 | A_51_P509573 | 8.97 | 7.31 | 9.91 | 12.71 | 10.67 | 11.32 |
| Ccl6 | A_51_P460954 | 12.44 | 9.41 | 13.37 | 13.66 | 10.81 | 9.74 |
| Cd9 | A_51_P320852 | 1.79 | 1.83 | 2.41 | 1.69 | 1.59 | 2.58 |
| Cd14 | A_51_P172853 | 2.74 | 3.20 | 3.82 | 2.57 | 3.63 | 3.30 |
| Cd37 | A_55_P2118570 | 2.31 | 2.09 | 3.18 | 2.16 | 2.71 | 2.74 |
| Cd37 | A_55_P2174490 | 1.98 | 1.96 | 2.90 | 1.90 | 4.28 | 2.09 |
| Cd48 | A_55_P2185605 | 2.21 | 2.74 | 2.46 | 2.45 | 3.43 | 3.74 |

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|---------------|---------------|-------|-------|--------|--------|--------|--------|
| Cd48 | A_55_P2132549 | 1.86 | 2.37 | 3.00 | 2.10 | 3.46 | 2.79 |
| Cd52 | A_51_P151126 | 5.00 | 5.76 | 9.37 | 6.84 | 6.34 | 9.90 |
| Cd68 | A_55_P1961943 | 5.21 | 3.01 | 10.46 | 5.78 | 6.19 | 7.20 |
| Cd84 | A_55_P2054445 | 3.10 | 3.08 | 2.79 | 2.89 | 2.88 | 4.31 |
| Cd86 | A_55_P1971951 | 1.78 | 2.31 | 2.50 | 2.51 | 3.05 | 3.51 |
| Cd300lf | A_55_P2081164 | 2.34 | 4.71 | 3.00 | 2.51 | 5.35 | 3.80 |
| Cd300lf | A_52_P422494 | 2.27 | 3.84 | 2.72 | 2.70 | 4.80 | 3.18 |
| Cebpa | A_52_P168567 | 2.09 | 1.66 | 2.66 | 1.90 | 2.08 | 1.87 |
| Ch25h | A_55_P2008987 | 2.58 | 2.61 | 4.10 | 3.68 | 3.65 | 4.68 |
| Clec7a | A_51_P246653 | 12.10 | 34.95 | 30.86 | 15.93 | 32.21 | 32.47 |
| Col16a1 | A_55_P2124751 | 1.21 | 1.95 | 1.36 | 2.03 | 1.56 | 2.09 |
| Col16a1 | A_55_P2056739 | 1.63 | 2.18 | 1.79 | 2.07 | 2.07 | 1.88 |
| Csf1 | A_51_P195506 | 1.58 | 1.63 | 1.86 | 1.44 | 1.69 | 2.16 |
| Csf1 | A_51_P195506 | 1.47 | 1.46 | 1.93 | 1.48 | 1.56 | 2.01 |
| Csf1 | A_51_P195506 | 1.54 | 1.44 | 1.72 | 1.42 | 1.62 | 1.99 |
| Csf1 | A_51_P195506 | 1.48 | 1.62 | 1.95 | 1.56 | 1.39 | 2.17 |
| Csf1 | A_51_P195506 | 1.55 | 1.61 | 1.97 | 1.70 | 1.40 | 2.22 |
| Csf1 | A_51_P195506 | 1.40 | 1.50 | 1.83 | 1.38 | 1.56 | 2.02 |
| Csf1 | A_51_P195506 | 1.44 | 1.73 | 1.82 | 1.35 | 1.53 | 2.50 |
| Csf1 | A_51_P195506 | 1.47 | 1.54 | 1.76 | 1.49 | 1.50 | 2.09 |
| Csf1 | A_51_P195506 | 1.46 | 1.63 | 1.81 | 1.51 | 1.42 | 2.24 |
| Csf1 | A_51_P195506 | 1.52 | 1.55 | 1.87 | 1.48 | 1.48 | 2.22 |
| Csf1r | A_52_P602091 | 2.17 | 2.47 | 1.68 | 1.84 | 2.40 | 2.07 |
| Csf1r | A_55_P2025078 | 1.83 | 1.88 | 1.89 | 2.19 | 1.70 | 2.51 |
| Csf1r | A_55_P2025073 | 1.42 | 1.40 | 1.26 | 1.30 | 1.71 | 1.03 |
| Csf2rb | A_52_P52618 | 2.12 | 2.07 | 2.26 | 2.02 | 2.41 | 3.06 |
| Cst7 | A_51_P137419 | 74.71 | 63.46 | 140.15 | 100.48 | 118.36 | 145.84 |
| Ctsa | A_55_P1955841 | 1.50 | 1.69 | 1.74 | 1.75 | 1.20 | 2.07 |
