**Table S2. Bioinformatic analyses.** Variants in bold represent the intronic variants that were significantly associated with OS. The remaining variants represent those that were selected for luciferase assays based upon their LD with the bolded variant, and compelling evidence of a possible effects on gene regulatory function. Data were obtained from multiple bioinformatic sources to inform predictions regarding variant function (1-5). In the luciferase assays, variants with an LD of r2>0.8 were included in the construct to increase the likelihood to identify other variants with functional effects. Abbreviations: LD, linkage disequilibrium; TF, transcription factor.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **SNP** | **Gene** | **Regulome DB score** | **Enhancer Histone Marks** | **DNAse** | **Proteins Bound** | **TF Motifs Altered** |
| **rs1885657 (T>C)** | *VEGFA* | 4 | 12 tissues | 18 tissues | 4 | AP-2, CEBPB, HEY-1, NRSF, Rad21 |
| rs943070 (C>G)  High LD with rs1885657 (r2=1.0) | *VEGFA* | 4 | 13 tissues | 28 tissues | 7 | ATF3, BDP1 |
| rs58159269 (T>C)  High LD with rs1885657 (r2=1.0) | *VEGFA* | 4 | 6 tissues | 30 tissues | 13 | AP-2, BDP1, CCNT2, CTCF, Ets, GR, HNF4, Hic1, Nrf1, Rad21, SMC3, SP1, p300 |
| **rs3024987 (C>T)**  Moderate LD with rs1885657 (r2=0.61) | *VEGFA* | 4 | 15 tissues | 3 tissues | None | CTCF, Myf, Rad21, SMC3, SinAk-20 |
| **rs8047917 (T>A)** | *WWOX* | 5 | 6 tissues | 1 tissue | None | E4F1, HMG-IY, XBP |
| rs77533819  (T>C)  High LD with rs8047917 (r2=1.0) | *WWOX* | 6 | 4 tissues | None | None | CDP7, ERalpha, PAX-4, RXRA, Sin3Ak-20 |
| rs7190335  (T>C)  High LD with rs8047917 (r2=0.96) | *WWOX* | 6 | 2 tissues | 2 tissues | None | Evi-1, GATA, Hoxa9, Hoxd10, Irf |
| **rs3816375 (A>G)** | *ITGAV* | No data | 2 tissues | 1 tissue | None | Cart1, DMRT7, Nanog, Pou5f1 |

**References**

1. Boyle AP, Hong EL, Hariharan M, Cheng Y, Schaub MA, Kasowski M, et al. Annotation of functional variation in personal genomes using RegulomeDB. *Genome research*. **2012**;22(9):1790-7.

2. Cunningham F, Amode MR, Barrell D, Beal K, Billis K, Brent S, et al. Ensembl 2015. *Nucleic acids research*. **2015**;43(Database issue):D662-9.

3. Kent WJ, Sugnet CW, Furey TS, Roskin KM, Pringle TH, Zahler AM, et al. The human genome browser at UCSC. *Genome research*. **2002**;12(6):996-1006.

4. Rahmani M, Nguyen TK, Dent P, Grant S. The multikinase inhibitor sorafenib induces apoptosis in highly imatinib mesylate-resistant bcr/abl+ human leukemia cells in association with signal transducer and activator of transcription 5 inhibition and myeloid cell leukemia-1 down-regulation. *Molecular pharmacology*. **2007**;72(3):788-95.

5. Ward LD, Kellis M. HaploReg: a resource for exploring chromatin states, conservation, and regulatory motif alterations within sets of genetically linked variants. *Nucleic acids research*. **2012**;40(Database issue):D930-4.