| Ctsc | A_52_P195839 | 1.95 | 1.94 | 1.96 | 1.77 | 2.07 | 2.40 |
| Ctsd | A_51_P384629 | 3.04 | 3.02 | 3.79 | 3.23 | 3.08 | 3.48 |
| Ctsd | A_65_P13209 | 2.97 | 4.44 | 2.41 | 2.83 | 3.72 | 3.14 |
| Ctsh | A_52_P51078 | 1.85 | 1.52 | 1.66 | 2.01 | 1.94 | 2.11 |
| Ctss | A_55_P2024888 | 3.03 | 3.32 | 2.88 | 3.40 | 3.75 | 4.04 |
| Ctsz | A_51_P256202 | 2.71 | 3.02 | 3.85 | 3.02 | 3.78 | 4.33 |
| Cx3cr1 | A_52_P99810 | 1.99 | 1.01 | 3.01 | 2.10 | 2.64 | 2.00 |
| Cx3cr1 | A_55_P2007964 | 1.98 | 1.64 | 1.61 | 2.16 | 2.03 | 2.30 |
| Cxcl10 | A_55_P2016462 | 2.86 | 3.42 | 3.02 | 2.50 | 3.77 | 5.35 |
| Cyba | A_55_P1979341 | 3.08 | 2.72 | 4.63 | 2.69 | 2.44 | 4.68 |
| Cyba | A_51_P131800 | 2.33 | 1.57 | 3.73 | 2.38 | 2.37 | 3.05 |
| Cyth4 | A_55_P2113210 | 2.03 | 2.13 | 2.57 | 1.79 | 1.47 | 2.42 |
| Emr1 | A_55_P2018934 | 1.52 | 1.26 | 1.62 | 1.61 | 2.02 | 1.85 |
| Emr1 | A_55_P2144386 | 1.61 | 1.57 | 1.40 | 1.93 | 1.68 | 2.37 |
| F420015M19Rik | A_55_P2041584 | 1.63 | -1.55 | 3.13 | 2.15 | 1.47 | 2.03 |
| Fam167b | A_52_P326657 | 1.52 | 1.49 | 1.89 | 2.20 | 1.97 | 1.89 |
| Fam46c | A_51_P447976 | 2.92 | 2.77 | 4.88 | 3.69 | 2.40 | 5.96 |
| Fblim1 | A_55_P2038757 | 1.47 | 1.51 | 2.61 | 1.59 | 4.68 | 2.78 |

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|---------|---------------|------|------|-------|------|-------|------|
| Fcer1g | A_51_P405476 | 3.28 | 2.42 | 5.04 | 3.57 | 3.98 | 3.83 |
| Fcgr2b | A_51_P130095 | 1.60 | 1.67 | 3.82 | 1.97 | 3.38 | 4.16 |
| Fcgr2b | A_51_P130095 | 1.58 | 1.69 | 3.46 | 2.35 | 3.07 | 5.25 |
| Fcgr2b | A_51_P130095 | 1.52 | 1.68 | 3.48 | 2.32 | 2.41 | 5.58 |
| Fcgr2b | A_51_P130095 | 1.42 | 1.70 | 3.90 | 2.50 | 2.14 | 6.25 |
| Fcgr2b | A_51_P130095 | 1.52 | 1.79 | 3.73 | 1.95 | 3.29 | 5.97 |
| Fcgr2b | A_51_P130095 | 1.54 | 1.51 | 3.93 | 2.19 | 2.57 | 4.97 |
| Fcgr2b | A_51_P130095 | 1.54 | 1.85 | 3.56 | 1.76 | 3.96 | 5.48 |
| Fcgr2b | A_51_P130095 | 1.46 | 1.67 | 3.00 | 2.41 | 3.34 | 4.86 |
| Fcgr2b | A_51_P130095 | 1.55 | 1.59 | 3.05 | 2.22 | 3.03 | 5.27 |
| Fcgr2b | A_51_P130095 | 1.44 | 1.66 | 3.69 | 2.72 | 2.80 | 4.72 |
| Fes | A_52_P365011 | 2.05 | 1.91 | 1.90 | 1.88 | 2.13 | 1.96 |
| Fes | A_52_P635338 | 1.96 | 2.38 | 2.22 | 2.66 | 1.95 | 3.13 |
| Fyb | A_55_P2006869 | 1.75 | 2.15 | 1.83 | 1.63 | 1.54 | 2.75 |
| Gal3st2 | A_55_P2026547 | 1.76 | 1.89 | 1.86 | 2.01 | 1.48 | 2.65 |
| Gfap | A_55_P2157245 | 3.37 | 6.08 | 4.36 | 2.20 | 2.97 | 5.37 |
| Gfap | A_52_P52303 | 5.16 | 8.37 | 5.01 | 2.85 | 3.12 | 4.46 |
| Gfap | A_55_P2157250 | 8.08 | 8.58 | 11.81 | 3.99 | 7.98 | 3.50 |
| Glipr1 | A_51_P371051 | 1.98 | 1.77 | 1.54 | 1.47 | 1.66 | 1.56 |
| Gm5637 | A_55_P2166555 | 2.14 | 2.07 | 2.60 | 2.27 | 2.07 | 2.92 |
| Gngt2 | A_55_P2151986 | 1.83 | 1.77 | 3.02 | 2.62 | 2.32 | 3.46 |
| Gpnmb | A_51_P438967 | 1.76 | 3.44 | 2.37 | 1.97 | 5.68 | 3.70 |
| Gpr34 | A_55_P2039684 | 1.98 | 1.92 | 2.12 | 2.36 | 2.05 | 2.63 |
| Gpr65 | A_51_P108459 | 2.30 | 2.92 | 2.67 | 2.28 | 2.75 | 3.50 |
| Gpr65 | A_51_P108459 | 2.34 | 2.54 | 2.76 | 1.86 | 2.10 | 3.19 |
| Gpr65 | A_51_P108459 | 2.74 | 1.37 | 2.75 | 2.51 | 2.95 | 2.01 |
| Gpr65 | A_51_P108459 | 2.89 | 2.96 | 2.89 | 2.87 | 2.84 | 4.53 |
| Gpr65 | A_51_P108459 | 2.54 | 3.34 | 2.64 | 2.44 | 3.13 | 4.62 |
| Gpr65 | A_51_P108459 | 2.49 | 3.17 | 2.48 | 2.11 | 1.92 | 3.97 |
| Gpr65 | A_51_P108459 | 2.69 | 2.92 | 2.64 | 2.81 | -1.38 | 3.49 |
| Gpr65 | A_51_P108459 | 2.44 | 3.05 | 2.61 | 2.96 | 2.88 | 3.51 |
| Gpr65 | A_51_P108459 | 2.13 | 2.72 | 2.41 | 1.84 | 2.70 | 3.09 |
| Gpr65 | A_51_P108459 | 2.61 | 2.79 | 2.44 | 2.67 | 2.75 | 3.61 |
| Gpr84 | A_55_P2044932 | 2.78 | 2.85 | 3.78 | 3.10 | 2.22 | 5.77 |
| Gpsm3 | A_55_P1957633 | 1.79 | 1.49 | 2.47 | 1.83 | 1.90 | 2.10 |
| Grn | A_51_P192800 | 2.55 | 2.33 | 2.64 | 2.20 | 3.03 | 2.47 |
| Gsdmd | A_51_P172231 | 1.25 | 1.62 | 1.58 | 1.38 | 2.04 | 1.60 |
| Gsdmd | A_51_P172231 | 1.45 | 1.71 | 1.54 | 1.26 | 2.16 | 1.51 |
| Gsdmd | A_51_P172231 | 1.32 | 1.66 | 1.54 | 1.44 | 1.76 | 1.68 |
| Gsdmd | A_51_P172231 | 1.63 | 1.74 | 1.62 | 1.45 | 2.21 | 1.82 |
| Gsdmd | A_51_P172231 | 1.48 | 1.88 | 1.61 | 1.34 | 2.21 | 1.83 |
| Gsdmd | A_51_P172231 | 1.43 | 1.59 | 1.67 | 1.42 | 2.20 | 1.87 |
| Gsdmd | A_51_P172231 | 1.43 | 1.75 | 1.64 | 1.37 | 2.84 | 1.84 |
| Gsdmd | A_51_P172231 | 1.54 | 1.77 | 1.39 | 1.62 | 1.73 | 1.85 |
| Gsdmd | A_51_P172231 | 1.51 | 1.92 | 1.50 | 1.52 | 2.24 | 1.57 |
| Gsdmd | A_51_P172231 | 1.47 | 1.66 | 1.45 | 1.33 | 1.86 | 1.66 |

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|--------|---------------|------|-------|------|------|------|-------|
| Gusb | A_51_P211491 | 2.49 | 3.17 | 3.24 | 3.05 | 3.61 | 3.89 |
| Gusb | A_51_P211491 | 2.92 | 2.90 | 2.85 | 2.93 | 3.07 | 3.64 |
| Gusb | A_51_P211491 | 2.67 | 3.41 | 3.30 | 3.09 | 3.30 | 4.19 |
| Gusb | A_51_P211491 | 2.55 | 3.46 | 3.16 | 3.14 | 2.76 | 3.82 |
| Gusb | A_51_P211491 | 2.80 | 3.38 | 3.33 | 2.88 | 2.67 | 4.20 |
| Gusb | A_51_P211491 | 2.72 | 3.04 | 3.11 | 2.83 | 2.85 | 3.54 |
| Gusb | A_51_P211491 | 2.62 | 3.56 | 3.14 | 3.09 | 2.96 | 4.59 |
| Gusb | A_51_P211491 | 2.77 | 3.42 | 3.17 | 2.96 | 3.26 | 4.13 |
| Gusb | A_52_P160936 | 1.33 | 1.45 | 1.54 | 1.63 | 1.32 | 2.00 |
| Gusb | A_51_P211491 | 2.66 | 2.95 | 3.33 | 3.12 | 3.42 | 3.80 |
| Gusb | A_51_P211491 | 2.73 | 3.41 | 3.11 | 2.98 | 2.98 | 3.90 |
| H2-M2 | A_51_P191463 | 1.54 | 1.31 | 1.51 | 1.44 | 3.51 | -1.08 |
| H2-M2 | A_51_P191463 | 1.11 | 1.70 | 1.47 | 1.33 | 2.70 | 1.41 |
| H2-M2 | A_51_P191463 | 1.24 | 1.42 | 1.55 | 1.46 | 2.60 | 1.63 |
| H2-M2 | A_51_P191463 | 1.54 | 1.29 | 1.53 | 1.55 | 2.42 | 1.60 |
| H2-M2 | A_51_P191463 | 1.48 | 1.41 | 1.28 | 1.37 | 2.56 | 1.51 |
| H2-M2 | A_51_P191463 | 1.55 | 1.21 | 1.59 | 1.37 | 2.76 | 1.49 |
| H2-M2 | A_51_P191463 | 1.35 | 1.35 | 1.57 | 1.25 | 2.62 | 1.34 |
| H2-M2 | A_51_P191463 | 1.40 | 1.42 | 1.43 | 1.53 | 3.10 | 1.33 |
| H2-M2 | A_51_P191463 | 1.37 | 1.24 | 1.34 | 1.32 | 2.57 | 1.35 |
| H2-M2 | A_51_P191463 | 1.05 | 1.29 | 1.80 | 1.37 | 2.69 | 1.36 |
| H2-Q8 | A_55_P1978465 | 2.03 | 3.34 | 2.68 | 1.51 | 5.38 | 3.35 |
| Haa0 | A_55_P2074035 | 2.04 | 1.51 | 1.86 | 1.50 | 1.57 | 1.50 |
| Havcr2 | A_55_P1965659 | 2.14 | 2.41 | 2.75 | 2.75 | 2.09 | 2.89 |
| Hcls1 | A_51_P297679 | 2.08 | 2.50 | 2.33 | 2.29 | 2.27 | 3.37 |
| Hcst | A_55_P1984886 | 1.85 | 1.84 | 3.68 | 2.90 | 2.26 | 3.69 |
| Hexa | A_51_P282667 | 1.90 | 2.01 | 2.31 | 1.72 | 2.33 | 2.39 |
| Hexb | A_51_P453111 | 2.49 | 2.04 | 3.20 | 2.81 | 2.04 | 3.28 |
| Hk2 | A_51_P204080 | 1.68 | 1.81 | 2.06 | 1.52 | 2.53 | 2.40 |
| Hmha1 | A_55_P2002103 | 2.01 | 2.58 | 2.36 | 2.51 | 2.09 | 3.16 |
| Hspb6 | A_55_P2039289 | 1.55 | 1.45 | 2.08 | 1.60 | 1.58 | 1.74 |
| Hvcn1 | A_55_P2025008 | 2.76 | 3.22 | 3.72 | 2.83 | 2.92 | 3.95 |
| Hvcn1 | A_55_P1960053 | 2.72 | 3.93 | 4.07 | 2.87 | 3.36 | 4.51 |
| Igf1 | A_55_P2085979 | 1.42 | -1.24 | 1.04 | 1.06 | 1.30 | -1.39 |
| Igf1 | A_55_P2085984 | 2.70 | 2.42 | 3.72 | 3.22 | 2.84 | 5.41 |
| Igf1 | A_55_P2085984 | 2.53 | 2.13 | 5.02 | 3.85 | 2.86 | 5.35 |
| Igf1 | A_55_P2031636 | 1.17 | 1.01 | 1.16 | 1.03 | 1.58 | 1.50 |
| Igf1 | A_55_P2031631 | 2.98 | 2.48 | 4.57 | 2.96 | 2.77 | 5.27 |
| Igf1 | A_55_P2031631 | 2.59 | 1.97 | 5.09 | 3.06 | 2.99 | 4.22 |
| Igsf6 | A_51_P258372 | 1.64 | 1.81 | 1.85 | 1.95 | 1.76 | 2.55 |
| Ikzf1 | A_66_P124139 | 1.33 | 1.35 | 1.29 | 1.76 | 1.71 | 1.79 |
| Ikzf1 | A_55_P2023607 | 1.47 | 1.55 | 1.76 | 2.09 | 1.75 | 2.56 |
| Il3ra | A_55_P2008181 | 1.79 | 2.21 | 2.12 | 1.85 | 1.82 | 2.12 |
| Inpp5d | A_51_P337125 | 1.67 | 1.87 | 2.00 | 2.11 | 1.99 | 3.47 |
| Irf5 | A_51_P346668 | 2.06 | 2.03 | 2.06 | 2.30 | 1.77 | 2.10 |
| Irf8 | A_52_P354823 | 3.17 | 3.20 | 4.29 | 3.70 | 3.96 | 4.24 |

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| Itgax | A_51_P303424 | 16.29 | 13.43 | 19.61 | 16.11 | 14.83 | 23.20 |
| Itgb2 | A_51_P262208 | 2.47 | 2.65 | 3.39 | 2.35 | 2.38 | 2.87 |
| Itgb5 | A_51_P327796 | 2.01 | 1.62 | 2.68 | 1.87 | 1.73 | 2.45 |
| Kcne2 | A_55_P1979242 | 3.69 | 1.49 | -1.63 | 1.69 | -2.03 | 3.19 |
| Klhl6 | A_51_P433615 | 2.07 | 2.69 | 1.56 | 1.66 | 2.11 | 2.75 |
| Krt85 | A_55_P1999364 | 2.62 | 3.10 | 5.40 | 2.58 | 3.36 | 3.78 |
| Lag3 | A_51_P264825 | 2.84 | 2.27 | 3.64 | 2.73 | 4.53 | 3.21 |
| Lair1 | A_55_P1991214 | 1.63 | 1.38 | 2.36 | 2.13 | 2.13 | 2.46 |
| Lat2 | A_51_P242930 | 1.72 | 1.94 | 2.20 | 1.86 | 2.39 | 1.97 |
| Lcp1 | A_55_P2066613 | 1.41 | 1.21 | 2.52 | 2.62 | 2.35 | 3.11 |
| Lcp1 | A_52_P56751 | 1.74 | 1.88 | 1.63 | 1.91 | 2.09 | 2.40 |
| Lgals3 | A_55_P2171116 | 1.91 | 2.96 | 4.24 | 1.79 | 2.73 | 5.69 |
| Lsp1 | A_55_P1957413 | 1.85 | 2.10 | 2.34 | 2.26 | 2.45 | 3.28 |
| Ly86 | A_51_P465350 | 3.55 | 4.47 | 4.02 | 4.15 | 4.41 | 4.71 |
| Lyl1 | A_51_P143190 | 1.51 | 1.66 | 1.94 | 1.61 | 1.71 | 2.11 |
| Man2b1 | A_51_P336161 | 2.20 | 2.43 | 2.17 | 2.16 | 2.27 | 2.53 |
| Mlph | A_66_P132222 | 1.61 | 2.29 | 1.72 | 1.93 | 2.48 | 1.59 |
| Mlxip1 | A_55_P2119957 | 2.22 | 2.52 | 2.22 | 2.56 | 2.74 | 2.45 |
| Mpeg1 | A_51_P390538 | 5.58 | 5.52 | 6.06 | 7.74 | 7.35 | 8.19 |
| Myo1f | A_66_P112305 | 2.32 | 2.79 | 3.30 | 3.64 | 2.68 | 4.98 |
| Myo1f | A_55_P2124273 | 2.59 | 3.59 | 3.20 | 2.95 | 4.26 | 3.19 |
| Naglu | A_52_P504361 | 2.07 | 2.06 | 2.17 | 1.66 | 2.24 | 2.03 |
| Naip2 | A_55_P1984243 | 2.20 | 2.80 | 2.37 | 2.12 | 2.21 | 3.19 |
| Naprt1 | A_51_P414115 | 1.64 | 1.75 | 1.76 | 1.54 | 1.48 | 1.57 |
| Ncf2 | A_55_P2184189 | 1.77 | 2.09 | 2.71 | 2.51 | 3.28 | 3.31 |
| Ncf4 | A_51_P377452 | 2.09 | 2.09 | 2.11 | 2.36 | 1.76 | 3.12 |
| Nckap1l | A_51_P119429 | 1.95 | 2.20 | 2.11 | 2.43 | 1.66 | 3.22 |
| Nckap1l | A_51_P119429 | 1.89 | 2.12 | 2.16 | 2.27 | 1.72 | 2.66 |
| Nckap1l | A_51_P119429 | 1.83 | 1.82 | 2.03 | 2.31 | 1.61 | 2.68 |
| Nckap1l | A_51_P119429 | 1.93 | 2.08 | 2.11 | 2.64 | 1.55 | 2.68 |
| Nckap1l | A_51_P119429 | 1.79 | 1.93 | 1.96 | 2.60 | 1.93 | 2.79 |
| Nckap1l | A_51_P119429 | 1.70 | 2.18 | 1.88 | 2.31 | 1.63 | 2.83 |
| Nckap1l | A_51_P119429 | 1.85 | 1.94 | 2.13 | 2.38 | 1.96 | 2.75 |
| Nckap1l | A_51_P119429 | 1.86 | 2.10 | 1.86 | 2.22 | 2.27 | 2.85 |
| Nckap1l | A_51_P119429 | 1.89 | 2.17 | 2.02 | 2.57 | 1.85 | 2.94 |
| Nckap1l | A_51_P119429 | 1.71 | 1.98 | 1.89 | 2.39 | 1.80 | 2.76 |
| Npc2 | A_51_P347961 | 1.85 | 2.27 | 1.96 | 1.63 | 1.99 | 2.51 |
| Olfml3 | A_51_P191782 | 2.24 | 1.92 | 1.87 | 2.00 | 1.90 | 1.62 |
| Osmr | A_51_P319460 | 1.65 | 2.71 | 3.06 | 2.47 | 3.05 | 5.29 |
| P2ry6 | A_51_P105124 | 2.45 | 1.61 | 1.96 | 1.70 | 1.71 | 2.44 |
| P2ry6 | A_51_P105124 | 1.70 | 1.96 | 2.03 | 2.15 | 1.93 | 2.38 |
| P2ry6 | A_51_P105124 | 1.87 | 2.06 | 2.09 | 1.96 | 1.82 | 2.43 |
| P2ry6 | A_51_P105124 | 1.89 | 1.80 | 2.21 | 1.80 | 1.97 | 2.55 |
| P2ry6 | A_51_P105124 | 1.65 | 1.80 | 2.17 | 2.08 | 1.99 | 2.42 |
| P2ry6 | A_51_P105124 | 1.78 | 1.71 | 1.94 | 2.03 | 2.18 | 2.33 |
| P2ry6 | A_51_P105124 | 1.74 | 1.66 | 2.05 | 1.99 | 1.74 | 2.43 |

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|----------|---------------|------|------|------|------|------|------|
| P2ry6 | A_51_P105124 | 1.57 | 1.84 | 2.15 | 1.99 | 2.02 | 2.44 |
| P2ry6 | A_51_P105124 | 1.76 | 1.97 | 2.15 | 2.06 | 1.90 | 2.52 |
| P2ry6 | A_51_P105124 | 1.77 | 1.74 | 2.22 | 2.17 | 1.75 | 2.59 |
| Pdcd1 | A_51_P285736 | 2.82 | 2.43 | 4.02 | 3.33 | 2.22 | 3.48 |
| Plcg2 | A_51_P279163 | 1.68 | 1.92 | 1.89 | 1.61 | 1.96 | 2.38 |
| Pld4 | A_52_P591153 | 1.97 | 2.32 | 1.62 | 2.12 | 2.69 | 1.59 |
| Plek | A_55_P1966194 | 2.15 | 2.76 | 2.63 | 2.99 | 3.14 | 4.18 |
| Pon3 | A_51_P256665 | 2.12 | 2.16 | 2.82 | 2.12 | 1.98 | 3.61 |
| Psmb8 | A_51_P345367 | 2.27 | 2.17 | 2.56 | 1.96 | 3.58 | 2.67 |
| Ptpn6 | A_52_P114722 | 2.60 | 3.15 | 3.47 | 2.99 | 2.76 | 3.73 |
| Ptpn18 | A_55_P2069306 | 2.03 | 2.05 | 3.28 | 2.42 | 2.27 | 4.07 |
| Ptprc | A_55_P1990324 | 2.05 | 1.66 | 2.05 | 2.00 | 2.14 | 2.48 |
| Pycard | A_51_P438821 | 1.95 | 1.90 | 2.35 | 2.63 | 1.89 | 2.60 |
| Rac2 | A_51_P121891 | 2.06 | 1.83 | 2.43 | 2.47 | 3.52 | 2.40 |
| Rac2 | A_51_P121891 | 2.15 | 2.07 | 2.35 | 1.98 | 3.24 | 2.45 |
| Rac2 | A_51_P121891 | 2.08 | 2.12 | 2.46 | 1.98 | 2.52 | 2.58 |
| Rac2 | A_51_P121891 | 2.27 | 2.33 | 2.50 | 2.39 | 3.02 | 2.74 |
| Rac2 | A_51_P121891 | 2.05 | 2.02 | 2.45 | 2.24 | 2.70 | 2.51 |
| Rac2 | A_51_P121891 | 2.07 | 2.45 | 2.74 | 2.15 | 2.78 | 2.64 |
| Rac2 | A_51_P121891 | 2.24 | 2.15 | 2.38 | 2.08 | 3.16 | 2.38 |
| Rac2 | A_51_P121891 | 2.10 | 2.11 | 2.35 | 2.61 | 3.45 | 2.26 |
| Rac2 | A_51_P121891 | 1.94 | 2.43 | 2.39 | 2.15 | 2.56 | 2.60 |
| Rac2 | A_51_P121891 | 2.09 | 2.23 | 2.44 | 2.24 | 3.07 | 2.53 |
| Rasal3 | A_52_P16873 | 1.84 | 2.54 | 2.16 | 2.22 | 1.78 | 2.26 |
| Renbp | A_55_P2013357 | 1.67 | 1.67 | 2.29 | 1.84 | 2.14 | 2.07 |
| Runx1 | A_51_P206585 | 1.64 | 1.51 | 1.71 | 1.35 | 1.04 | 2.02 |
| Runx1 | A_55_P2183438 | 1.14 | 1.14 | 1.48 | 1.52 | 1.79 | 1.67 |
| Samsn1 | A_55_P2010271 | 2.32 | 2.28 | 3.11 | 3.84 | 3.11 | 3.63 |
| Selplg | A_55_P1976212 | 1.64 | 1.55 | 2.07 | 1.78 | 2.37 | 1.47 |
| Selplg | A_51_P131358 | 2.13 | 1.91 | 2.05 | 2.01 | 1.95 | 1.81 |
| Serpinf2 | A_55_P1956497 | 1.90 | 2.32 | 3.41 | 2.60 | 4.81 | 7.43 |
| Sh3bp2 | A_55_P2042823 | 1.75 | 2.03 | 2.60 | 1.83 | 1.89 | 3.00 |
| Siglec5 | A_55_P2043277 | 2.10 | 2.27 | 1.95 | 1.81 | 1.54 | 2.71 |
| Slamf9 | A_51_P246066 | 4.57 | 4.97 | 4.47 | 4.22 | 3.55 | 4.60 |
| Slc11a1 | A_51_P186476 | 3.60 | 5.16 | 4.09 | 5.26 | 8.50 | 4.61 |
| Slc14a1 | A_51_P312336 | 1.92 | 2.54 | 3.06 | 1.67 | 1.92 | 2.81 |
| Slc15a3 | A_52_P467389 | 3.81 | 4.84 | 4.26 | 4.27 | 9.07 | 4.38 |
| Slc16a3 | A_55_P2067505 | 1.85 | 2.81 | 2.07 | 1.90 | 2.11 | 2.25 |
| Slc16a3 | A_55_P1959425 | 1.83 | 2.50 | 2.12 | 1.70 | 2.13 | 1.90 |
| Slc37a2 | A_55_P2350617 | 1.64 | 1.94 | 2.05 | 2.08 | 2.02 | 2.72 |
| Slc7a7 | A_51_P472249 | 1.67 | 1.62 | 2.11 | 2.35 | 1.81 | 2.15 |
| Slco2b1 | A_55_P2079009 | 1.71 | 1.86 | 1.83 | 1.97 | 1.94 | 2.47 |
| Slco2b1 | A_55_P2030155 | 1.46 | 1.75 | 1.94 | 1.63 | 2.25 | 2.10 |
| Snx20 | A_51_P309158 | 1.65 | 1.60 | 1.65 | 1.99 | 1.67 | 1.71 |
| Sp110 | A_55_P2152566 | 1.75 | 2.17 | 1.95 | 1.90 | 2.16 | 2.85 |
| Stard4 | A_52_P384574 | 1.63 | 1.47 | 1.87 | 1.89 | 1.57 | 2.23 |

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|-----------|---------------|------|-------|-------|------|------|-------|
| Syngn1 | A_51_P270733 | 3.03 | 2.22 | 4.17 | 3.06 | 3.82 | 3.18 |
| Syt10 | A_51_P318830 | 7.28 | -3.34 | 2.47 | 3.89 | 2.15 | -2.29 |
| Tbxas1 | A_51_P448664 | 2.52 | 2.85 | 3.17 | 3.92 | 3.83 | 3.15 |
| Tcigr1 | A_51_P241861 | 1.51 | 1.75 | 1.86 | 1.68 | 2.06 | 1.46 |
| Tgfbr2 | A_55_P2107288 | 1.30 | 1.68 | 2.45 | 1.70 | 1.44 | 2.19 |
| Tgfbr2 | A_51_P450573 | 1.91 | 2.06 | 2.27 | 2.20 | 1.98 | 3.68 |
| Tgif1 | A_55_P2092526 | 1.71 | 1.77 | 2.28 | 2.15 | 1.74 | 3.65 |
| Timp2 | A_65_P12392 | 1.84 | 1.76 | 2.62 | 1.95 | 2.10 | 1.99 |
| Tlr1 | A_51_P495581 | 2.30 | 1.72 | 1.56 | 2.32 | 3.14 | 1.61 |
| Tlr2 | A_51_P452629 | 2.71 | 3.59 | 3.33 | 3.25 | 3.58 | 5.12 |
| Tlr2 | A_51_P452629 | 2.86 | 3.40 | 3.57 | 3.20 | 2.72 | 4.94 |
| Tlr2 | A_51_P452629 | 2.60 | 3.86 | 3.20 | 3.85 | 3.44 | 4.69 |
| Tlr2 | A_51_P452629 | 2.87 | 4.38 | 3.56 | 3.81 | 3.57 | 6.09 |
| Tlr2 | A_51_P452629 | 2.75 | 4.21 | 3.33 | 3.38 | 2.79 | 6.21 |
| Tlr2 | A_51_P452629 | 2.65 | 4.22 | 3.03 | 3.45 | 2.16 | 4.86 |
| Tlr2 | A_51_P452629 | 2.65 | 4.15 | 3.44 | 3.34 | 3.62 | 5.15 |
| Tlr2 | A_51_P452629 | 2.51 | 3.63 | 3.35 | 3.61 | 4.22 | 5.47 |
| Tlr2 | A_51_P452629 | 2.89 | 3.76 | 3.36 | 3.47 | 3.68 | 5.74 |
| Tlr2 | A_51_P452629 | 2.59 | 3.08 | 3.12 | 2.97 | 4.50 | 4.40 |
| Tlr7 | A_55_P2050932 | 1.34 | 1.41 | 1.48 | 1.81 | 1.43 | 1.41 |
| Tlr7 | A_55_P2129047 | 1.56 | 1.80 | 2.19 | 2.11 | 4.14 | 2.68 |
| Tlr12 | A_66_P114333 | 2.04 | 2.00 | 2.15 | 2.29 | 2.80 | 3.01 |
| Tlr13 | A_55_P2048279 | 1.91 | 1.89 | 2.32 | 2.29 | 1.96 | 2.91 |
| Tnfaip8l2 | A_51_P150678 | 1.66 | 2.15 | 2.35 | 1.77 | 1.49 | 2.67 |
| Tnfrsf1a | A_52_P192426 | 1.36 | 1.69 | 1.98 | 1.38 | 1.60 | 2.73 |
| Tnfrsf1a | A_52_P192426 | 1.42 | 1.83 | 2.15 | 1.59 | 1.90 | 2.92 |
| Tnfrsf1a | A_52_P192426 | 1.45 | 2.01 | 2.32 | 1.68 | 1.65 | 3.38 |
| Tnfrsf1a | A_52_P192426 | 1.46 | 1.73 | 2.18 | 1.48 | 1.37 | 3.19 |
| Tnfrsf1a | A_52_P192426 | 1.53 | 1.82 | 2.24 | 1.68 | 1.66 | 3.04 |
| Tnfrsf1a | A_52_P192426 | 1.35 | 2.03 | 2.34 | 1.56 | 2.22 | 3.30 |
| Tnfrsf1a | A_52_P192426 | 1.48 | 1.97 | 2.24 | 1.47 | 1.74 | 3.09 |
| Tnfrsf1a | A_55_P2051099 | 1.31 | 1.45 | 1.91 | 1.41 | 2.07 | 1.29 |
| Tnfrsf1a | A_52_P192426 | 1.61 | 1.68 | 2.09 | 1.61 | 1.81 | 2.89 |
| Tnfrsf1a | A_52_P192426 | 1.41 | 1.89 | 2.14 | 1.42 | 1.74 | 2.77 |
| Tnfrsf1a | A_52_P192426 | 1.49 | 1.60 | 2.16 | 1.38 | 1.65 | 2.77 |
| Tnfsf8 | A_55_P2179463 | 1.87 | 1.56 | 2.44 | 2.58 | 1.48 | 2.92 |
| Tnni2 | A_55_P2040893 | 2.40 | 2.00 | 3.49 | 2.96 | 2.56 | 2.75 |
| Tox4 | A_55_P2121618 | 4.35 | -2.72 | 2.12 | 3.32 | 1.62 | -1.55 |
| Trem2 | A_55_P1962937 | 7.05 | 4.23 | 10.78 | 9.00 | 5.53 | 11.92 |
| Tubb6 | A_51_P421140 | 1.62 | 1.67 | 1.54 | 1.78 | 1.74 | 3.02 |
| Tyrobp | A_51_P261517 | 5.82 | 6.44 | 6.40 | 5.74 | 5.11 | 7.24 |
| Ucp2 | A_51_P297105 | 1.91 | 1.60 | 2.58 | 1.84 | 2.79 | 1.75 |
| Ucp3 | A_66_P108247 | 2.18 | 1.84 | 2.29 | 1.69 | 2.68 | 2.00 |
| Unc93b1 | A_52_P507382 | 2.42 | 1.78 | 2.50 | 2.20 | 1.98 | 2.42 |
| Vav1 | A_51_P154780 | 1.66 | 1.92 | 1.77 | 1.98 | 1.48 | 2.04 |
| Vav1 | A_55_P2036567 | 2.02 | 1.96 | 2.64 | 2.59 | 1.75 | 3.71 |

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|-------|--------------|------|------|------|------|------|------|
| Vim | A_51_P392687 | 1.58 | 1.64 | 2.69 | 1.59 | 2.03 | 4.63 |
| Was | A_51_P327121 | 1.67 | 1.57 | 1.64 | 2.20 | 2.76 | 1.79 |
| Wdfy4 | A_52_P199614 | 1.65 | 1.58 | 1.87 | 2.02 | 2.07 | 3.00 |